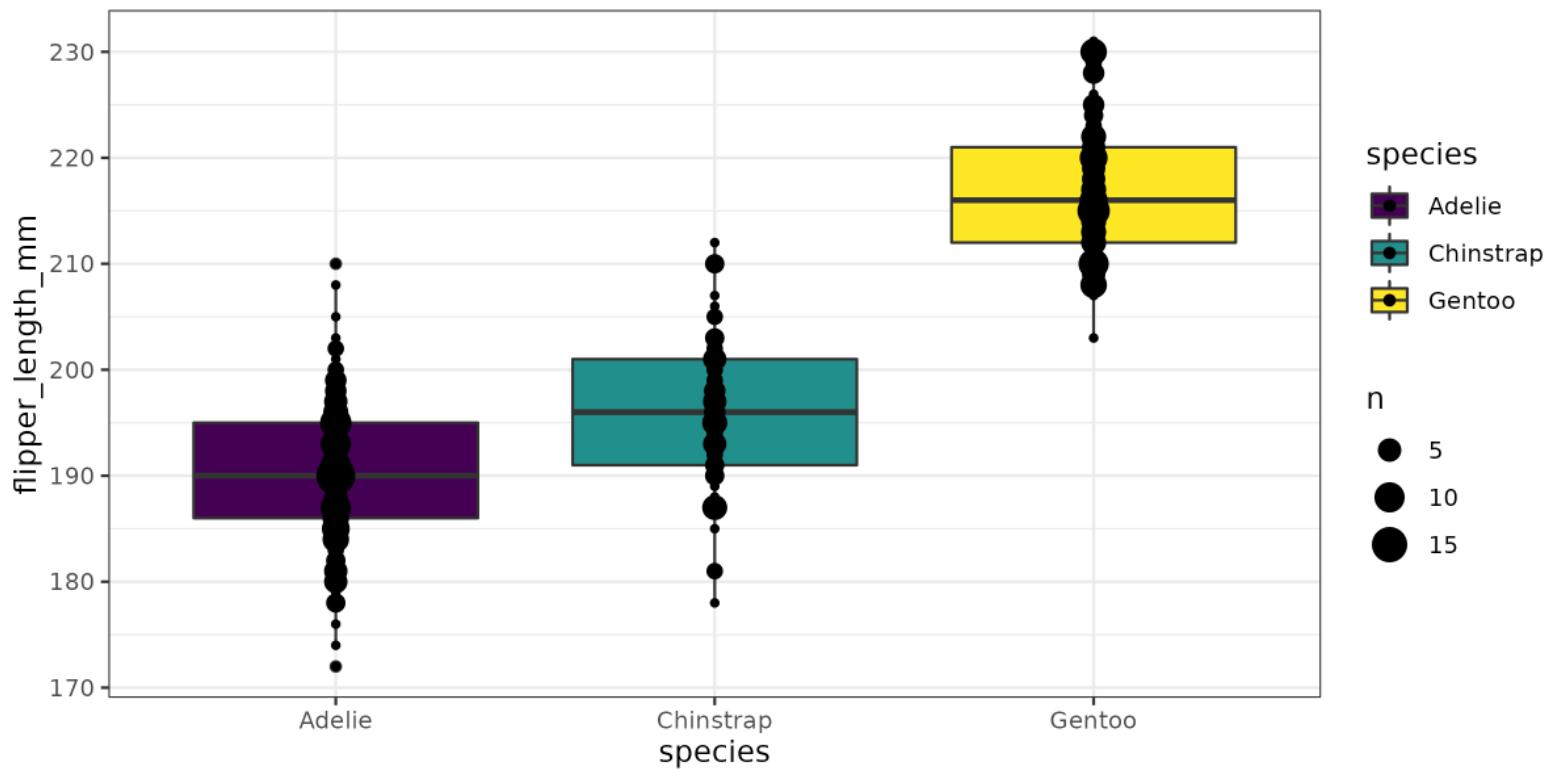


Visualizing Data in R

A primer on `ggplot2`



First things first

Save previous script (consider names like **intro.R** or **1_getting_started.R**)

Open New File

(make sure you're in the RStudio Project)

Add **library(tidyverse)** to the top

Save this new script

consider names like **figs.R** or **2_figures.R**

Outline

1. Figures with `ggplot2` (A `tidyverse` package)

- Basic plot
- Common plot types
- Plotting by categories
- Adding statistics
- Customizing plots
- Annotating plots

2. Combining figures with `patchwork`

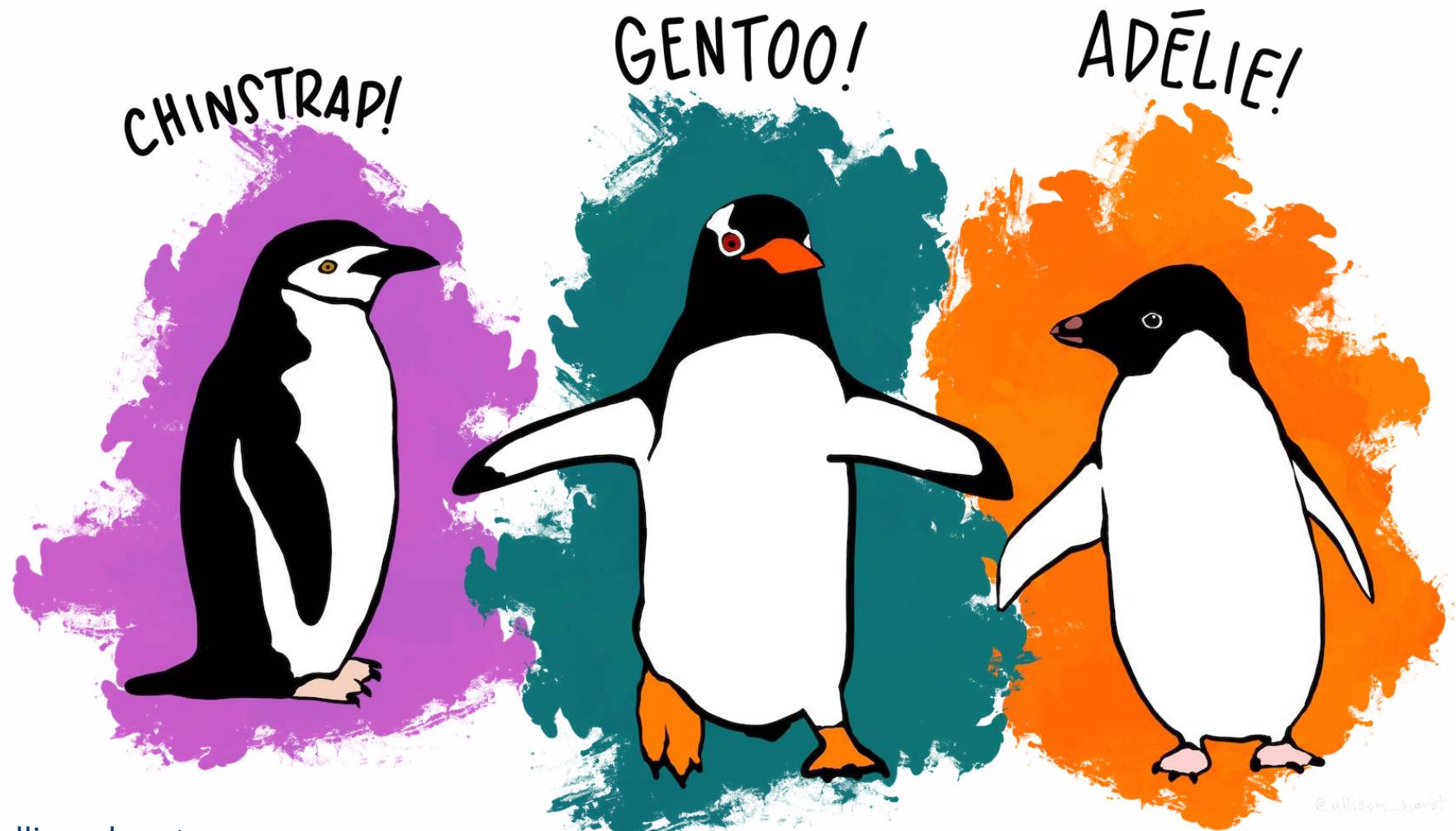
3. Saving figures

gg plot 2:

Build a data
MASTERpiece



Our data set: Palmer Penguins!

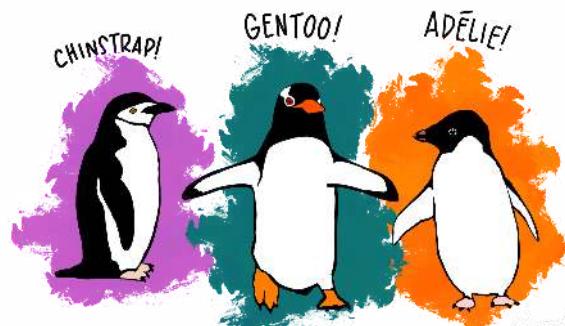


Our data set: Palmer Penguins!



```
library(palmerpenguins)  
penguins
```

```
## # A tibble: 344 × 8  
##   species island   bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex  year  
##   <fct>   <fct>        <dbl>          <dbl>            <int>        <int> <fct> <int>  
## 1 Adelie  Torgersen     39.1           18.7            181       3750 male   2007  
## 2 Adelie  Torgersen     39.5           17.4            186       3800 female 2007  
## 3 Adelie  Torgersen     40.3            18              195       3250 female 2007  
## 4 Adelie  Torgersen      NA             NA              NA         NA <NA>  2007  
## 5 Adelie  Torgersen     36.7           19.3            193       3450 female 2007  
## 6 Adelie  Torgersen     39.3           20.6            190       3650 male   2007  
## 7 Adelie  Torgersen     38.9           17.8            181       3625 female 2007  
## 8 Adelie  Torgersen     39.2           19.6            195       4675 male   2007  
## # ... with 336 more rows
```





Our data set: Palmer Penguins!

```
library(palmerpenguins)  
penguins
```

```
## # A tibble: 344 × 8  
##   species island   bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex  year  
##   <fct>   <fct>          <dbl>           <dbl>            <int>        <int> <fct> <int>  
## 1 Adelie  Torgersen     39.1            18.7             181      3750 male   2007  
## 2 Adelie  Torgersen     39.5            17.4             186      3800 female 2007  
## 3 Adelie  Torgersen     40.3            18               195      3250 female 2007  
## 4 Adelie  Torgersen     NA              NA               NA       NA <NA>  2007  
## 5 Adelie  Torgersen     36.7            19.3             193      3450 female 2007  
## 6 Adelie  Torgersen     39.3            20.6             190      3650 male   2007  
## 7 Adelie  Torgersen     38.9            17.8             181      3625 female 2007  
## 8 Adelie  Torgersen     39.2            19.6             195      4675 male   2007  
## # ... with 336 more rows
```

Your turn!

1. Run this code and look at the output in the console
2. Run `view(penguins)` to see the output in the built-in spreadsheet viewer



Side Note

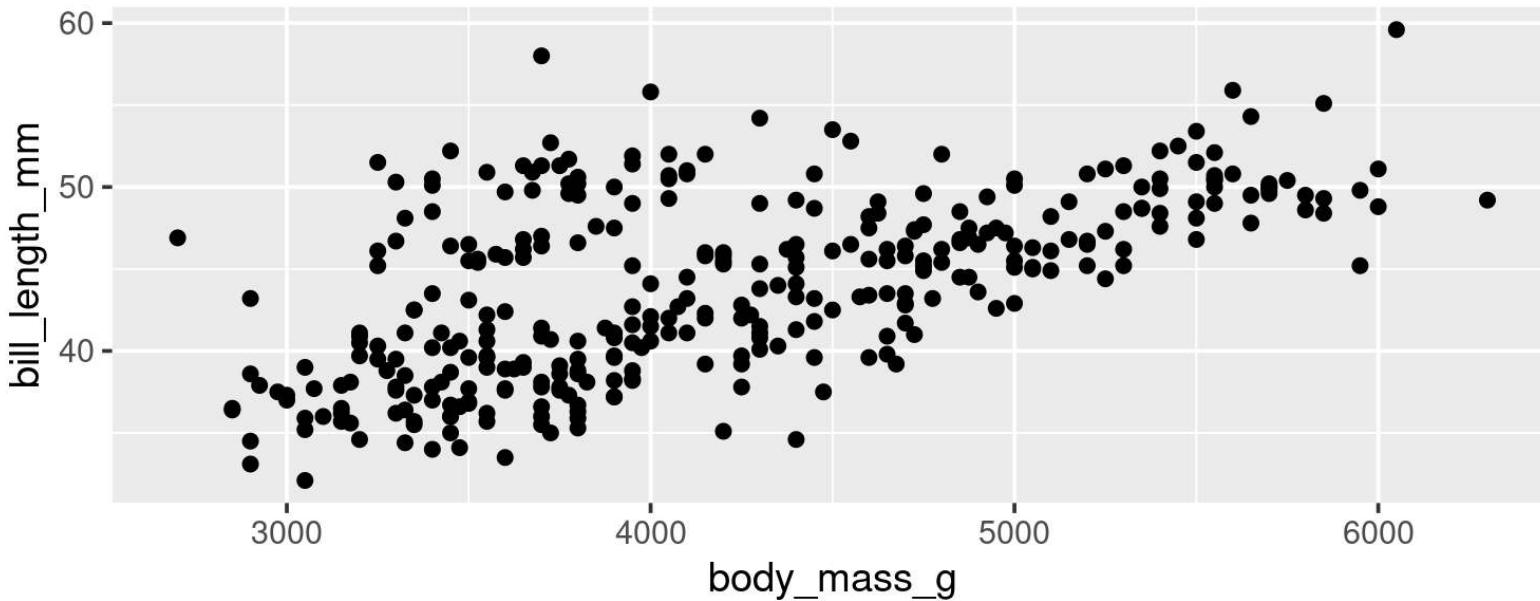
Where did the `penguins` data set come from?

- Sometimes R packages contain data
- If you load a package (i.e. `library(palmerpenguins)`) you can use the data
- **Note** that here the data object is called `penguins` (not `palmerpenguins`)
- **Note** this is NOT how you'll load your own data

A basic plot

```
library(palmerpenguins)
library(tidyverse)

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



Break it down

```
library(palmerpenguins)
library(tidyverse)

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

library(palmerpenguins)

- Load the **palmerpenguins** package so we have access to **penguins** data

Break it down

```
library(palmerpenguins)
library(tidyverse)

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

library(tidyverse)

- Load the **tidyverse** package (which loads the **ggplot2** package and gives us access to the **ggplot()** function among others)

Break it down

```
library(palmerpenguins)
library(tidyverse)

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

ggplot()

- Set the attributes of your plot
- **data** = Dataset
- **aes** = Aesthetics (how the data are used)
- Think of this as your plot defaults

Break it down

```
library(palmerpenguins)
library(tidyverse)

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

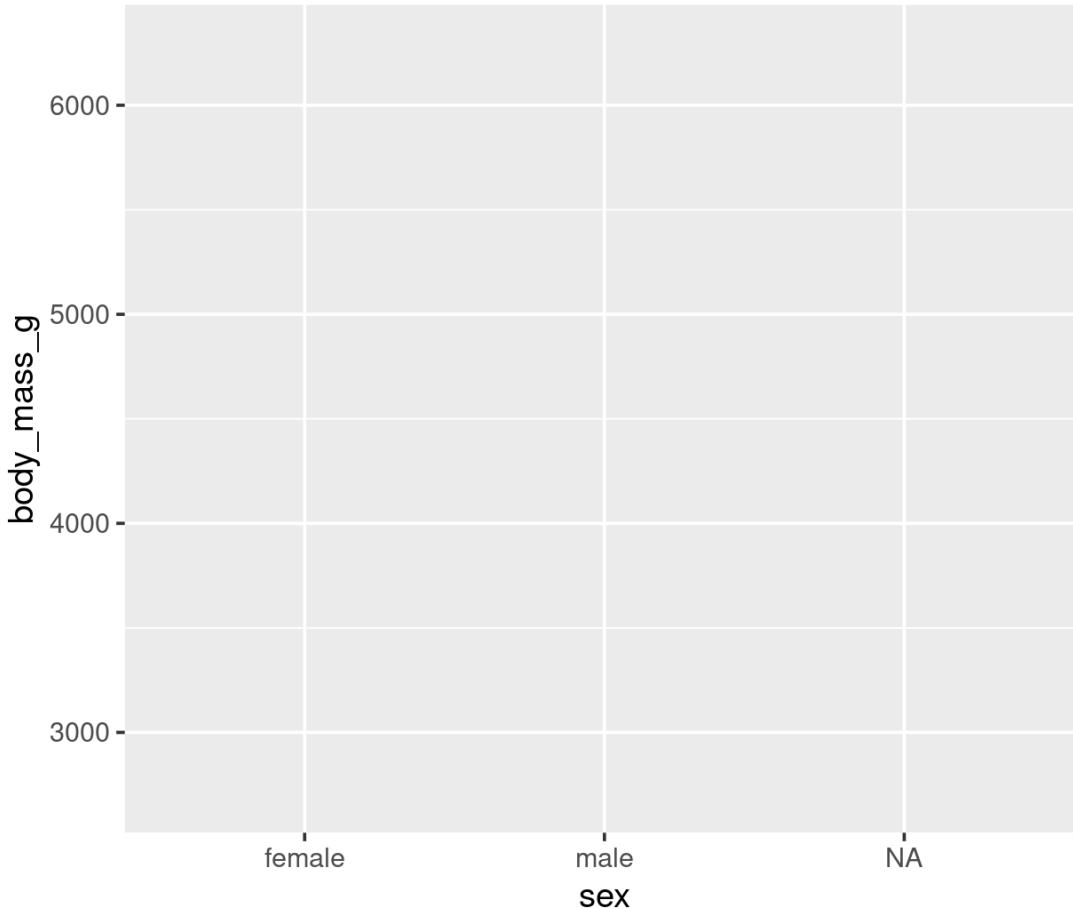
geom_point()

- Choose a **geom** function to display the data
- Always *added* to a **ggplot()** call with **+**

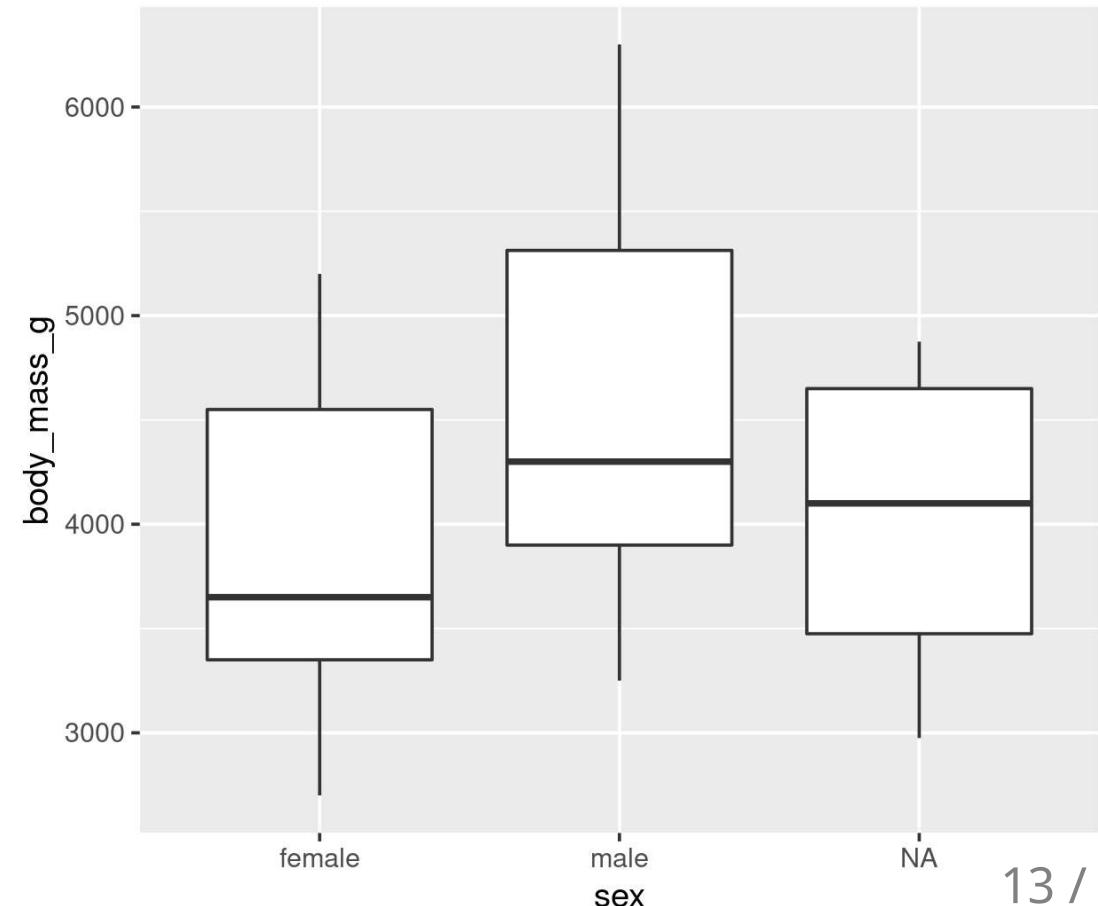
ggplots are essentially layered objects, starting with a call to **ggplot()**

Plots are layered

```
ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

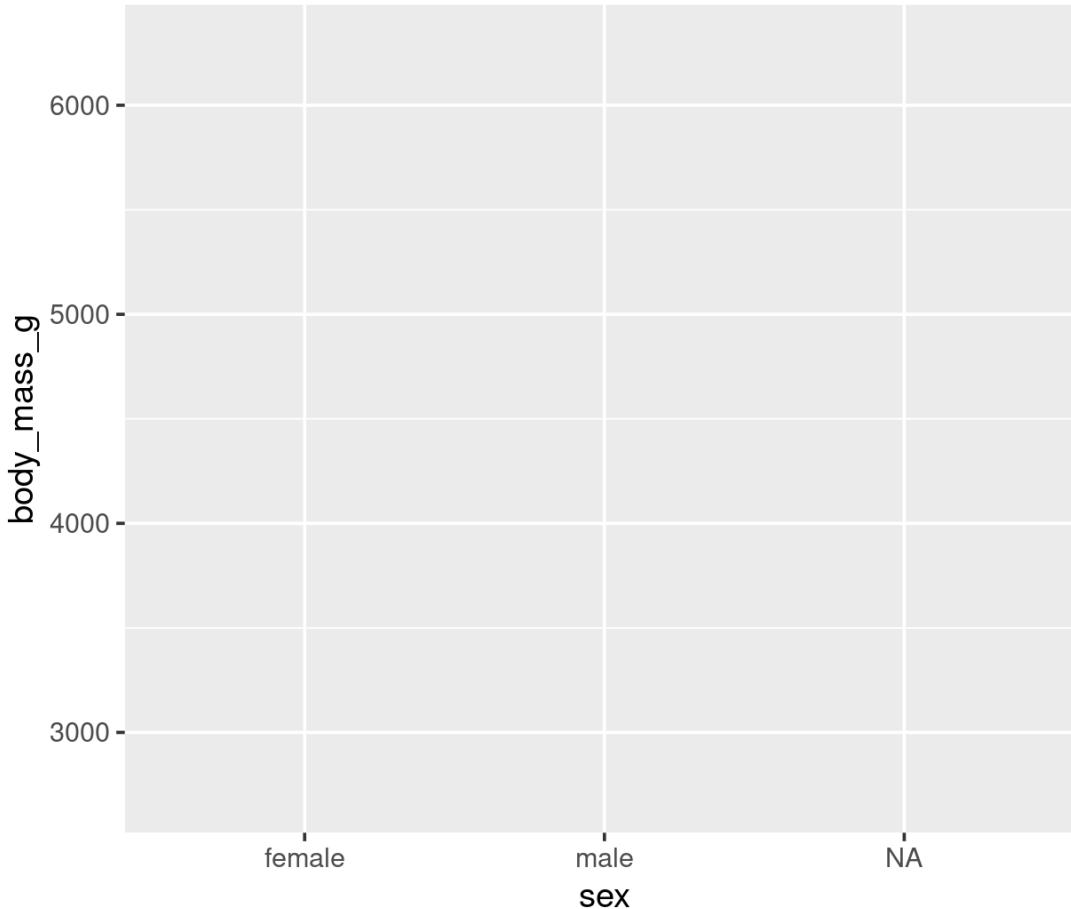


```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  geom_boxplot()
```

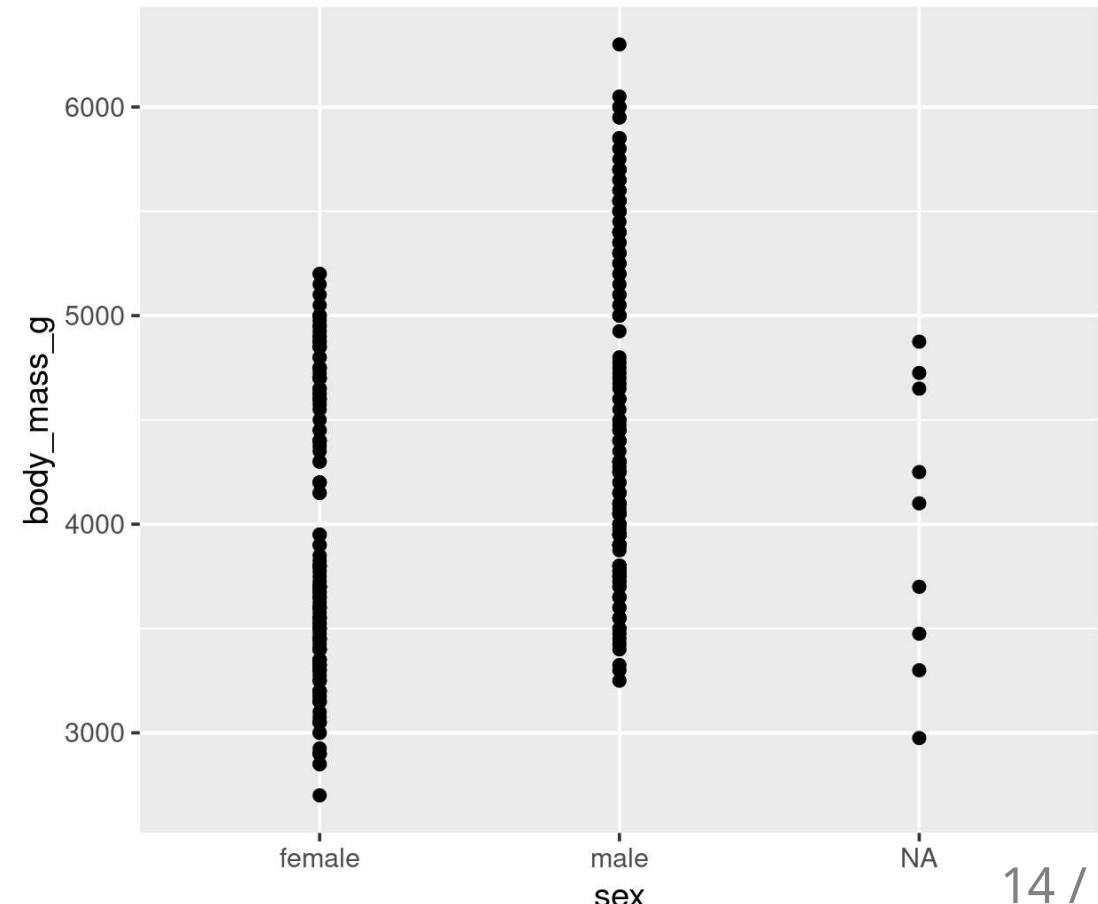


Plots are layered

```
ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

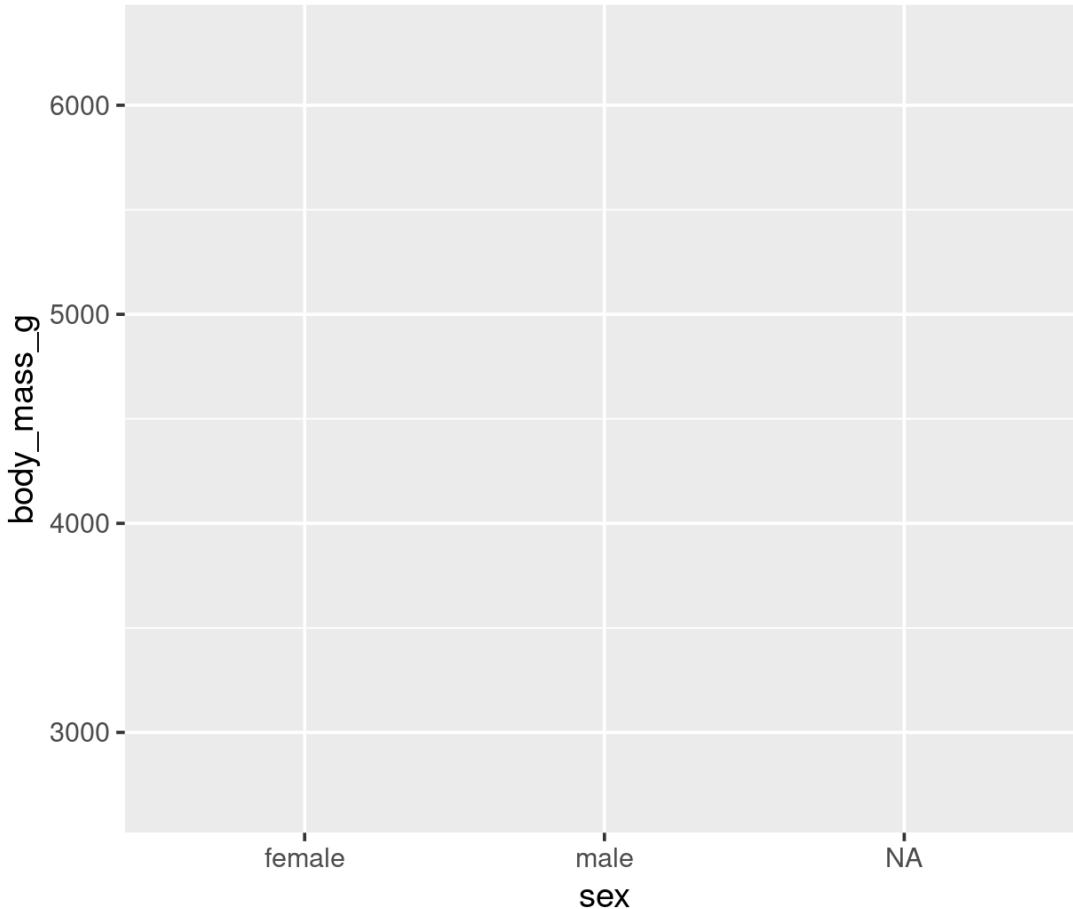


```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  geom_point()
```

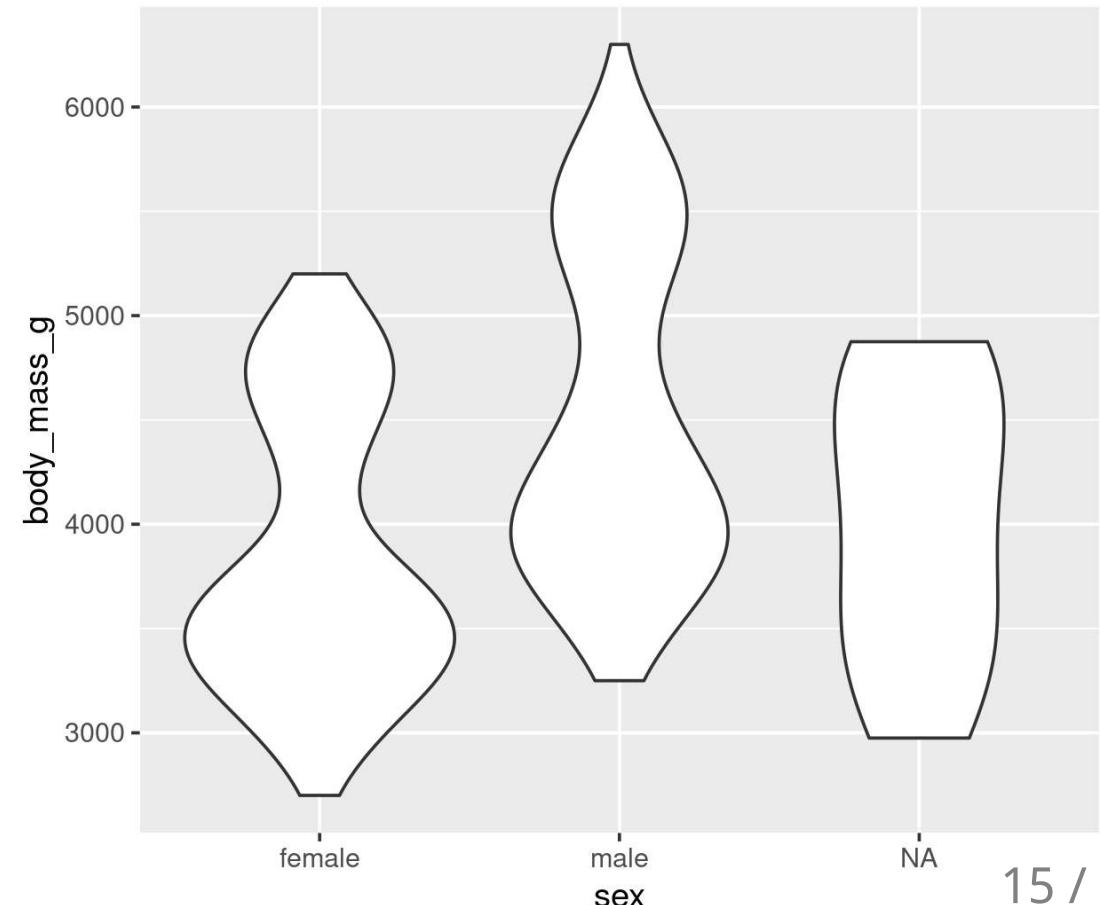


Plots are layered

