

Creating Figures as an Intro to R

Using the **ggplot2** package

Steffi LaZerte



Artwork by [@allison_horst](#)

Introductions

Instructor

Dr. Steffi LaZerte

- Background in Biology (Animal Behaviour)
- Working with R since 2007
- Professional R programmer/consultant since 2017



Introductions

Assistant

Dr. Alex Koiter

- Physical Geographer
- Working with R since 2010
- Assistant Professor in Geography and Environment, Brandon University



What about you?

- Name
- Background (Area of study, etc.)
- Familiarity with R (or other programming languages)
 - I've heard of R
 - I've used R
 - I use R all the time

Outline

1. A little about R

2. Creating figures with `ggplot2`

3. Combining figures with `patchwork`

4. Saving figures

Outline

1. A little about R

2. Creating figures with `ggplot2`

3. Combining figures with `patchwork`

4. Saving figures

Taken this or a similar workshop before?

During activities consider...

- Extra activities labeled "Too Easy?"
- Using your own data
- Exploring other aspects of `ggplot2` that interest you

Feel free to ask questions even if it's not the "official" activity!

What is R?

R is Programming language

A programming **language** is a way to give instructions in order to get a computer to do something

- You need to know the language (i.e., the code)
- Computers don't know what you mean, only what you type (unfortunately)
- Spelling, punctuation, and capitalization all matter!

For example

R, what is 56 times 5.8?

```
56 * 5.8
```

```
## [1] 324.8
```

Use code to tell R what to do

R, what is the average of numbers 1, 2, 3, 4?

```
mean(c(1, 2, 3, 4))
```

```
## [1] 2.5
```

Use code to tell R what to do

R, what is the average of numbers 1, 2, 3, 4?

```
mean(c(1, 2, 3, 4))
```

```
## [1] 2.5
```

R, save this value for later

```
steffis_mean <- mean(c(1, 2, 3, 4))
```

Use code to tell R what to do

R, what is the average of numbers 1, 2, 3, 4?

```
mean(c(1, 2, 3, 4))
```

```
## [1] 2.5
```

R, save this value for later

```
steffis_mean <- mean(c(1, 2, 3, 4))
```

R, multiply this value by 6

```
steffis_mean * 6
```

```
## [1] 15
```

Why R?

R is hard

```
# Get in circle around city
circle <- data.frame()
cutoff <- 10
for(i in unique(gps$region)) {
  n <- nrow(gps[gps$region == i,]) ##number of IDs
  if(i == "wil") tmp <- geocode("Williams Lake, Canada")
  if(i == "kam") tmp <- geocode("Kamloops, Canada")
  if(i == "kel") tmp <- geocode("Kelowna, Canada")
  temp <- data.frame()
  for(a in 1:n){
    if(a <= cutoff) temp <- rbind(temp, gcDestination(lon = tmp$lon,
                                                       lat = tmp$lat,
                                                       bearing = (a*(360/(cutoff))-360/(cutoff)),
                                                       dist = 20,
                                                       dist.units = "km",
                                                       model = "WGS84"))
    if(a > cutoff) temp <- rbind(temp, gcDestination(lon = tmp$lon,
                                                       lat = tmp$lat,
                                                       bearing = ((a-cutoff)*(360/(max(table(gps$region
)))-10))-360/(max(table(gps$region))-cutoff)),
                                                       dist = 35,
                                                       dist.units = "km",
                                                       model = "WGS84"))
  }
  circle <- rbind(circle, cbind(temp,
                                 region = i,
                                 hab = gps$hab[gps$region == i],
                                 spl = gps$spl.orig[gps$region == i],
                                 lon = tmp$lon,
                                 lat = tmp$lat)))
}
circle
```

Why R?

But R is powerful (and reproducible)!

