# Queen Elizabeth Scholarship - Advanced Scholars Program: R Workshop #2

## The tidyverse

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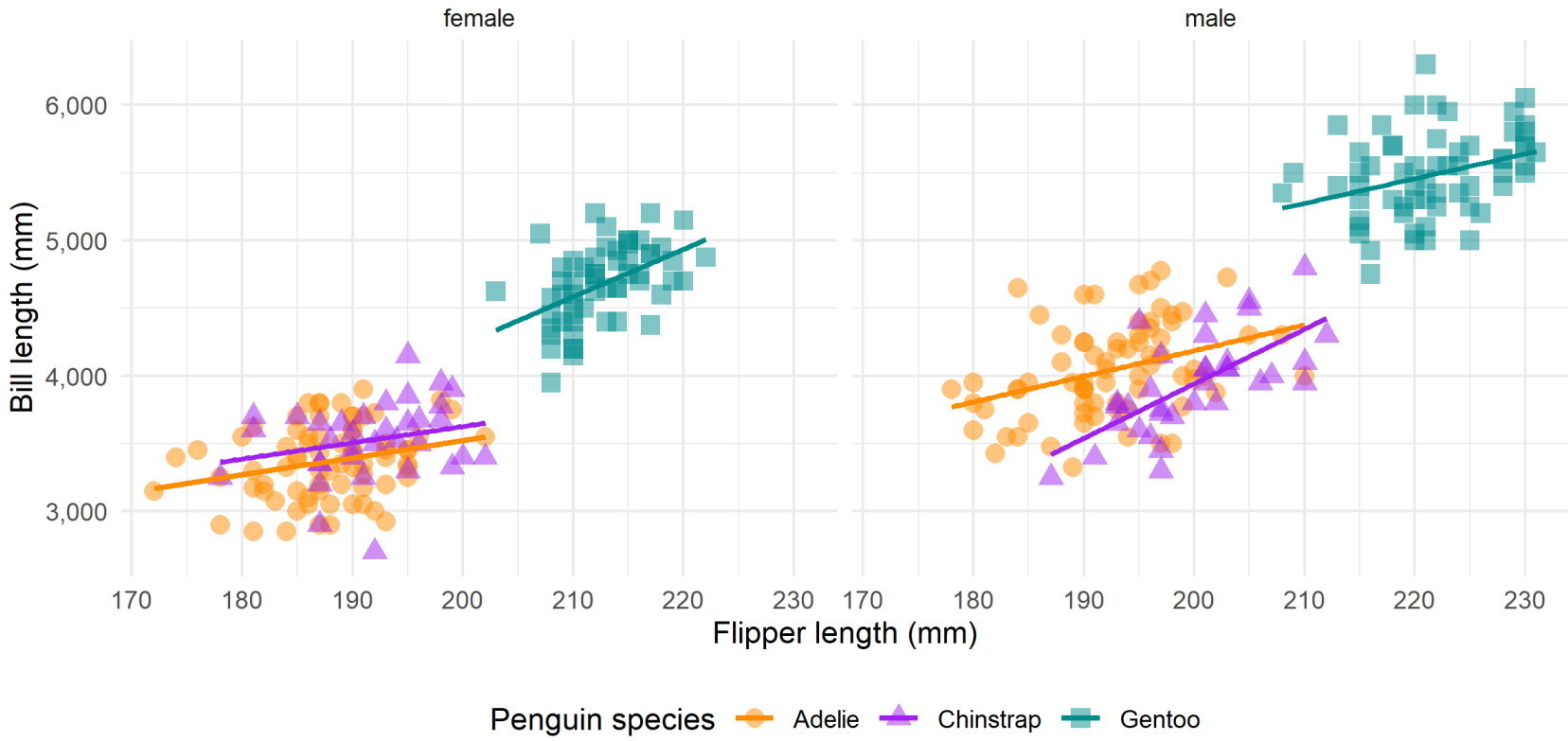
# Today's workshop

- Review of key concepts from Workshop #1
- An example of how to use R to perform data analysis on a dataset



# The code for today

The code for today's workshop is available at the following link: https://github.com/melissavanbussel/QES-AS-R-Workshops

Instructions:

1. Open RStudio
2. File > New File > R Script
3. Copy/paste the code from GitHub into the R Script
4. Save the script onto your computer (Ctrl+S)

# Review of key concepts from Workshop 1

# R Scripts vs. the R console

- Code that is run in the console only does not get saved when you close RStudio.
- If you type the code in your R Script and save the file, you will be able to run that code again in the future.
- The console is great for quick calculations, but anything that you'd like to run again should be saved in your R script.

# Comments

Any lines of code that start with hashtags are comments and do not get evaluated as code.

```
# This is a comment, it does not get evaluated as code
# You can write anything you want in a comment!
# The line below does not start with a hashtag, so it is evaluated
print("Hello, world!")
```

```
## [1] "Hello, world!"
```

# Variable assignment

To assign an object to a variable in R, use the ← assignment operator.

```
years ← c(2010, 2020, 2021)
```

Any line of code that has the assignment operator will have no output. Type the name of the variable to see the contents of the variable.

```
years
```

```
## [1] 2010 2020 2021
```

# Functions in R

Just like in Mathematics, a function in R is something that takes some input(s) and returns an output.

They take the form `function_name(argument_1 = val_1, argument_2 = val_2, ...)`

```
mean(x = years)
```

```
## [1] 2017
```

If you pass the arguments to the function in the correct order, you don't need to name the arguments.

```
mean(years)
```

```
## [1] 2017
```

# Viewing documentation

To view the documentation for a function, type `?functionName`. The documentation will appear in the bottom right pane of RStudio.

```
?mean
```

# Missing values

Missing values are represented as `NA`s in R. If there is even just one `NA` included in a calculation, the result will be `NA`.

```
mean(c(1, 2, 3)) # No problem
```

```
## [1] 2
```

```
mean(c(1, NA, 3)) # Result is NA
```

```
## [1] NA
```

Similar results occur for other summary functions, such as:

- `max`
- `min`
- `median`

One option is to use the option `na.rm = TRUE` inside of these summary functions.

```
mean(c(1, NA, 3), na.rm = TRUE)
```

```
## [1] 2
```

# Packages

There are a lot of functions that are "built in" to R (they are automatically available when R is installed).

Sometimes, we want to use more advanced techniques. We could write this code ourselves, but this is time-consuming. Rather than re-inventing the wheel, we install a package that someone else has created.

Packages typically contain functions, but can also include other things like datasets (for example).

```
# Only needs to be done once
install.packages("tidyverse")

# Needs to be done each time RStudio is opened
# (if you want to use the package)
library(tidyverse)
```

# Using packageName::functionName

Sometimes, you may see R code on the internet that takes the form packageName::functionName.

This allows you to use the functionName function from the packageName package, without loading the packageName package.