```
ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```



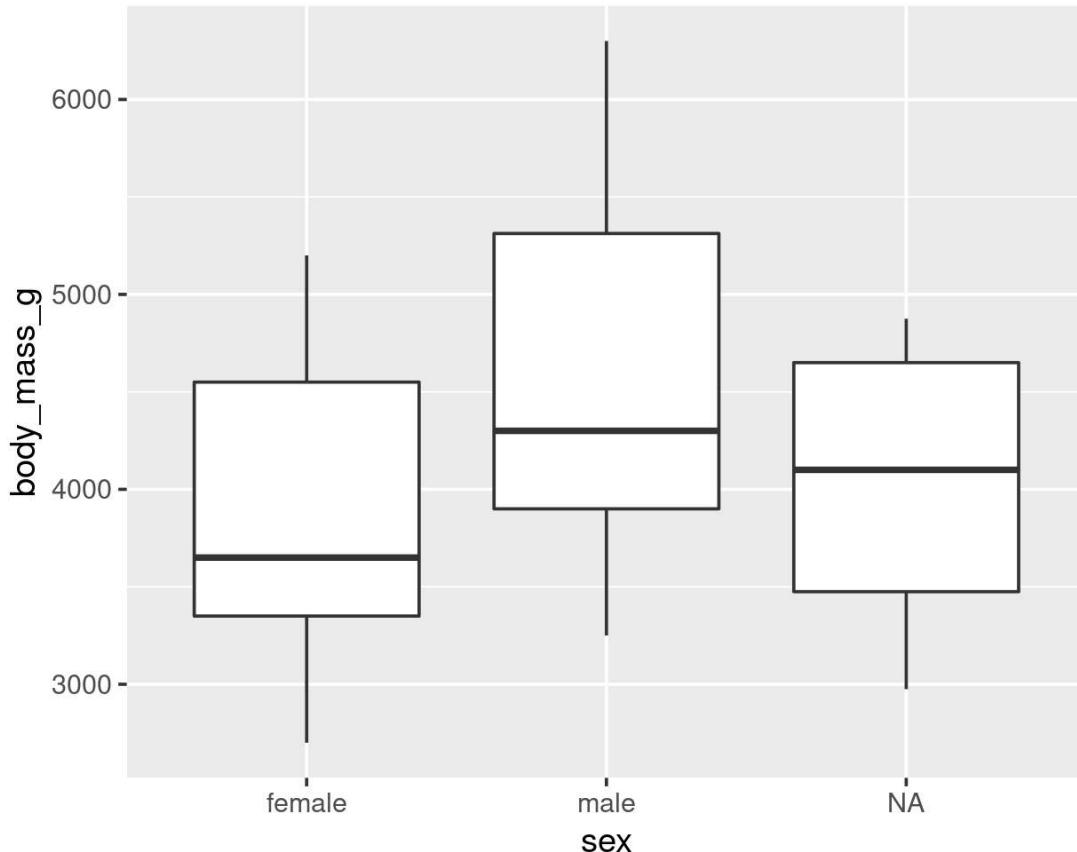
```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  geom_violin()
```



Plots are layered

You can add multiple layers

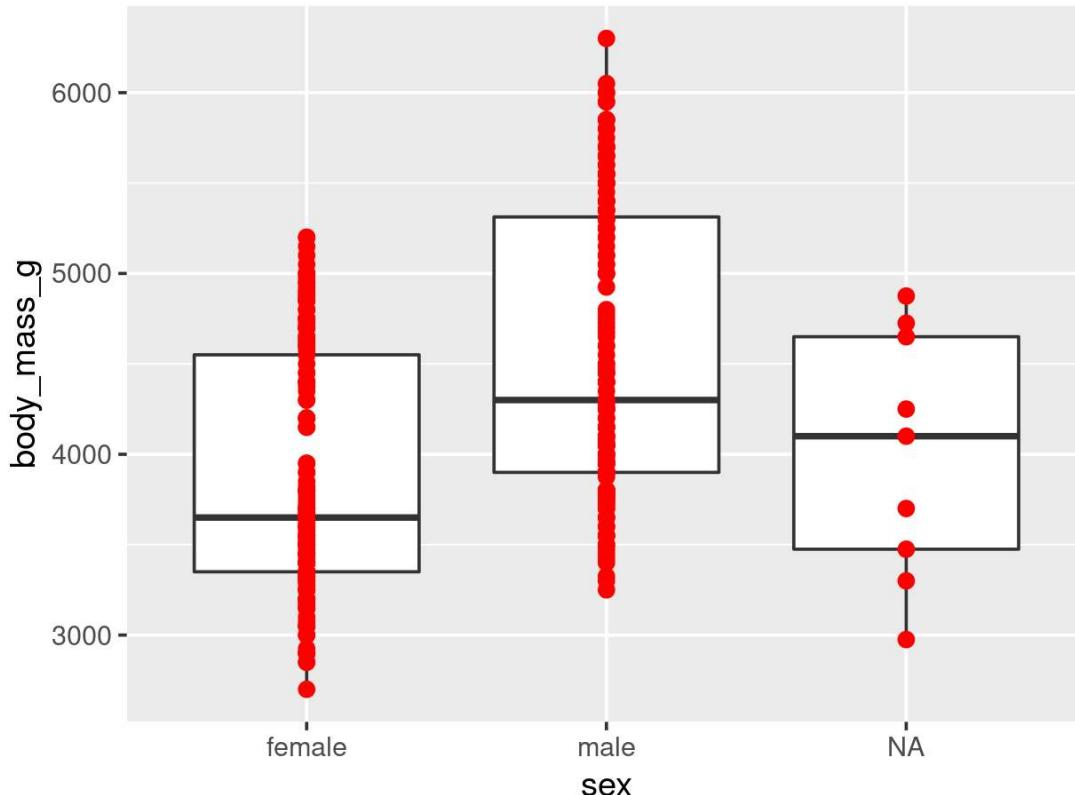
```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  geom_boxplot()
```



Plots are layered

You can add multiple layers

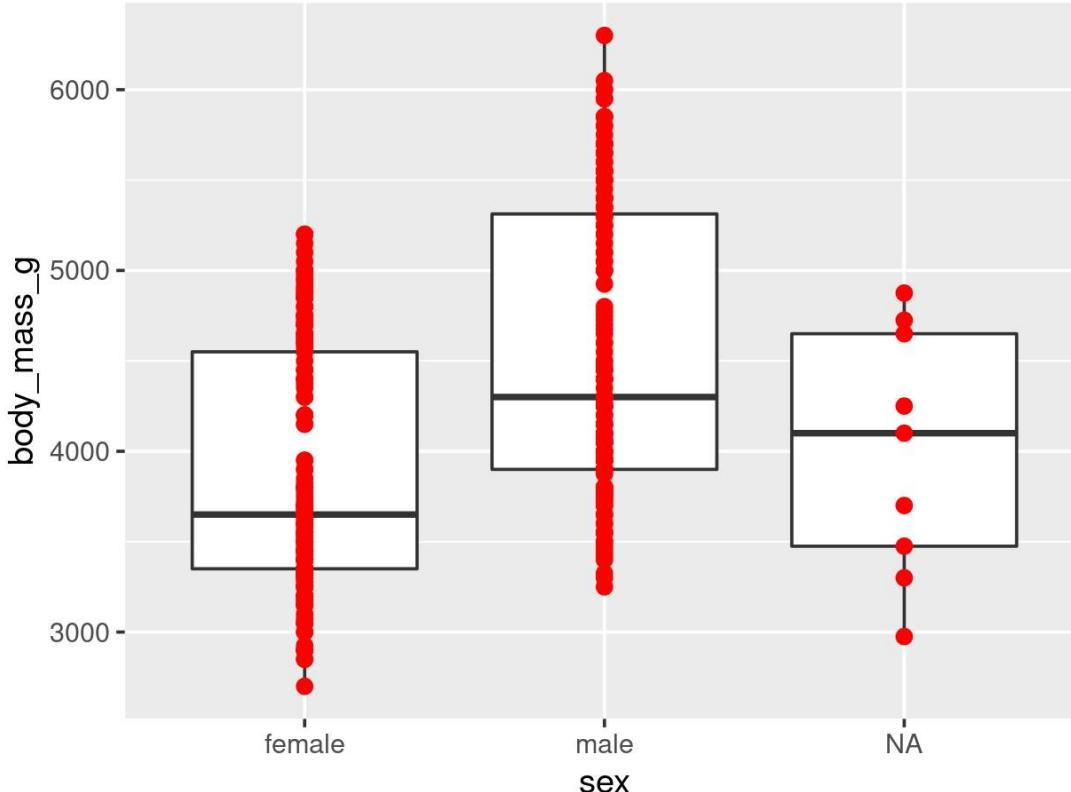
```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  geom_boxplot() +  
  geom_point(size = 2, colour = "red")
```



Plots are layered

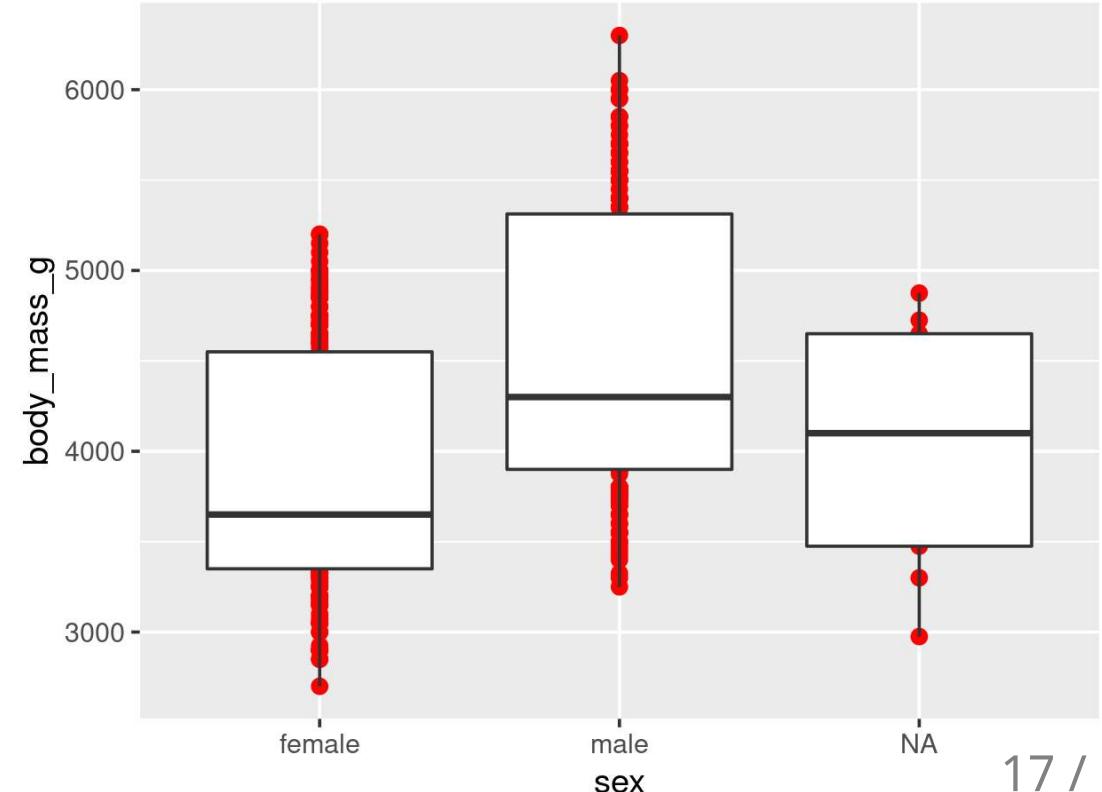
You can add multiple layers

```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  geom_boxplot() +  
  geom_point(size = 2, colour = "red")
```



Order matters

```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  geom_point(size = 2, colour = "red") +  
  geom_boxplot()
```



Plots are objects

Any ggplot can be saved as an object

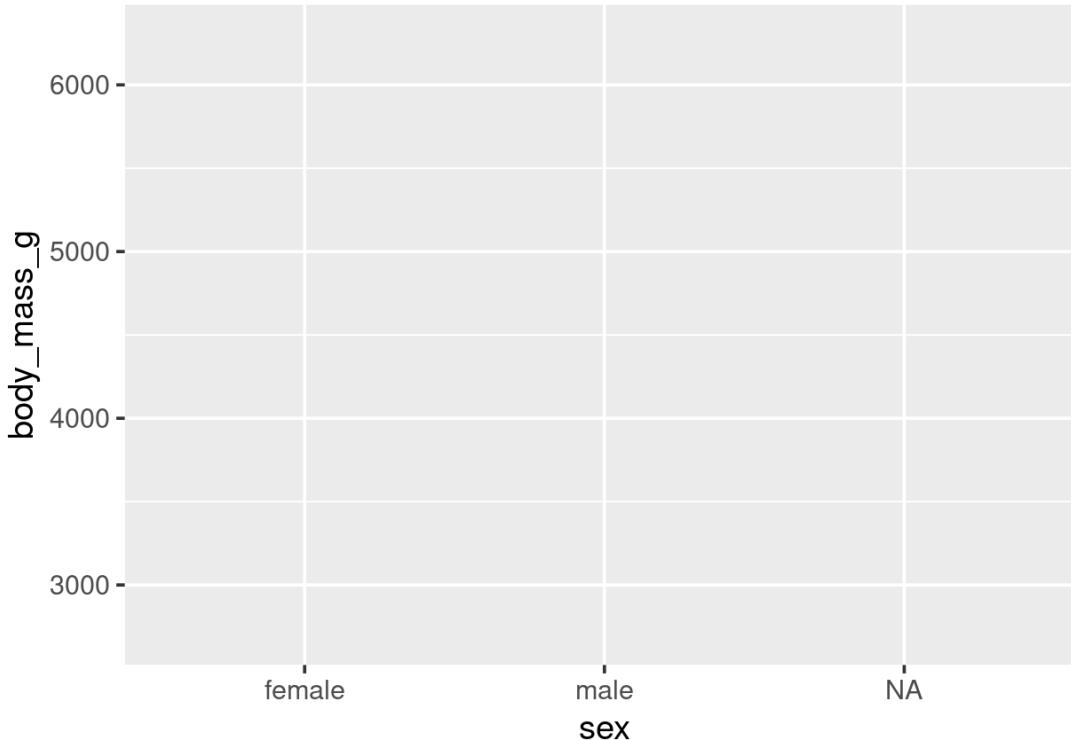
```
g <- ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

Plots are objects

Any ggplot can be saved as an object

```
g <- ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

```
g
```

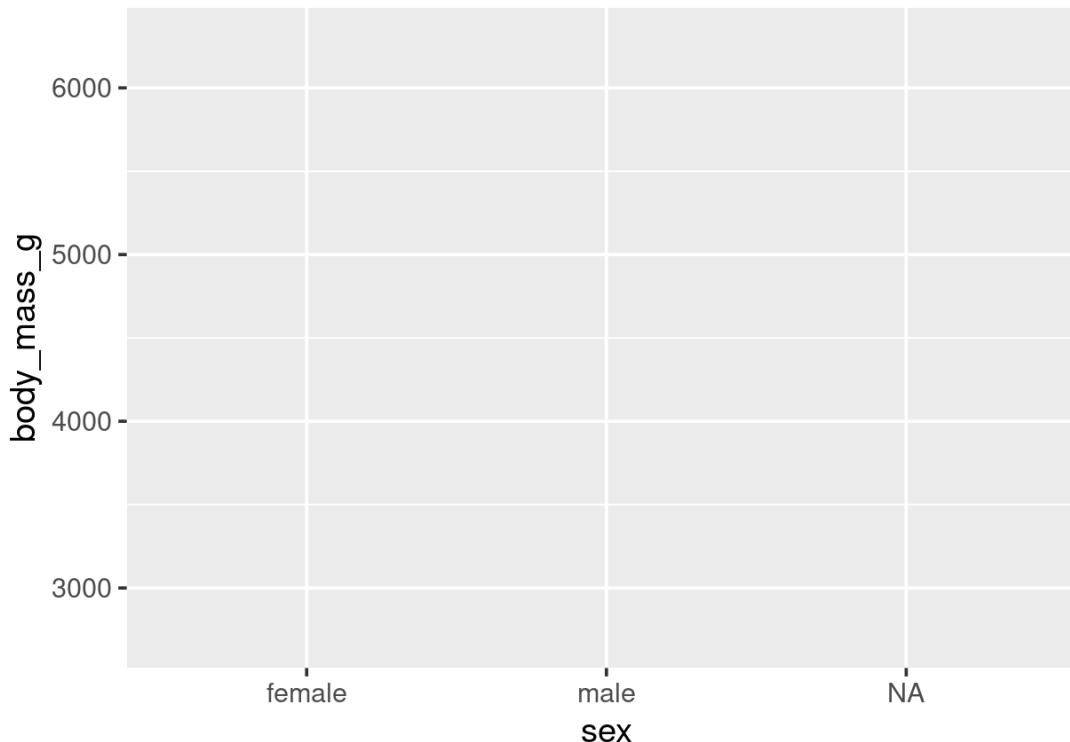


Plots are objects

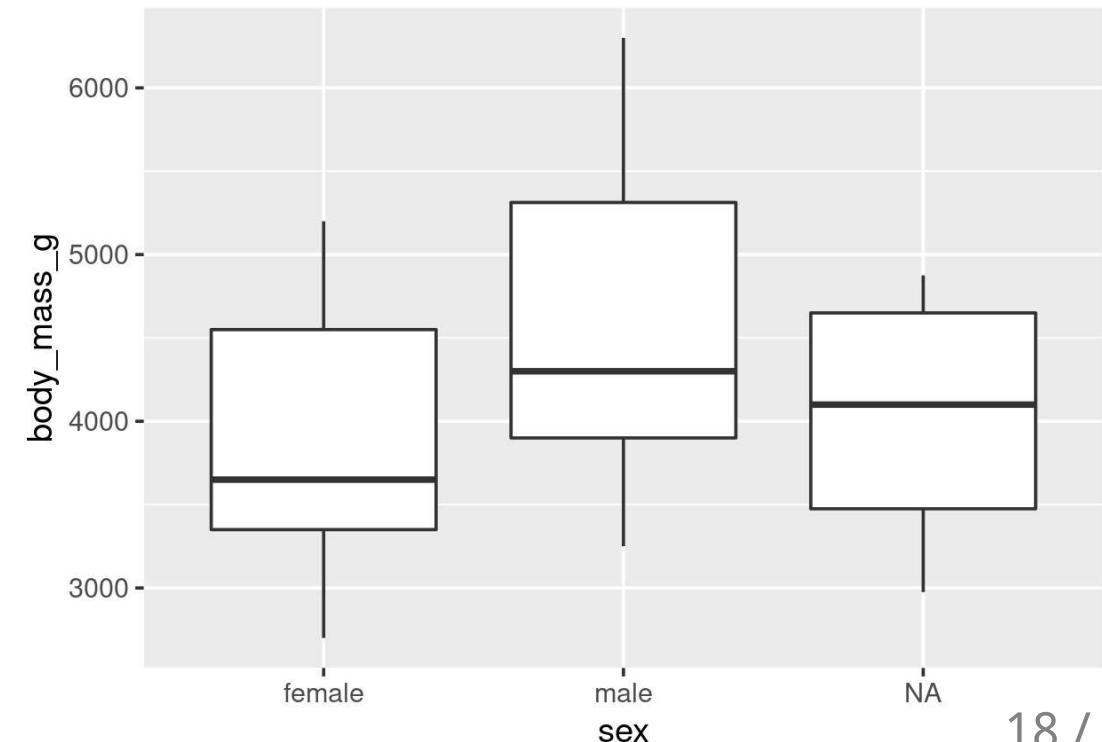
Any ggplot can be saved as an object

```
g <- ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

```
g
```



```
g + geom_boxplot()
```

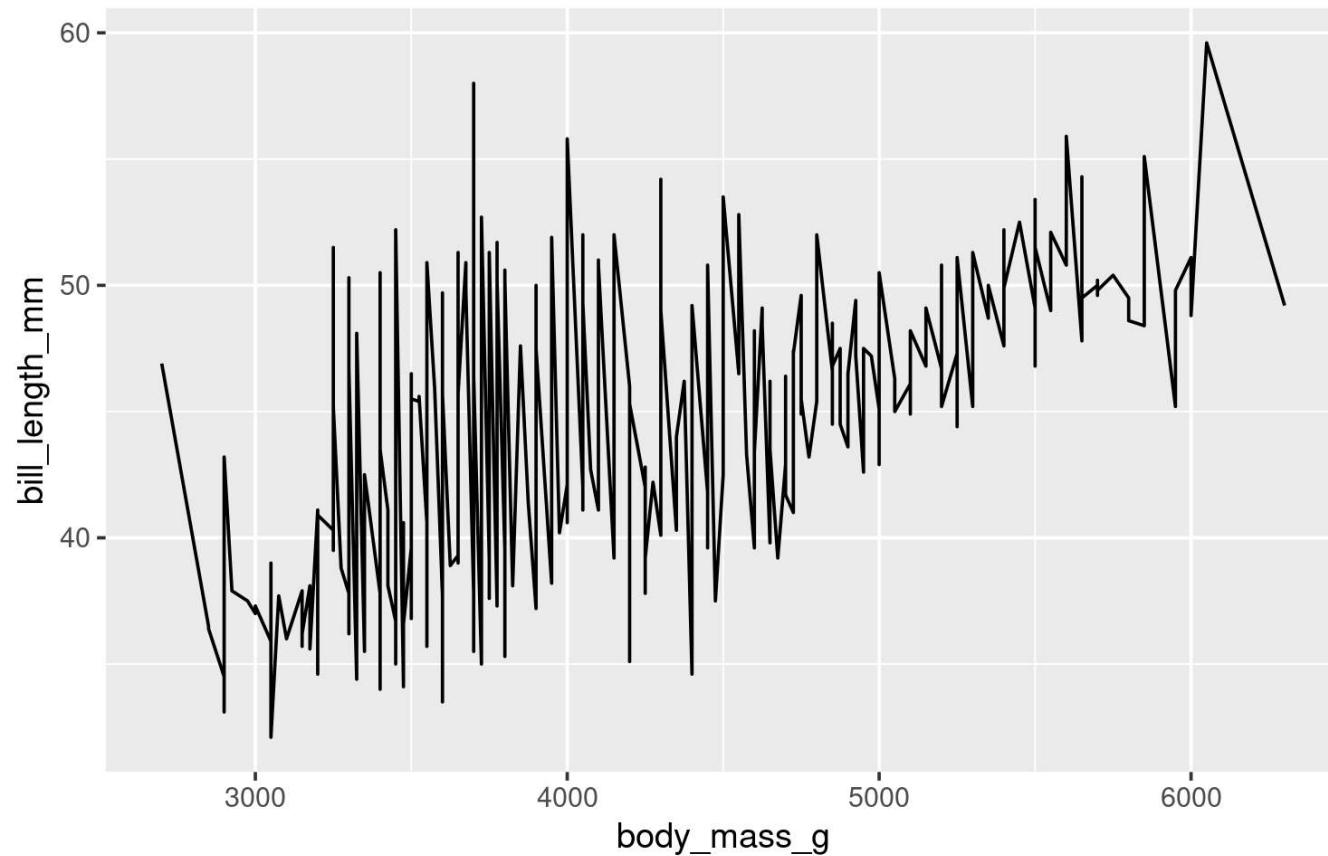


More Geoms

(Plot types)

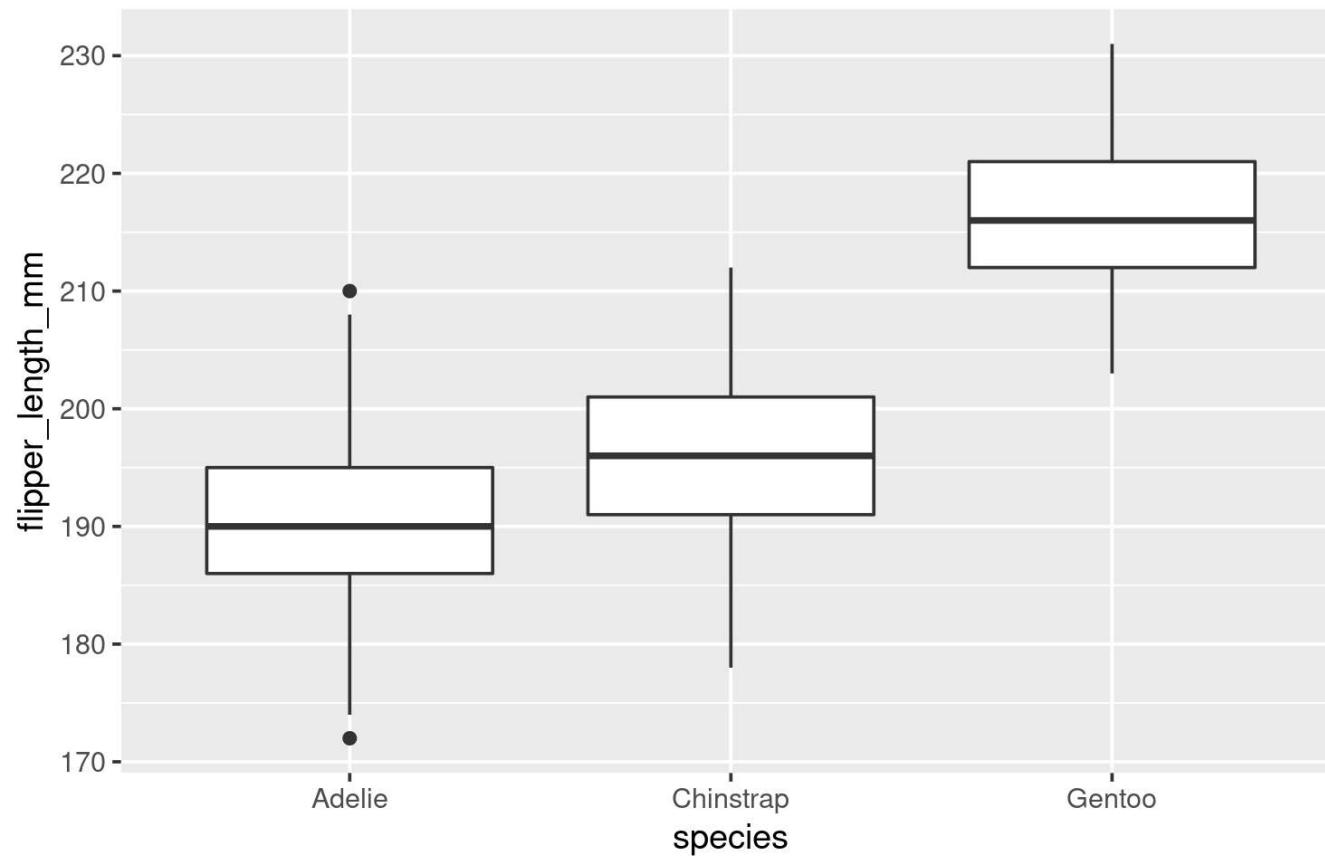
Geoms: Lines

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +  
  geom_line()
```



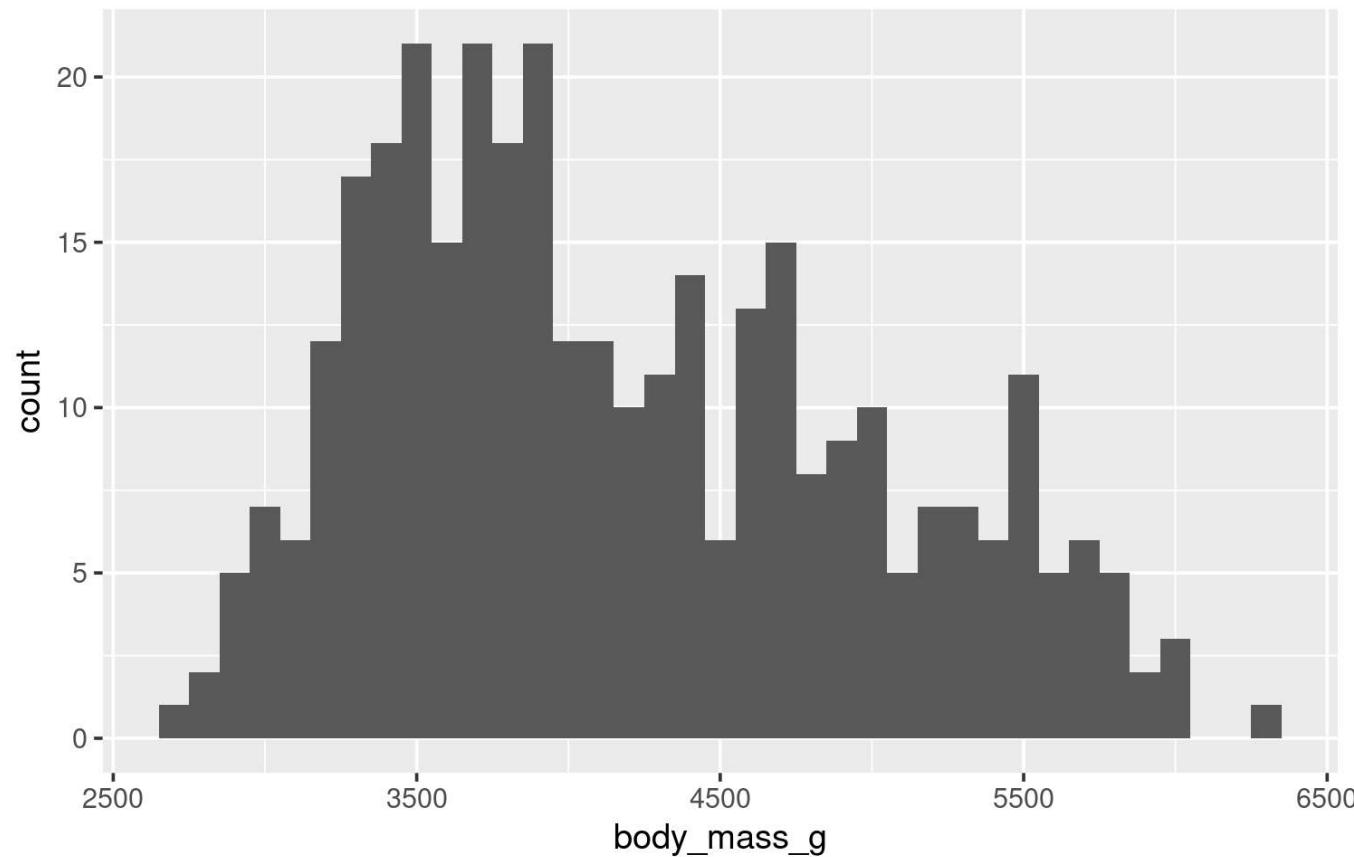
Geoms: Boxplots

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



Geoms: Histogram

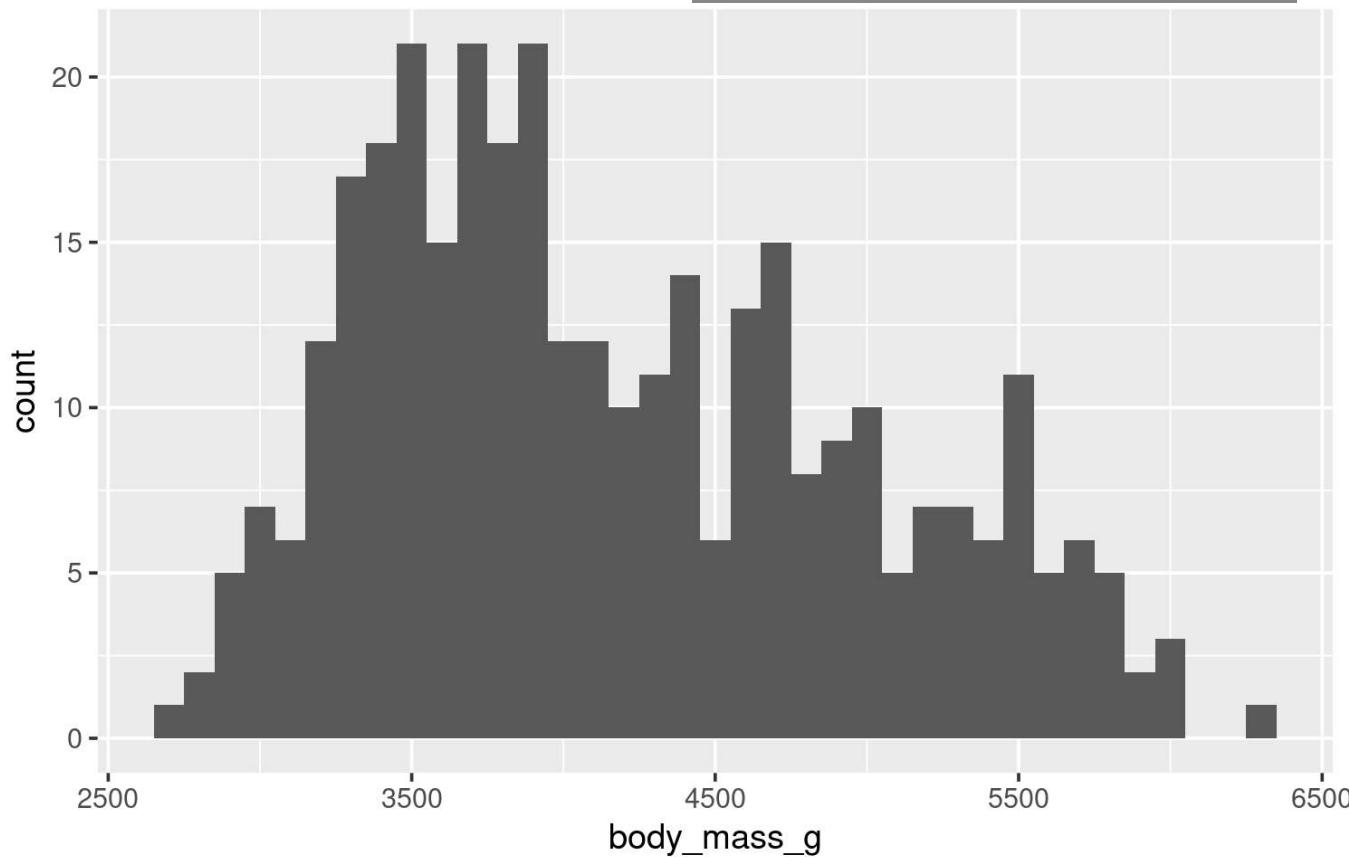
```
ggplot(data = penguins, aes(x = body_mass_g)) +  
  geom_histogram(binwidth = 100)
```



Geoms: Histogram

```
ggplot(data = penguins, aes(x = body_mass_g)) +  
  geom_histogram(binwidth = 100)
```