The screenshot shows the R Global Environment window. It has three main sections: Data, Values, and Functions. The Data section contains two entries: 'fish' and 'telem_total'. The 'fish' entry shows '172 obs. of 13 variables'. The 'telem_total' entry shows '12950046 obs. of 10 variables'. A large green oval highlights the 'telem_total' entry. The Values section contains one entry: 'tz' with the value '"Etc/GMT+8"'. The Functions section contains one entry: 'load_data' with the definition 'function (x)'.

Global Environment		
<input type="button" value="Search"/>		
Data		
 fish	172 obs. of 13 variables	
 telem_total	12950046 obs. of 10 variables	
Values		
tz	"Etc/GMT+8"	
Functions		
load_data	function (x)	

Why R?

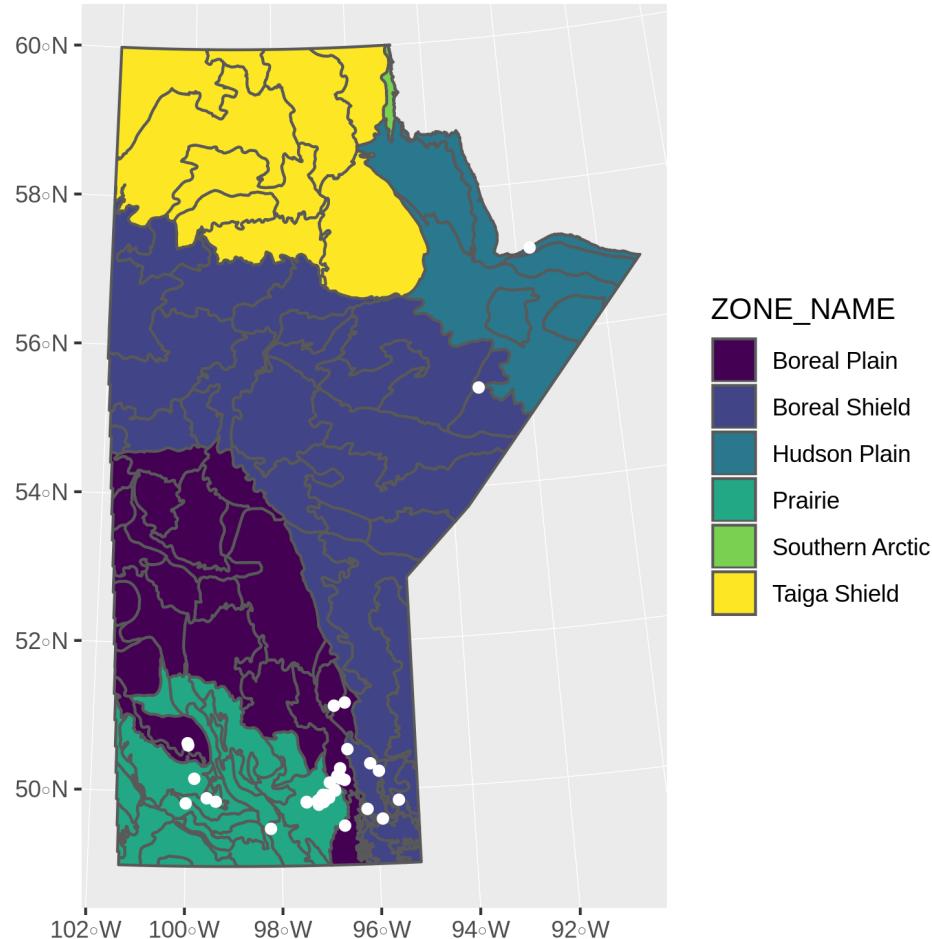
But R is powerful (and reproducible)!

The screenshot shows the R Global Environment window. It has three main sections: Data, Values, and Functions. The Data section contains two entries: 'fish' and 'telem_total'. The 'fish' entry shows '172 obs. of 13 variables'. The 'telem_total' entry shows '12950046 obs. of 10 variables'. A large green oval highlights the 'telem_total' entry. The Values section contains one entry: 'tz' with the value '"Etc/GMT+8"'. The Functions section contains one entry: 'load_data' with the definition 'function (x)'.