This is also typically used if there is more than one package with the same function name. In this case, it is useful to explicitly state which package you're using.

```
scales::dollar(123456)
```

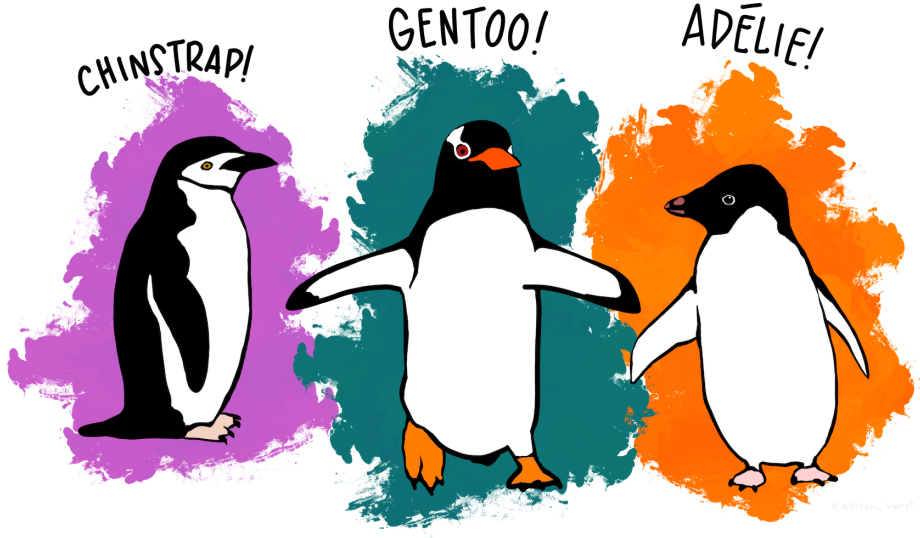
```
## [1] "$123,456"
```

# Data frames and the View function

A data frame is a table (two-dimensional) with columns and rows. We can examine the contents of a data frame by using the `View` function.

Recall the `penguins` dataset from the `palmerpenguins` package from Workshop 1:

- 344 observations of 7 variables
- Information about Adelie, Chinstrap, and Gentoo penguins
- Observed on islands near Palmer Station in Antarctica




```
library(palmerpenguins)
View(penguins)
```

# Tibbles

The `str` function shows us the **structure** of a data frame. It tells us:

- The number of rows and columns
- The data types of each of the variables
- A preview of the data (first few rows)

```
str(penguins)
```

```
## tibble [344 x 8] (S3: tbl_df/tbl/data.frame)
##  $ species          : Factor w/ 3 levels "Adelie","Chinstrap",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ island           : Factor w/ 3 levels "Biscoe","Dream",..: 3 3 3 3 3 3 3 3 3 3 ...
##  $ bill_length_mm   : num [1:344] 39.1 39.5 40.3 NA 36.7 39.3 38.9 39.2 34.1 42 ...
##  $ bill_depth_mm    : num [1:344] 18.7 17.4 18 NA 19.3 20.6 17.8 19.6 18.1 20.2 ...
##  $ flipper_length_mm: int [1:344] 181 186 195 NA 193 190 181 195 193 190 ...
##  $ body_mass_g      : int [1:344] 3750 3800 3250 NA 3450 3650 3625 4675 3475 4250 ...
##  $ sex              : Factor w/ 2 levels "female","male": 2 1 1 NA 1 2 1 2 NA NA ...
##  $ year             : int [1:344] 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 ...
```

We can see that the `penguins` dataset is both a "tibble" and a "data frame". Tibbles are a type of data frame.

- They are "simpler" (and therefore faster)
- They work great with the tidyverse, which we will learn about in a second!

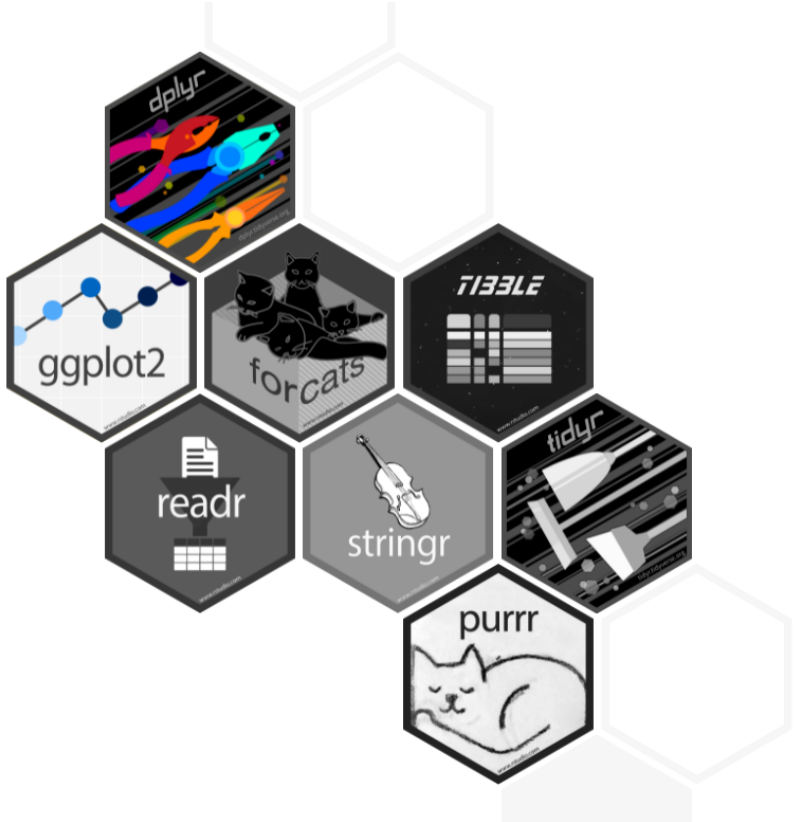
# Introduction to the tidyverse

# What is the tidyverse?


The tidyverse is a set of packages in R.

- `dplyr`
- `tidyr`
- `ggplot2`
- `readr`
- `stringr`
- etc...

# What is the tidyverse?




Today, we will focus on `dplyr` and `ggplot2`.

# Why use the tidyverse?

- Consistency (common underlying philosophy)
- Speed (many tasks implemented in C++)
- Easier to learn (learning one package = learning many)

# Loading the tidyverse

By installing (or loading) the tidyverse, we're actually installing (or loading) many packages at once, all with one line of code.

```
# If not already installed
install.packages("tidyverse")

# Equivalent to
install.packages("dplyr")
install.packages("ggplot2")
install.packages("stringr")
 ...

# Once installed
library(tidyverse)

# Equivalent to:
library(dplyr)
library(ggplot2)
library(stringr)
 ...
```

# Using dplyr for data exploration

# The `select` function

- `select`: select a subset of **columns** from a data frame

```
library(tidyverse)
select(.data = penguins, bill_length_mm, bill_depth_mm)
```

```
## # A tibble: 344 x 2
##    bill_length_mm bill_depth_mm
##             <dbl>         <dbl>
##  1           39.1          18.7
##  2           39.5          17.4
##  3           40.3          18
##  4           NA            NA
##  5           36.7          19.3
##  6           39.3          20.6
##  7           38.9          17.8
##  8           39.2          19.6
##  9           34.1          18.1
## 10           42            20.2
## #  ... with 334 more rows
```