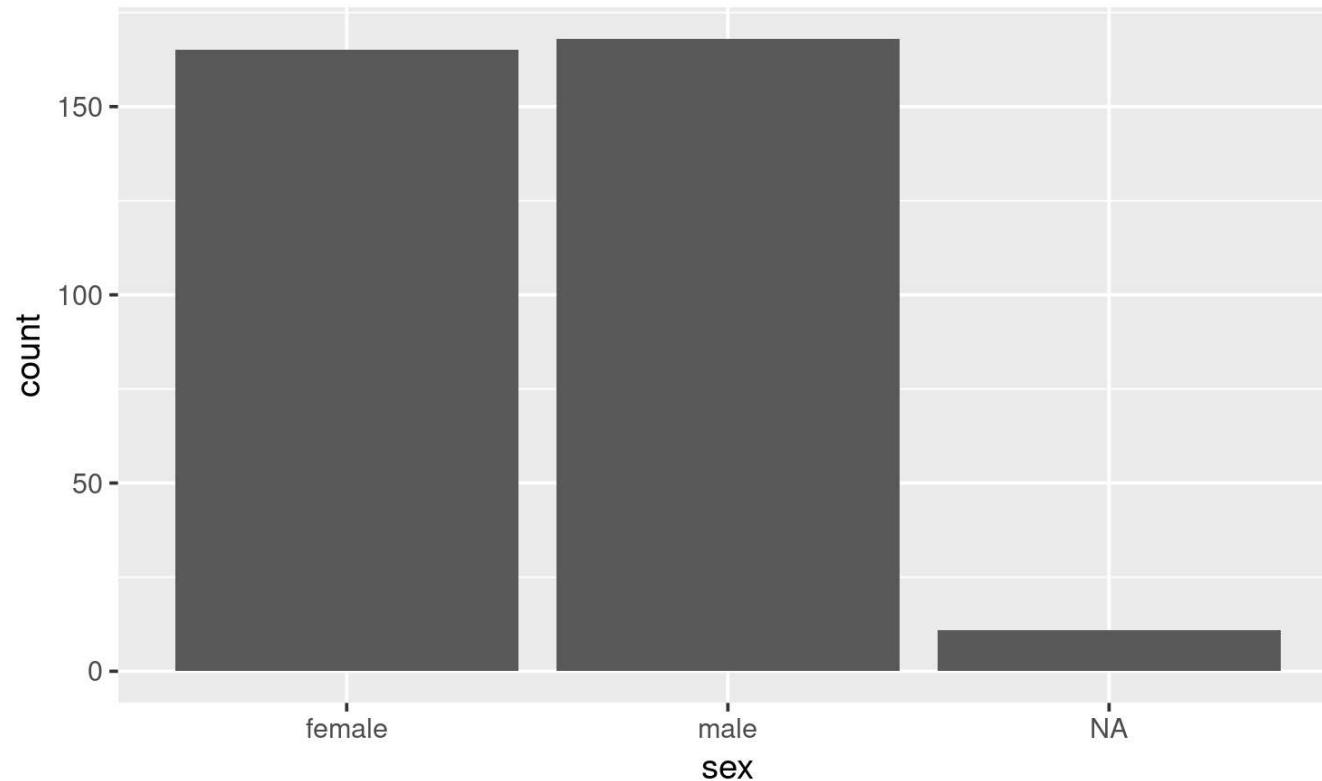
Note: We only need 1 aesthetic here (x)



Geoms: Barplots

Let **ggplot** count your data

```
ggplot(data = penguins, aes(x = sex)) +  
  geom_bar()
```

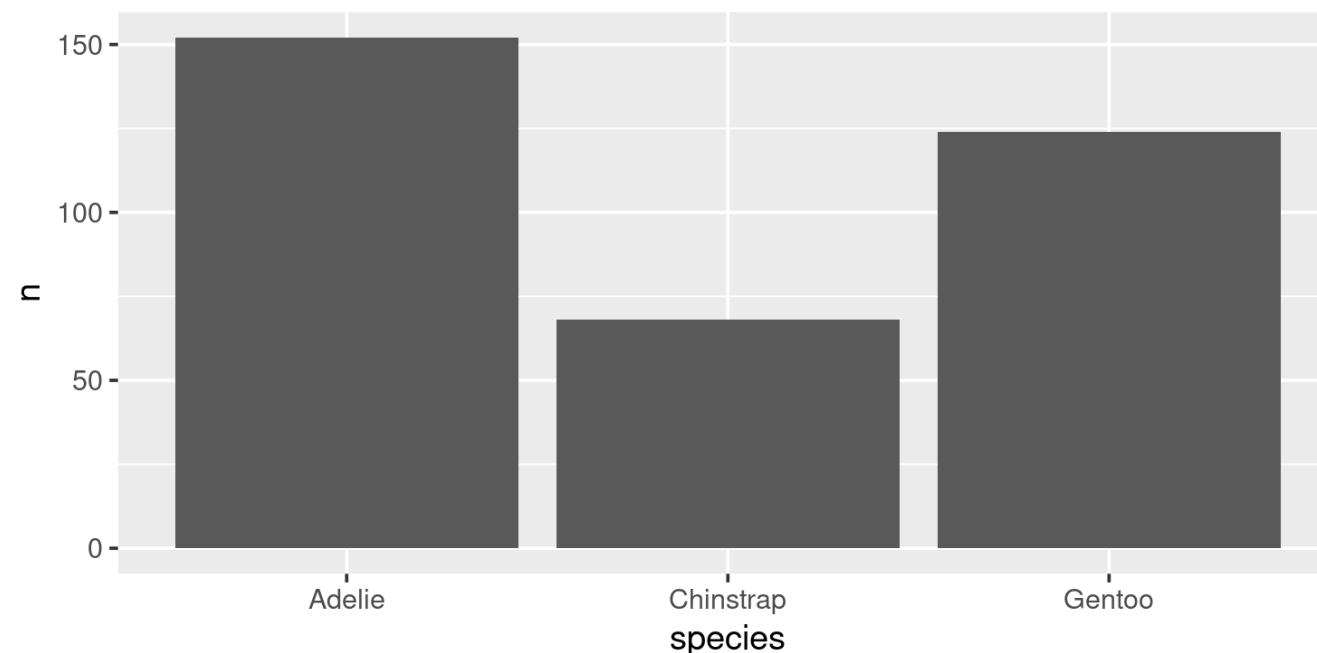


Geoms: Barplots

You can also provide the counts

```
# Create our own data frame of counts
species <- count(penguins, species)

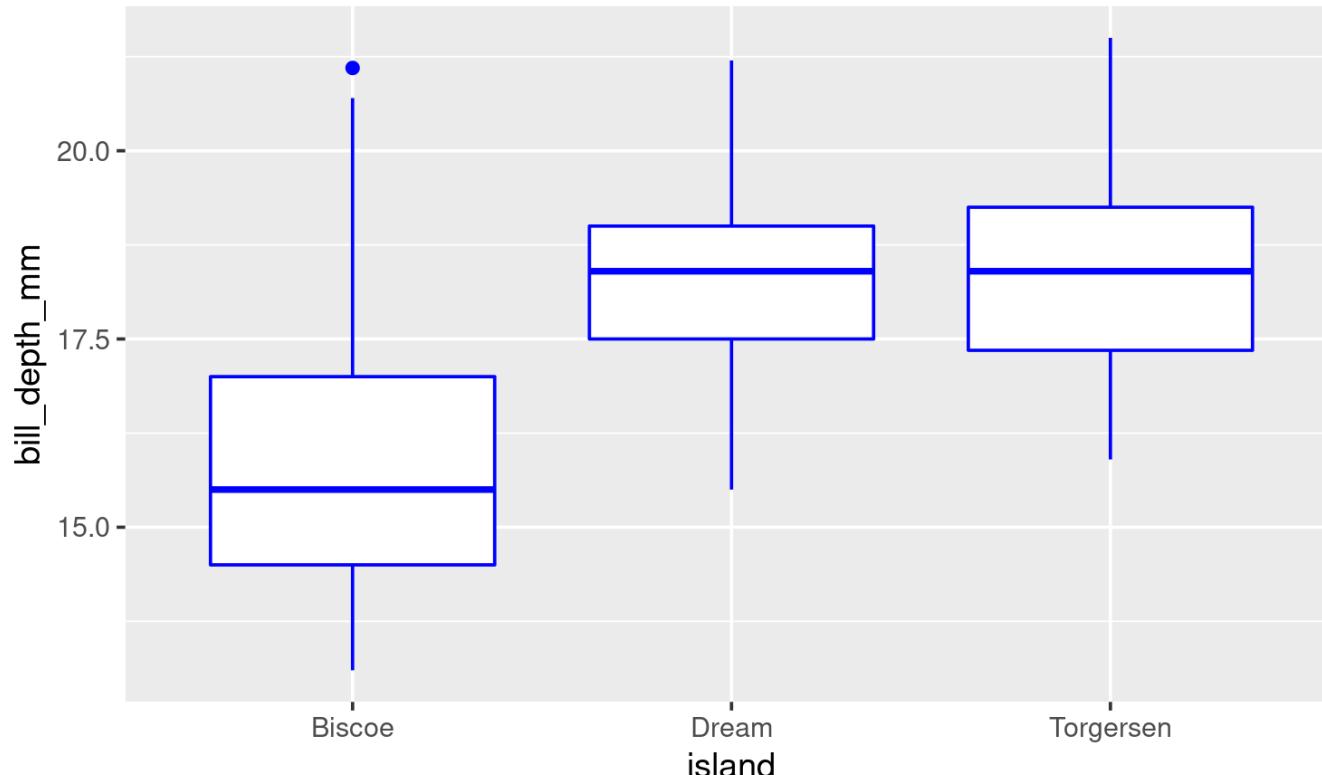
ggplot(data = species, aes(x = species, y = n)) +
  geom_bar(stat = "identity")
```



Your Turn: Create this plot

```
library(tidyverse)  
  
ggplot(data = [REDACTED], aes(x = [REDACTED], y = [REDACTED])) +  
  geom_[REDACTED]([REDACTED])
```

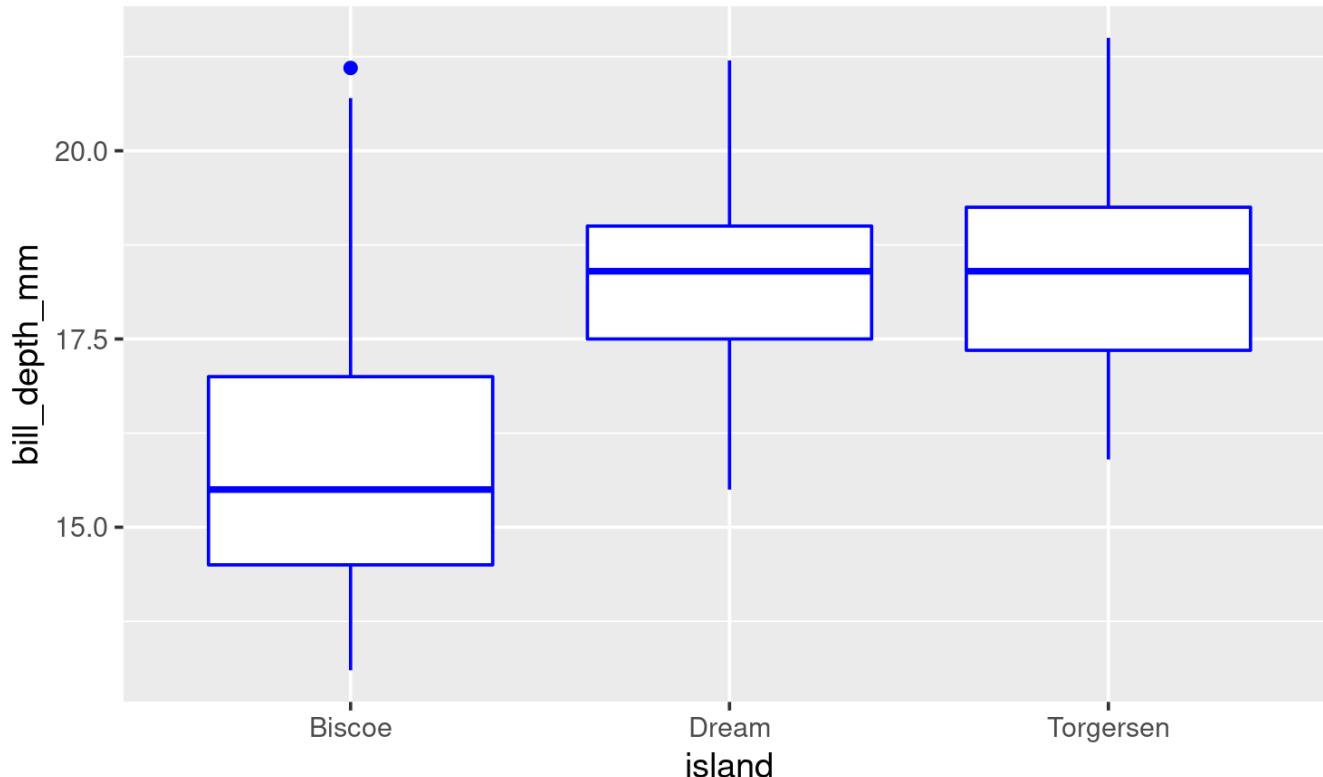
Extra Challenge
Plot points on top



Your Turn: Create this plot

```
library(tidyverse)  
  
ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +  
  geom_boxplot(colour = "blue")
```

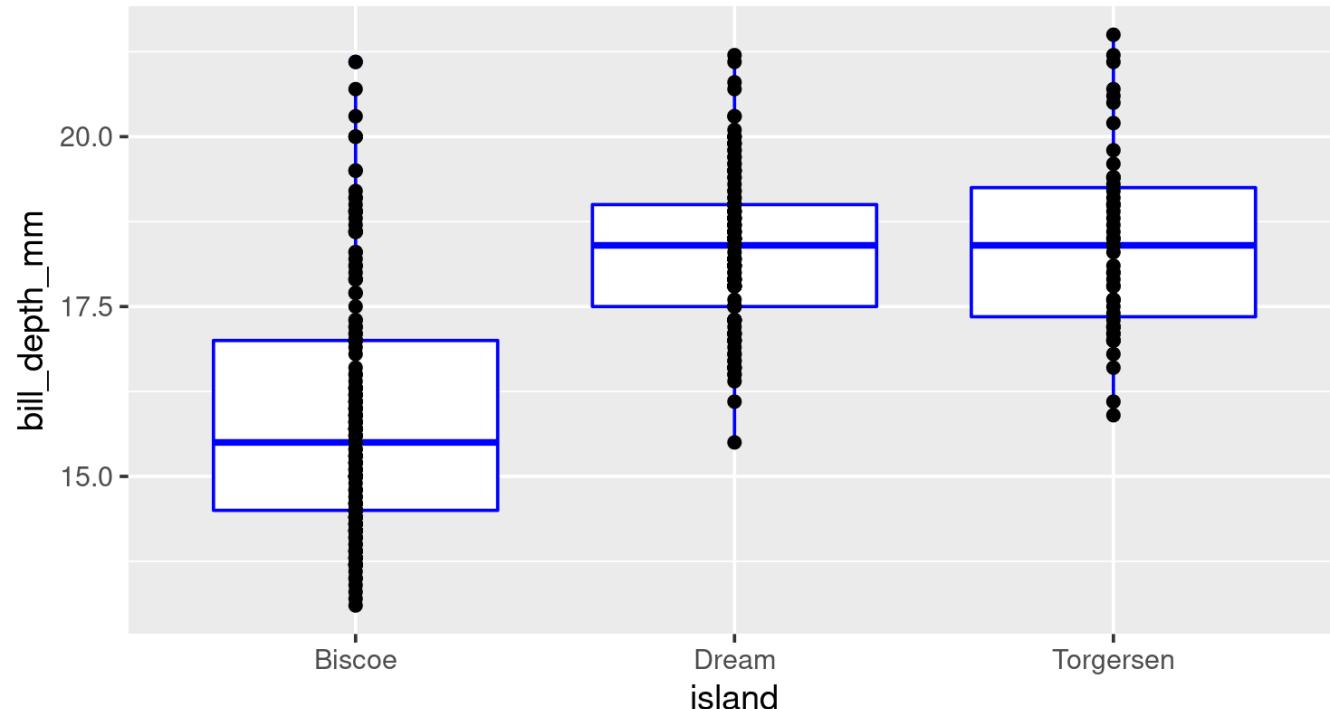
Extra Challenge
Plot points on top



Your Turn: Create this plot (Extra Challenge)

```
library(tidyverse)  
  
ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +  
  geom_boxplot(colour = "blue") +  
  geom_point()
```

Extra Challenge
Plot points on top

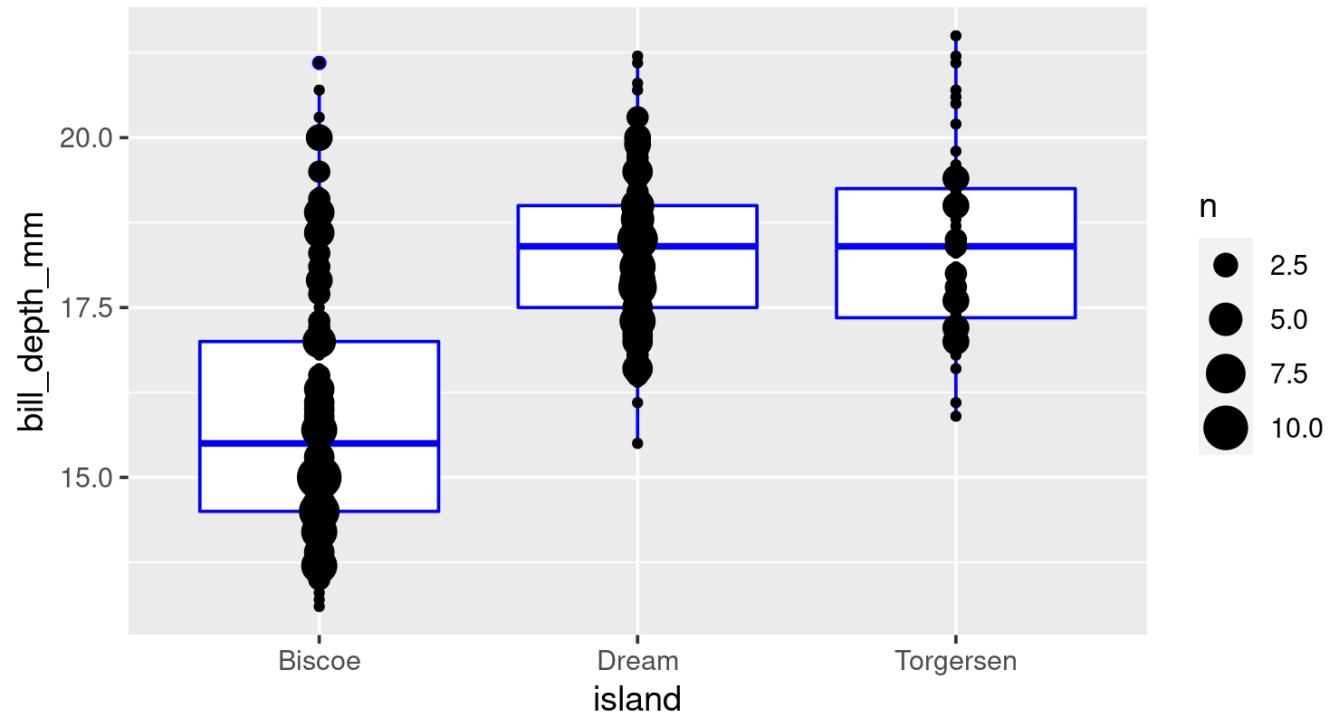


Your Turn: Create this plot (Extra Challenge)

```
library(tidyverse)

ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +
  geom_boxplot(colour = "blue") +
  geom_count()
```

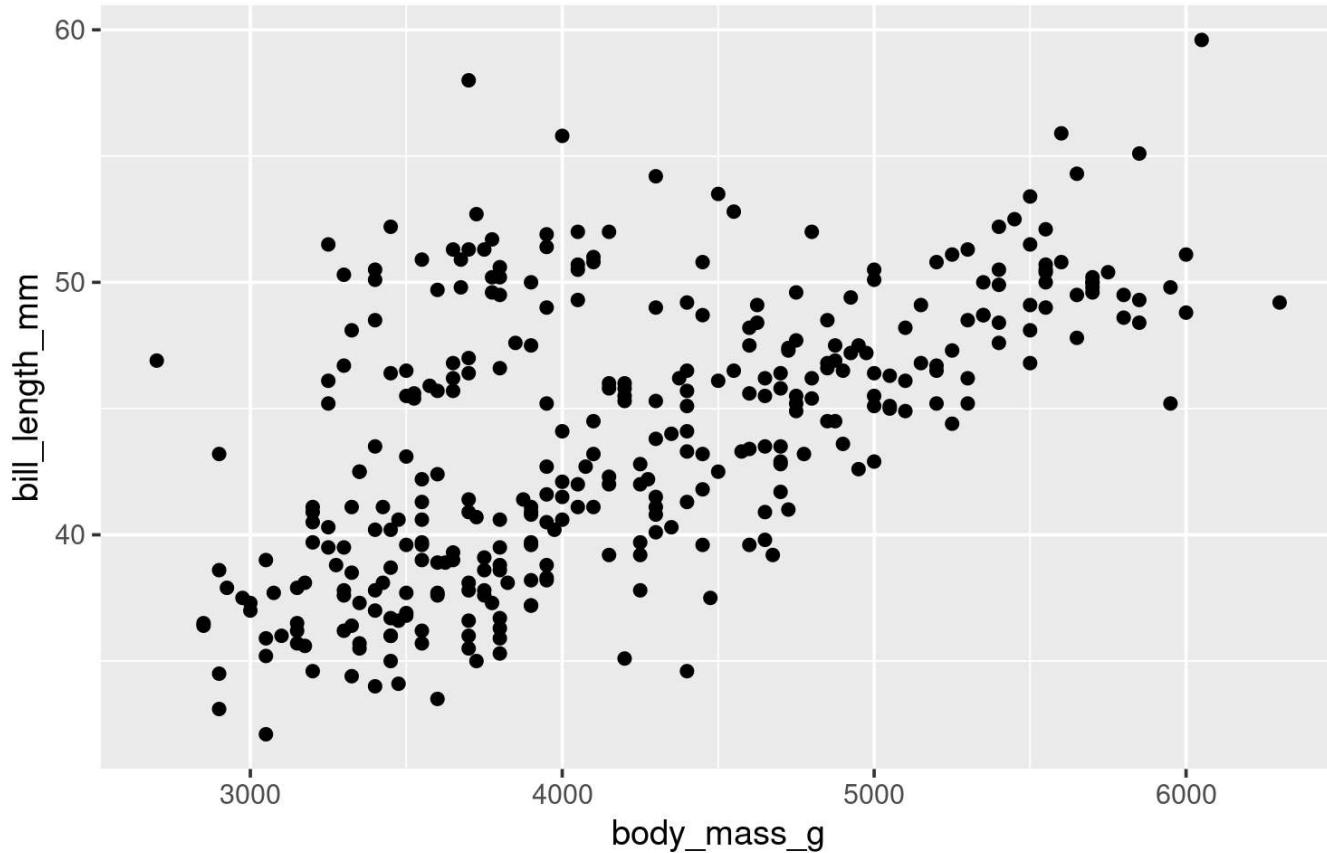
Extra Challenge
Plot points on top



Showing data by group

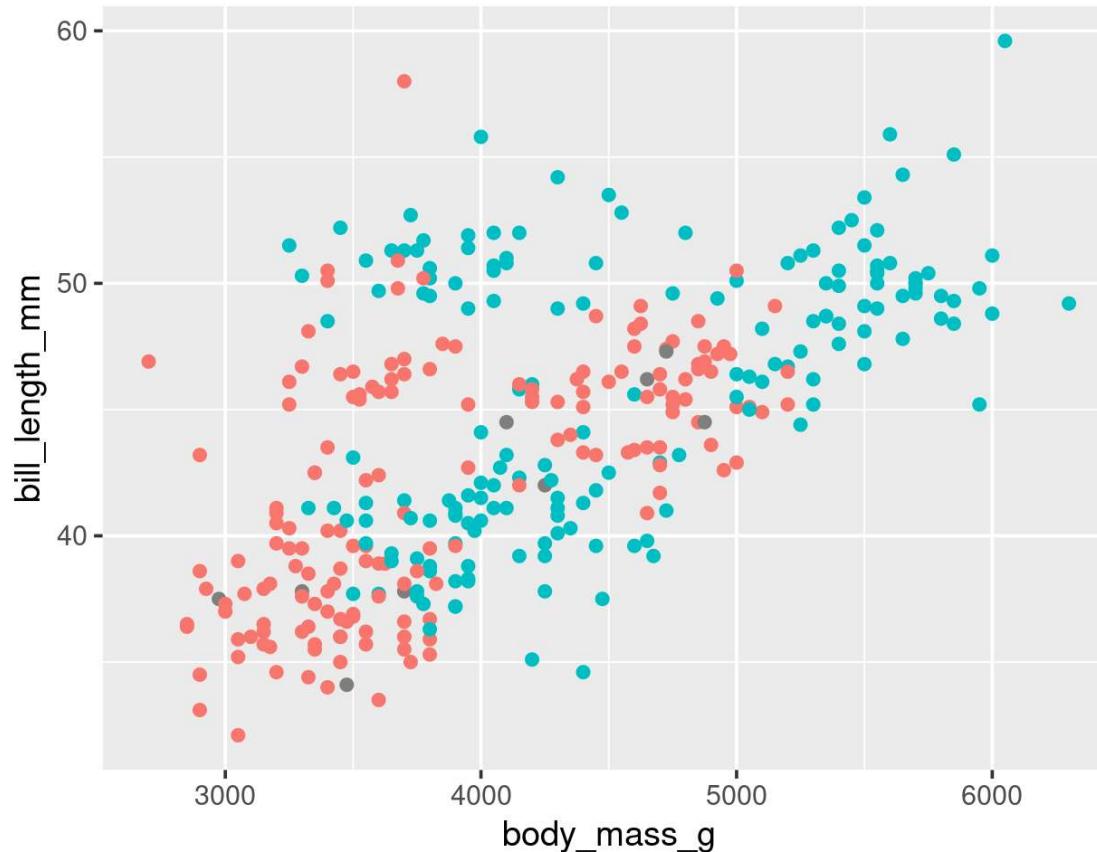
Mapping aesthetics

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



Mapping aesthetics

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
  geom_point()
```



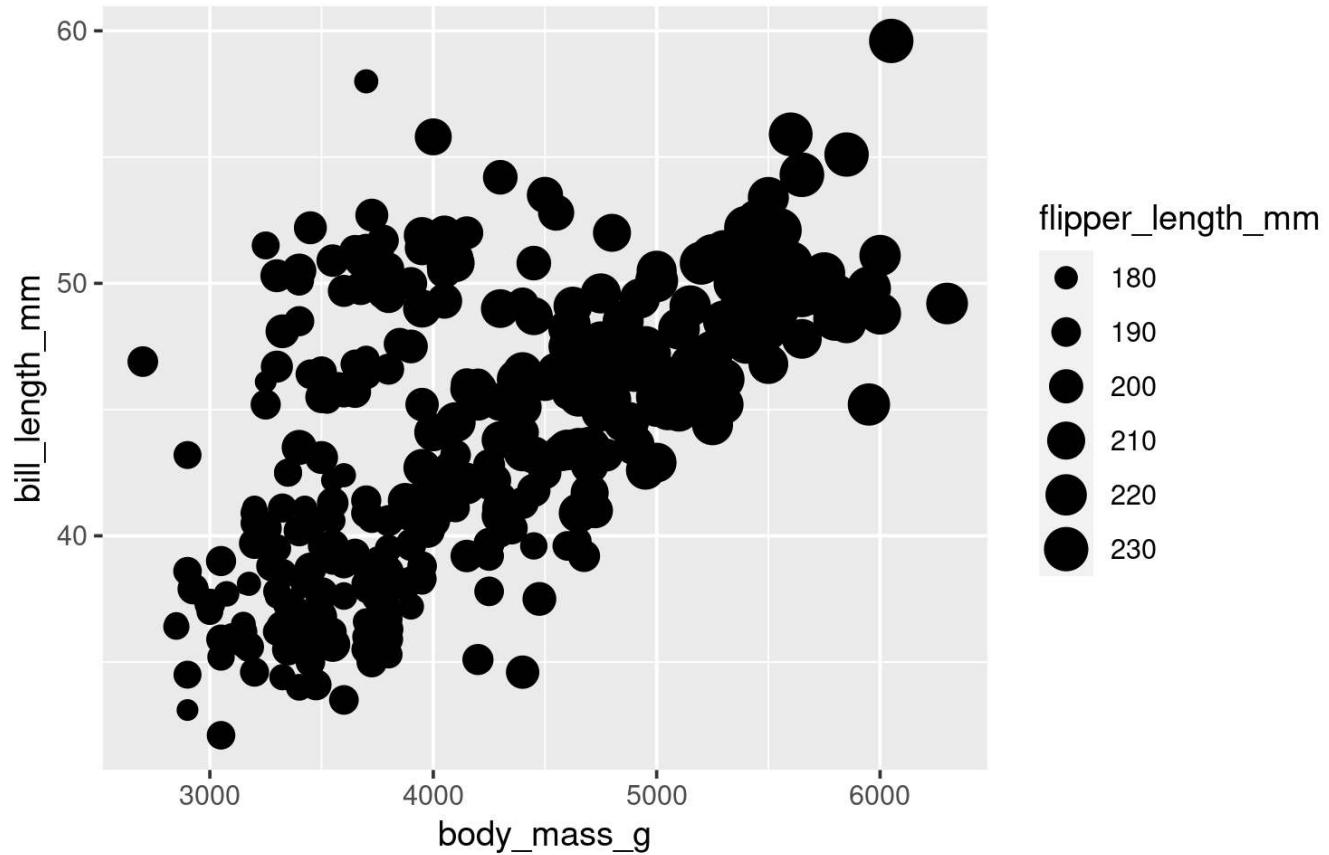
ggplot() automatically creates legends

sex

- female
- male
- NA

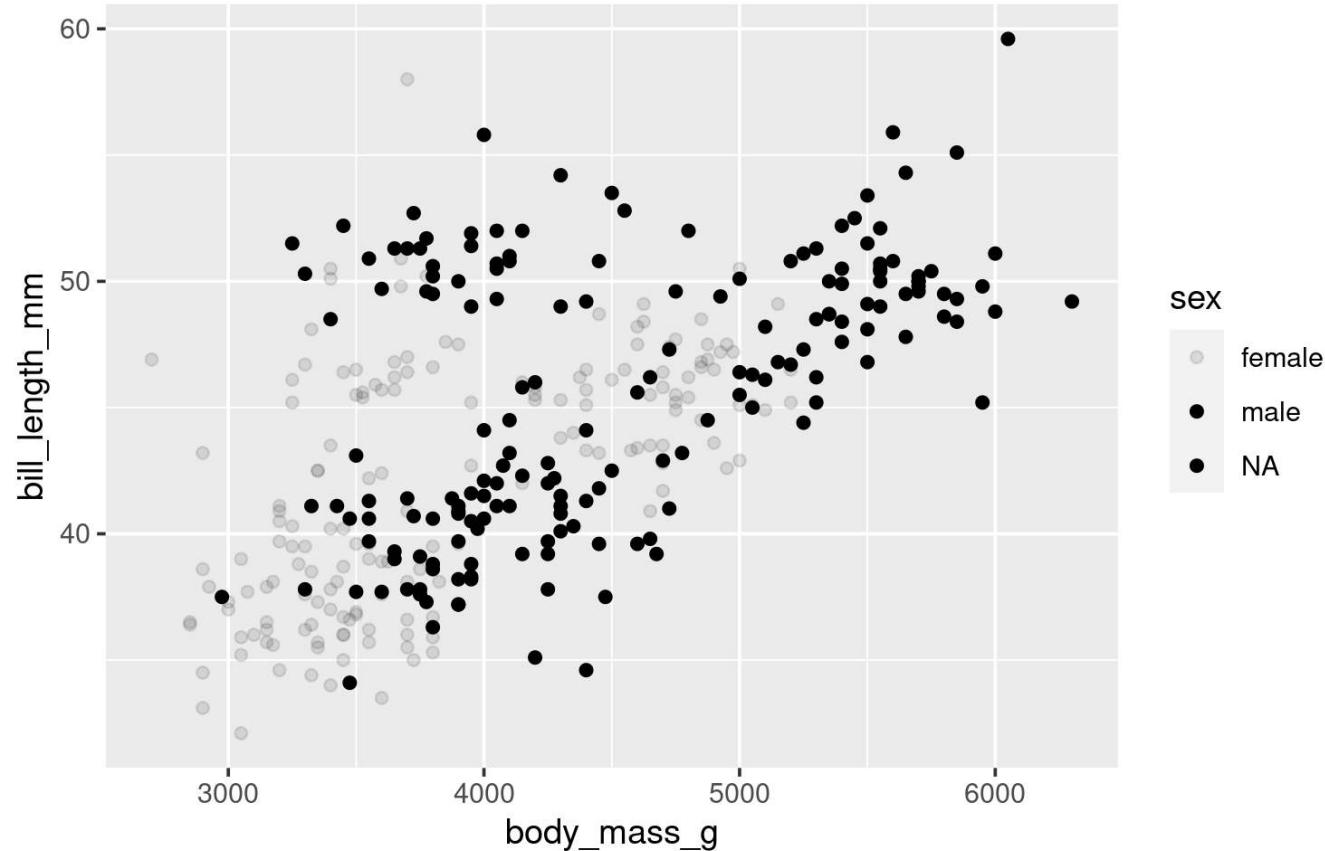
Mapping aesthetics

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



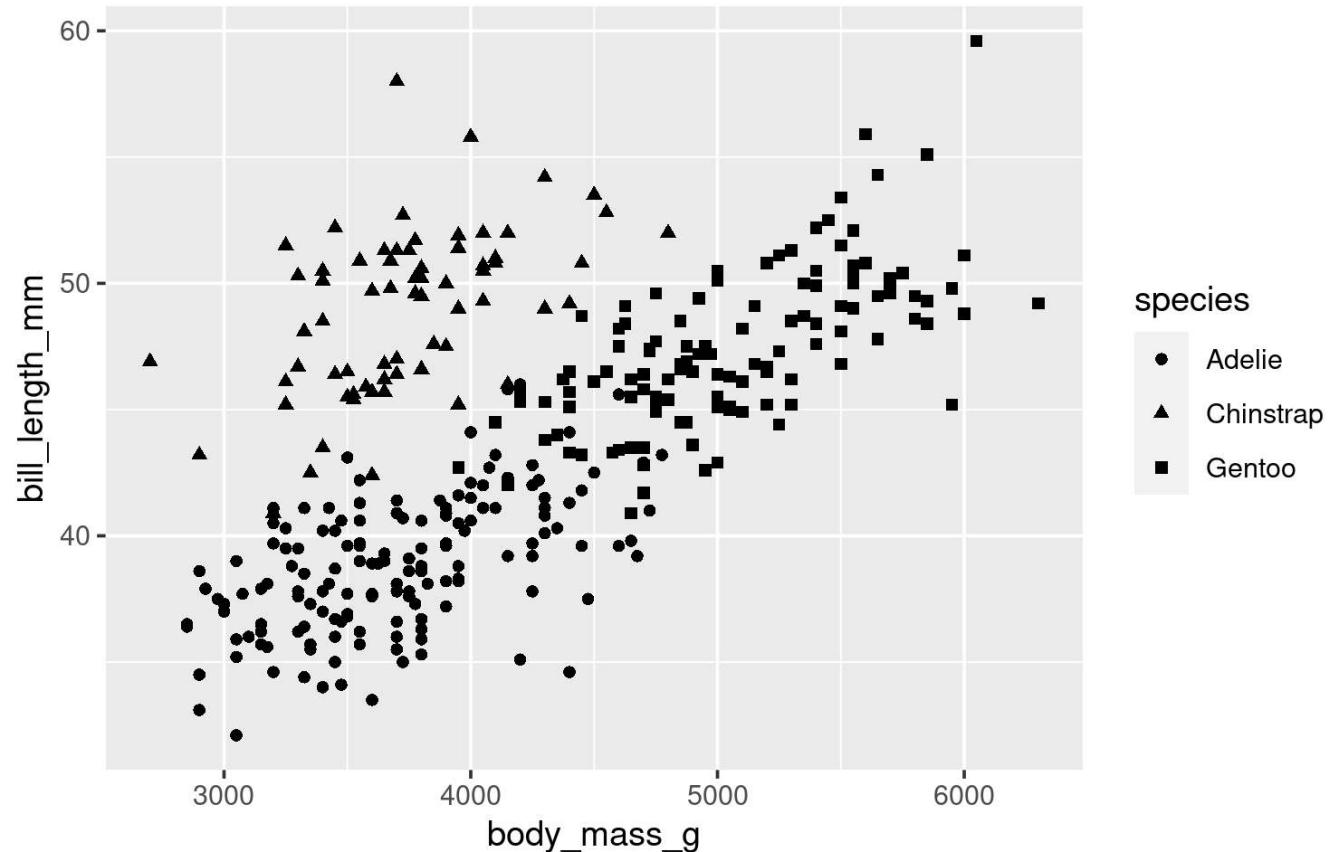
Mapping aesthetics

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, alpha = sex)) +  
  geom_point()
```