Global Environment	
Data	
 fish	172 obs. of 13 variables
 telem_total	12950046 obs. of 10 variables
Values	
tz	"Etc/GMT+8"
Functions	
load_data	function (x)

Why R?

R is also beautiful



Why R?

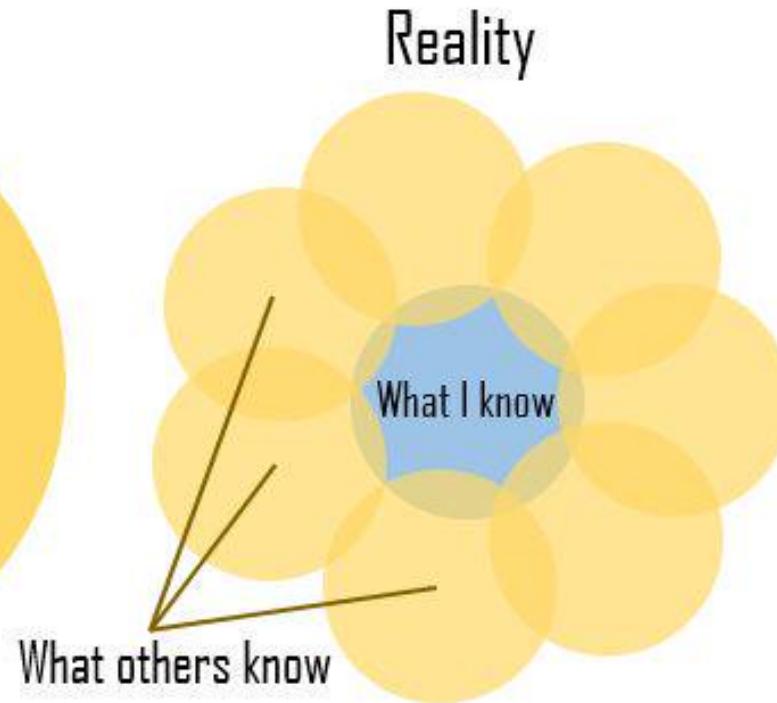
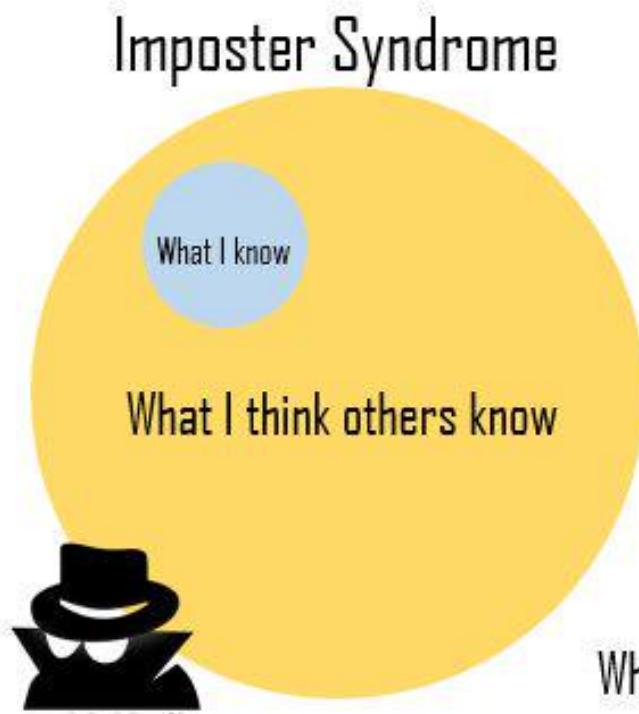
R is affordable (i.e., free!)