# The `select` function

To select all columns **except** for ones we specify, use the minus sign:

```
select(.data = penguins, -species)
```

```
## # A tibble: 344 x 7
##    island  bill_length_mm bill_depth_mm flipper_length_~ body_mass_g sex    year
##    <fct>            <dbl>         <dbl>             <int>       <int> <fct> <int>
##  1 Torger~           39.1          18.7               181        3750 male   2007
##  2 Torger~           39.5          17.4               186        3800 fema~  2007
##  3 Torger~           40.3          18                 195        3250 fema~  2007
##  4 Torger~           NA            NA                  NA          NA <NA>   2007
##  5 Torger~           36.7          19.3               193        3450 fema~  2007
##  6 Torger~           39.3          20.6               190        3650 male   2007
##  7 Torger~           38.9          17.8               181        3625 fema~  2007
##  8 Torger~           39.2          19.6               195        4675 male   2007
##  9 Torger~           34.1          18.1               193        3475 <NA>   2007
## 10 Torger~           42            20.2               190        4250 <NA>   2007
## #  ... with 334 more rows
```

The result is all columns in the `penguins` data frame, other than the `species` column.

# The `filter` function

- `filter`: select a subset of **rows** from a data frame

A logical condition is specified, and R checks if the condition is true for each row in the data frame. Only rows where the condition is `TRUE` are returned:

```
filter(.data = penguins, bill_length_mm ⩾ 55)
```

```
## # A tibble: 5 x 8
##   species island bill_length_mm bill_depth_mm flipper_length_~ body_mass_g sex
##   <fct>   <fct>           <dbl>         <dbl>             <int>       <int> <fct>
## 1 Gentoo  Biscoe           59.6          17                 230        6050 male
## 2 Gentoo  Biscoe           55.9          17                 228        5600 male
## 3 Gentoo  Biscoe           55.1          16                 230        5850 male
## 4 Chinst~ Dream            58            17.8               181        3700 fema~
## 5 Chinst~ Dream            55.8          19.8               207        4000 male
## # ... with 1 more variable: year <int>
```

# Relational and logical operators in R

There are many other relational operators in R:

| Operator | Description |
|---|---|
| < | Less than |
| > | Greater than |
| <= | Less than or equal to |
| >= | Greater than or equal to |
| == | Equal to |
| != | Not equal to |

Multiple conditions can be combined by using logical operators such as & ("AND") or | ("OR").

For example: `bill_length_mm ⩽ 180 | bill_length_mm ⩾ 200`

# The pipe operator (%>%)

The pipe operator takes the object on the left of the %>% and feeds it as input to the first argument of the function on the right of the %>%.

The code on the left and the code on the right will produce the **exact** same output, but using the pipe operator (left) is much faster to write and easier to read.

With the pipe operator (one step)

```
penguins %>%
  select(bill_length_mm, bill_depth_mm) %>%
  filter(bill_length_mm ⩾ 55)
```

Without the pipe operator (two steps)

```
step1 ← select(.data = penguins,
                bill_length_mm,
                bill_depth_mm)
filter(step1, bill_length_mm ⩾ 55)
```

# The pipe operator (%>%)

```
penguins %>%
  select(bill_length_mm, bill_depth_mm) %>%
  filter(bill_length_mm ⩾ 55)
```

```
## # A tibble: 5 x 2
##   bill_length_mm bill_depth_mm
##            <dbl>         <dbl>
## 1           59.6          17
## 2           55.9          17
## 3           55.1          16
## 4           58            17.8
## 5           55.8          19.8
```

TIP: When reading the code in your head, replace the %>% with the word "THEN".

# Challenge problem

**Which of the following will result in a data frame that only contains observations about male penguins?**

A:

```
penguins %>%
  select(bill_length_mm, bill_depth_mm) %>%
  filter(sex == "male")
```

B:

```
penguins %>%
  filter(sex == "male") %>%
  select(bill_length_mm, bill_depth_mm)
```

C: All of the above

# The `mutate` function

- `mutate`: create a new variable based on existing variables

Create a new variable called `bill_length_m` that expresses the bill lengths in metres rather than in millimetres:

```
penguins %>%
  mutate(bill_length_m = bill_length_mm / 1000) %>%
  select(bill_length_m, bill_length_mm)
```

```
## # A tibble: 344 x 2
##    bill_length_m bill_length_mm
##            <dbl>          <dbl>
##  1        0.0391           39.1
##  2        0.0395           39.5
##  3        0.0403           40.3
##  4       NA                NA
##  5        0.0367           36.7
##  6        0.0393           39.3
##  7        0.0389           38.9
##  8        0.0392           39.2
##  9        0.0341           34.1
## 10        0.042            42
## #  ... with 334 more rows
```

# The `group_by` and `summarise` functions

- The `group_by` and `summarise` functions are often used together
  - `group_by` splits the data into groups (user-specified categorical variable)
  - `summarise` returns a summary value for each group
  - When used together, the resulting data frame has one row per group

```
penguins %>%
  group_by(species) %>%
  summarise(num_penguins = n())
```

```
## # A tibble: 3 x 2
##   species   num_penguins
## * <fct>            <int>
## 1 Adelie             152
## 2 Chinstrap           68
## 3 Gentoo             124
```

Some things to note:

- You can group by more than one variable as well
- You can use the `summarise` function to compute more than just one summary value
- While using the `group_by` and `summarise` functions together is quite common, it is possible to use them separately.

# The `arrange` function

- `arrange`: sorts the data frame by a specified variable
- By default, it sorts in ascending order (smallest to largest)

```
penguins %>%
  group_by(species) %>%
  summarise(num_penguins = n()) %>%
  arrange(num_penguins)
```

```
## # A tibble: 3 x 2
##   species   num_penguins
##   <fct>            <int>
## 1 Chinstrap           68
## 2 Gentoo             124
## 3 Adelie             152
```

# The `arrange` function

- To sort in descending order (largest to smallest), use the `desc` function

```
penguins %>%
  group_by(species) %>%
  summarise(num_penguins = n()) %>%
  arrange(desc(num_penguins))
```

```
## # A tibble: 3 x 2
##   species   num_penguins
##   <fct>            <int>
## 1 Adelie             152
## 2 Gentoo             124
## 3 Chinstrap           68
```

# The `count` function

- The `count` function is a shortcut for `summarise(n = n())`
- Therefore, the `count` function names the variable "`n`"

```
penguins %>%
  group_by(species) %>%
  count() %>%
  arrange(desc(n))
```

```
## # A tibble: 3 x 2
## # Groups:   species [3]
##   species       n
##   <fct>     <int>
## 1 Adelie      152
## 2 Gentoo      124
## 3 Chinstrap    68
```

# Missing values

Recall that missing values are represented as `NA`s in R.

```
penguins %>%
  group_by(species) %>%
  summarise(mean_body_mass = mean(body_mass_g))
```

```
## # A tibble: 3 x 2
##   species   mean_body_mass
## * <fct>              <dbl>
## 1 Adelie               NA
## 2 Chinstrap          3733.
## 3 Gentoo               NA
```

The `mean` function (as well as many other summary functions) returns `NA` if even one value in the calculation is `NA`.