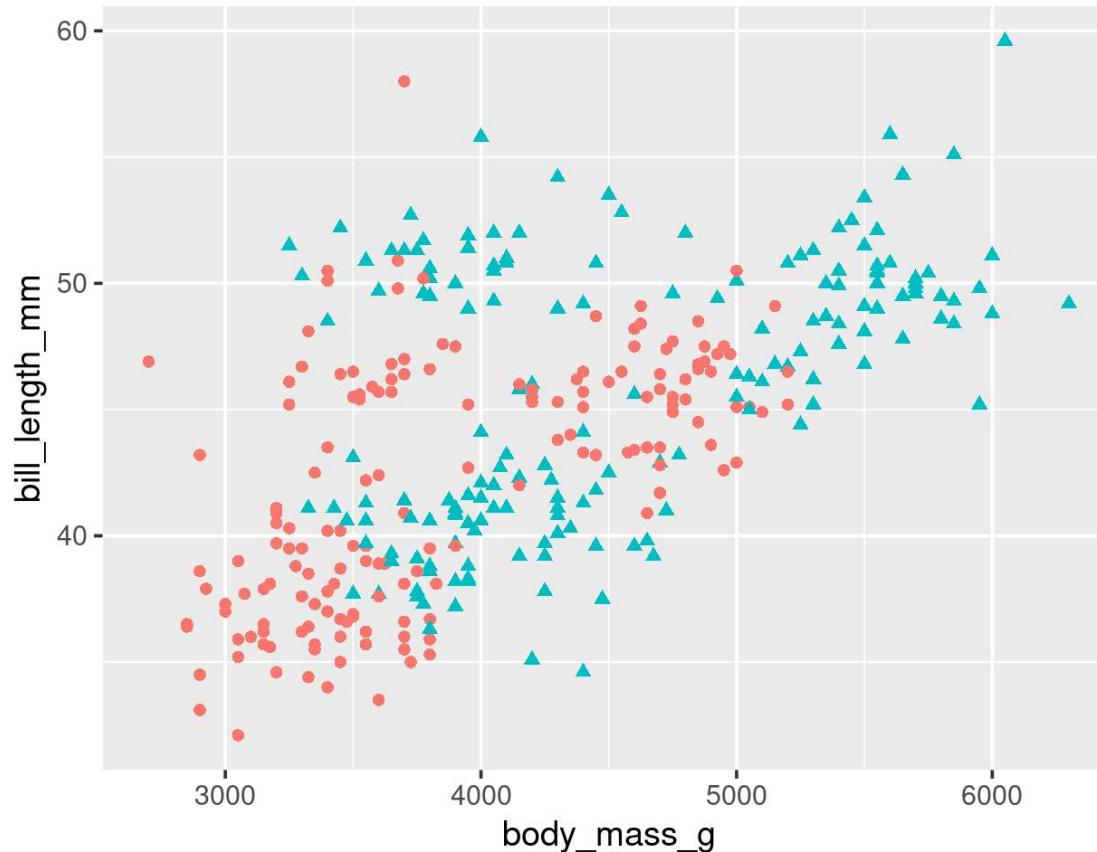
Mapping aesthetics

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



Mapping aesthetics

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex, shape = sex)) +  
  geom_point()
```



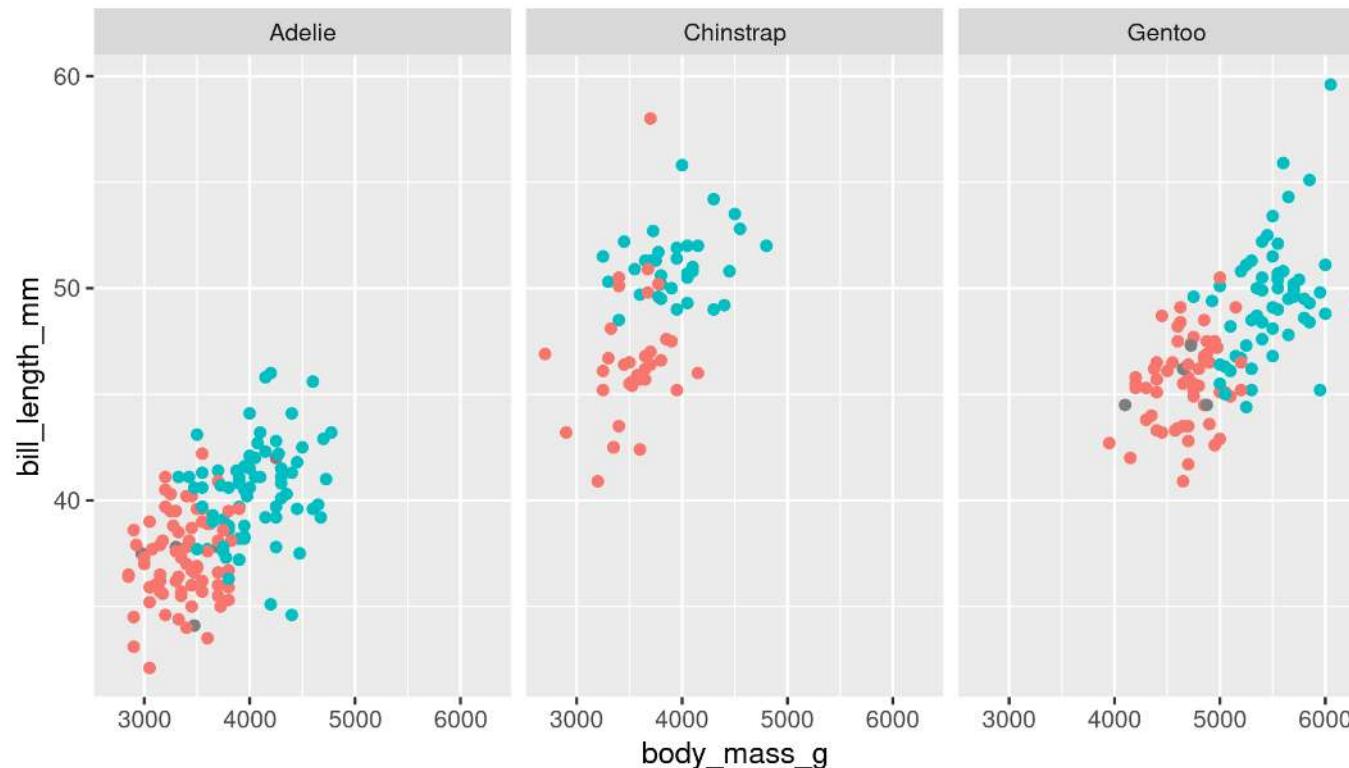
ggplot() combines legends where it can

sex

- female
- ▲ male
- NA

Faceting: facet_wrap()

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
  geom_point() +  
  facet_wrap(~ species)
```



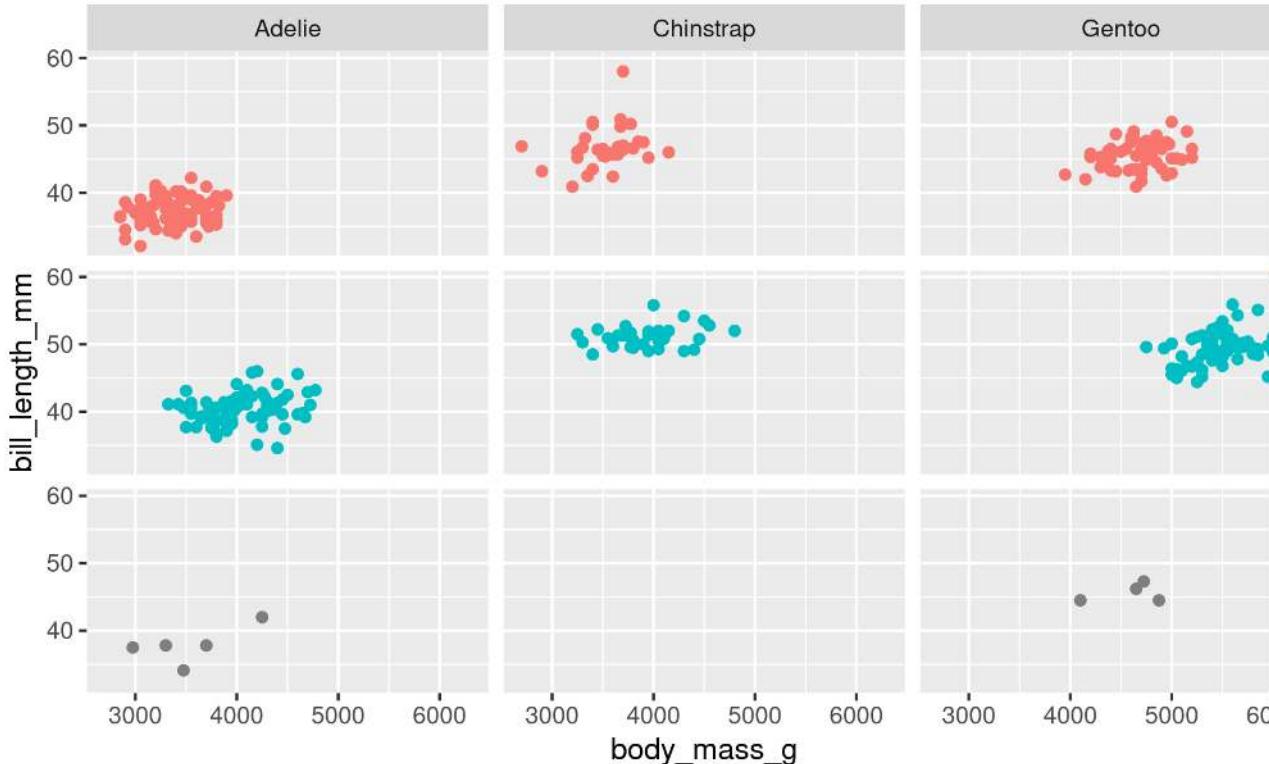
Split plots by wrapping
Generally for one grouping variable

sex

- female
- male
- NA

Faceting: facet_grid()

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



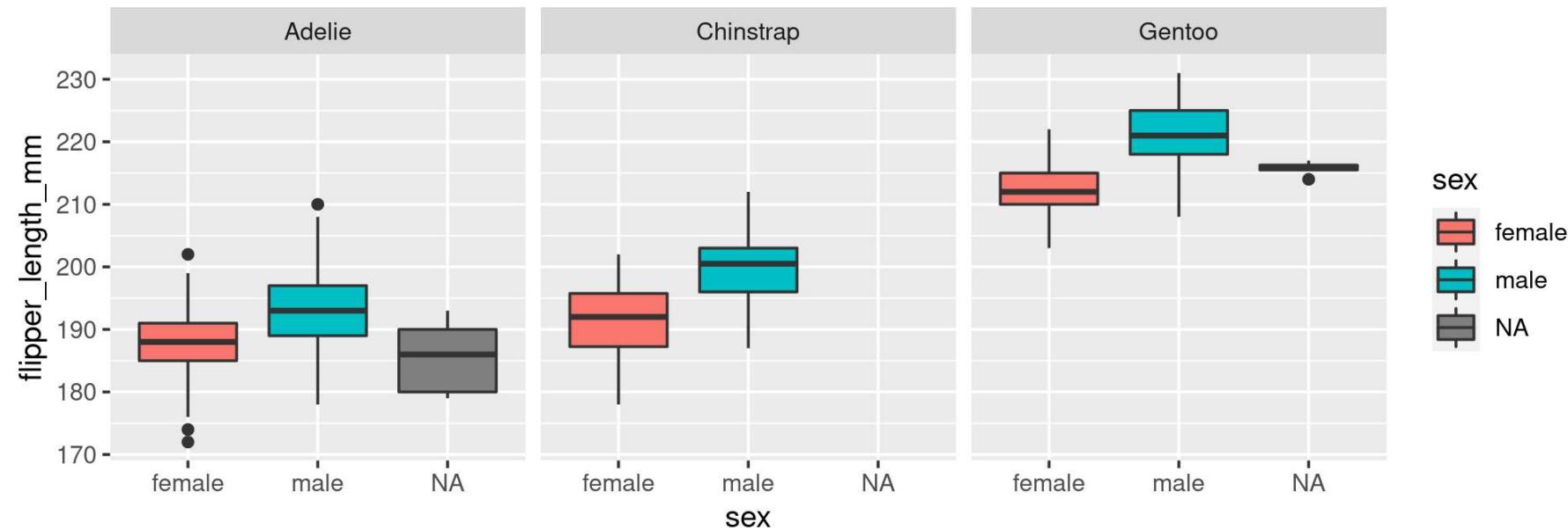
Split plots by **two** grouping variables on a grid

sex

- female
- male
- NA

Your Turn: Create this plot

```
ggplot(data = [REDACTED], aes([REDACTED])) +  
  [REDACTED] +  
  [REDACTED]
```

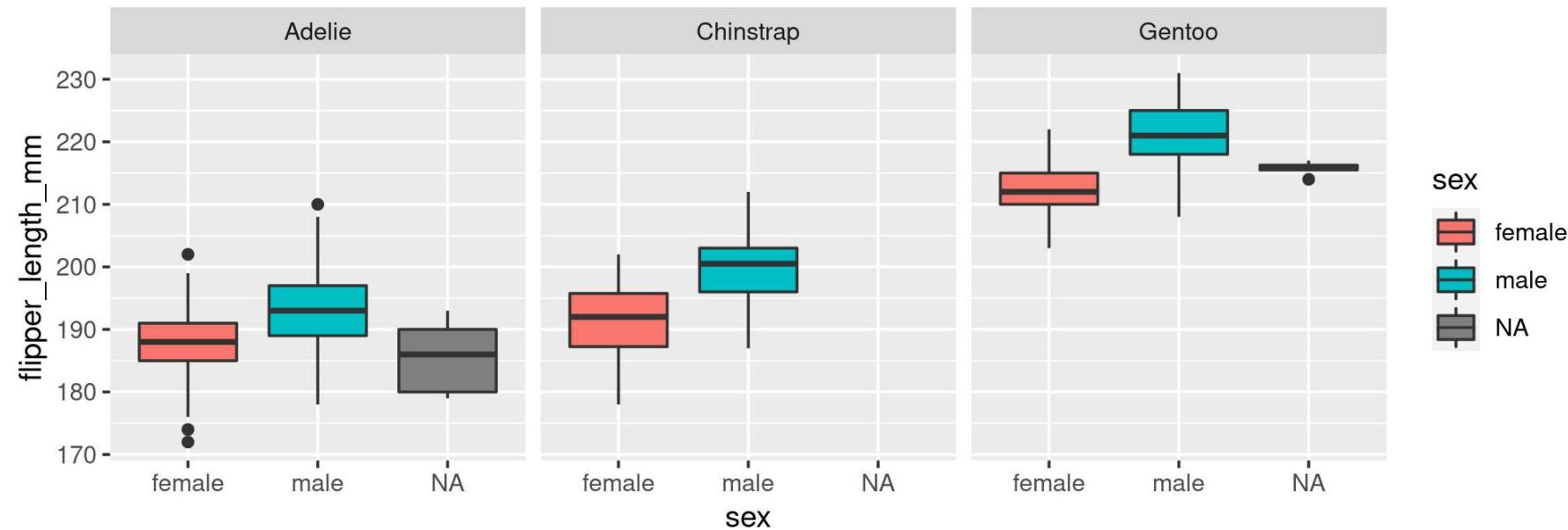


Hint: `colour` is for outlining with a colour, `fill` is for 'filling' with a colour

Extra Challenge: Split boxplots by sex **and** island

Your Turn: Create this plot

```
ggplot(data = penguins, aes(x = sex, y = flipper_length_mm, fill = sex)) +  
  geom_boxplot() +  
  facet_wrap(~ species)
```

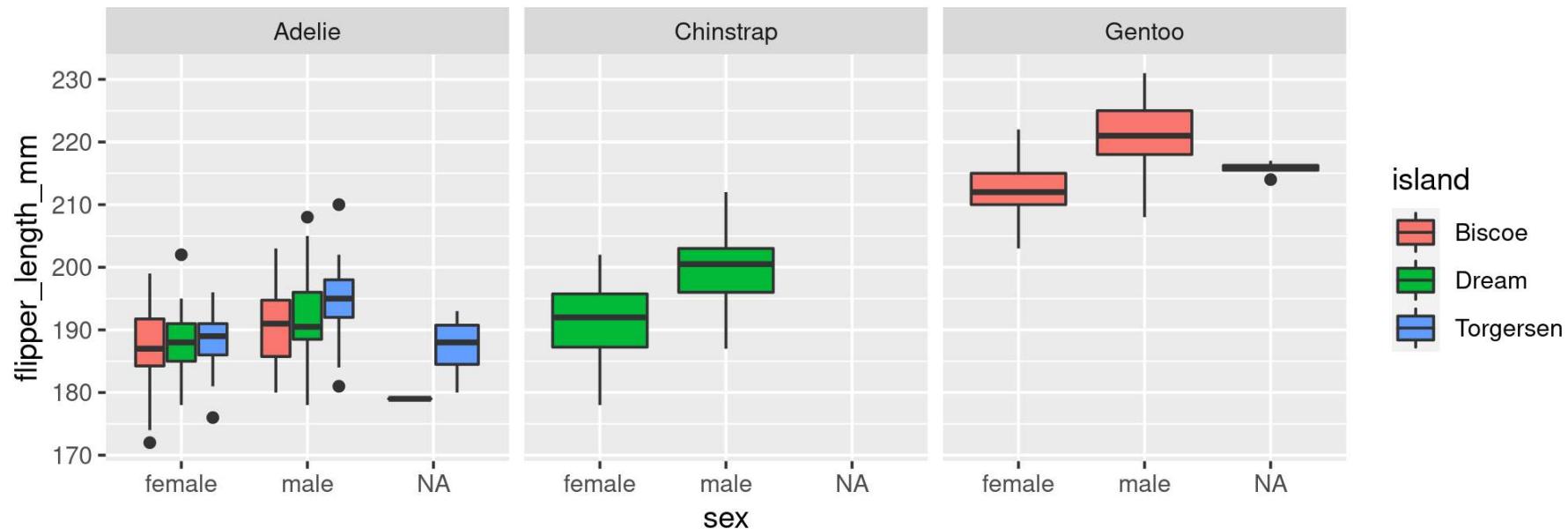


Hint: `colour` is for outlining with a colour, `fill` is for 'filling' with a colour

Extra Challenge: Split boxplots by sex **and** island

Your Turn: Create this plot (Extra Challenge)

```
ggplot(data = penguins, aes(x = sex, y = flipper_length_mm, fill = island)) +  
  geom_boxplot() +  
  facet_wrap(~ species)
```

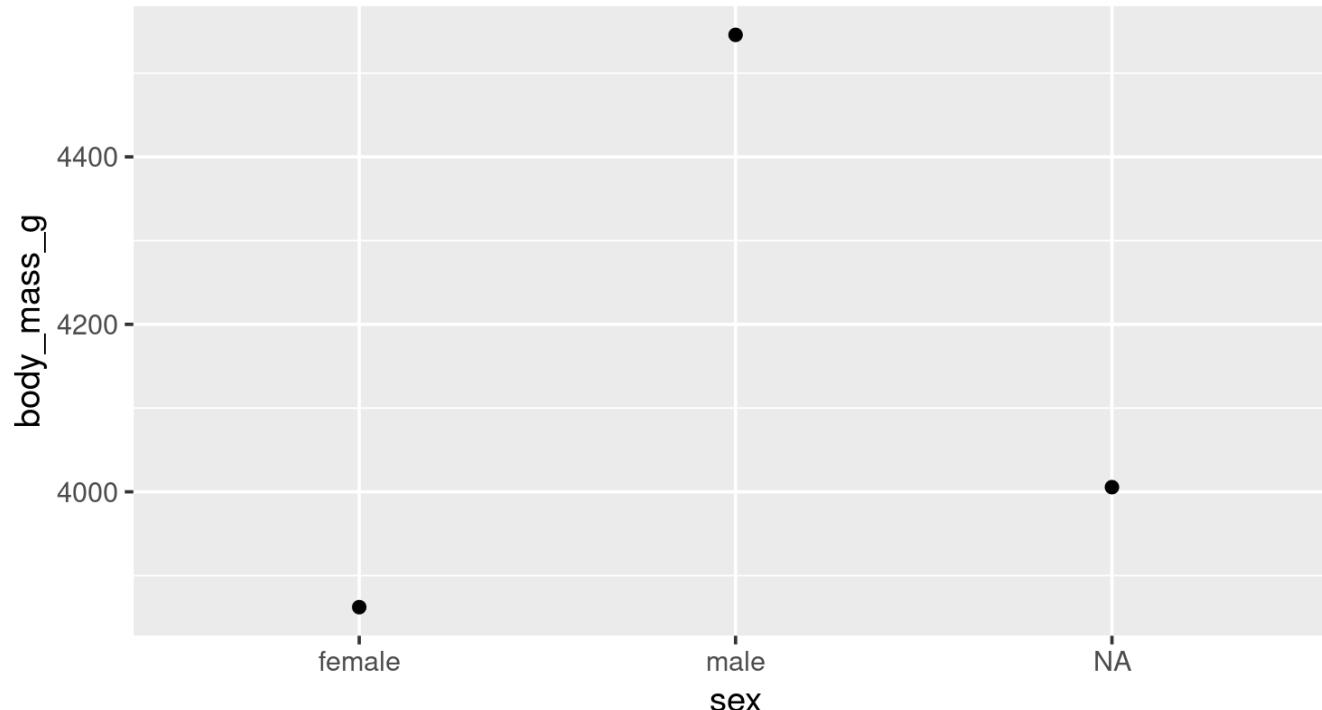


Small change (**fill = sex** to **fill = island**) results in completely different plot

Summarizing data

Add data means as points

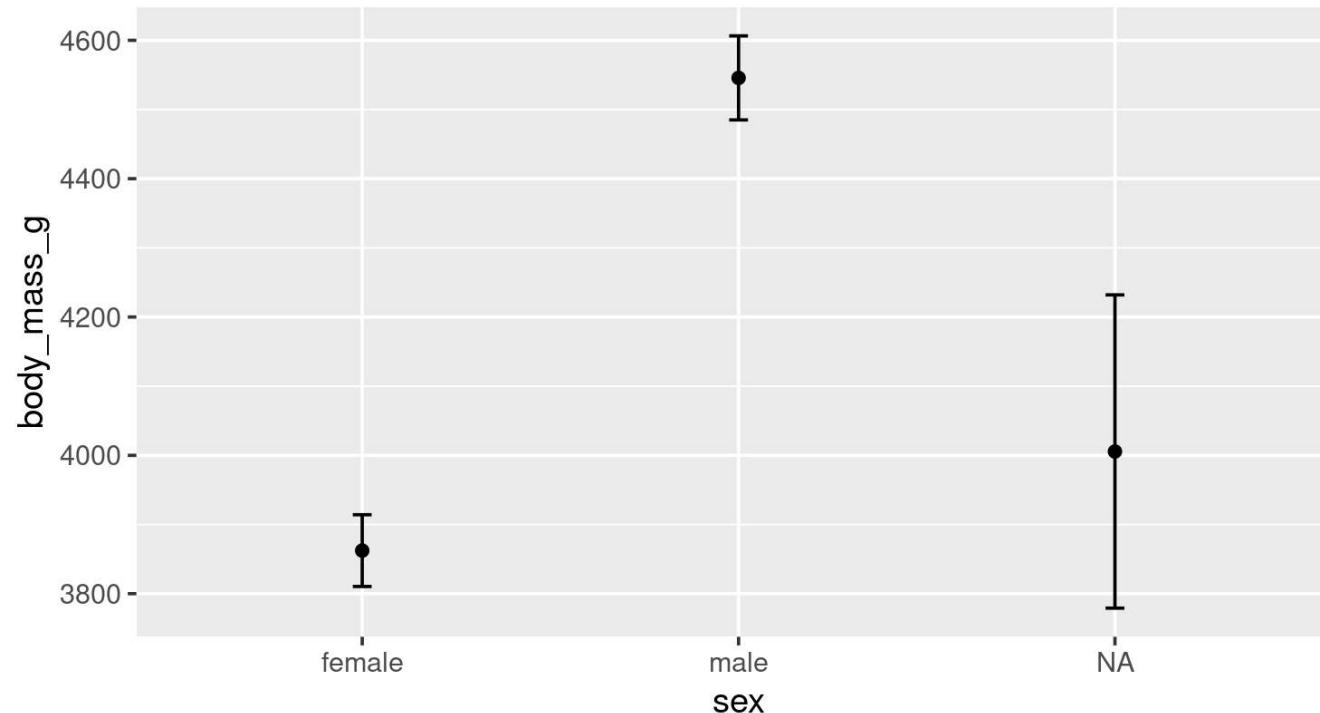
```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  stat_summary(geom = "point", fun = mean)
```



Summarizing data

Add error bars, calculated from the data

```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  stat_summary(geom = "point", fun = mean) +  
  stat_summary(geom = "errorbar", width = 0.05, fun.data = mean_se)
```

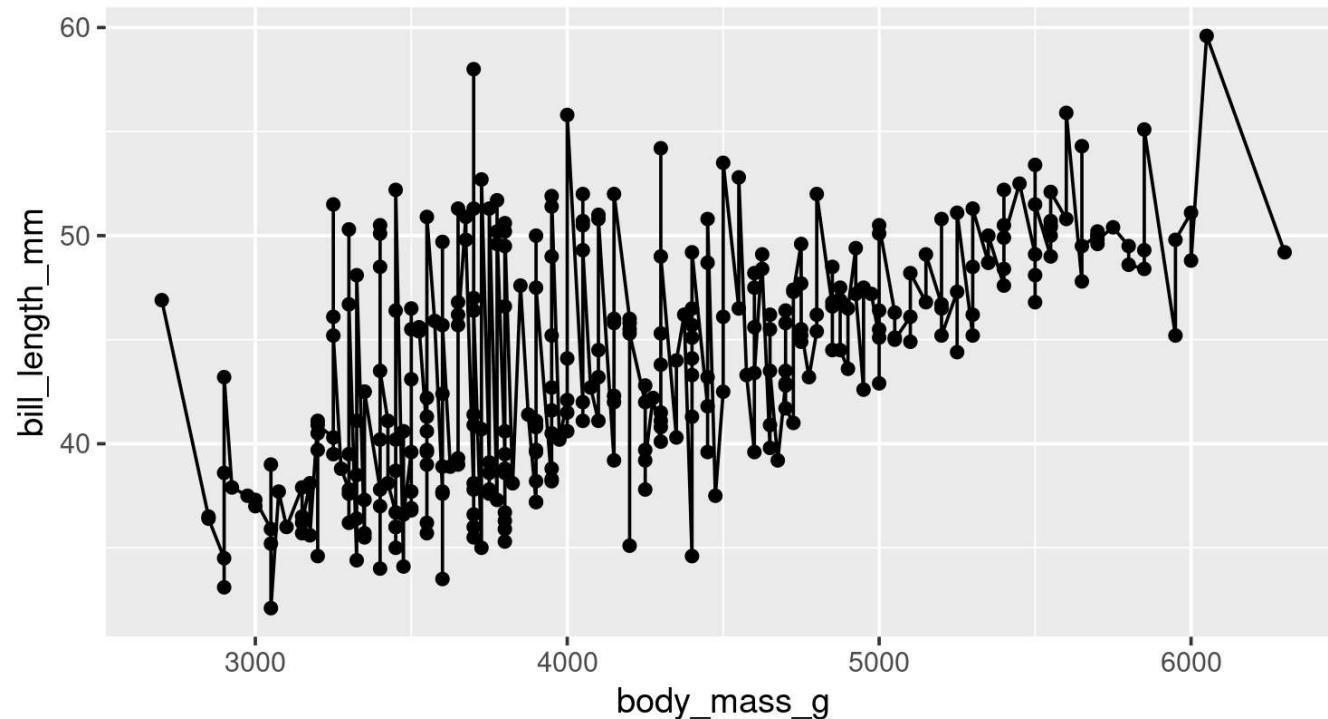


Trendlines / Regression Lines

Trendlines / Regression lines

geom_line() is connect-the-dots, not a trend or linear model

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +  
  geom_point() +  
  geom_line()
```

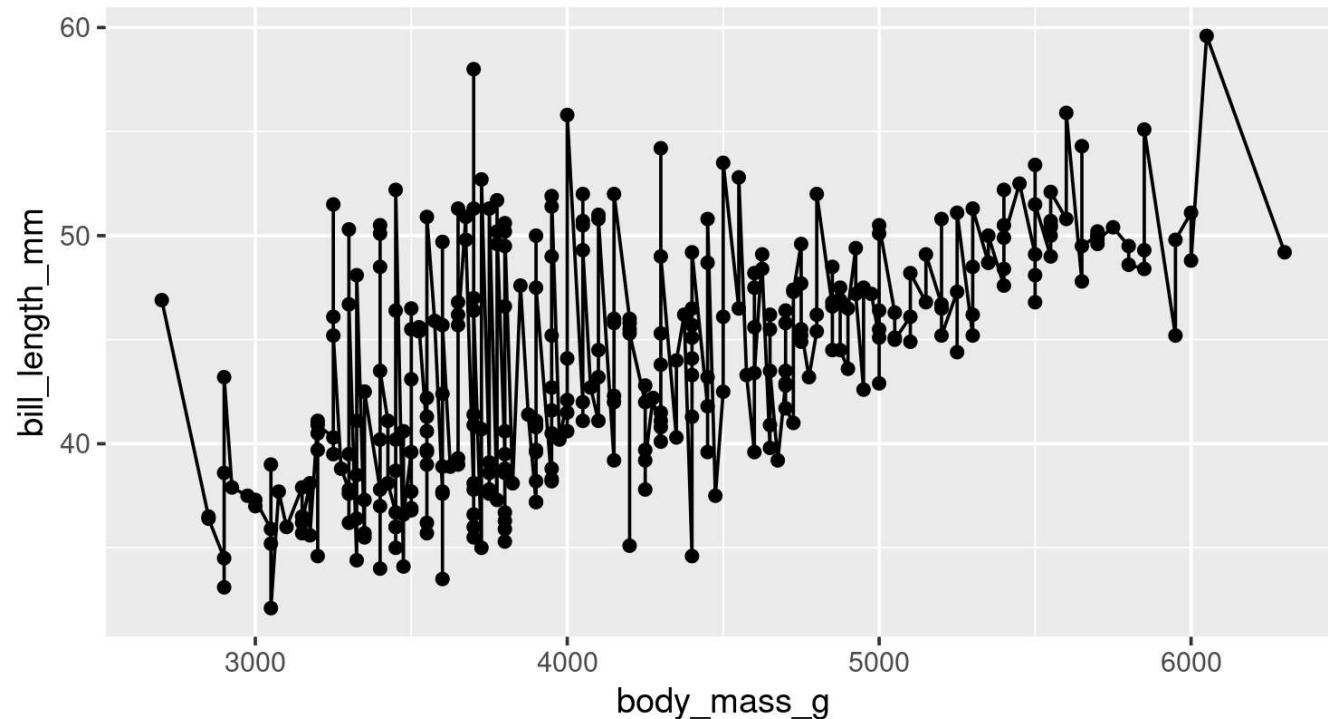


Trendlines / Regression lines

geom_line() is connect-the-dots, not a trend or linear model

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +  
  geom_point() +  
  geom_line()
```