R is available as Free Software under the terms of the [Free Software Foundation's GNU General Public License](#) in source code form. It compiles and runs on a wide variety of UNIX platforms and similar systems (including FreeBSD and Linux), Windows and MacOS.

ImpostR Syndrome

ImpostR
Syndrome

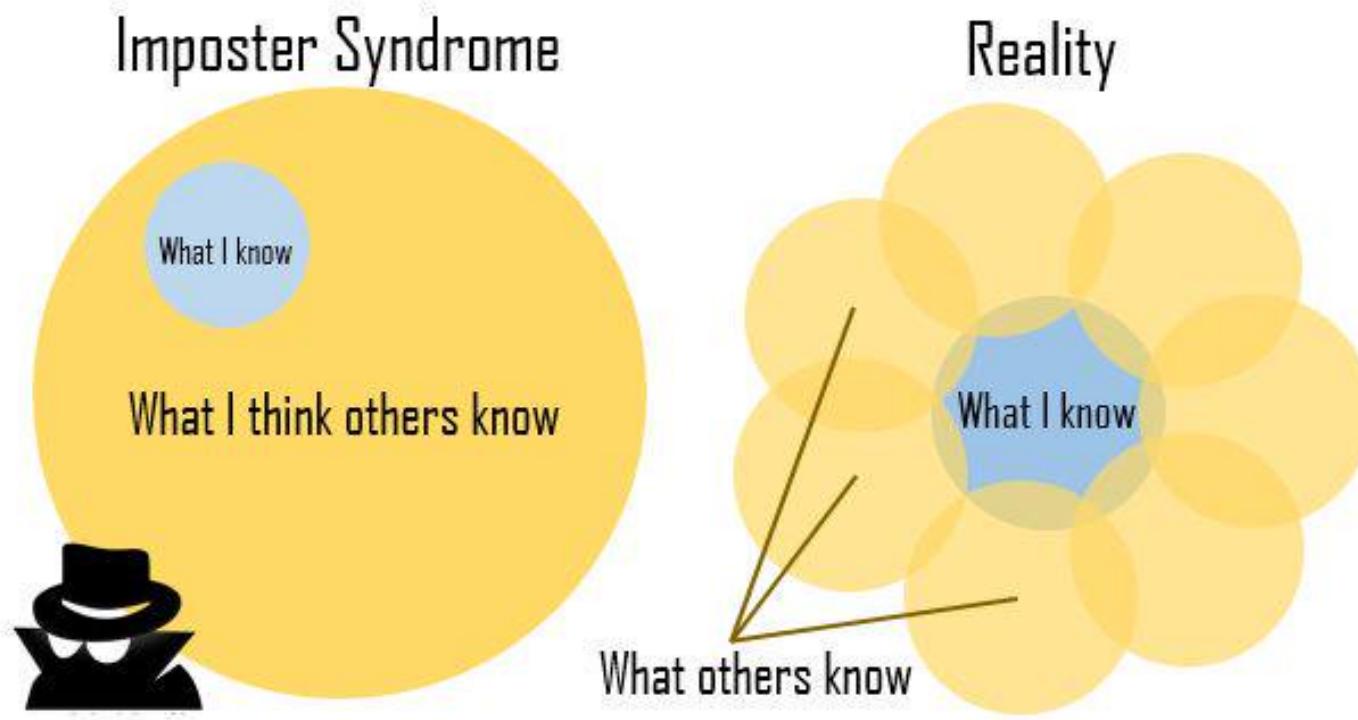
ImpostR Syndrome



David Whittaker

ImpostR
Syndrome

ImpostR Syndrome



David Whittaker

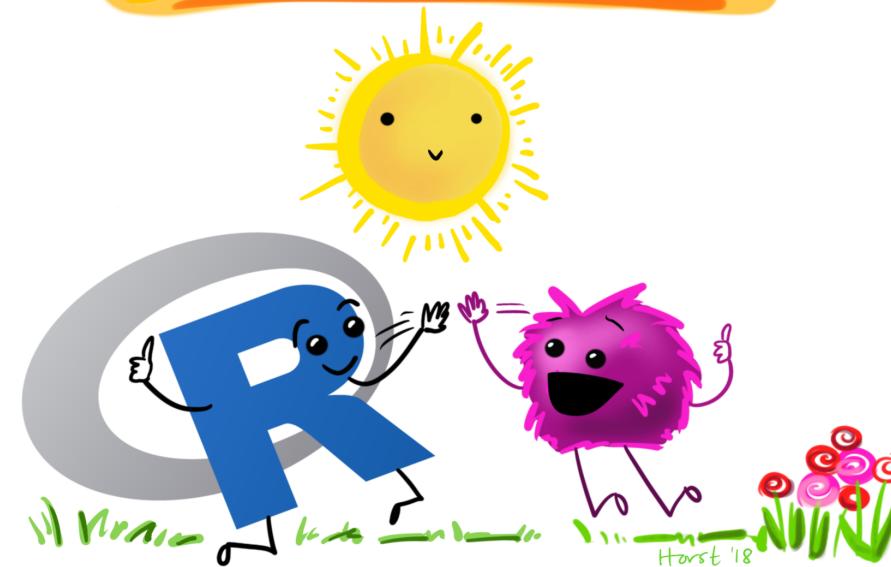
Impost^R
Syndrome

Moral of the story?

Make friends, code in groups, learn together and don't beat yourself up



...but now it's like...



About R

Code, Output, Scripts

Code

- The actual commands

Output

- The result of running code or a script

Script

- A text file full of code that you want to run
- You should always keep your code in a script

Code, Output, Scripts

Code

- The actual commands

Output

- The result of running code or a script

Script

- A text file full of code that you want to run
- You should always keep your code in a script

For example:

```
mean(c(1, 2, 3, 4))
```

Code

```
## [1] 2.5
```

Output

```
4_analysis.R x
15 #! # Setup
16 ## @knitr setup
17 library(tidyverse)
18 library(stringr)
19 library(gridExtra)