# Missing values

There are many different ways to deal with missing values (this is an entire topic in itself!). Today, we will just exclude the missing values from our calculations.

**Option 1**: The `na.rm = TRUE` option (only removes for the `body_mass_g` variable)

```
penguins %>%
  group_by(species) %>%
  summarise(mean_body_mass = mean(body_mass_g, na.rm = TRUE))
```

```
## # A tibble: 3 x 2
##   species   mean_body_mass
## * <fct>              <dbl>
## 1 Adelie             3701.
## 2 Chinstrap          3733.
## 3 Gentoo             5076.
```

# Missing values

**Option 2**: Removing **any** observations with missing values via the `drop_na` function (what we will do for the remainder of today's workshop)

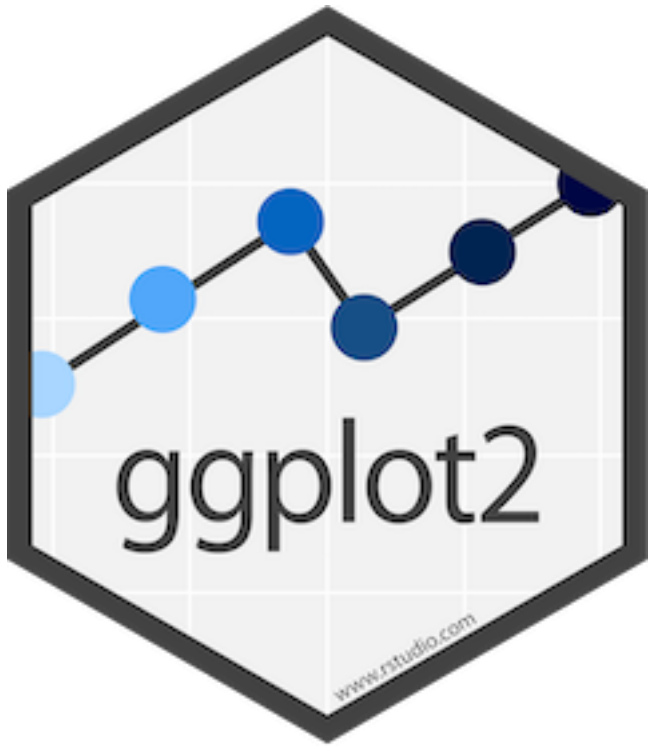
```
penguins2 ← penguins %>%
  drop_na()
penguins2 %>%
  group_by(species) %>%
  summarise(mean_body_mass = mean(body_mass_g))
```

```
## # A tibble: 3 x 2
##   species   mean_body_mass
## * <fct>              <dbl>
## 1 Adelie             3706.
## 2 Chinstrap          3733.
## 3 Gentoo             5092.
```

# Data Visualization with `ggplot2`

# The `ggplot2` package

- Part of the tidyverse
- For producing data visualizations
- Understanding ggplot = understanding the "grammar of graphics"



# The Grammar of Graphics

- Language has grammatical elements; combining them together creates a meaningful sentence

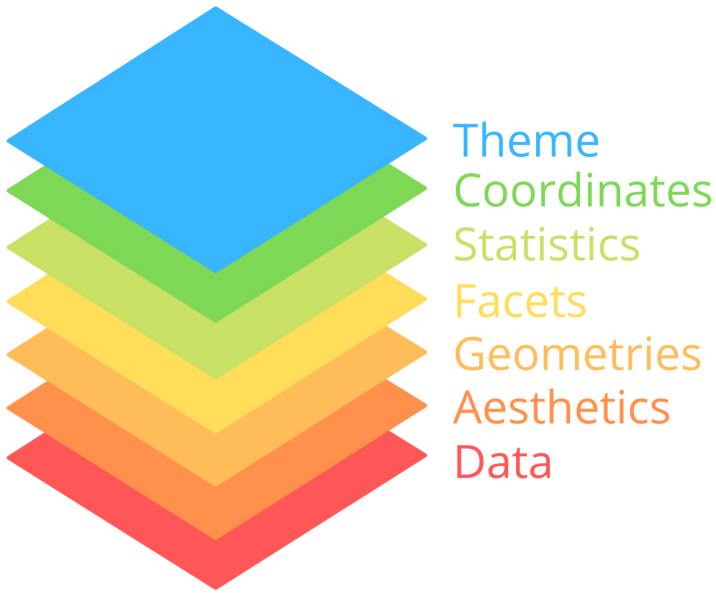

- Data visualizations have their own grammatical elements; combining them together creates a meaningful plot

## All Grammatical Elements

| Element | Description |
|---|---|
| Data | The dataset being plotted. |
| Aesthetics | The scales onto which we *map* our data. |
| Geometries | The visual elements used for our data. |
| Facets | Plotting small multiples. |
| Statistics | Representations of our data to aid understanding. |
| Coordinates | The space on which the data will be plotted. |
| Themes | All non-data ink. |