Not what we're
looking for

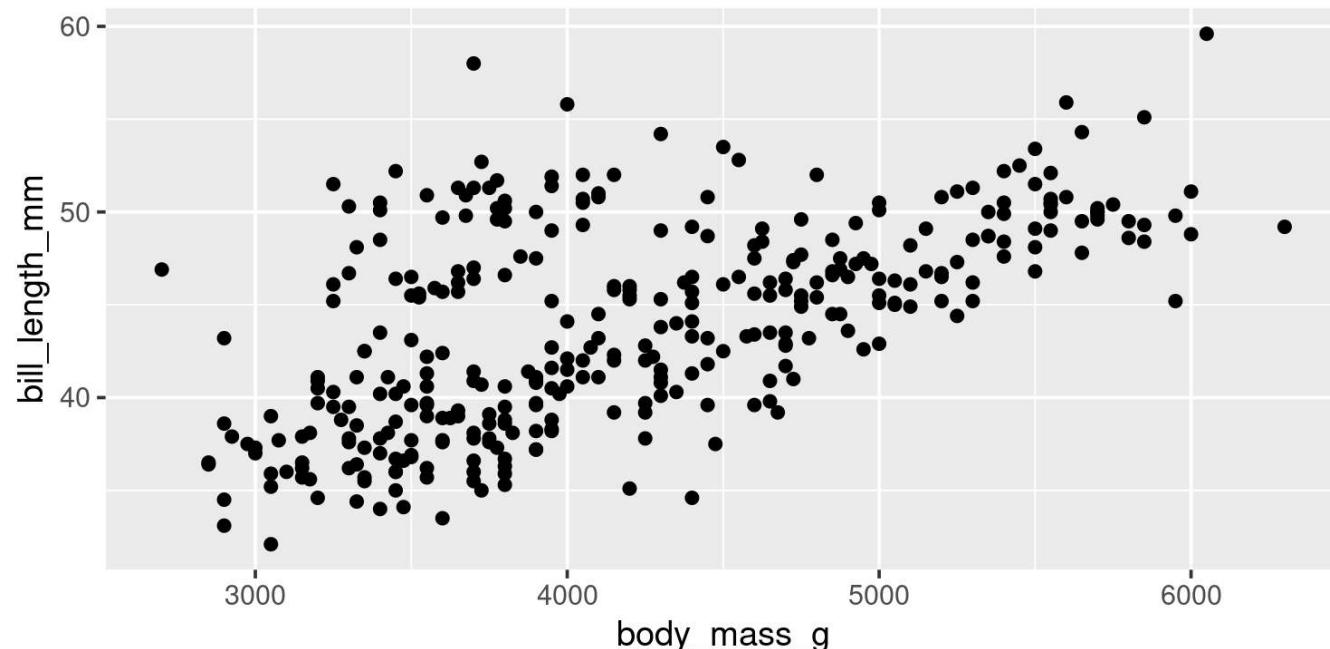


Trendlines / Regression lines

Let's add a trend line properly

Start with basic plot:

```
g <- ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +  
  geom_point()  
g
```

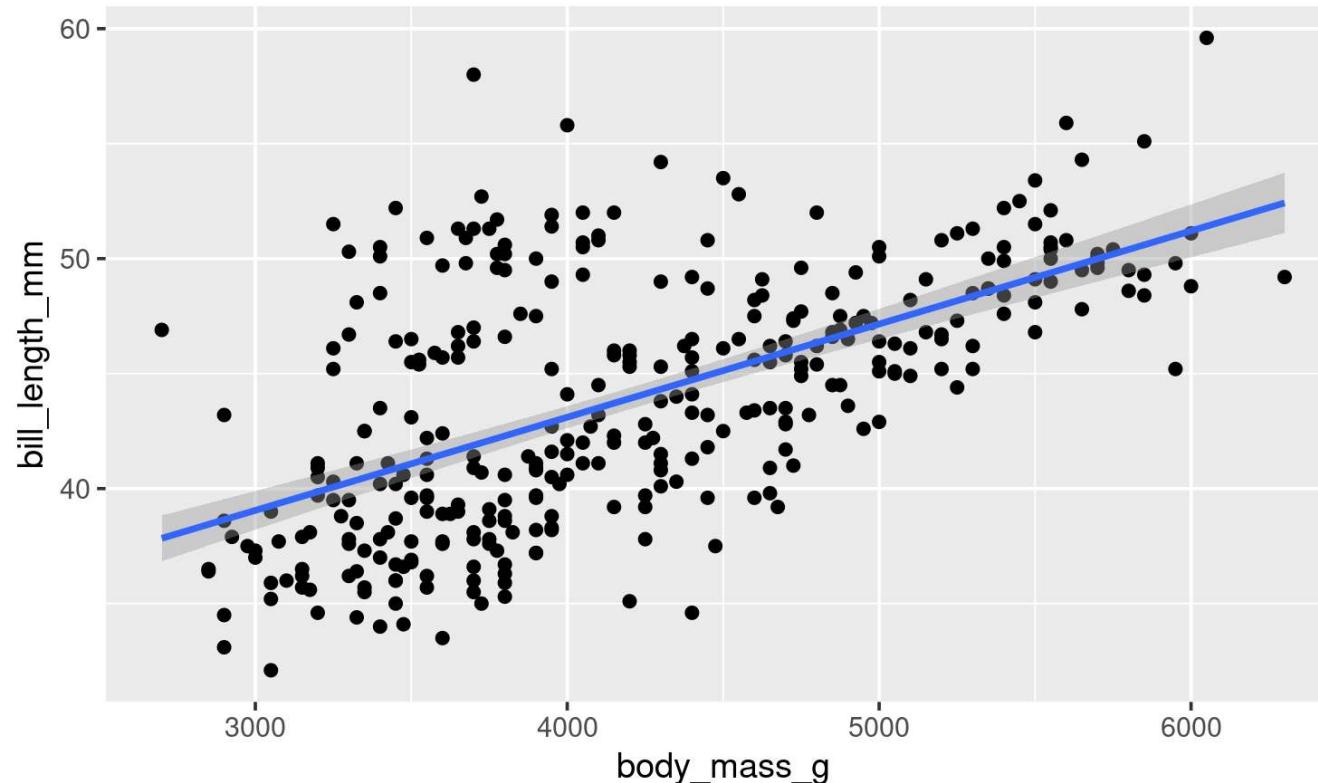


Trendlines / Regression lines

Add the `stat_smooth()`

```
g + stat_smooth(method = "lm")
```

- `lm` is for "linear model" (i.e. trendline)
- grey ribbon = standard error

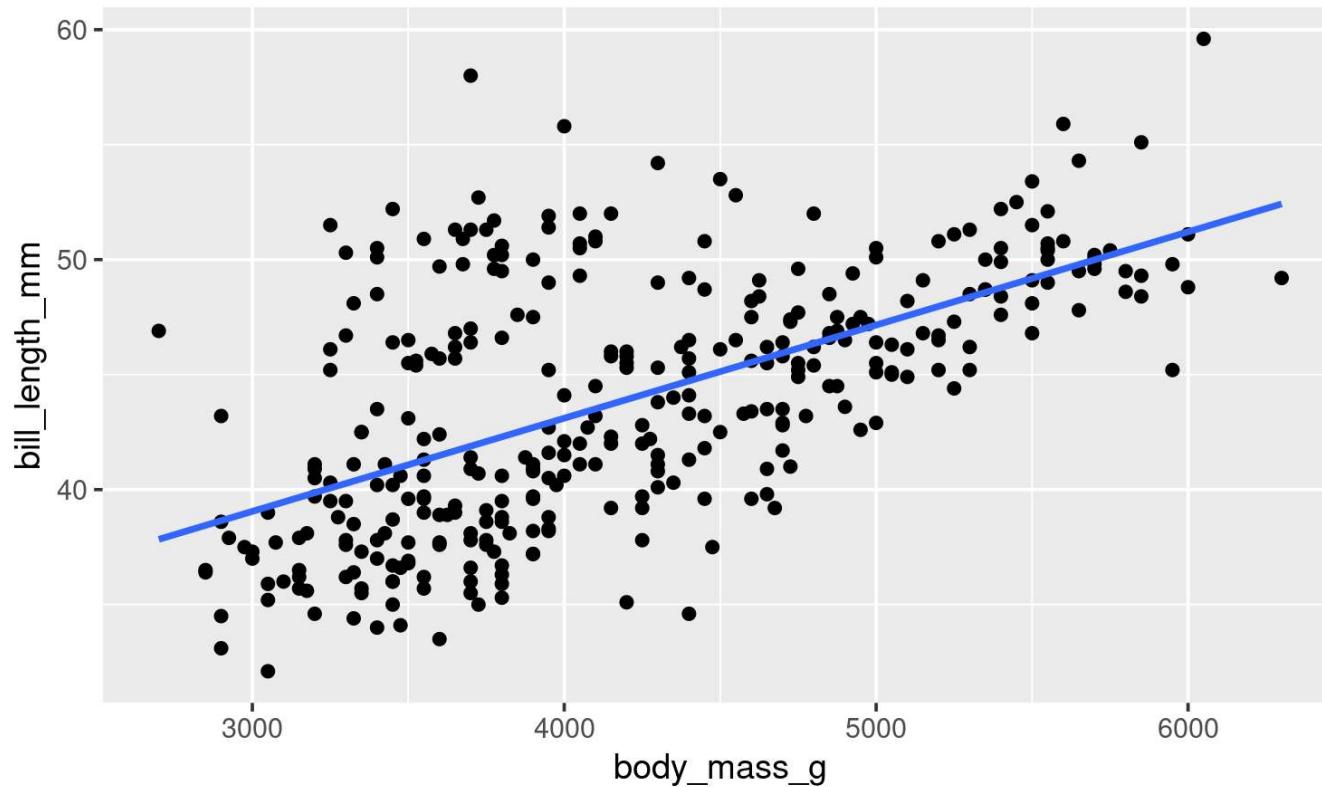


Trendlines / Regression lines

Add the `stat_smooth()`

```
g + stat_smooth(method = "lm", se = FALSE)
```

- remove the grey ribbon `se = FALSE`

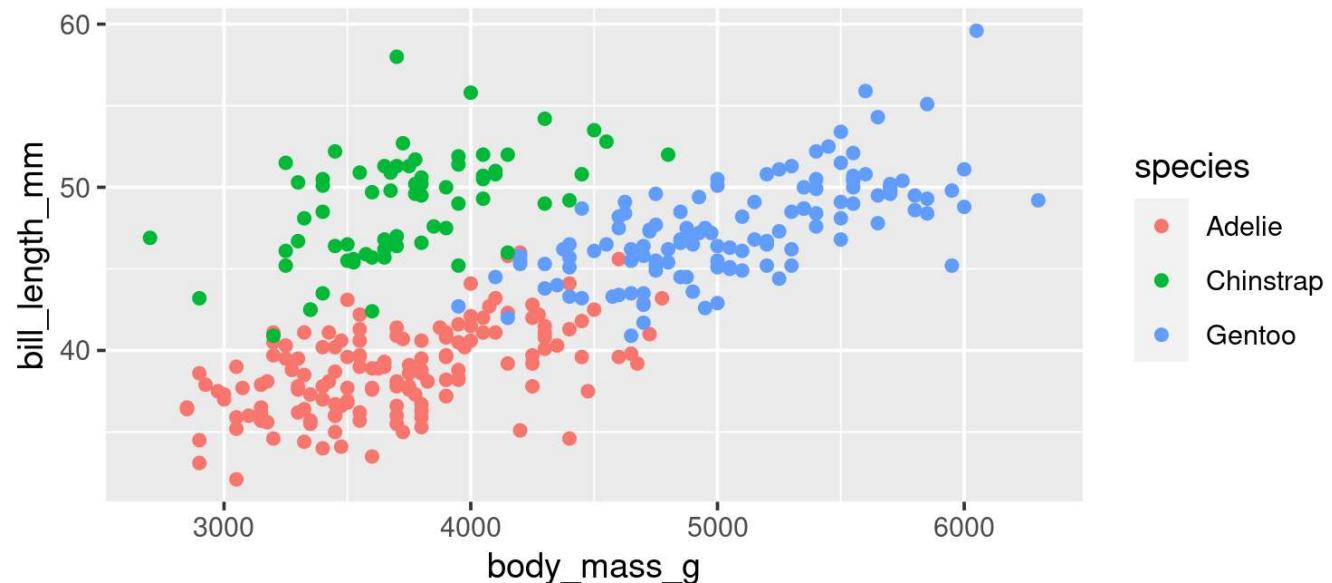


Trendlines / Regression lines

A line for each group

- Specify group (here we use **colour** to specify **species**)

```
g <- ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point()  
  
g
```

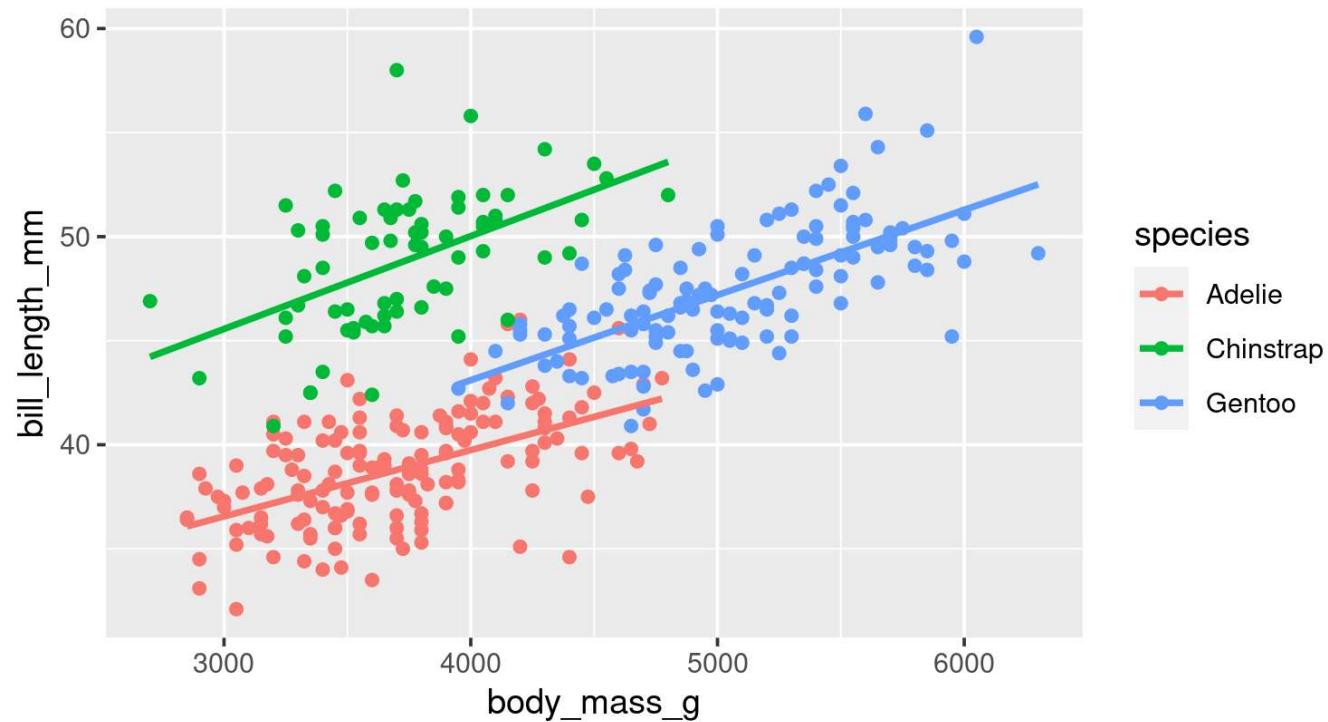


Trendlines / Regression lines

A line for each group

- `stat_smooth()` automatically uses the same grouping

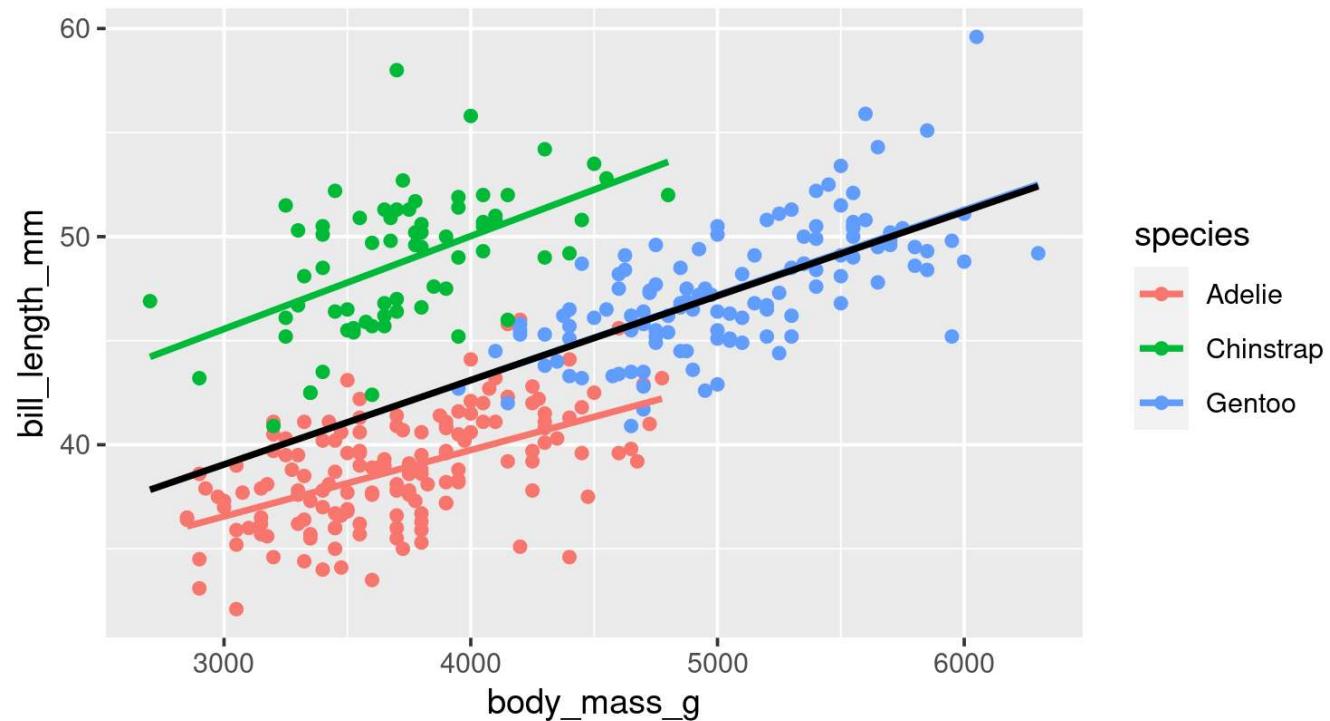
```
g + stat_smooth(method = "lm", se = FALSE)
```



Trendlines / Regression lines

A line for each group AND overall

```
g +
  stat_smooth(method = "lm", se = FALSE) +
  stat_smooth(method = "lm", se = FALSE, colour = "black")
```



Your Turn: Create this plot

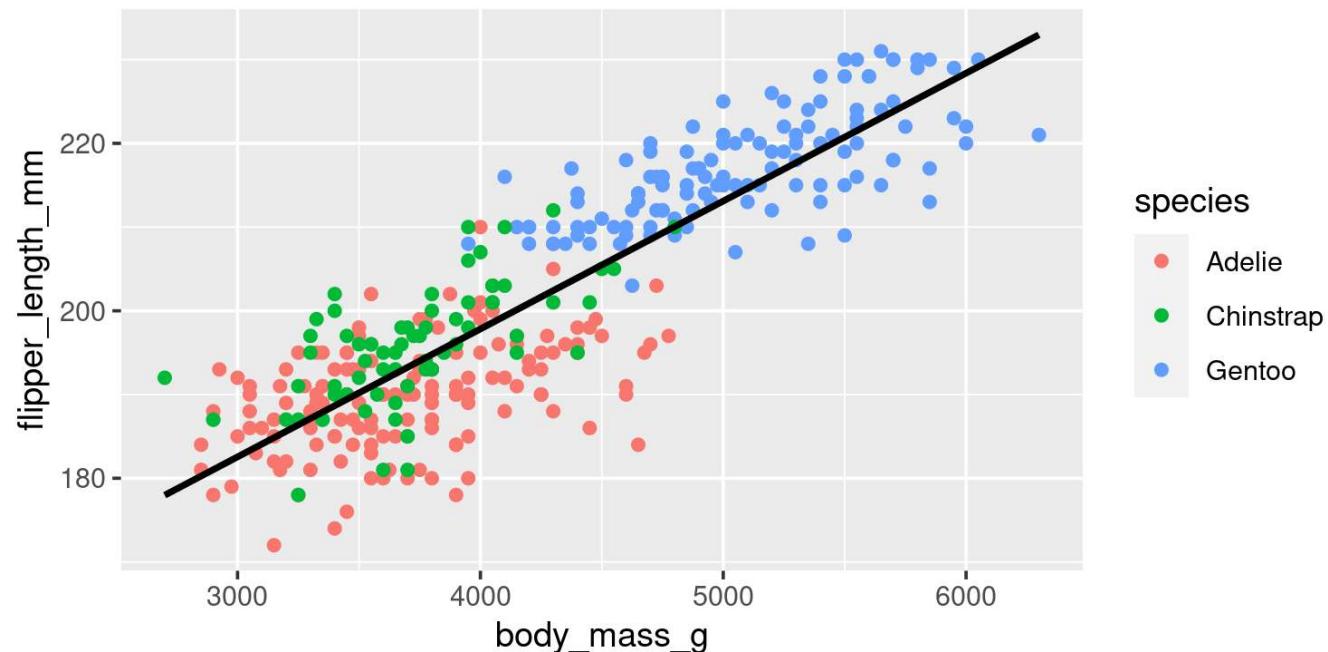
- A scatter plot: **Flipper Length** by **Body Mass** grouped by **Species**
- With *a single regression line for the overall trend*

Extra Challenge: Create a separate plot for each sex as well

Your Turn: Create this plot

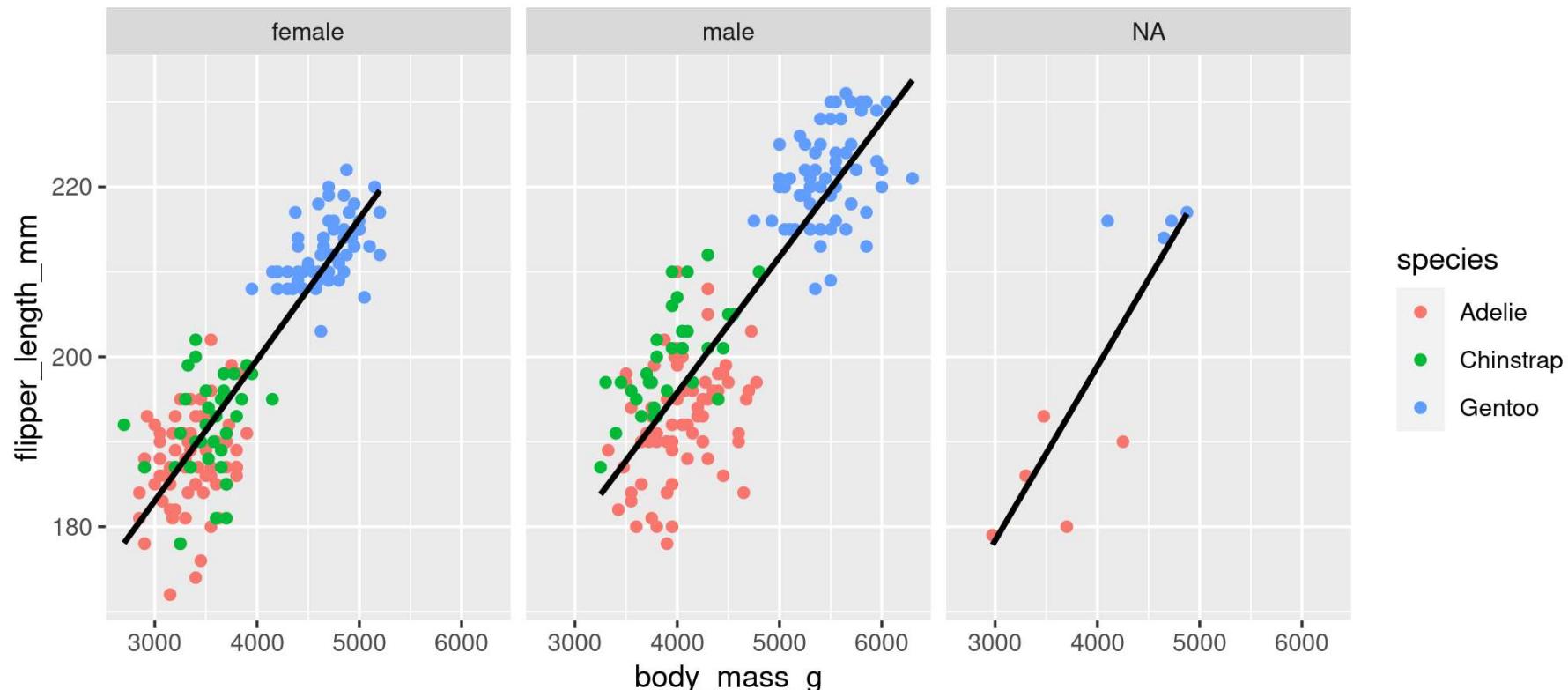
- A scatter plot: **Flipper Length** by **Body Mass** grouped by **Species**
- With *a single regression line for the overall trend*

```
ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
  geom_point() +  
  stat_smooth(se = FALSE, colour = "black", method = "lm")
```



Your Turn: Create this plot (Extra Challenge)

```
ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
  geom_point() +  
  stat_smooth(se = FALSE, colour = "black", method = "lm") +  
  facet_wrap(~sex)
```

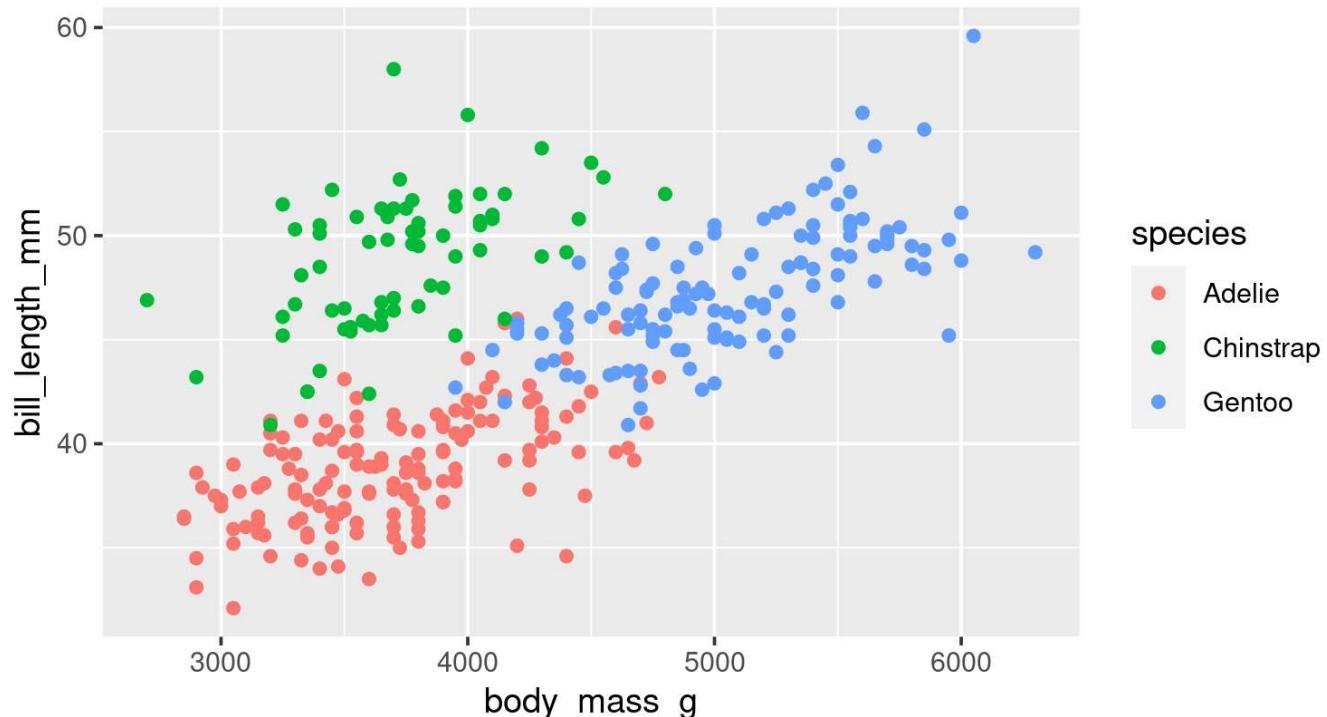


Customizing plots

Customizing: Starting plot

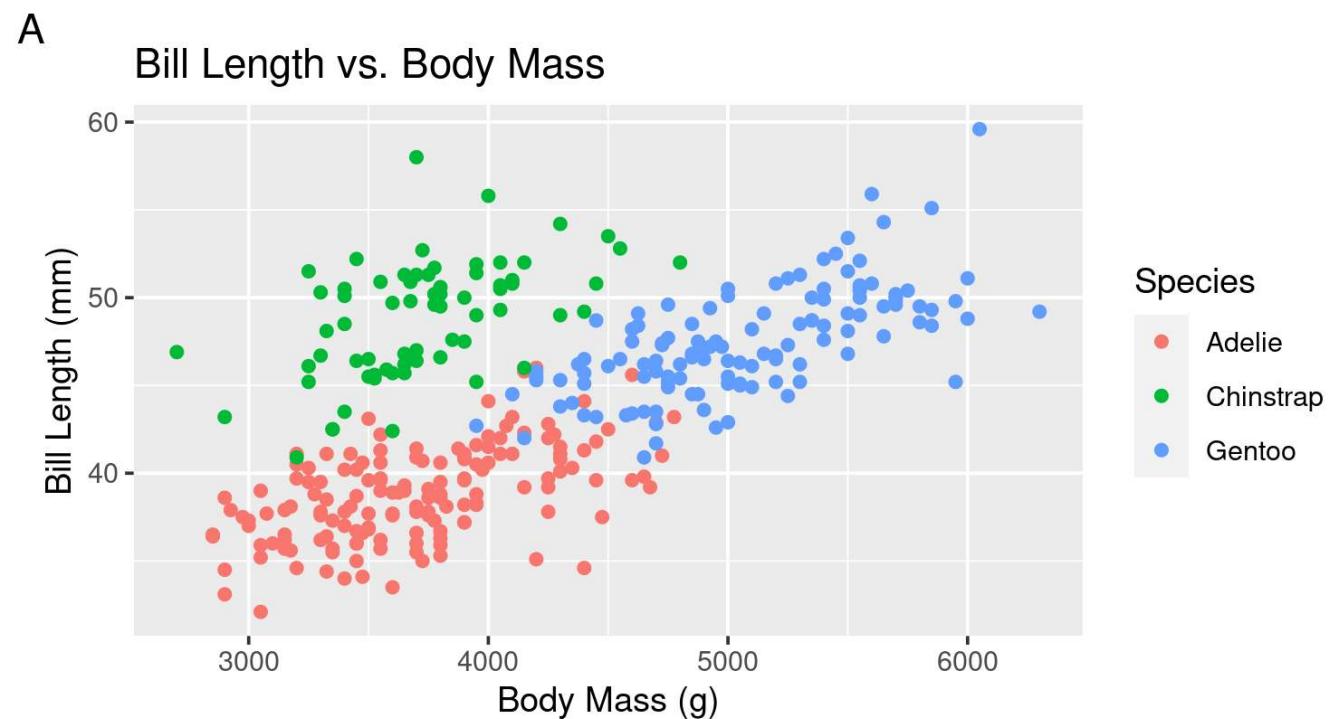
Let's work with this plot

```
g <- ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point()
```



Customizing: Labels

```
g + labs(title = "Bill Length vs. Body Mass",  
         x = "Body Mass (g)",  
         y = "Bill Length (mm)",  
         colour = "Species", tag = "A")
```