20 library(grid)
21 library(boot)
22
23 theme_cust <- theme_bw() +
24   theme(panel.grid = element_blank())
25
26 #' Load data
27 d <- read_csv("../Data/Datasets/pca.csv") %>%
28   mutate(hab_c = ifelse(hab > 0, "Urban", "Rural"))
29
30 summary(d$hab)
31
32 #' # Plotting
33 d_sum <- d %>%
34   group_by(hab_c) %>%
35   summarize(prop = sum(atypical_c) / length(atypical_c))
36
37 d_n <- count(d, atypical_c, hab_c)
38
39 #' # Sample sizes
40 ## @knitr sample_size
41 count(d, hab_c)
42 count(d, atypical_c)
43 count(d, lowhigh, monotone, freq_sweep)
44
45 count(d, region)
46 count(d, project = ifelse(str_detect(id, "MC[BC]{1}[0-9]{2}"), "Steffi",
```

Script

RStudio vs. R



RStudio



R

- **RStudio** is not **R**
- RStudio is a User Interface or IDE (integrated development environment)
 - (i.e., Makes coding simpler)

functions() - Do things, Return things

mean(), read_csv(), ggplot(), c(), etc.

functions() - Do things, Return things

`mean()`, `read_csv()`, `ggplot()`, `c()`, etc.

- Always have ()
- Can take **arguments** (think 'options')
 - `mean(x = c(2, 10, 45))`,
 - `mean(x = c(NA, 10, 2, 65), na.rm = TRUE)`

functions() - Do things, Return things

`mean()`, `read_csv()`, `ggplot()`, `c()`, etc.