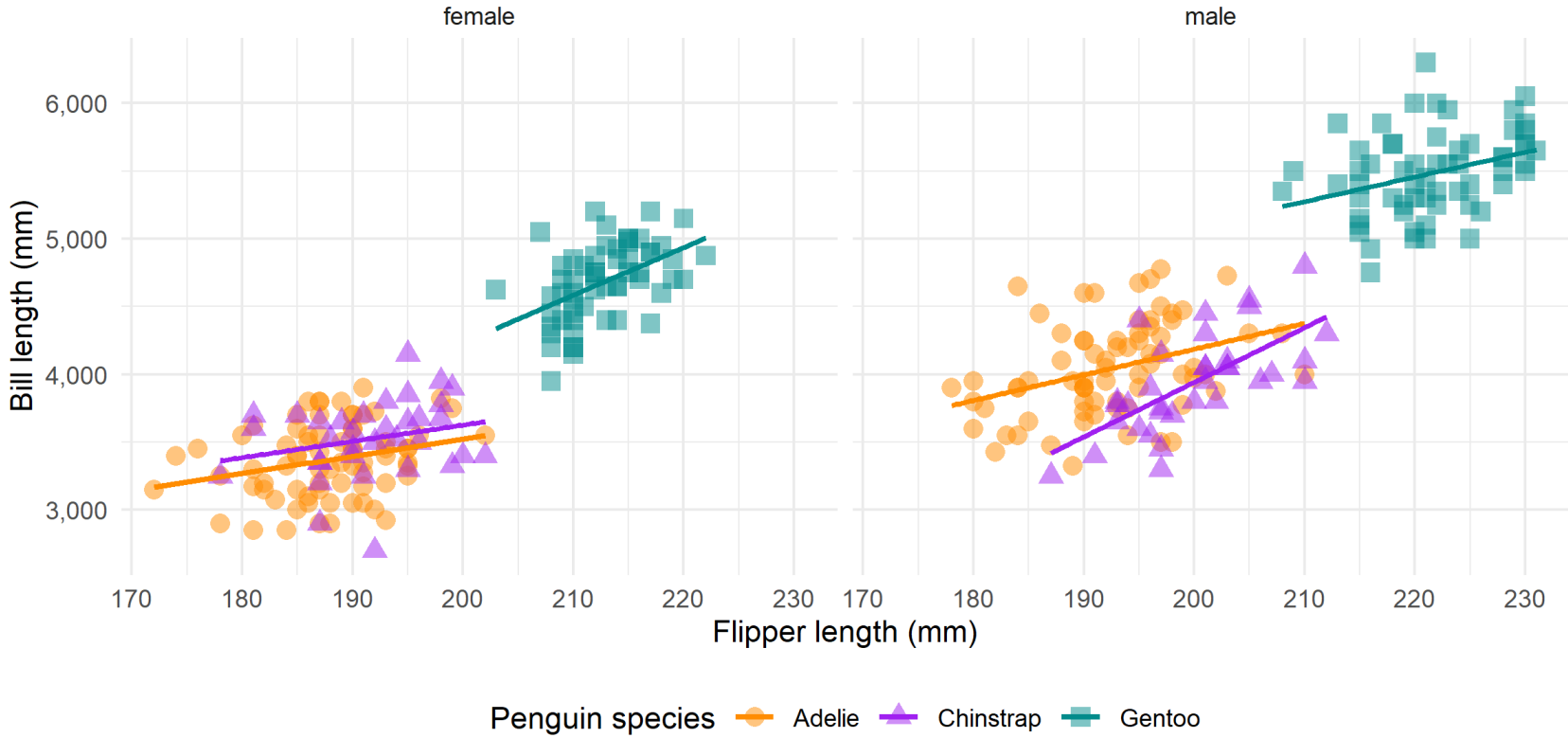
# Grammatical elements

- There are a total of 7 grammatical elements for graphics
- We combine these grammatical elements to communicate meaningfully through data visualizations
- We layer these grammatical elements on top of one another, typically with one layer per grammatical element



# Example

In the next few slides, we'll build the plot below, one layer at a time.



# Layer 1: Data

- The data layer is where we define which dataset we'll use for our visualization
- For `ggplot`, this must be a data frame
- This differs from creating plots using base R

```
# The penguins dataset is a tibble, which is a type of data frame
head(penguins)
```

```
## # A tibble: 6 x 8
##   species island bill_length_mm bill_depth_mm flipper_length_~ body_mass_g sex
##   <fct>   <fct>           <dbl>         <dbl>             <int>       <int> <fct>
## 1 Adelie  Torge~           39.1          18.7               181        3750 male
## 2 Adelie  Torge~           39.5          17.4               186        3800 fema~
## 3 Adelie  Torge~           40.3          18                 195        3250 fema~
## 4 Adelie  Torge~           NA            NA                  NA          NA <NA>
## 5 Adelie  Torge~           36.7          19.3               193        3450 fema~
## 6 Adelie  Torge~           39.3          20.6               190        3650 male
## # ... with 1 more variable: year <int>
```

# Layer 1: Data

```
# Equivalent to ggplot(data = penguins2)
penguins2 %>%
  ggplot()
```

# Layer 2: Aesthetics

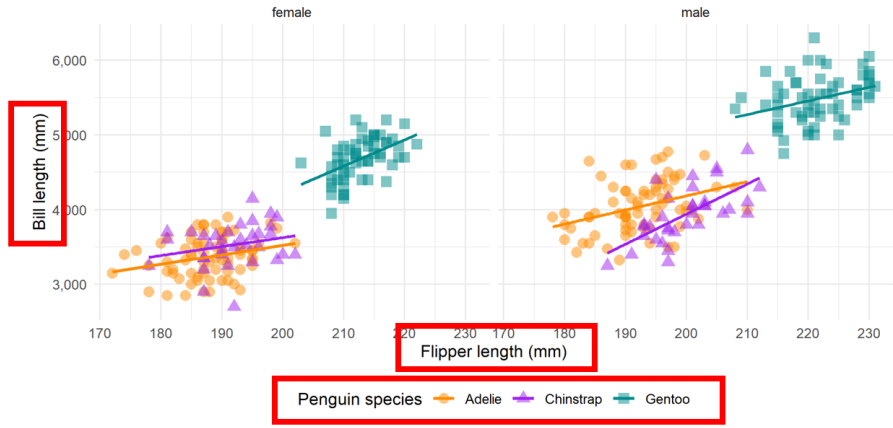
We "map" variables from our dataset onto "aesthetics" on our plot.

`flipper_length_mm` ⇒ x-axis

`body_mass_g` ⇒ y-axis

`species` ⇒ colour

`species` ⇒ shape

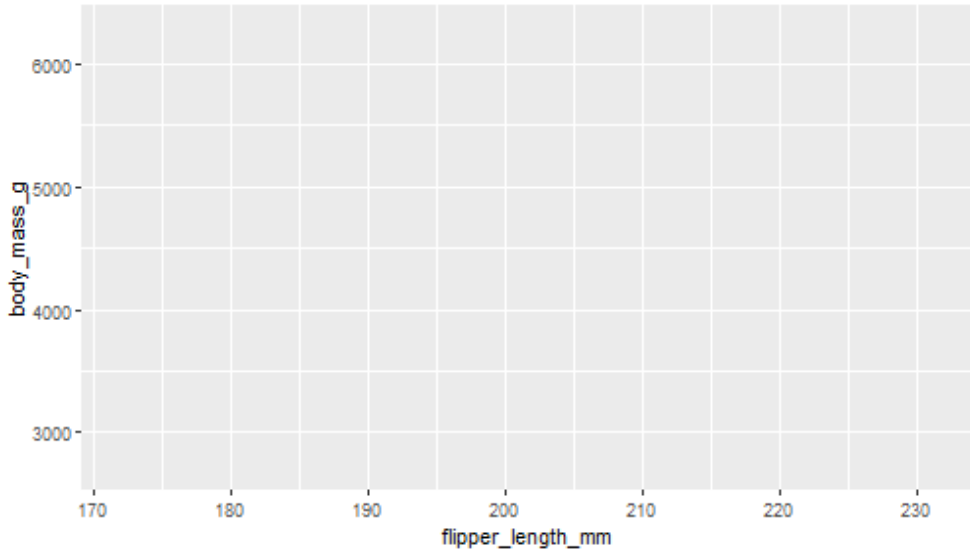



Notice how a variable can be mapped to more than one aesthetic.