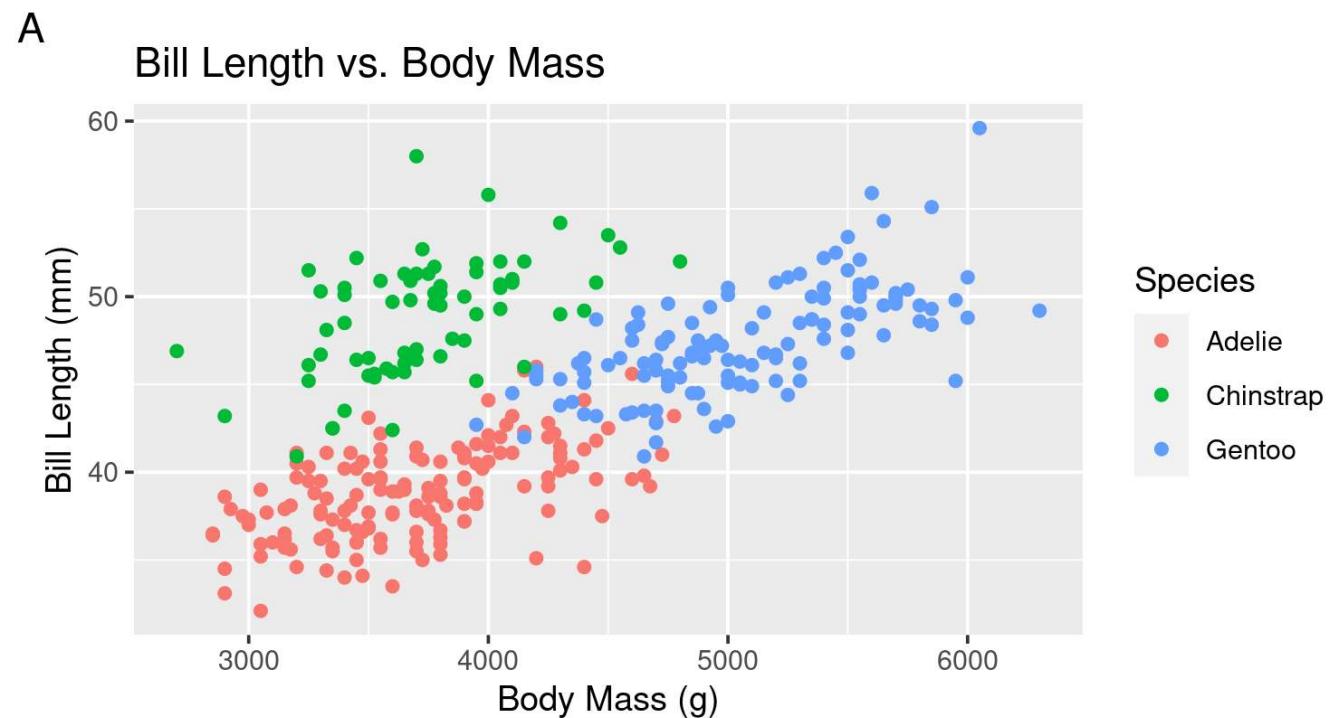


Customizing: Labels

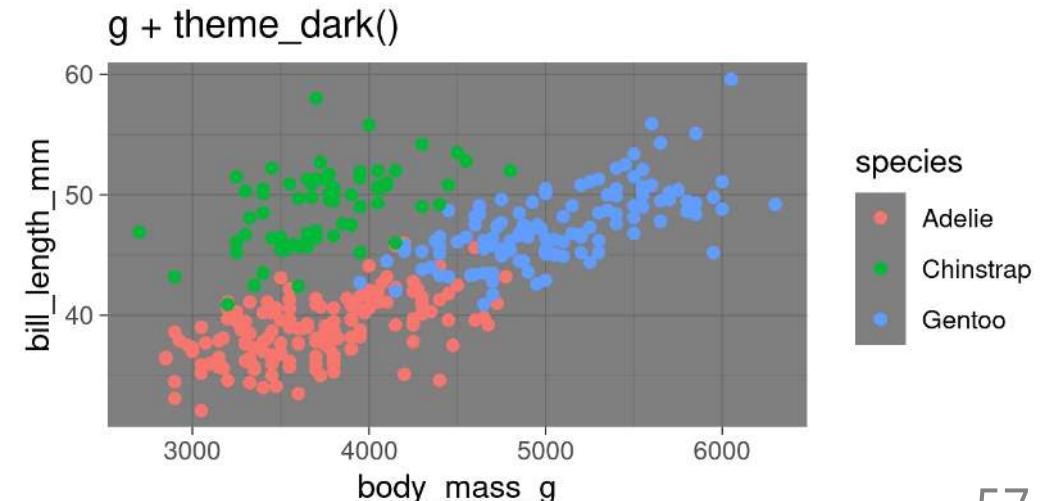
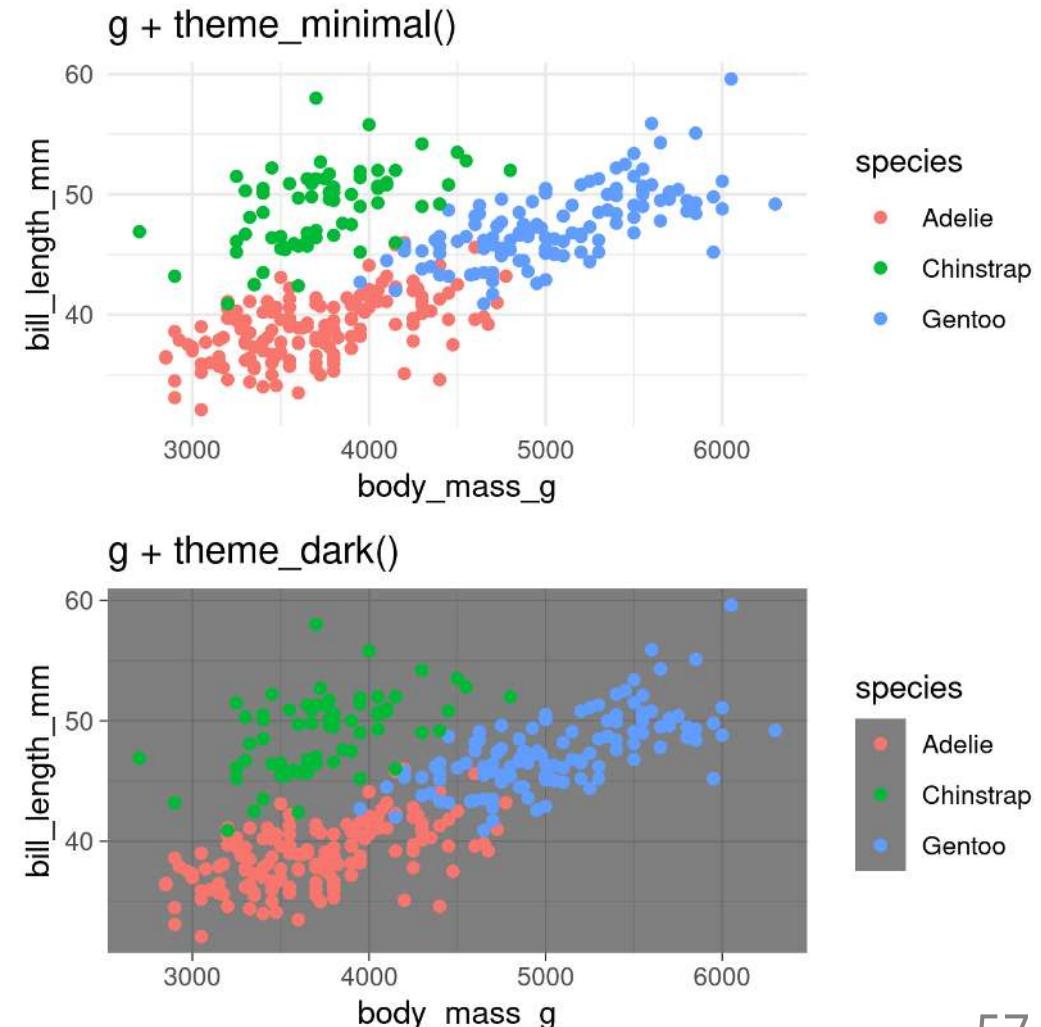
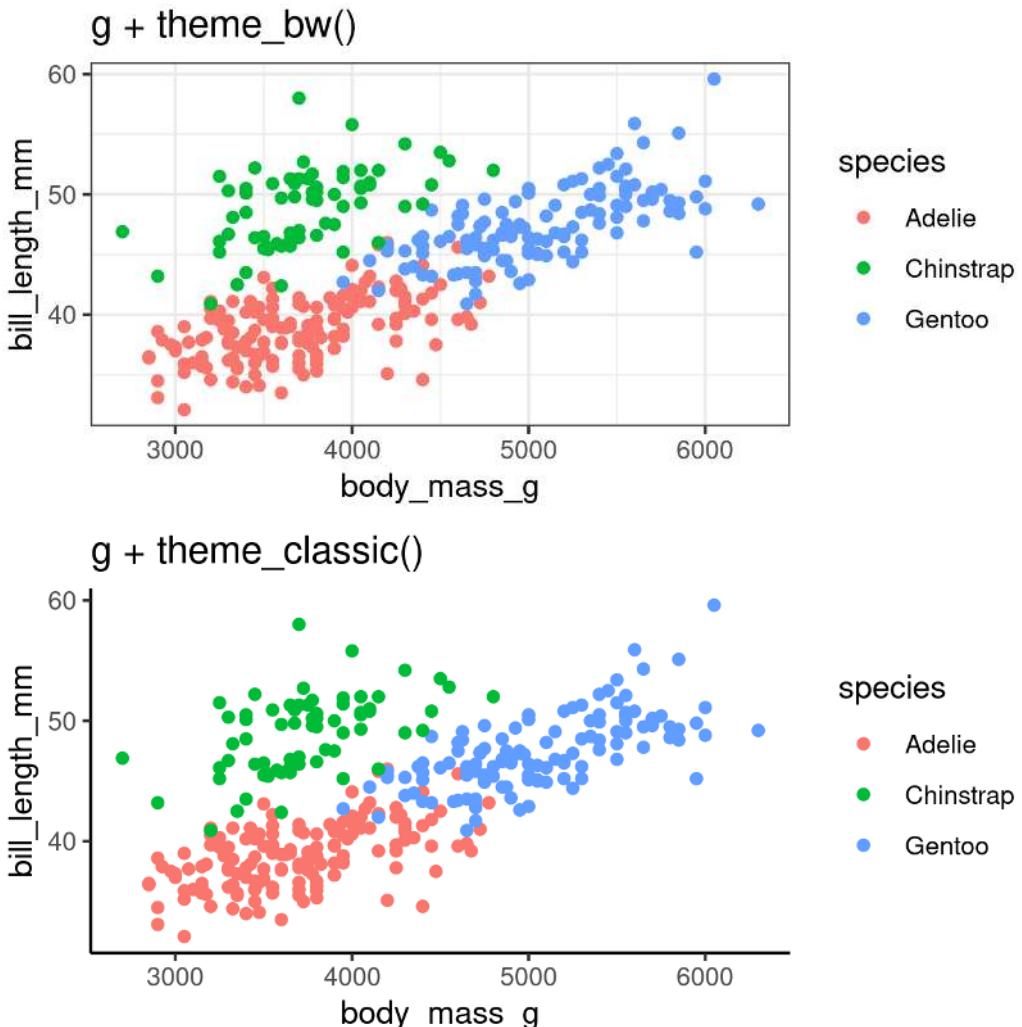
```
g + labs(title = "Bill Length vs. Body Mass",  
        x = "Body Mass (g)",  
        y = "Bill Length (mm)",  
        colour = "Species", tag = "A")
```

Your Turn:

Add proper labels to one of your previous plots



Customizing: Built-in themes



Customizing: Axes

scale_ + (x or y) + type (**continuous, discrete, date, datetime**)

- **scale_x_continuous()**
- **scale_y_discrete()**
- etc.

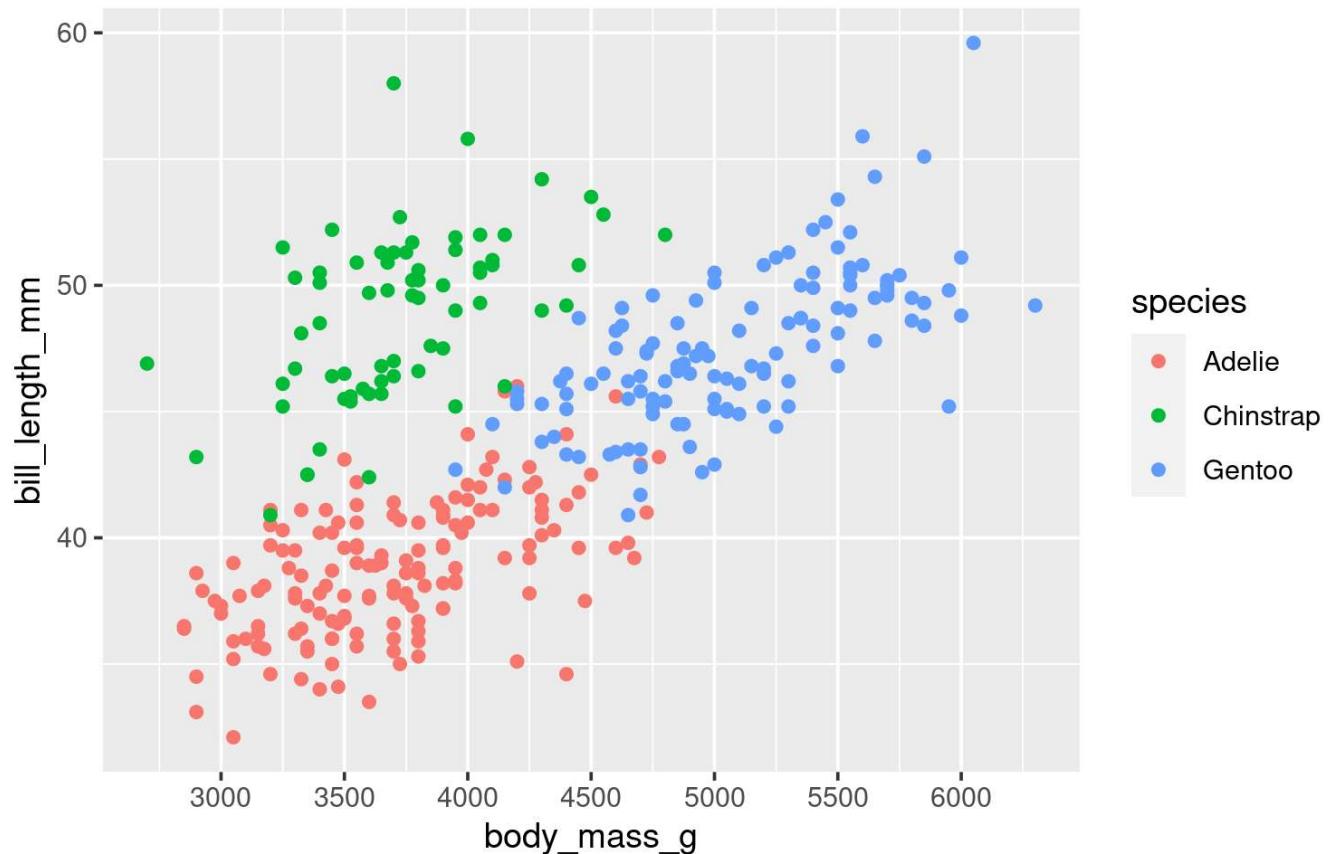
Common arguments

```
g + scale_x_continuous(breaks = seq(0, 20, 10)) # Tick breaks  
g + scale_x_continuous(limits = c(0, 15))        # xlim() is a shortcut for this  
g + scale_x_continuous(expand = c(0, 0))         # Space between axis and data
```

Customizing: Axes

Breaks

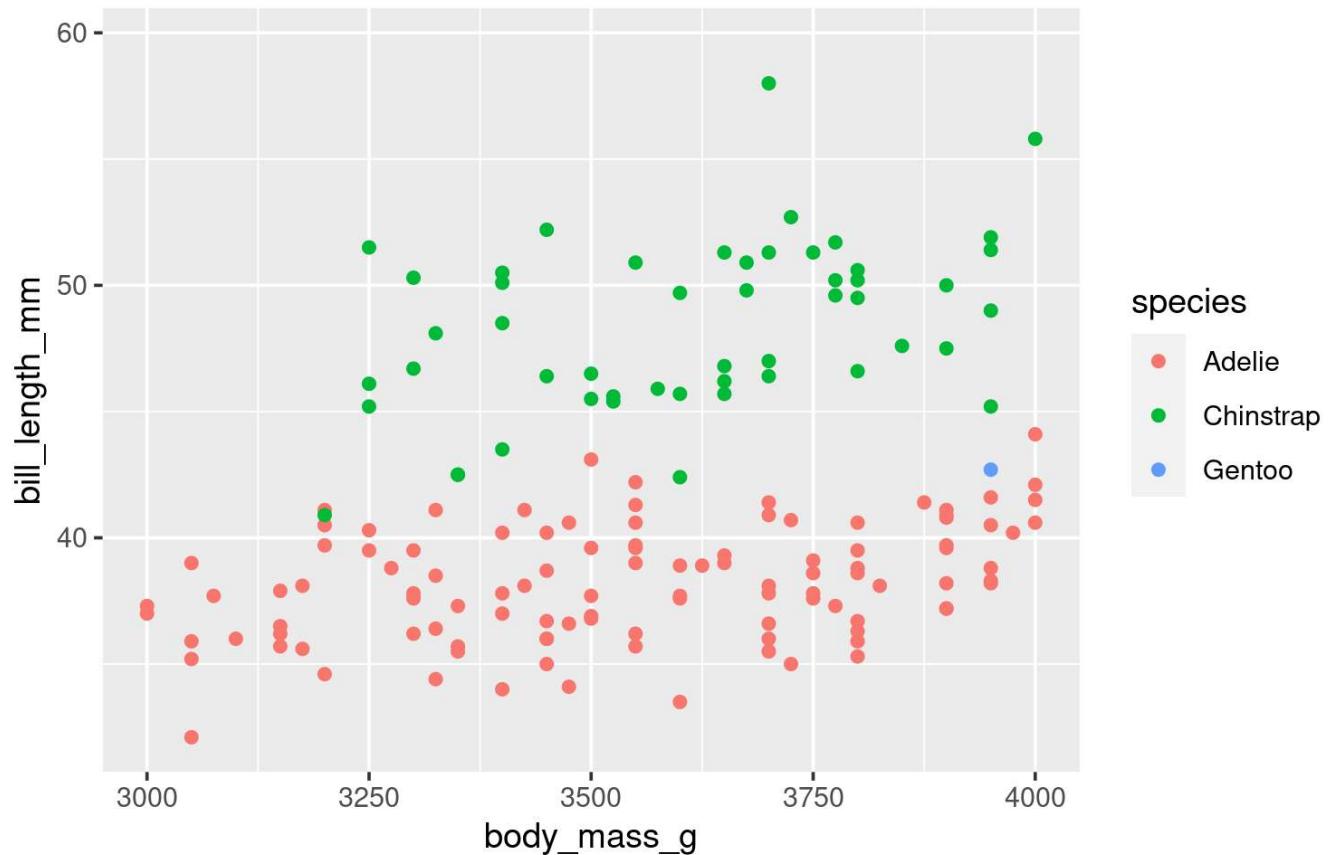
```
g + scale_x_continuous(breaks = seq(2500, 6500, 500))
```



Customizing: Axes

Limits

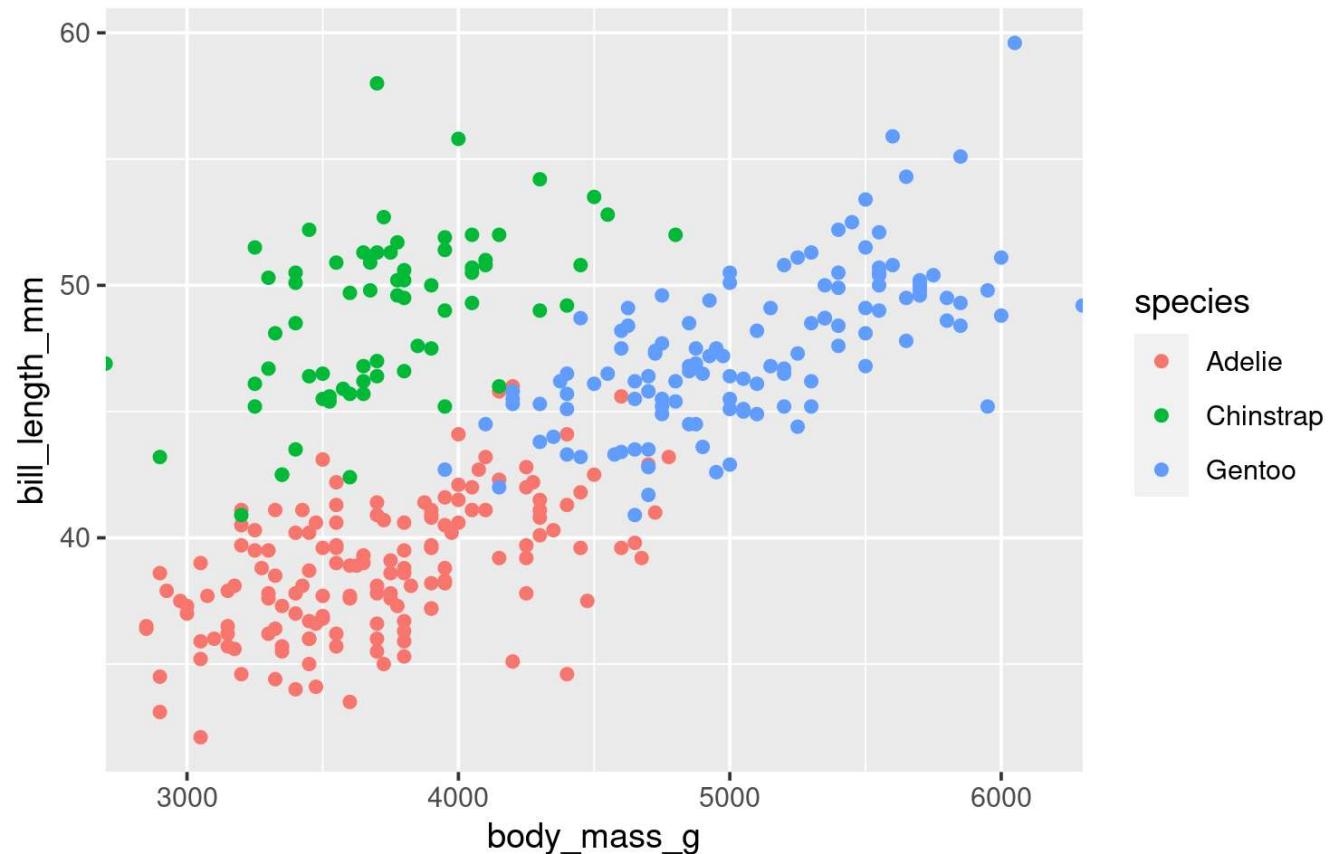
```
g + scale_x_continuous(limits = c(3000, 4000))
```



Customizing: Axes

Space between origin and axis start

```
g + scale_x_continuous(expand = c(0, 0))
```

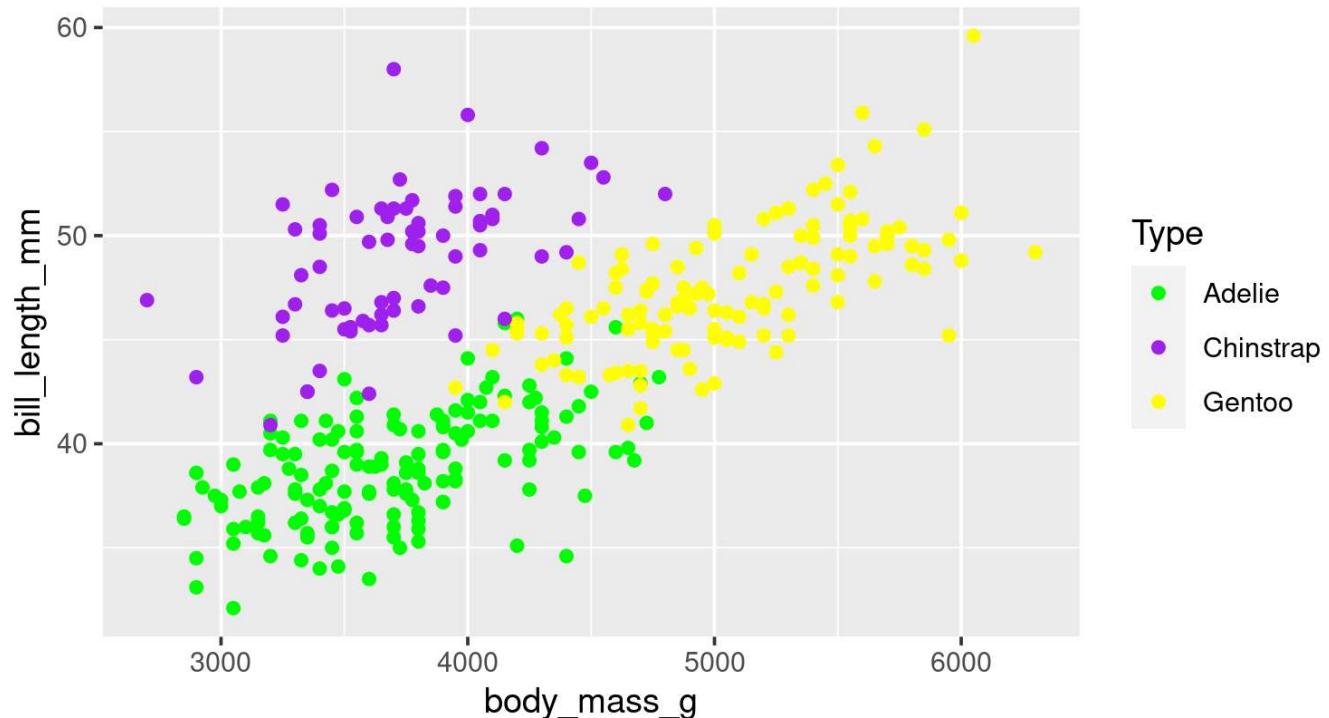


Customizing: Aesthetics

Using scales

`scale_` + aesthetic (`colour`, `fill`, `size`, etc.) + type (`manual`, `continuous`, `datetime`, etc.)

```
g + scale_colour_manual(name = "Type", values = c("green", "purple", "yellow"))
```

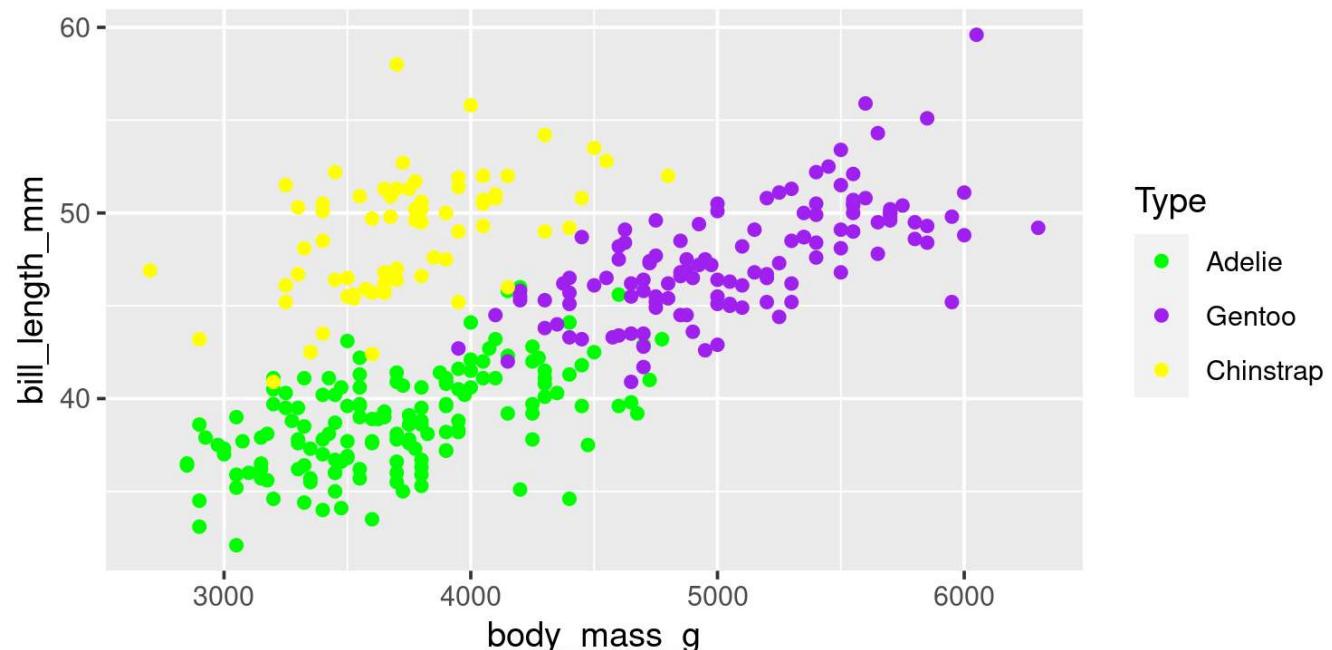


Customizing: Aesthetics

Using scales

Or be very explicit:

```
g + scale_colour_manual(name = "Type", na.value = "black", values = c("Adelie" = "green",
"Chinstrap" = "yellow"))
```

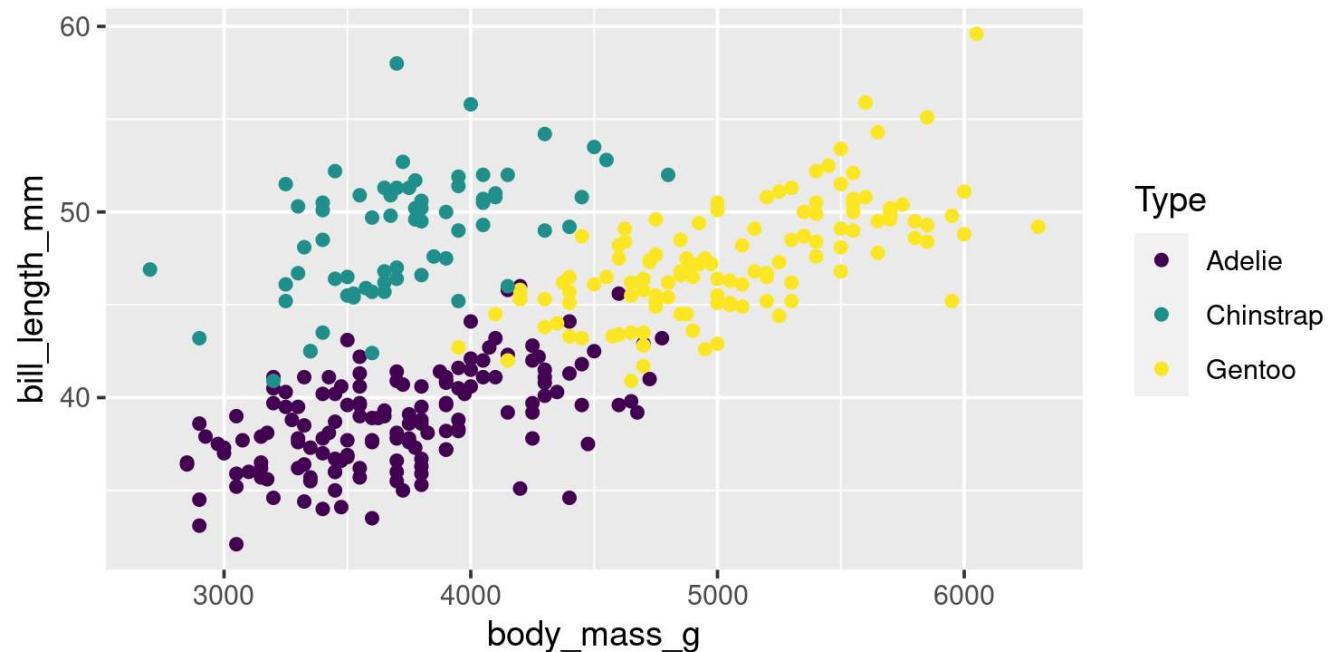


Customizing: Aesthetics

For colours, consider colour-blind-friendly scale

`viridis_d` for "discrete" data

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point() +  
  scale_colour_viridis_d(name = "Type")
```

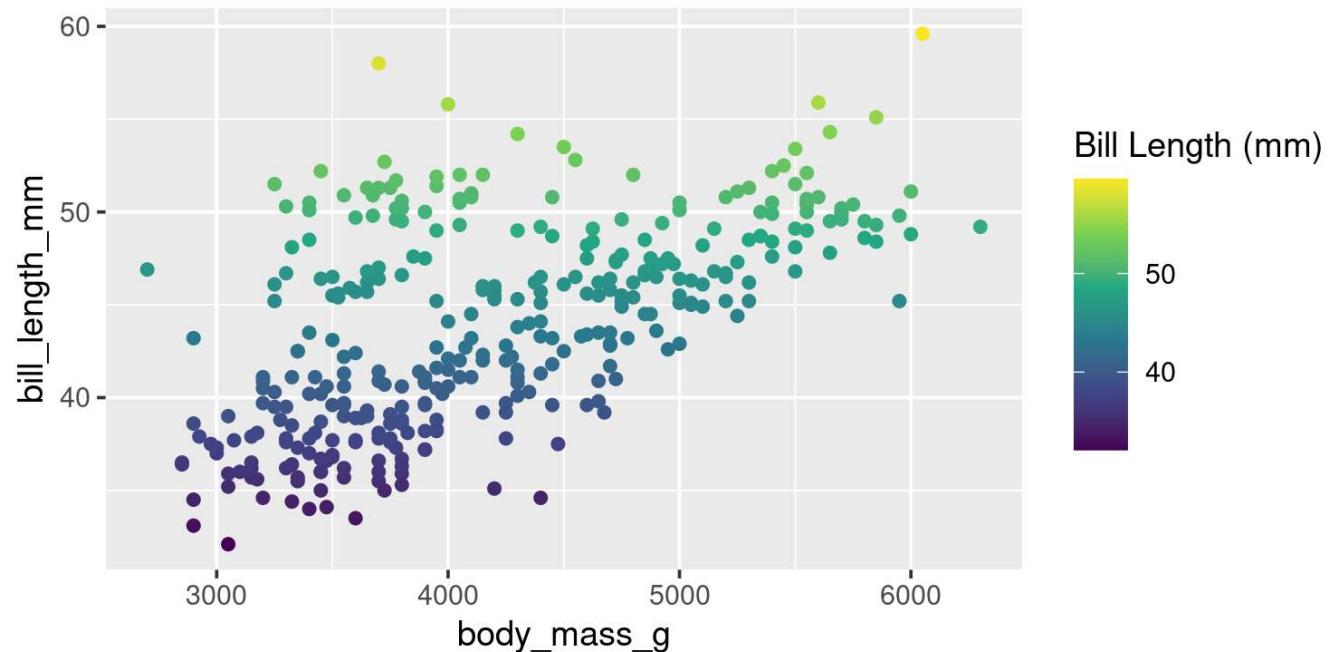


Customizing: Aesthetics

For colours, consider colour-blind-friendly scale

`viridis_c` for "continuous" data

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = bill_length_mm)) +  
  geom_point() +  
  scale_colour_viridis_c(name = "Bill Length (mm)")
```

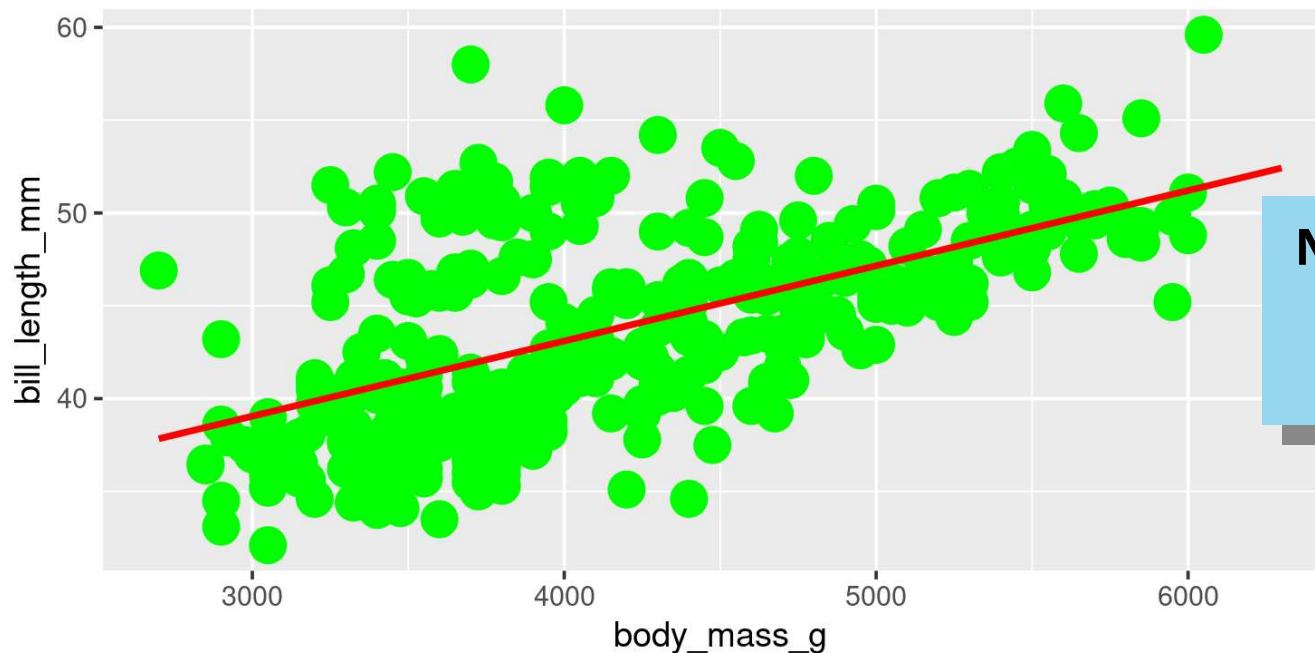


Customizing: Aesthetics

Forcing

Remove the association between a variable and an aesthetic

```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
  geom_point(colour = "green", size = 5) +  
  stat_smooth(method = "lm", se = FALSE, colour = "red")
```