- Always have ()
- Can take **arguments** (think 'options')
 - `mean(x = c(2, 10, 45))`,
 - `mean(x = c(NA, 10, 2, 65), na.rm = TRUE)`
- Arguments defined by **name** or by **position**
- With correct position, do not need to specify by name

By name:

```
mean(x = c(1, 5, 10))
```

```
## [1] 5.333333
```

By position:

```
mean(c(1, 5, 10))
```

```
## [1] 5.333333
```

R documentation

?mean

R documentation

?mean

mean {base}

R Documentation

Arithmetic Mean

Description

Generic function for the (trimmed) arithmetic mean.

Usage

```
mean(x, ...)  
## Default S3 method:  
mean(x, trim = 0, na.rm = FALSE, ...)
```

Arguments

- x An R object. Currently there are methods for numeric/logical vectors and [date](#), [date-time](#) and [time interval](#) objects. Complex vectors are allowed for trim = 0, only.
- trim the fraction (0 to 0.5) of observations to be trimmed from each end of x before the mean is computed. Values of trim outside that range are taken as the nearest endpoint.
- na.rm a logical value indicating whether NA values should be stripped before the computation proceeds.
- ... further arguments passed to or from other methods.

Data

Generally kept in **vectors** or **data.frames**

- These are objects with names (like functions)
- We can use `<-` to assign values to objects (assignment)

Vector (1 dimension)

```
my_data <- c("a", 100, "c")
my_data
## [1] "a"   "100" "c"
```

Data frame (2 dimensions)

```
my_data <- data.frame(site = c("s1", "s2", "s3"),
                      count = c(101, 102, 103),
                      treatment = c("a", "b", "c"))
my_data
```

```
##   site count treatment
## 1   s1    101         a
## 2   s2    102         b
## 3   s3    103         c
```

rows X
columns

Your first *real* code!

First Code

```
# First load the packages  
library(palmerpenguins)  
library(ggplot2)  
  
# Now create the figure  
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point()
```

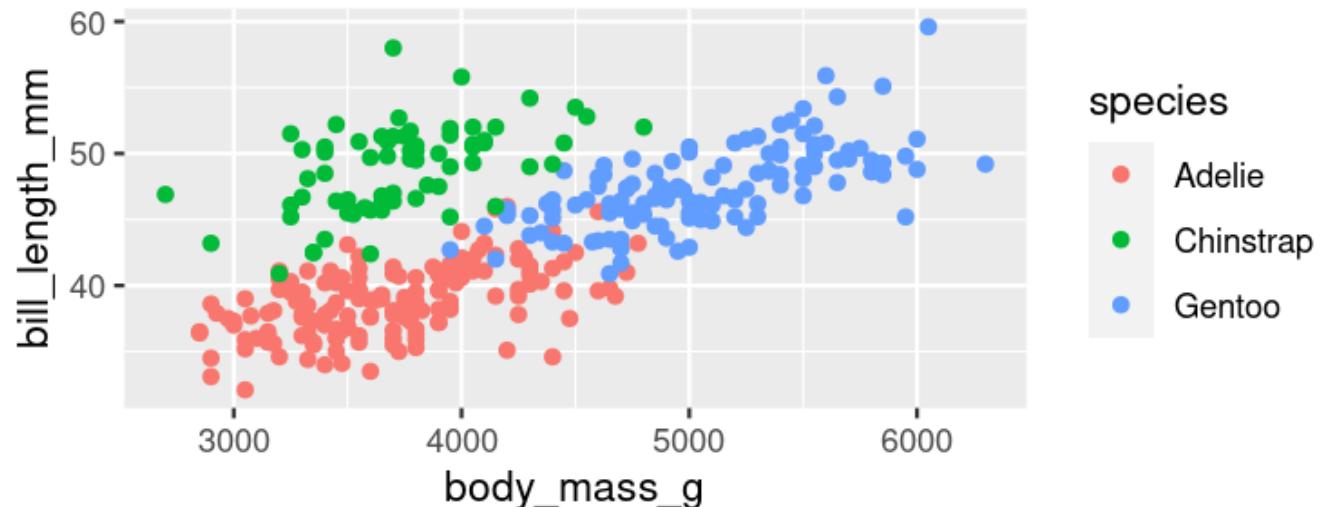
- Copy/paste or type this into the script window in RStudio
 - You may have to go to File > New File > R Script
- Click anywhere on the first line of code
- Use the 'Run' button to run this code, **or** use the short-cut **Ctrl-Enter**
 - Repeat until all the code has run