# Layer 2: Aesthetics

- We use the `aes` function inside of the `ggplot` function
- On the left hand side of the equals sign: aesthetic we're mapping to
- On the right hand side of the equals sign: variable name from our dataset

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species))
```




The resulting plot is still "empty", but we can see that the variables have now been mapped to the correct axes.

# Layer 3: Geometries

The geometries layer controls which type of data visualization we are creating.

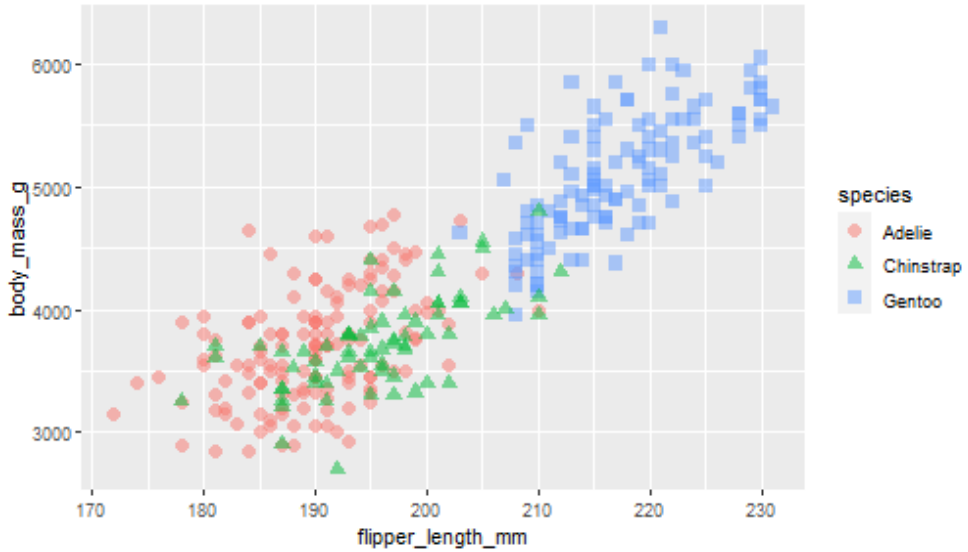
Some examples:

- `geom_boxplot()`: For creating boxplots
- `geom_point()`: For creating scatterplots
- `geom_line()`: For creating line plots
- `geom_histogram()`: For creating histograms

# Layer 3: Geometries

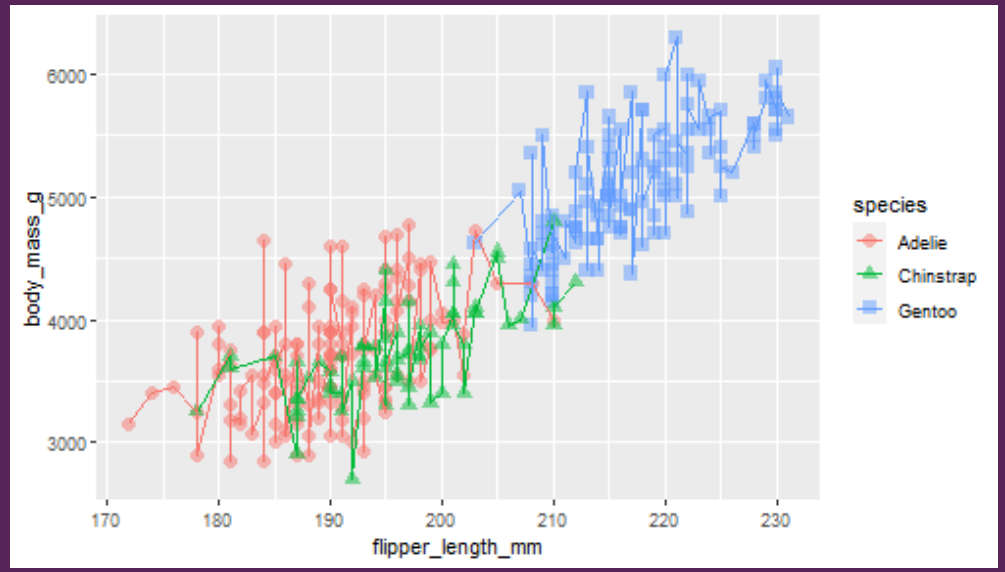
Notice that we use the addition sign after the `ggplot` function is finished.

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5)
```



# Challenge problem

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_line()
```




**We've added one more geometry compared to the previous slide, by using the `geom_line` function. Which of the following statements is true?**

a) The plot is obviously not a meaningful plot, but the code is correct.

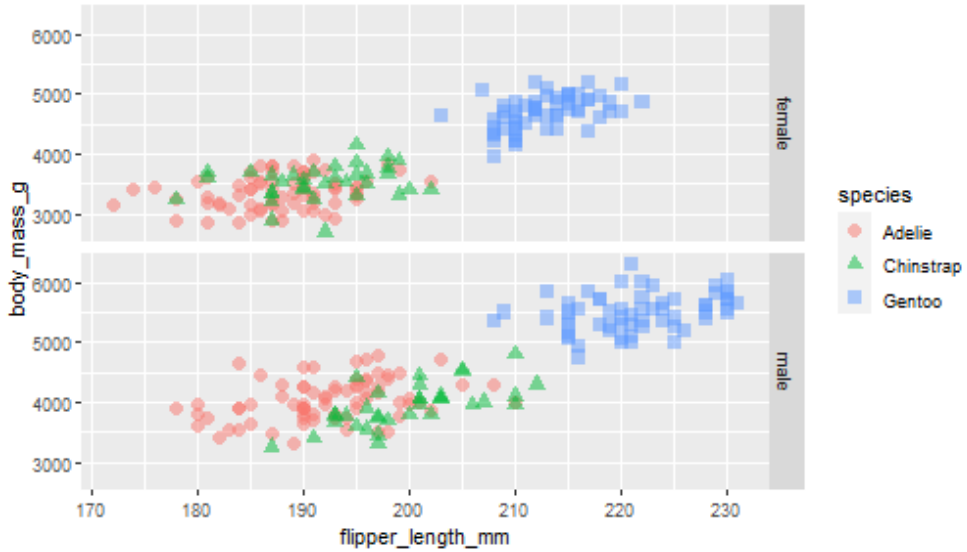
b) The plot is obviously not a meaningful plot, **and** the code is problematic as well -- we are on "Layer 3: Geometries" but we have 4 layers

# Layer 4: Facets

Facets allow us to create a grid of plots, one for each level of a categorical variable in our dataset.

For vertical facets, we use `variableName ~ .`

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(sex ~ .) # Vertical
```



# Layer 4: Facets

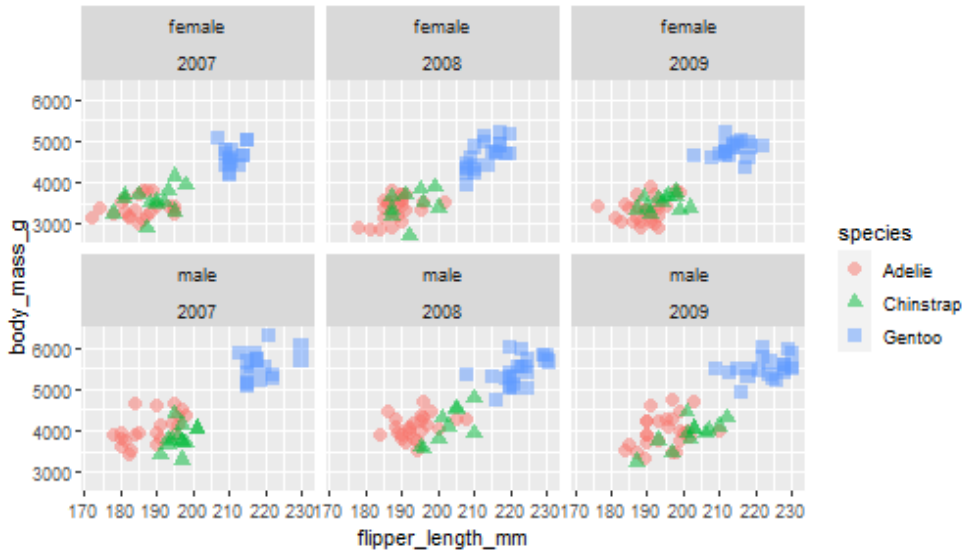
For horizontal facets, we use `. ~ variableName`

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(. ~ sex) # Horizontal
```

# Layer 4: Facets

We can also group by two variables by using the `facet_wrap` function.

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_wrap(. ~ sex + year)
# Row variable: sex; Column variable: year
```



# Layer 5: Statistics

The "statistics" grammatical elements allow us to perform statistical calculations on our existing ggplot.