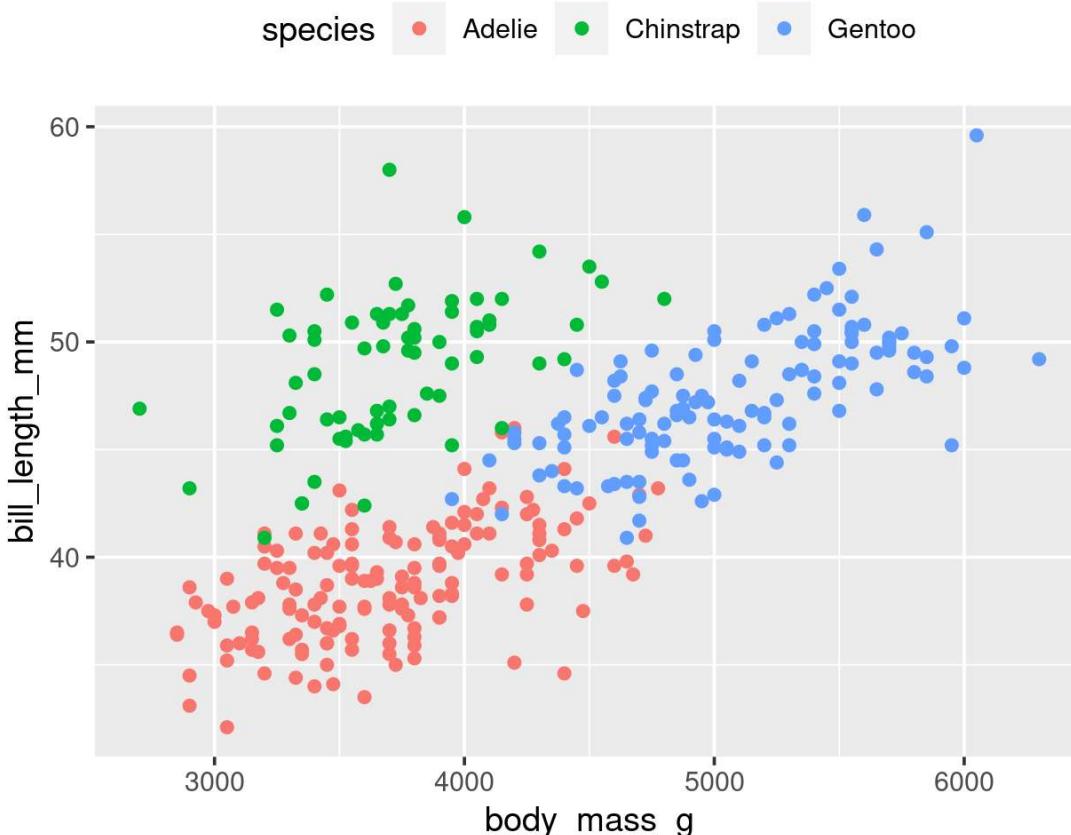


Note: When forcing,
aesthetic is not
inside **aes()**

Customizing: Legends placement

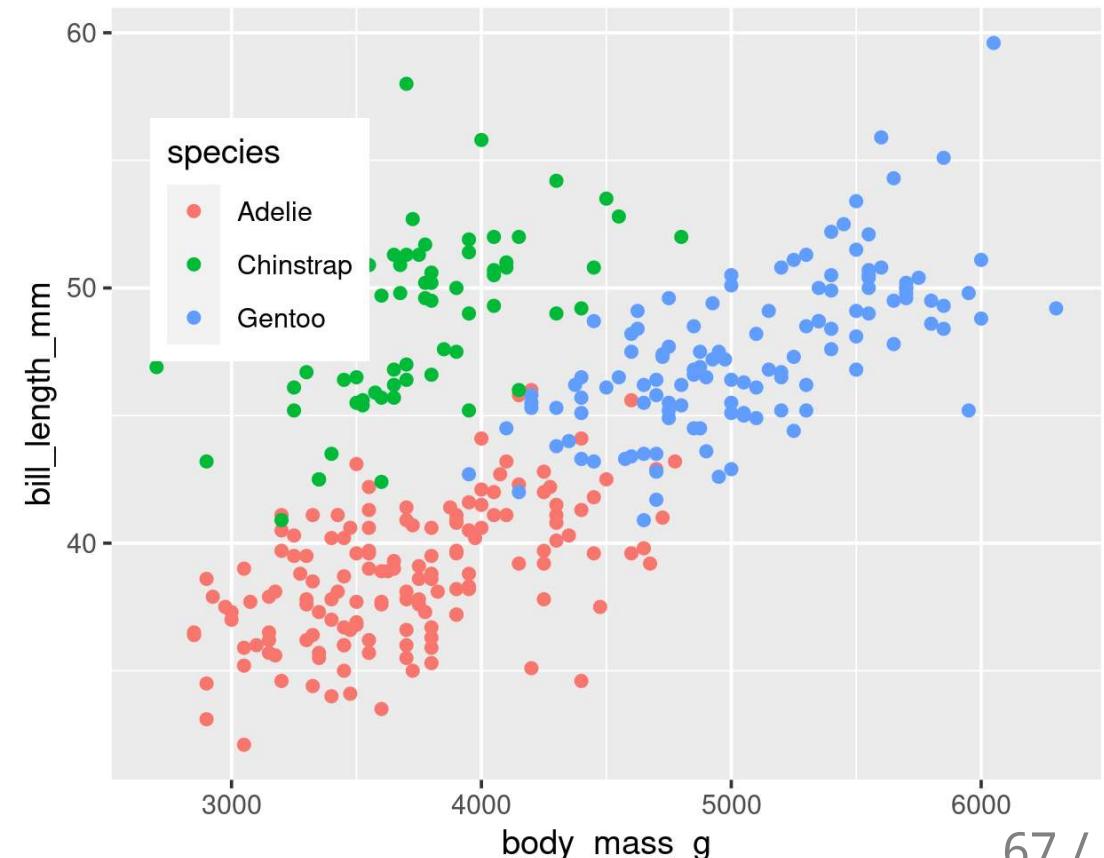
At the: top, bottom, left, right

```
g + theme(legend.position = "top")
```



Exactly here

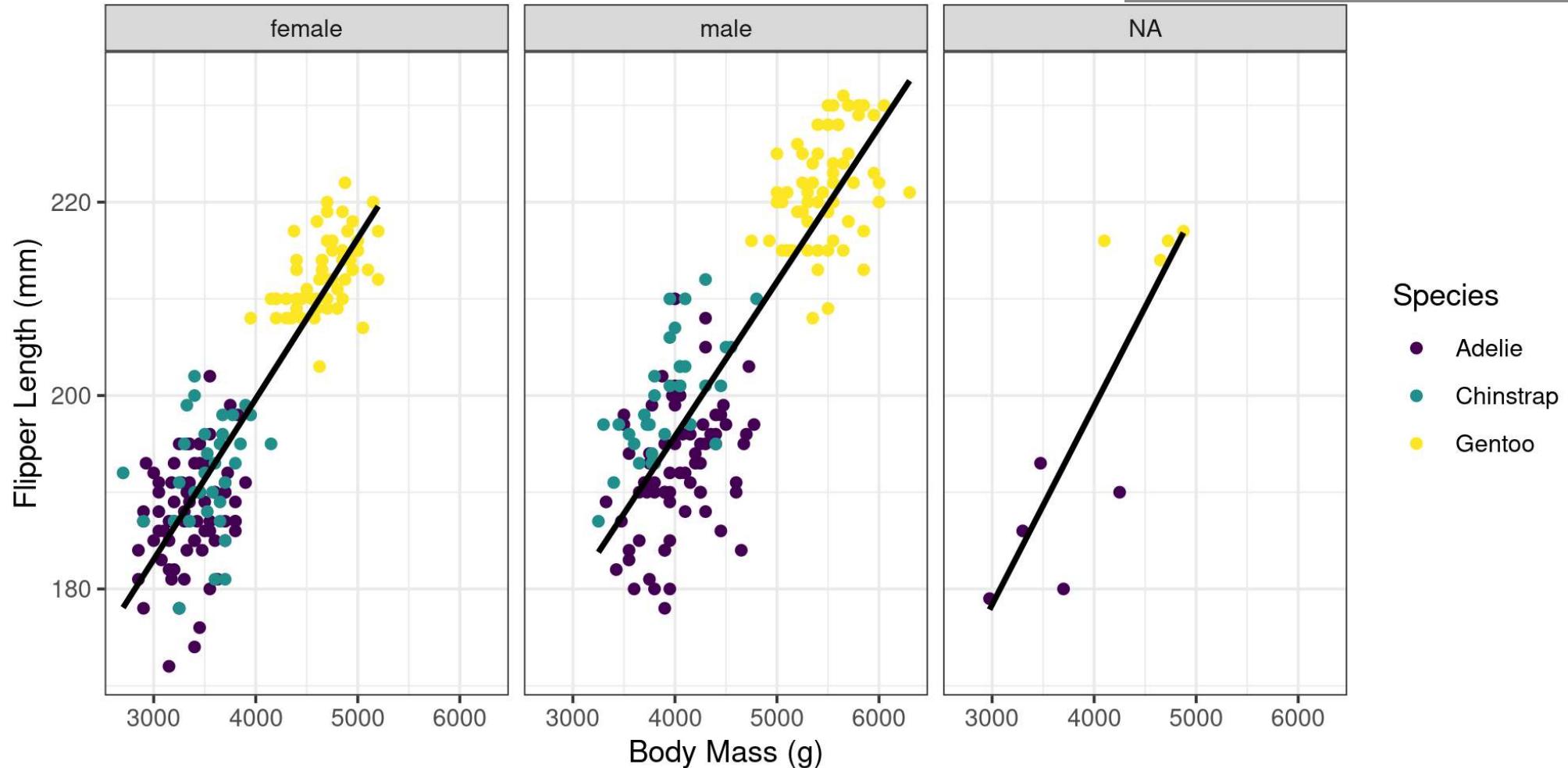
```
g + theme(legend.position = c(0.15, 0.7))
```



Your Turn: Create this plot

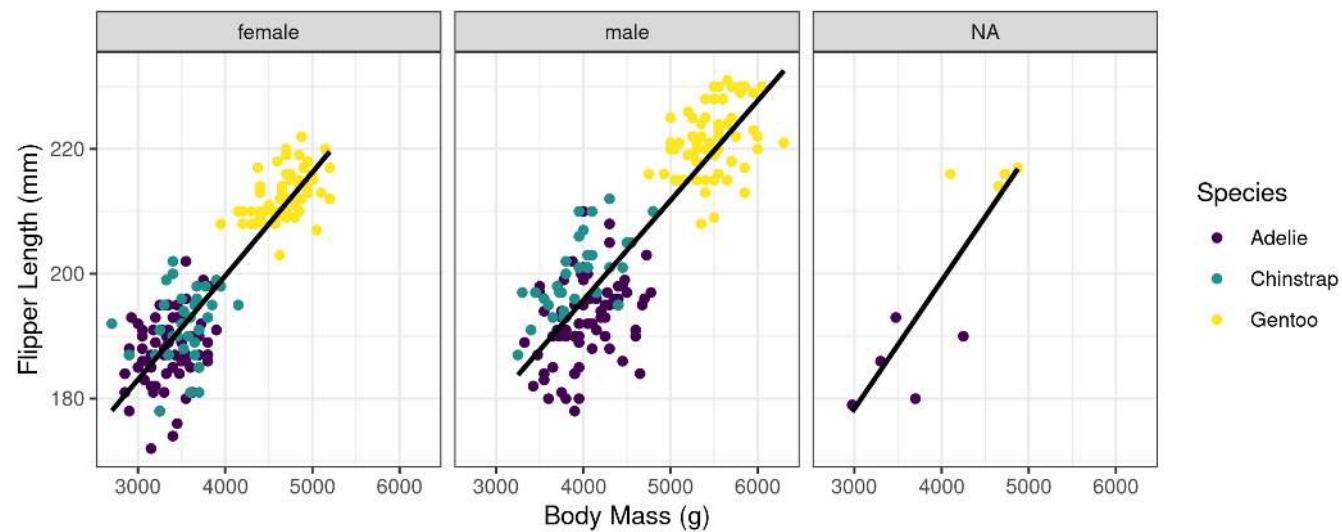
Extra Challenge

Create a plot of your own data



Your Turn: Create this plot

```
ggplot(penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
  theme_bw() +  
  geom_point() +  
  stat_smooth(method = "lm", se = FALSE, colour = "black") +  
  scale_colour_viridis_d() +  
  facet_wrap(~ sex) +  
  labs(x = "Body Mass (g)",  
       y = "Flipper Length (mm)",  
       colour = "Species")
```



Side note: Order of operations

Order of operations

Remember...

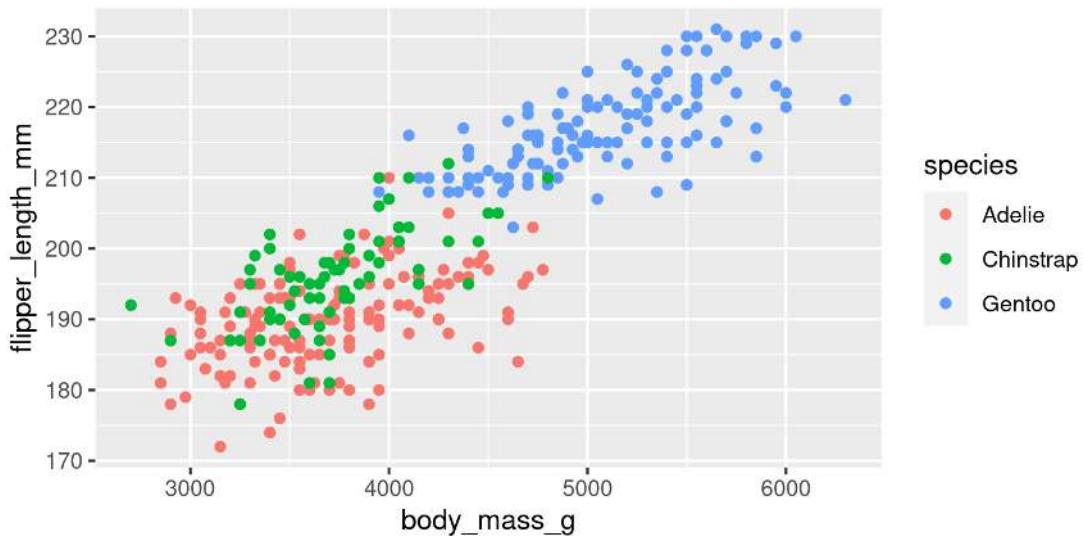
- **ggplot()** is the default line (all options passed down)
- The other lines are *added* with the **+** (options only apply to this line)

Order of operations

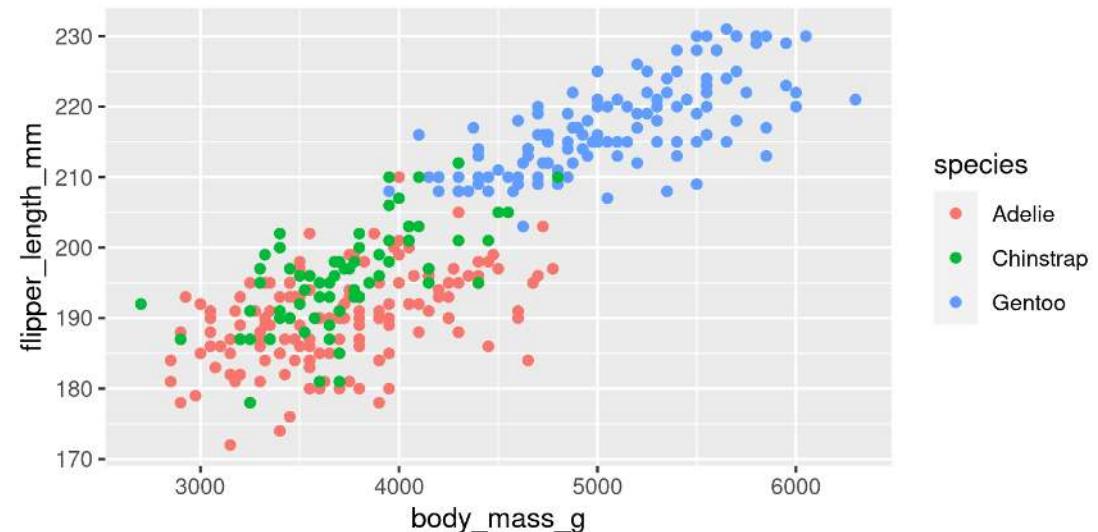
Where to put the aes()?

Sometimes it doesn't matter...

```
ggplot(penguins, aes(x = body_mass_g,  
                     y = flipper_length_mm,  
                     colour = species)) +  
  geom_point()
```



```
ggplot(penguins, aes(x = body_mass_g,  
                     y = flipper_length_mm)) +  
  geom_point(aes(colour = species))
```

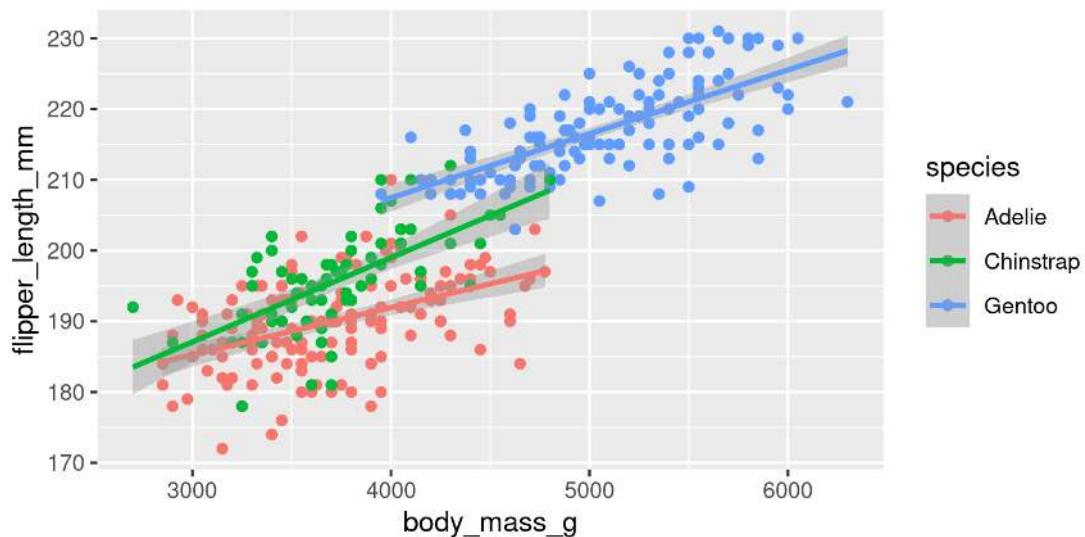


Order of operations

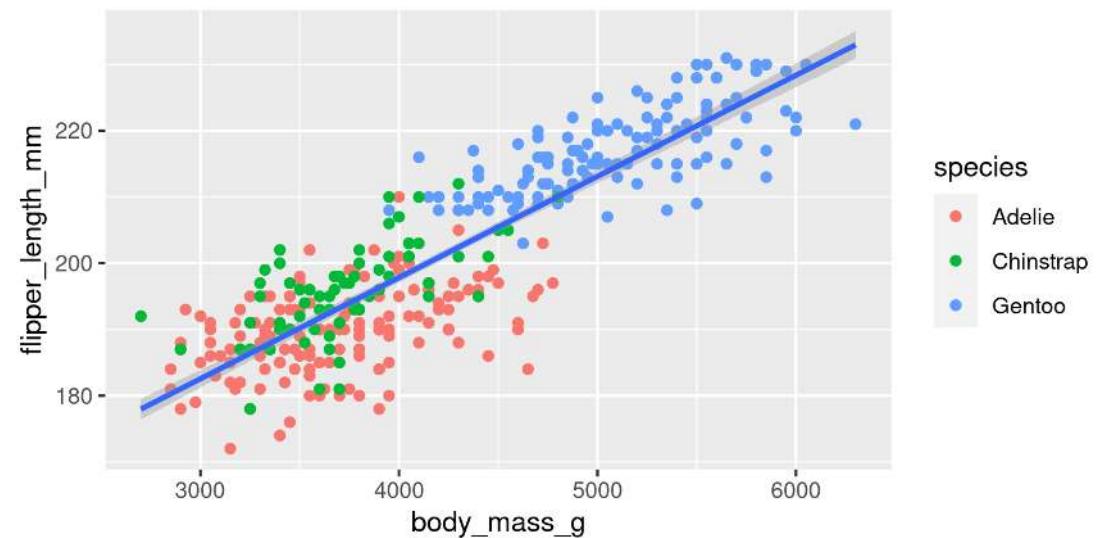
Where to put the aes()?

Sometimes it DOES matter...

```
ggplot(penguins, aes(x = body_mass_g,  
                     y = flipper_length_mm,  
                     colour = species)) +  
  geom_point() +  
  stat_smooth(method = "lm")
```



```
ggplot(penguins, aes(x = body_mass_g,  
                     y = flipper_length_mm)) +  
  geom_point(aes(colour = species)) +  
  stat_smooth(method = "lm")
```

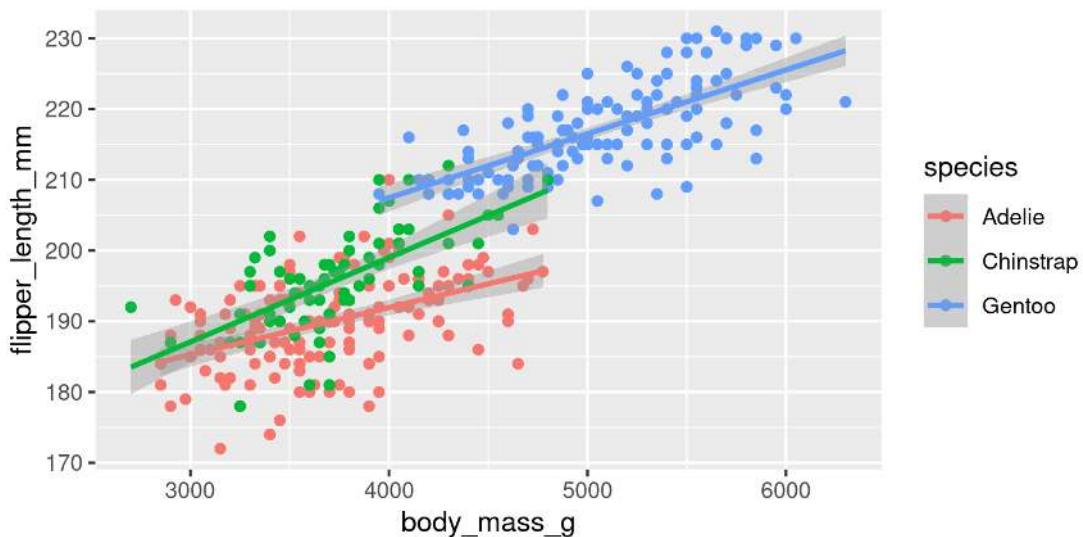


Order of operations

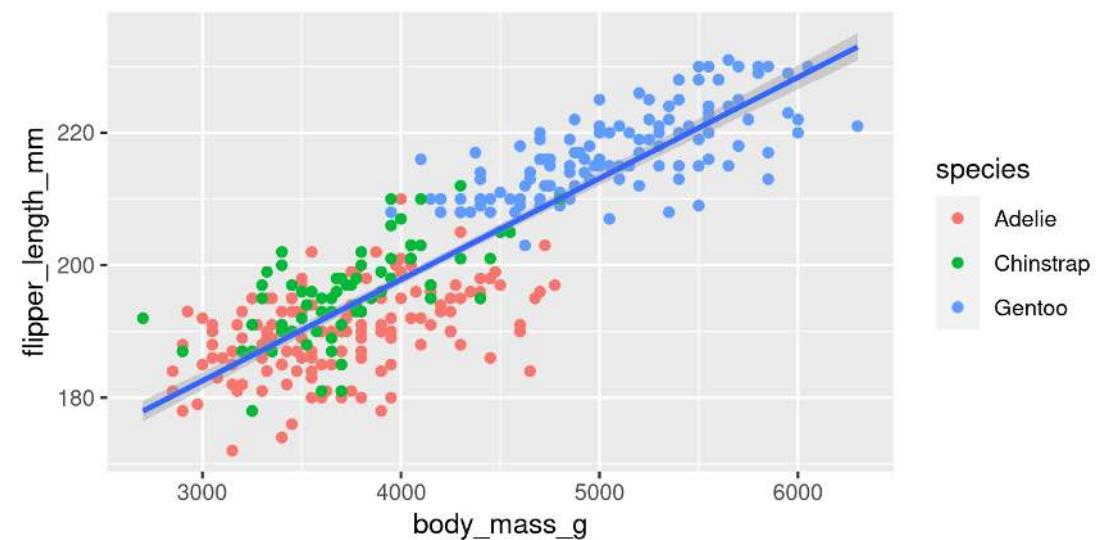
Where to put the aes()?

Applies to ALL lines in the ggplot
including **stat_smooth**

```
y = flipper_length_mm,  
colour = species)) +  
  
geom_point() +  
stat_smooth(method = "lm")
```



```
ggplot(penguins, aes(x = body_mass_g,  
y = flipper_length_mm)) +  
geom_point(aes(colour = species)) +  
stat_smooth(method = "lm")
```

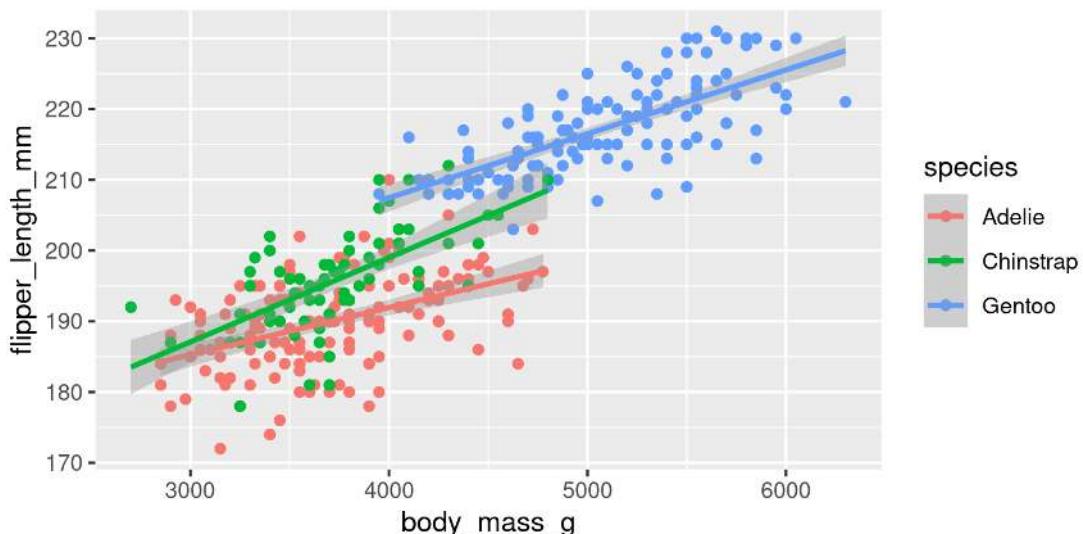


Order of operations

Where to put the aes()?

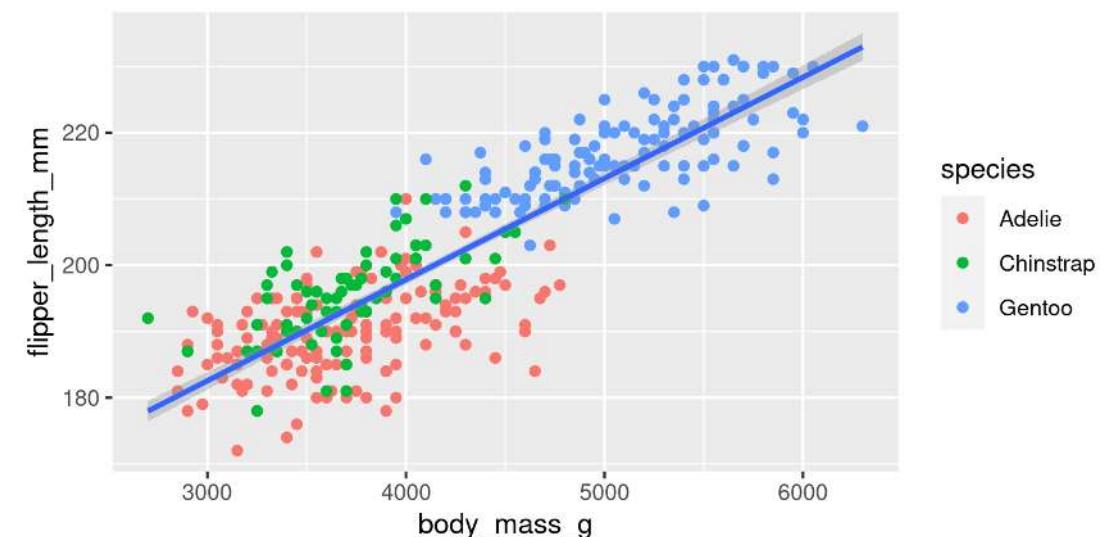
Applies to ALL lines in the ggplot
including **stat_smooth**

```
y = flipper_length_mm,  
colour = species)) +  
  
geom_point() +  
stat_smooth(method = "lm")
```



Applies to only the geom_point in the ggplot
not **stat_smooth**

```
y = flipper_length_mm)) +  
geom_point(aes(colour = species)) +  
stat_smooth(method = "lm")
```

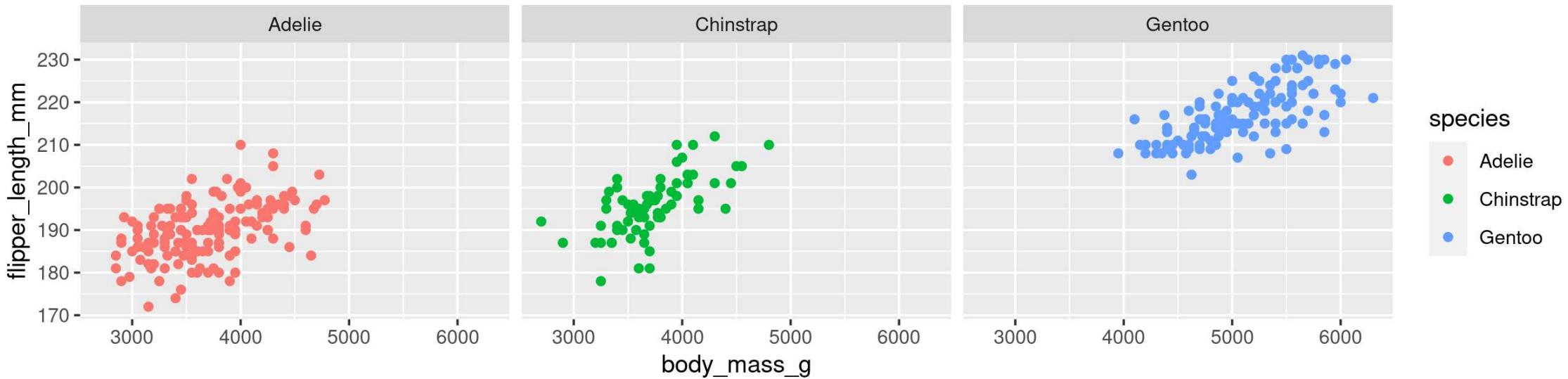


Annotating plots

Annotating

Plot to be annotated: Let's add sample sizes

```
ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
  geom_point() +  
  facet_grid(~ species)
```



Annotating

Create data to use in our annotations

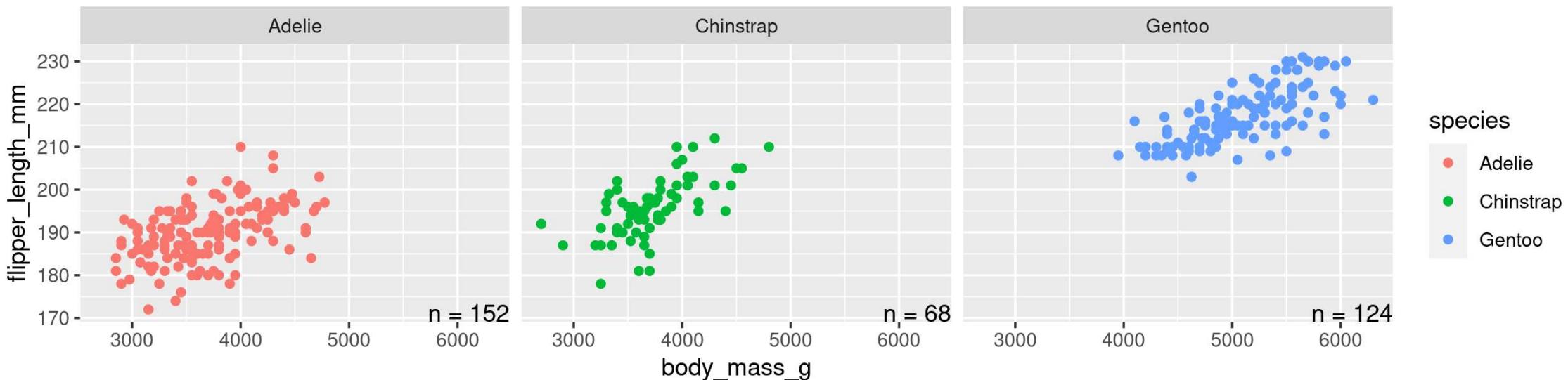
(**mutate()** is covered tomorrow!)

```
library(tidyverse)
n <- count(penguins, species)
n <- mutate(n, text = paste0("n = ", n))
n
```

```
## # A tibble: 3 × 3
##   species      n  text
##   <fct>     <int> <chr>
## 1 Adelie     152  n = 152
## 2 Chinstrap   68  n = 68
## 3 Gentoo    124  n = 124
```