First Code

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library(palmerpenguins)
library(ggplot2)

# Now create the figure
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +
  geom_point()
```

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



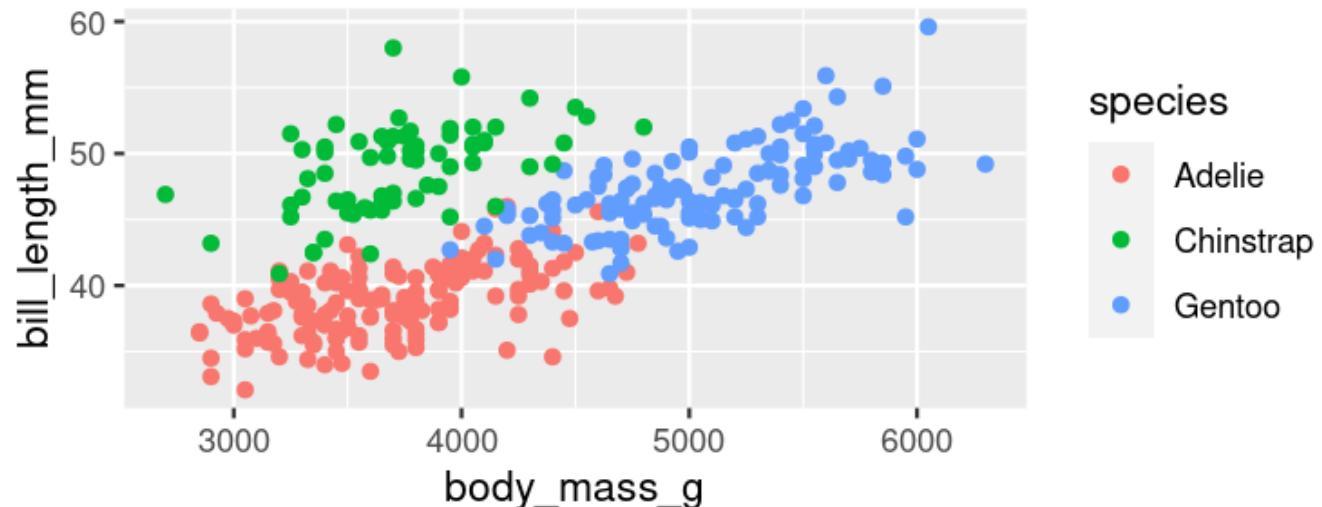
First Code

```
# First load the packages  
library(palmerpenguins)  
library(ggplot2)
```

Packages
ggplot2 and **palmerpenguins**