To add a least squares regression line, use `stat_smooth`:

- "lm" stands for "Linear Model"
- "se" stands for "Standard Error"

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(. ~ sex) +
  stat_smooth(method = "lm", se = FALSE)
```

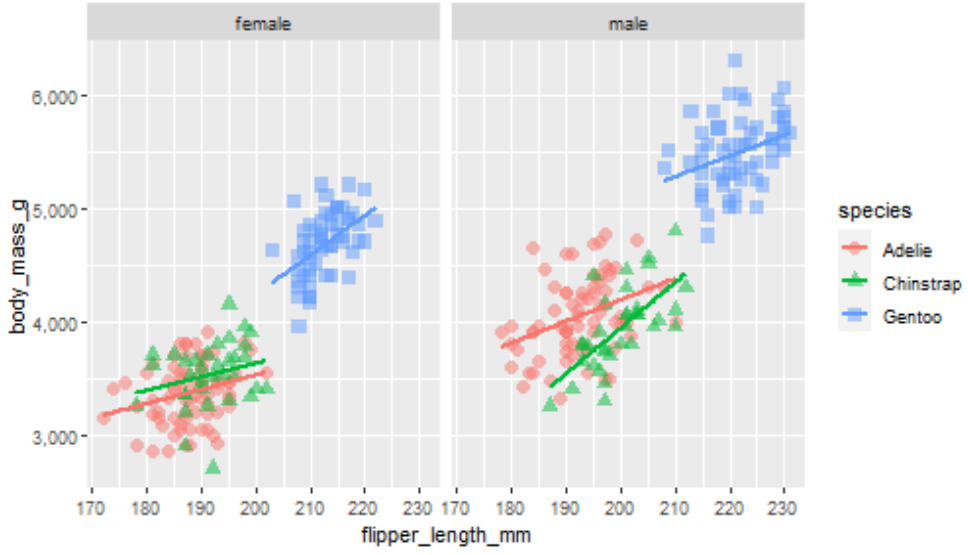
# Layer 6: Coordinates

The coordinates grammatical element allows us to control the way each coordinate (aesthetic) looks on our plot.

They take the form `scale_aestheticName_transformationType`.

To add commas to the values along the y-axis:

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(. ~ sex) +
  stat_smooth(method = "lm", se = FALSE) +
  scale_y_continuous(labels = scales::comma)
```

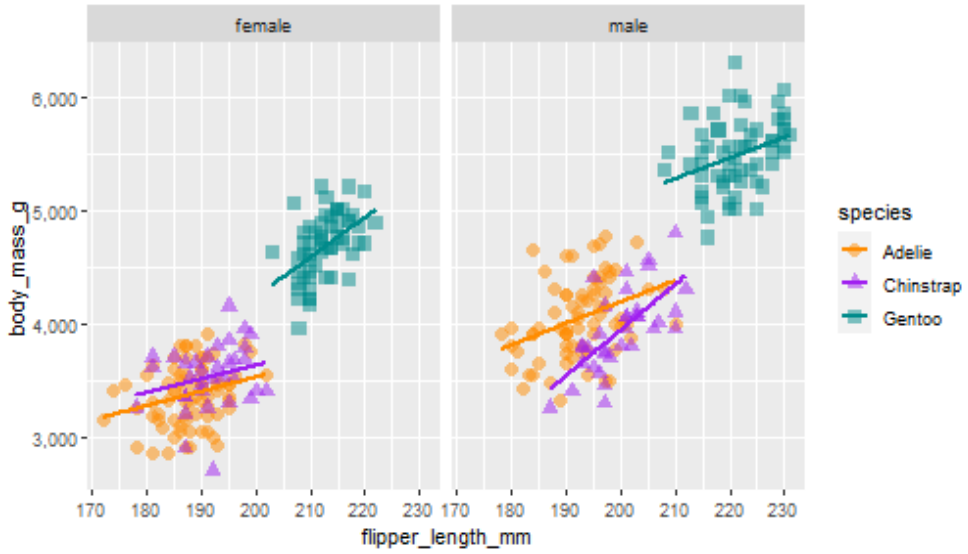



Since we previously mapped the `bill_length_mm` variable to the `y` aesthetic, `scale_y_continuous` changes the y-axis (which represents the bill length).

# Layer 6: Coordinates

To (manually) change the colours used for the `species` variable:

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(. ~ sex) +
  stat_smooth(method = "lm", se = FALSE) +
  scale_y_continuous(labels = scales::comma) +
  scale_colour_manual(values = c("darkorange",
                                 "purple", "cyan4"))
```



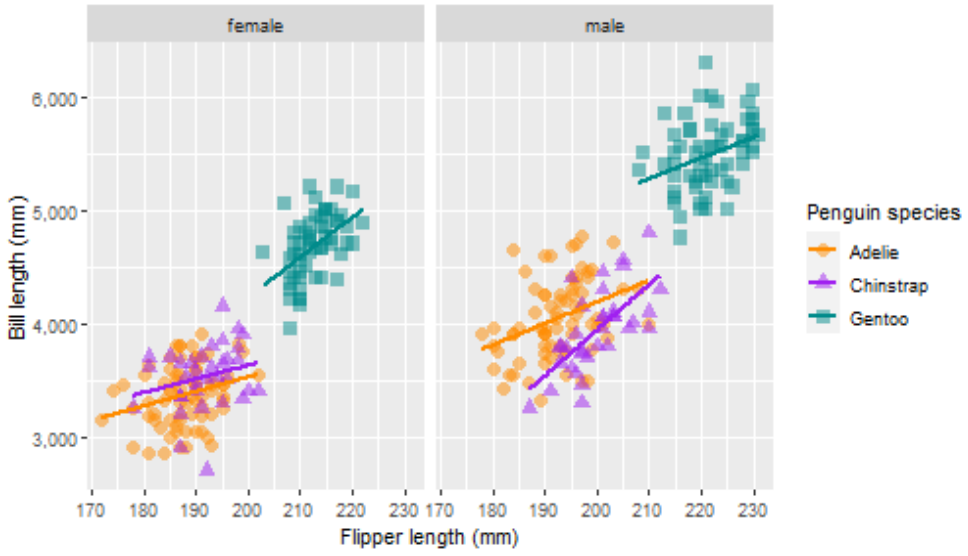

Since we previously mapped the `species` variable to the `colour` aesthetic, `scale_colour_manual` changes the colours for the `species` variable.

# Layer 7: Theme

- The "theme" grammatical elements control the non-data related aspects of the plot
- Changing the theme is useful for creating publication-ready plots

Let's start by changing the plot labels (aesthetic name goes on the left hand side of the equals sign, text to display goes on the right hand side of the equals sign):

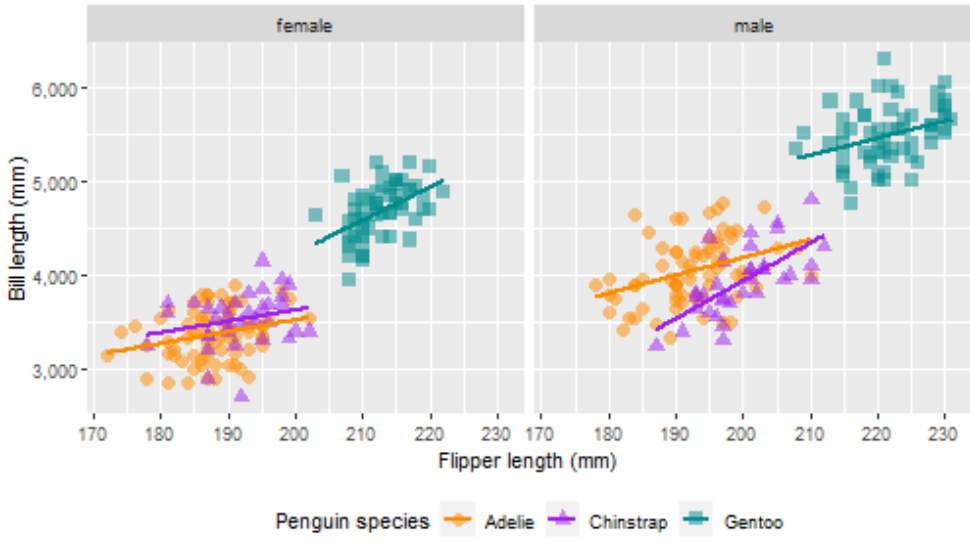
```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(. ~ sex) +
  stat_smooth(method = "lm", se = FALSE) +
  scale_y_continuous(labels = scales::comma) +
  scale_colour_manual(values = c("darkorange",
                                 "purple", "cyan4")
  labs(x = "Flipper length (mm)",
       y = "Bill length (mm)",
       colour = "Penguin species",
       shape = "Penguin species")
```



# Layer 7: Theme

We can change almost anything imaginable by using the `theme` function. Let's change the position of the legend:

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(. ~ sex) +
  stat_smooth(method = "lm", se = FALSE) +
  scale_y_continuous(labels = scales::comma) +
  scale_colour_manual(values = c("darkorange",
                                 "purple", "cyan4")
  labs(x = "Flipper length (mm)",
       y = "Bill length (mm)",
       colour = "Penguin species",
       shape = "Penguin species") +
  theme(legend.position = "bottom")
```

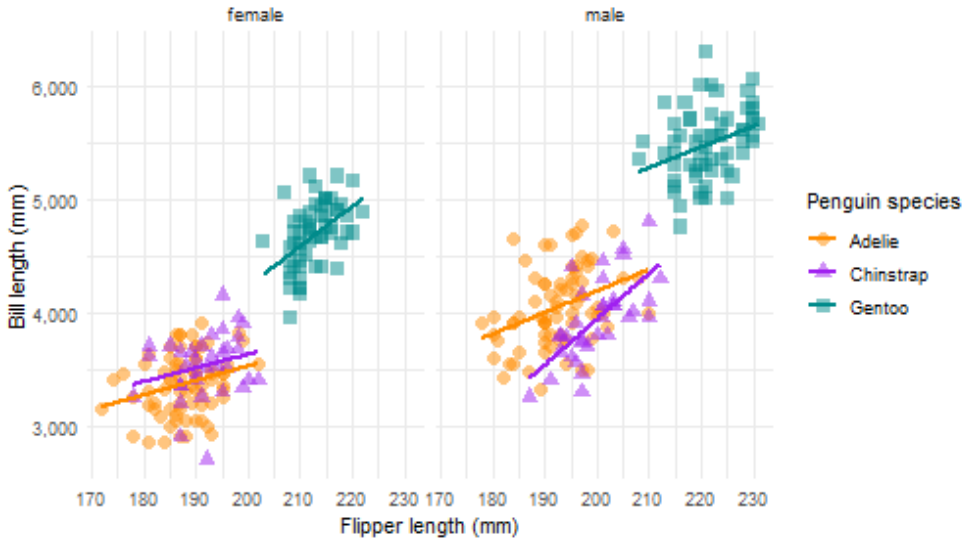



To see a full list of options that can be changed using the `theme` function, see ggplot2.tidyverse.org/reference/theme.html.

# Layer 7: Theme

There are also some pre-existing themes that you can use in order to save time. For example, the "minimal" theme removes the grey background:

```
penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(. ~ sex) +
  stat_smooth(method = "lm", se = FALSE) +
  scale_y_continuous(labels = scales::comma) +
  scale_colour_manual(values = c("darkorange",
                                 "purple", "cyan4")) +
  labs(x = "Flipper length (mm)",
       y = "Bill length (mm)",
       colour = "Penguin species",
       shape = "Penguin species") +
  theme_minimal()
```



# Challenge problem

**If we want to use the minimal theme AND change the legend position to "top", which of the following will do this?**

a) `theme_minimal() + theme(legend.position = "top")`

b) `theme(legend.position = "top") + theme_minimal()`

c) Both will give the desired result

# Saving a ggplot

To save a plot created using `ggplot`, use the `ggsave` function.

```
# Assign plot object to a variable
p ← penguins2 %>%
  ggplot(aes(x = flipper_length_mm,
             y = body_mass_g,
             colour = species,
             shape = species)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_grid(. ~ sex) +
  stat_smooth(method = "lm", se = FALSE) +
  scale_y_continuous(labels = scales::comma) +
  scale_colour_manual(values = c("darkorange",
                                 "purple", "cyan4")) +
  labs(x = "Flipper length (mm)",
       y = "Bill length (mm)",
       colour = "Penguin species",
       shape = "Penguin species") +
  theme_minimal() +
  theme(legend.position = "bottom")

# Use the ggsave function to save the plot
ggsave(plot = p,
       filename = "C:/Users/Melissa/Documents/ggplot.png",
       width = 8, height = 4,
       units = "in")
```

# Working directories

- On the last slide, we specified the entire file path
- This is fine if we're saving one plot, but becomes frustrating if we're saving many
- It's a good practice to set your working directory (the location on your computer where R will read in files and save files to)

```
# Determine current working directory
getwd()

# Set working directory
setwd("C:/Users/Melissa/Documents")

# Now we can save our plot without specifying the entire file path
ggsave(plot = p,
       filename = "ggplot.png",
       width = 8, height = 4,
       units = "in")
```

# Challenge problem

Can you re-create the following plot?

**Hint**: you will need to set the argument `position = "identity"` inside of the `geom_histogram` function.