Annotating

```
ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
  geom_point() +  
  facet_grid(~ species) +  
  geom_text(data = n,  
            x = +Inf, y = -Inf,  
            aes(label = text),  
            hjust = 1, vjust = 0,  
            colour = "black")  
  # Use 'n' data set  
  # Location relative to plot (right, bottom)  
  # Map 'text' to label  
  # Adjust horizontal and vertical placement  
  # black text
```



Combining plots

Combining plots with patchwork

Setup

- Load **patchwork**
- Create a couple of different plots

```
library(patchwork)

g1 <- ggplot(data = penguins, aes(x = bill_length_mm, y = bill_depth_mm, colour = species)) +
  geom_point()

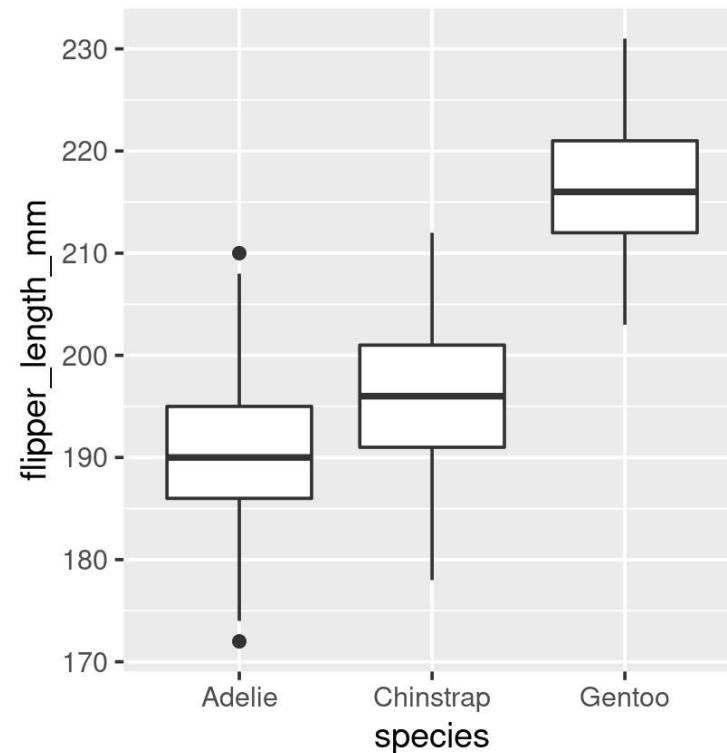
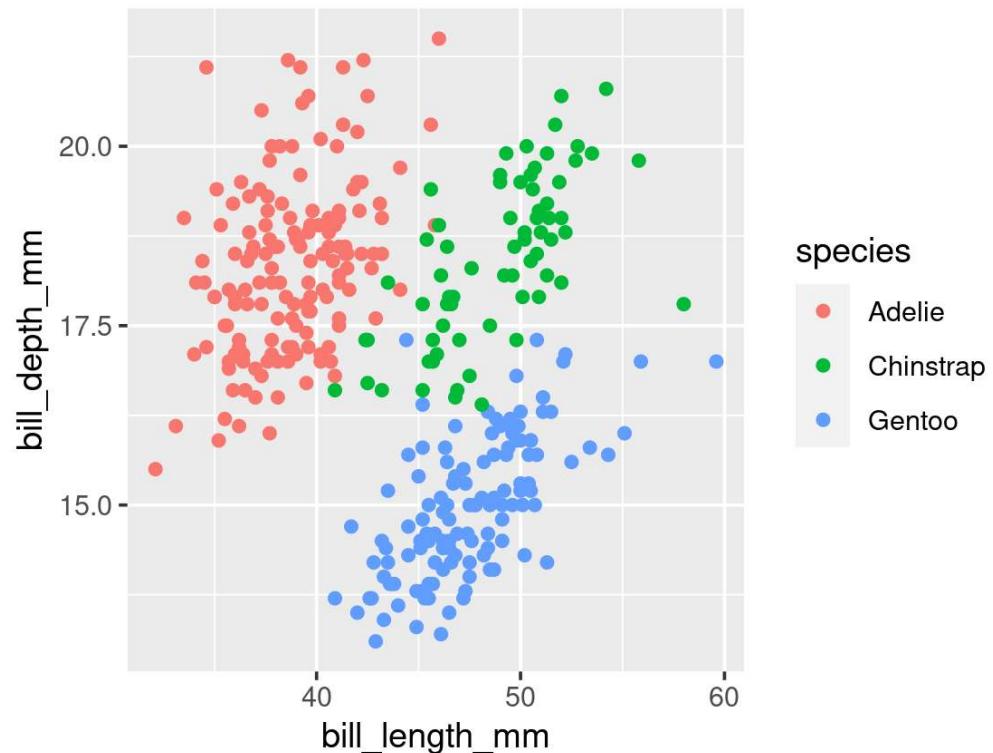
g2 <- ggplot(data = penguins, aes(x = species, y = flipper_length_mm)) +
  geom_boxplot()

g3 <- ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g, colour = species)) +
  geom_point()
```

Combining plots with patchwork

Side-by-Side 2 plots

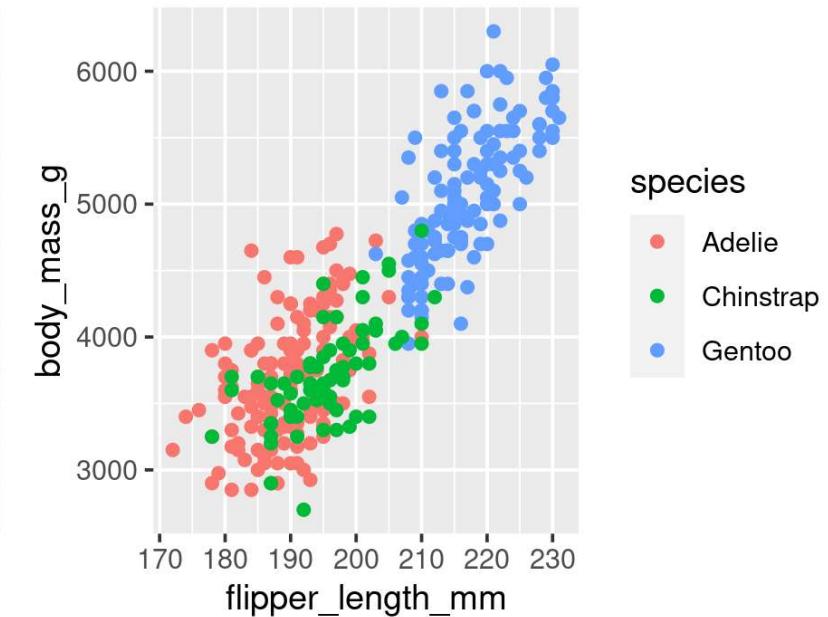
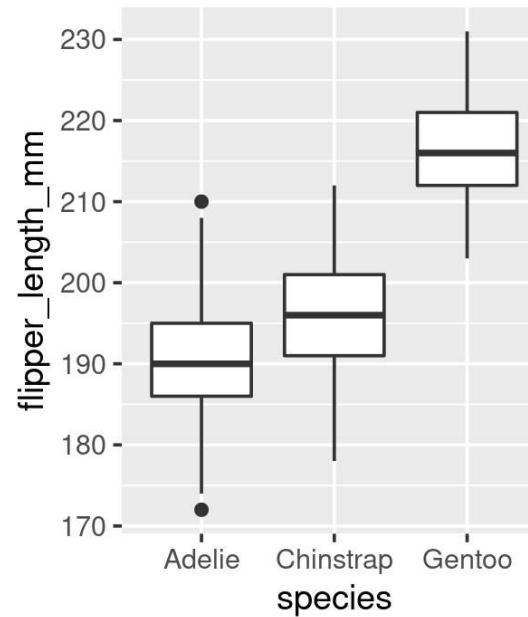
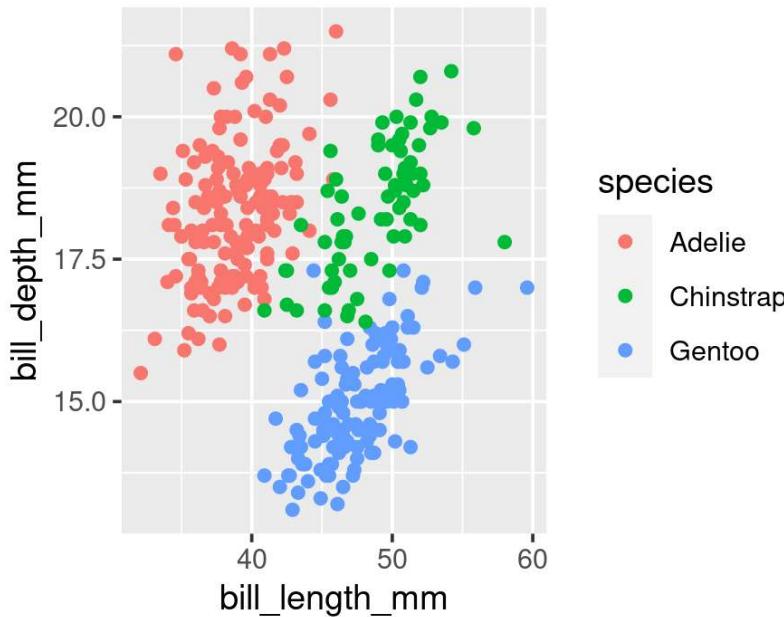
g1 + g2



Combining plots with patchwork

Side-by-Side 3 plots

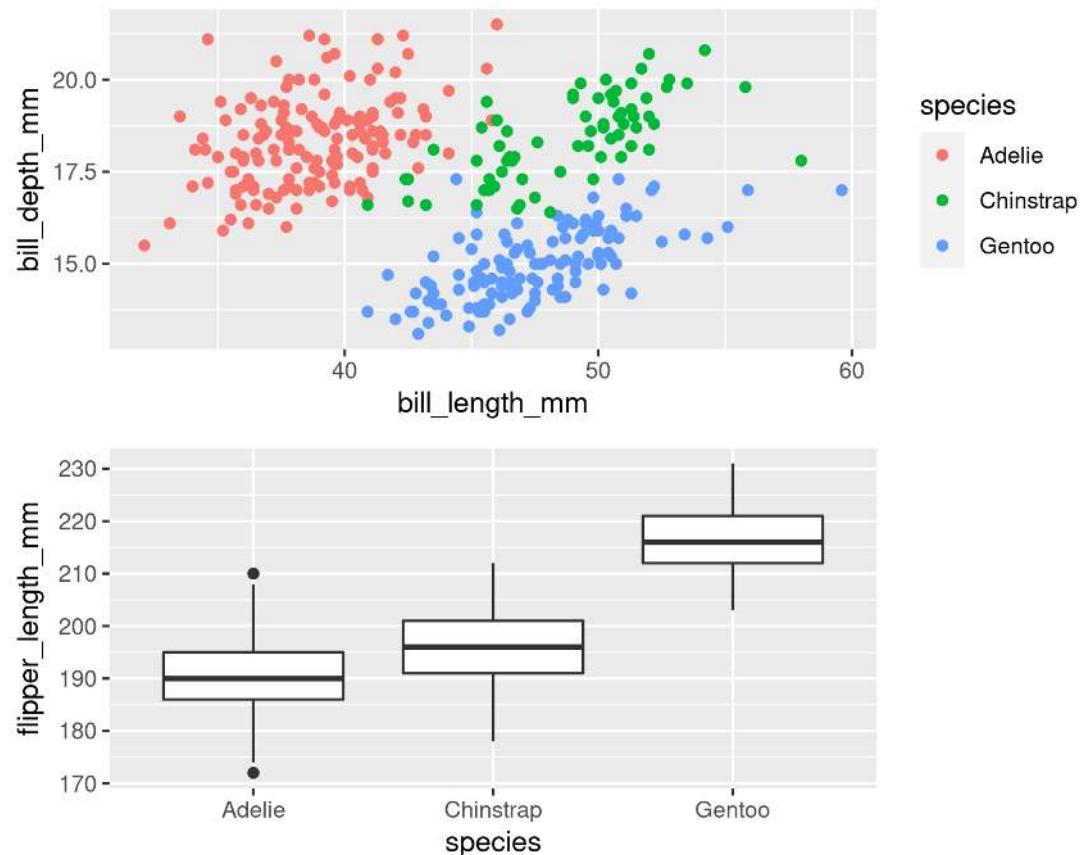
g1 + g2 + g3



Combining plots with patchwork

Stacked 2 plots

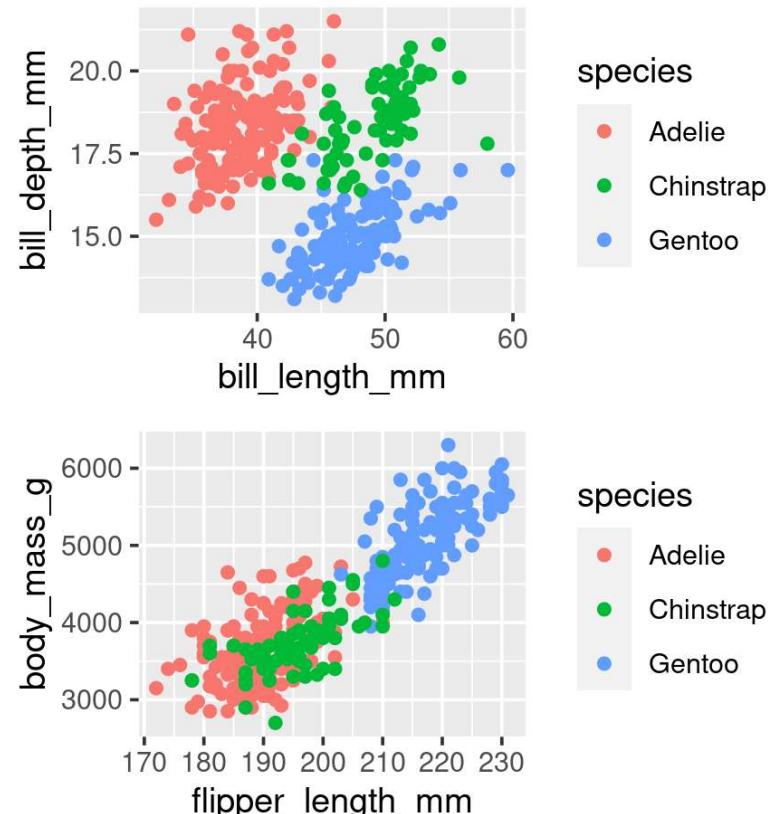
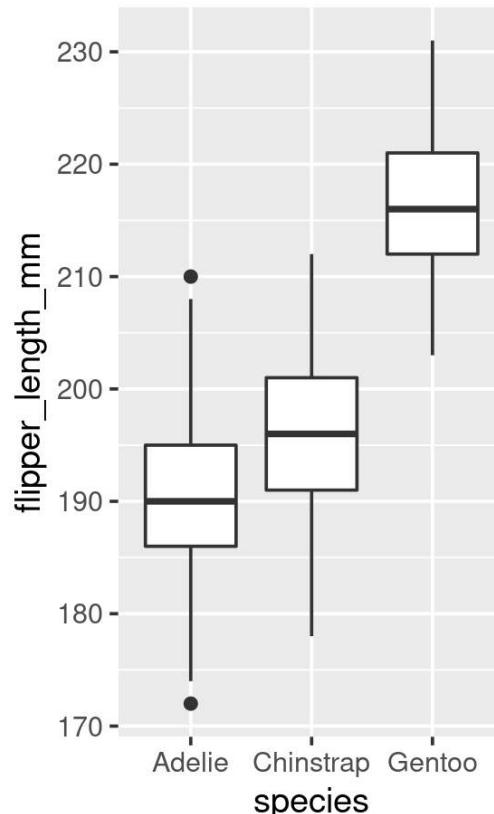
g1 / g2



Combining plots with patchwork

More complex arrangements

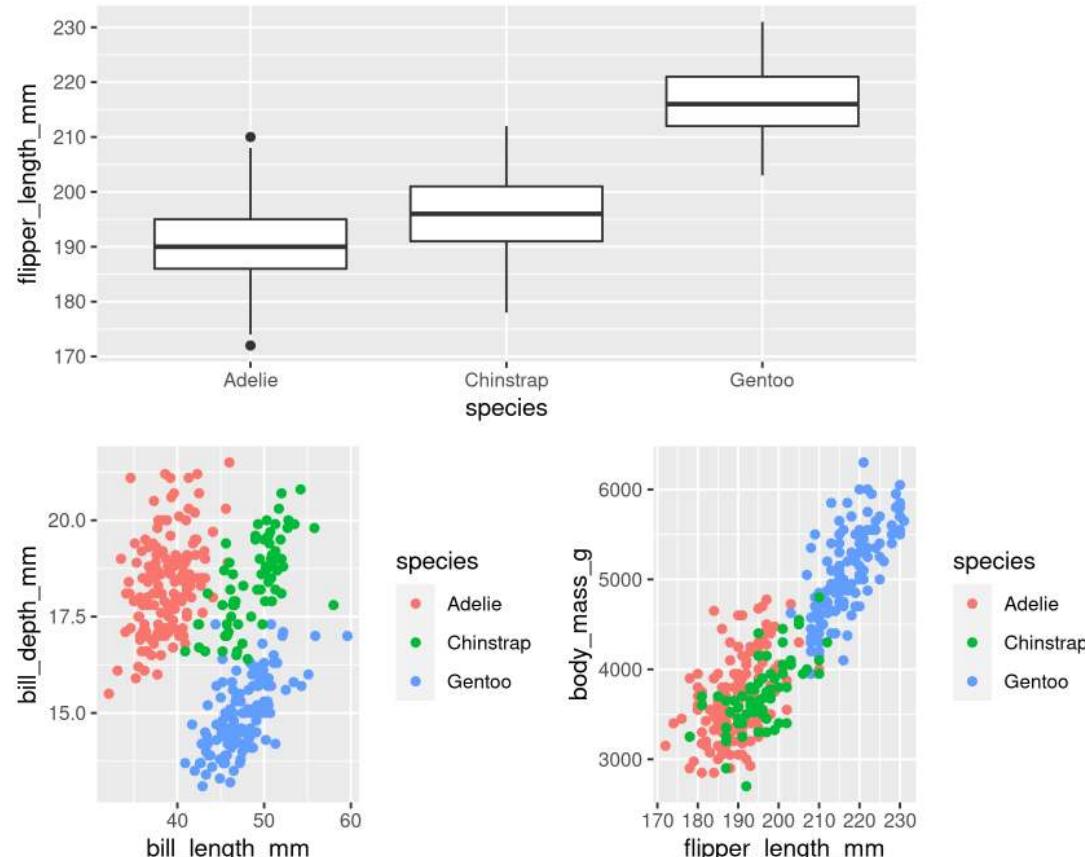
```
g2 + (g1 / g3)
```



Combining plots with patchwork

More complex arrangements

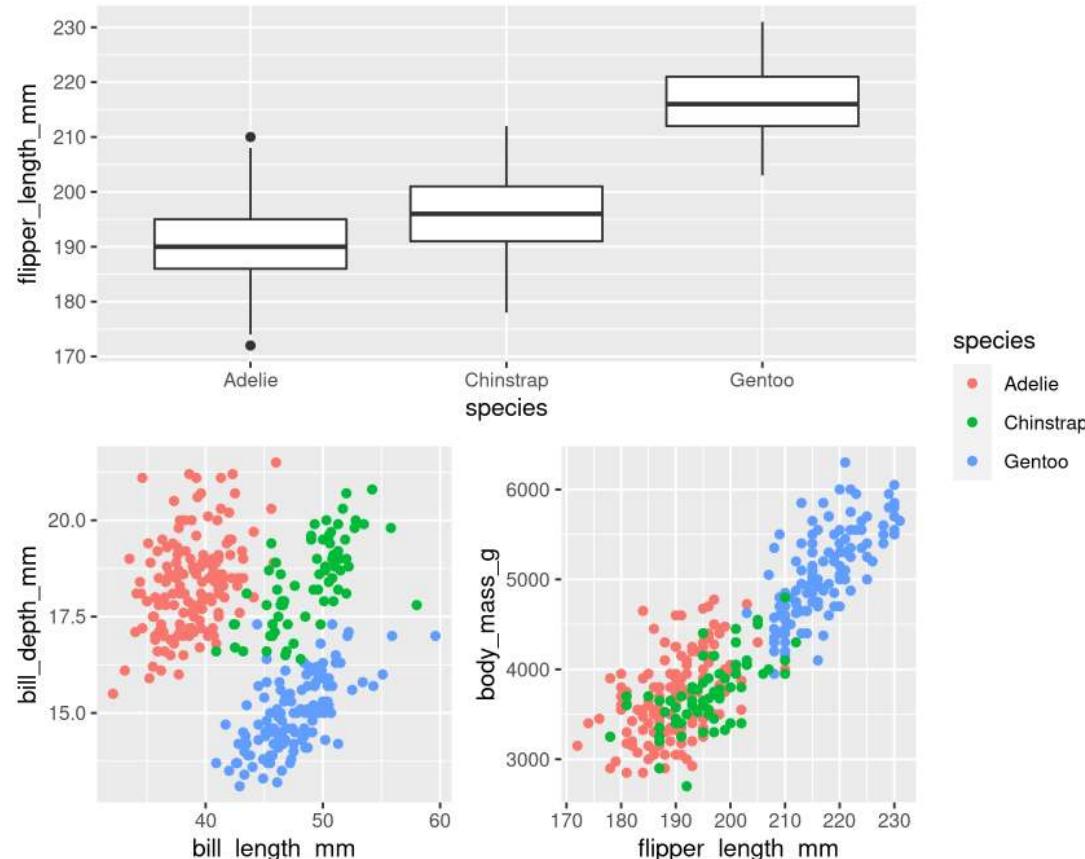
```
g2 / (g1 + g3)
```



Combining plots with patchwork

"collect" common legends

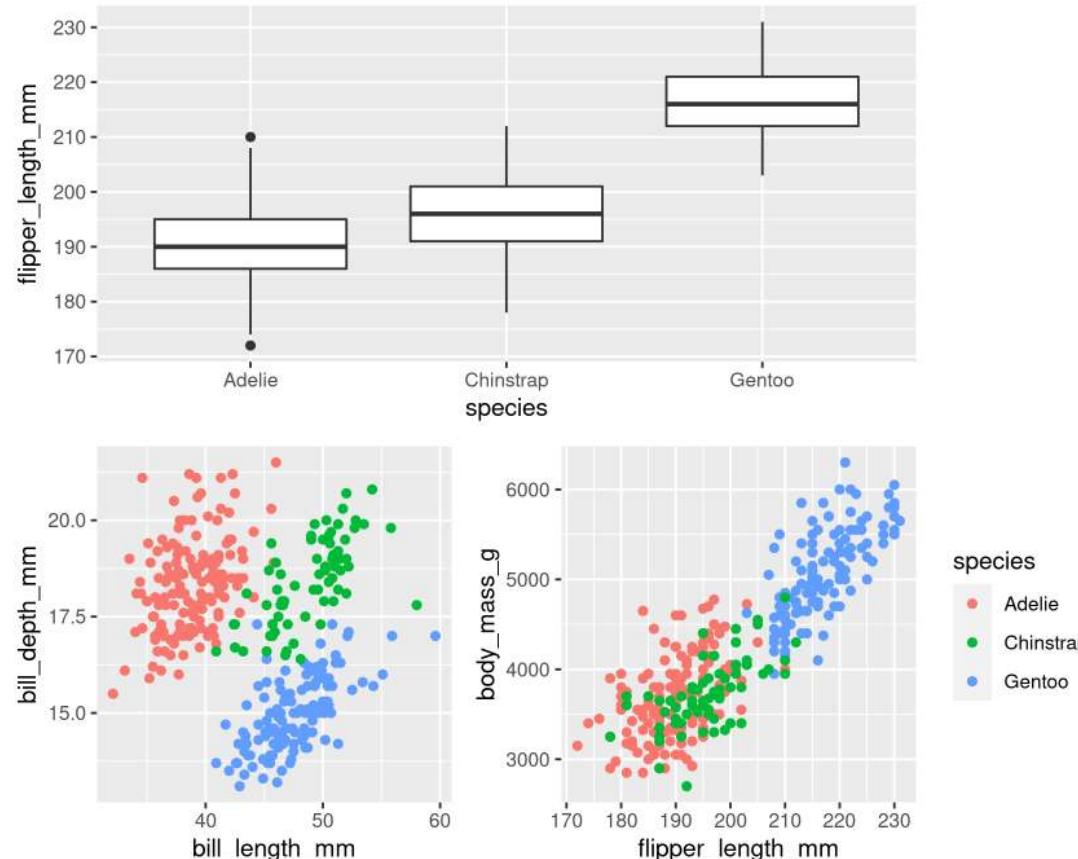
```
g2 / (g1 + g3) + plot_layout(guides = "collect")
```



Combining plots with patchwork

"collect" common legends

```
g2 / (g1 + g3 + plot_layout(guides = "collect"))
```



Combining plots with patchwork

Annotate

```
g2 / (g1 + g3) +
  plot_layout(guides = "collect") +
  plot_annotation(title = "Penguins Data Summary",
                  caption = "Fig 1. Penguins Data Summary",
                  tag_levels = "A",
                  tag_suffix = ")")
```

Penguins Data Summary

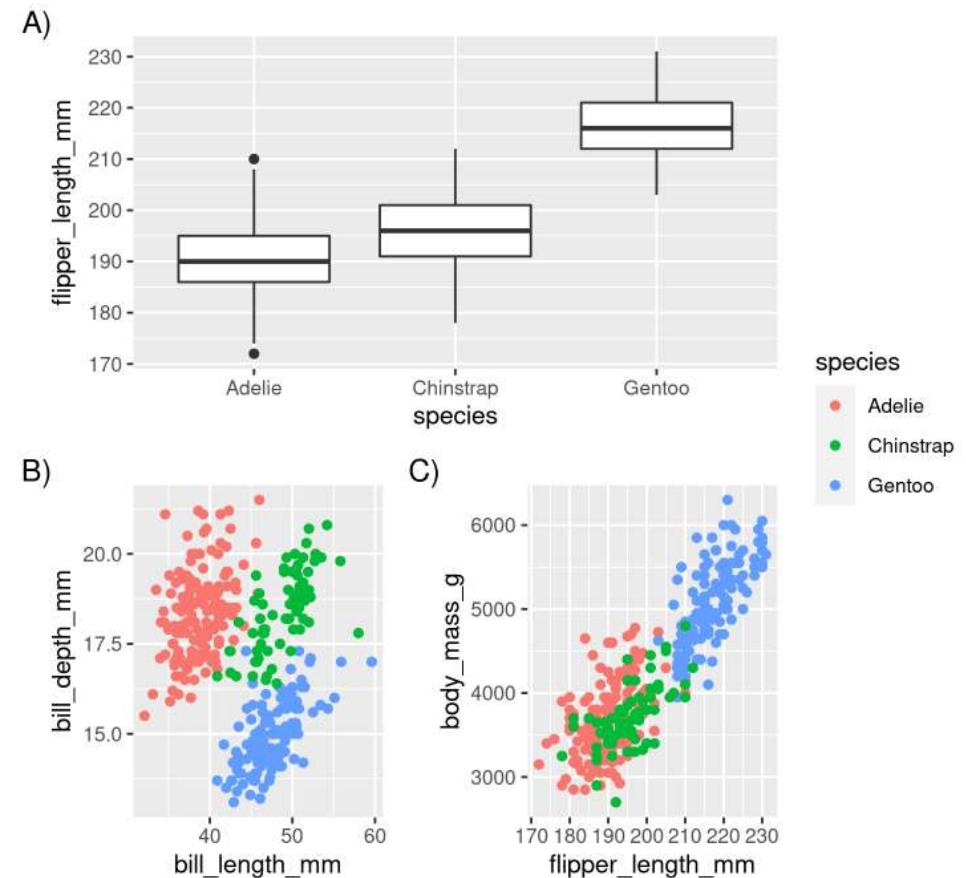


Fig 1. Penguins Data Summary

Combining plots with patchwork

Annotate

```
g2 / (g1 + g3) +  
  plot_layout(guides = "collect") +  
  plot_annotation(title = "Penguins Data Summary",  
                  caption = "Fig 1. Penguins Data Summary",  
                  tag_levels = "A",  
                  tag_suffix = ")")
```

Your Turn: Combine any 3 figures

Penguins Data Summary

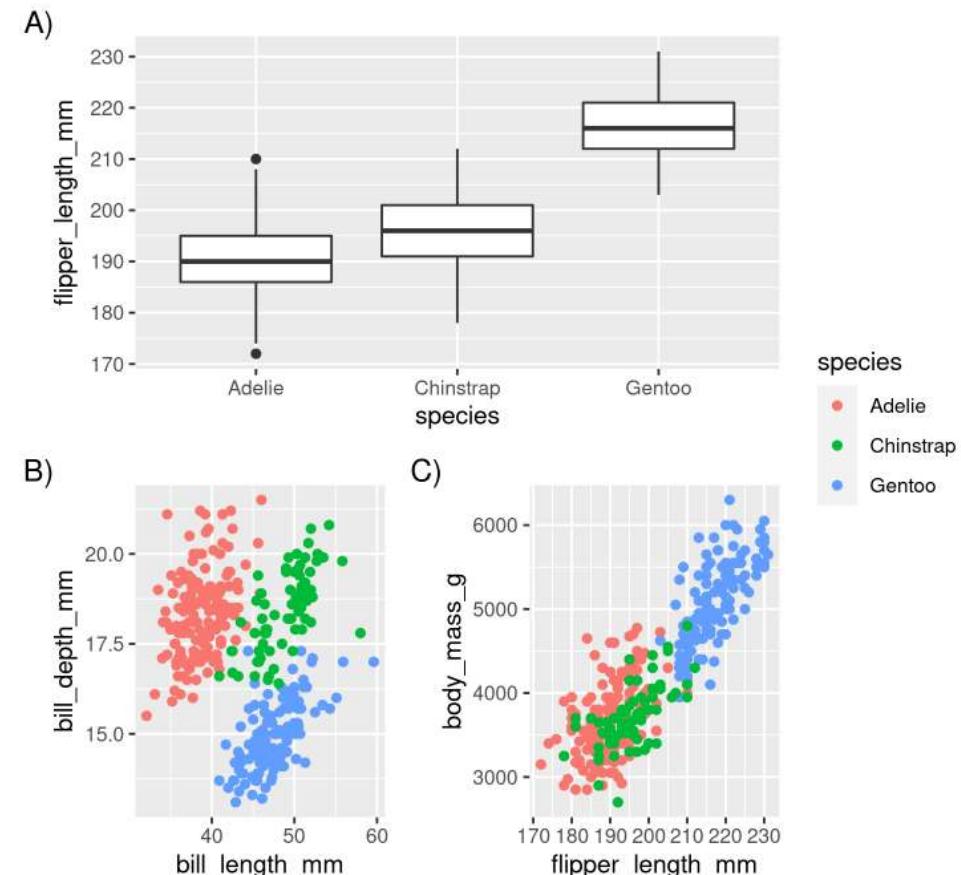


Fig 1. Penguins Data Summary

Saving plots

Saving plots

RStudio Export

Demo

Saving plots

RStudio Export

Demo

ggsave()

```
g <- ggplot(penguins, aes(x = sex, y = bill_length_mm, fill = year)) +  
  geom_boxplot()  
  
ggsave(filename = "penguins_mass.png", plot = g)
```

```
## Saving 6 x 3.9 in image
```

Saving plots

Publication quality plots

- Many publications require 'lossless' (pdf, svg, eps, ps) or high quality formats (tiff, png)
- Specific sizes corresponding to columns widths
- Minimum resolutions

```
g <- ggplot(penguins, aes(x = sex, y = body_mass_g)) +  
  geom_boxplot() +  
  labs(x = "Sex", y = "Body Mass (g)") +  
  theme(axis.text.x = element_text(angle = 45, hjust = 1))  
  
ggsave(filename = "penguins_mass.pdf", plot = g, dpi = 300,  
       height = 80, width = 129, units = "mm")
```

Wrapping up: Common mistakes

- The **package** is **ggplot2**, the function is just **ggplot()**
- Did you remember to put the **+** at the **end** of the line?
- Order matters! If you're using custom **theme()**'s, make sure you put these lines **after** bundled themes like **theme_bw()**, or they will be overwritten
- Variables like 'year' are treated as continuous, but are really categories
 - Wrap them in **factor()**, i.e. **ggplot(data = penguins, aes(x = factor(year), y = body_mass_g))**

Wrapping up: Common mistakes

I get an error regarding an object that can't be found or aesthetic length?

You are probably trying to plot two different datasets, and you make references to variables in the **ggplot()** call that don't exist in one of the datasets:

```
n <- count(penguins, island)

ggplot(data = penguins, aes(x = flipper_length_mm, y = bill_length_mm, colour = species)) +
  geom_point() +
  facet_wrap(~ island) +
  geom_text(data = n, aes(label = n),
            x = -Inf, y = +Inf, hjust = 0, vjust = 1)
```



```
## Error: Aesthetics must be either length 1 or the same as the data (3): colour
```

Wrapping up: Common mistakes

I get an error regarding an object that can't be found or aesthetic length?

Either move the aesthetic...

```
ggplot(penguins, aes(x = flipper_length_mm, y = bill_length_mm)) +  
  geom_point(aes(colour = species)) +  
  facet_wrap(~ island) +  
  geom_text(data = n, aes(label = n),  
            x = -Inf, y = +Inf, hjust = 0, vjust = 1)
```

Or assign it to NULL where it is missing...

```
ggplot(penguins, aes(x = flipper_length_mm, y = bill_length_mm, colour = species)) +  
  geom_point() +  
  facet_wrap(~ island) +  
  geom_text(data = n, aes(label = n, colour = NULL),  
            x = -Inf, y = +Inf, hjust = 0, vjust = 1)
```

Wrapping up: Further reading (all Free!)

- RStudio > Help > Cheatsheets > Data Visualization with ggplot2
- [**ggplot2 book v3**](#) by Hadley Wickham, Danielle Navarro, and Thomas Lin Pedersen
- [**R Graphics Cookbook**](#) by Winston Chang
- [**R for Data Science**](#) by Hadley Wickham and Garret Grolemund
 - [Chapter on Data Visualization](#)
- [**Data Visualization: A practical introduction**](#) by Kieran Healy
- [**patchwork website**](#)
- [**gridExtra Vignette: Arranging Multiple Grobs**](#)
 - Alternative to patchwork