```
# Now create the figure  
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point()
```

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```



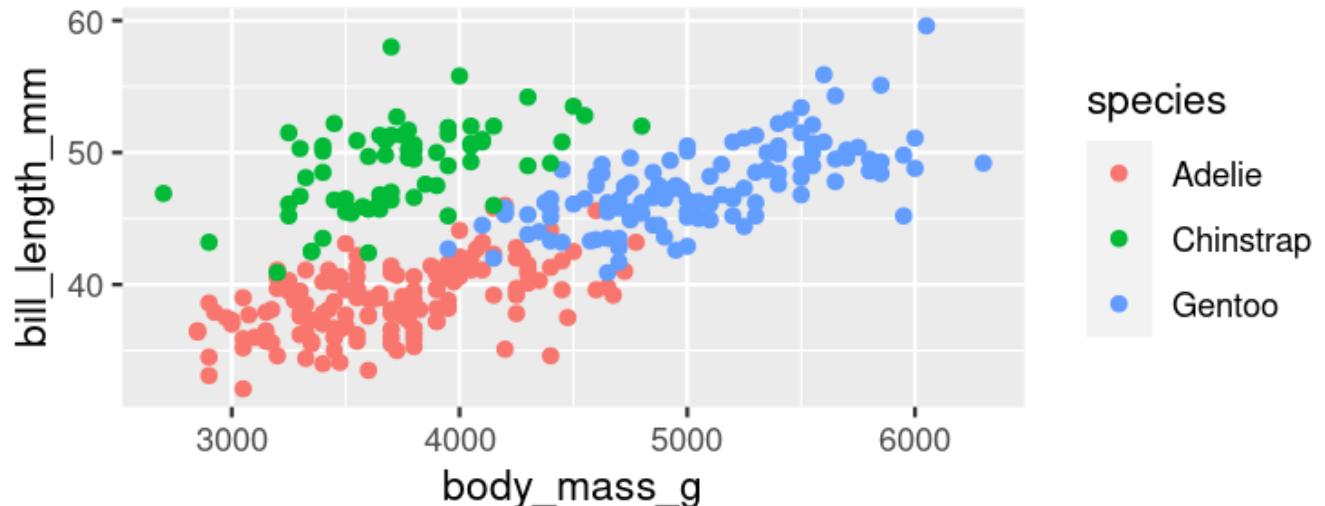
First Code

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```

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

Functions:
library(), **ggplot()**
aes(), and **geom_point()**



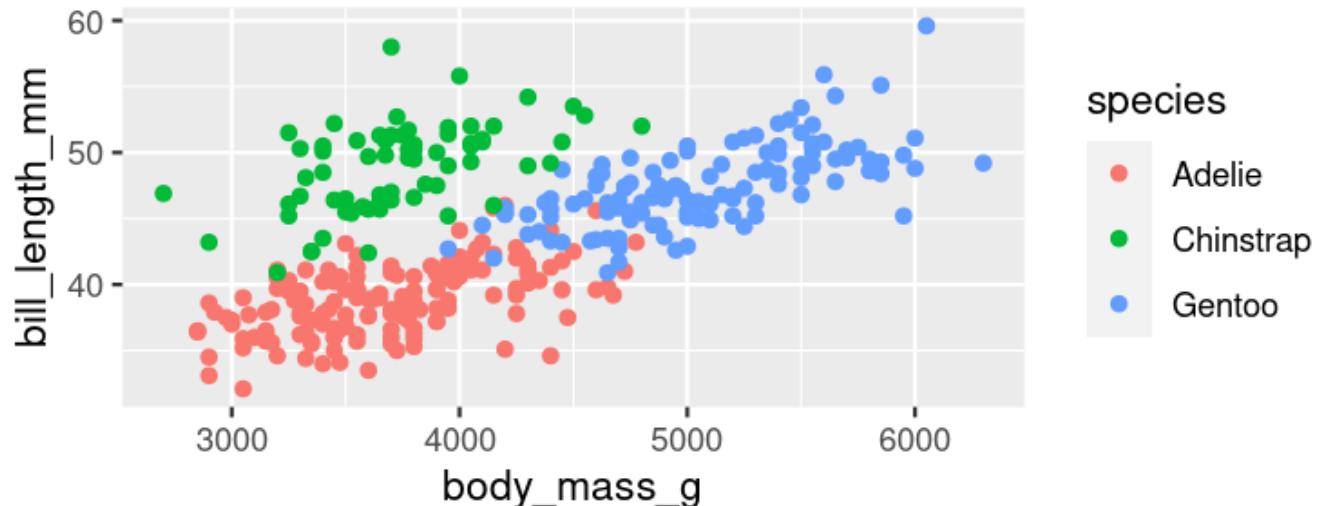
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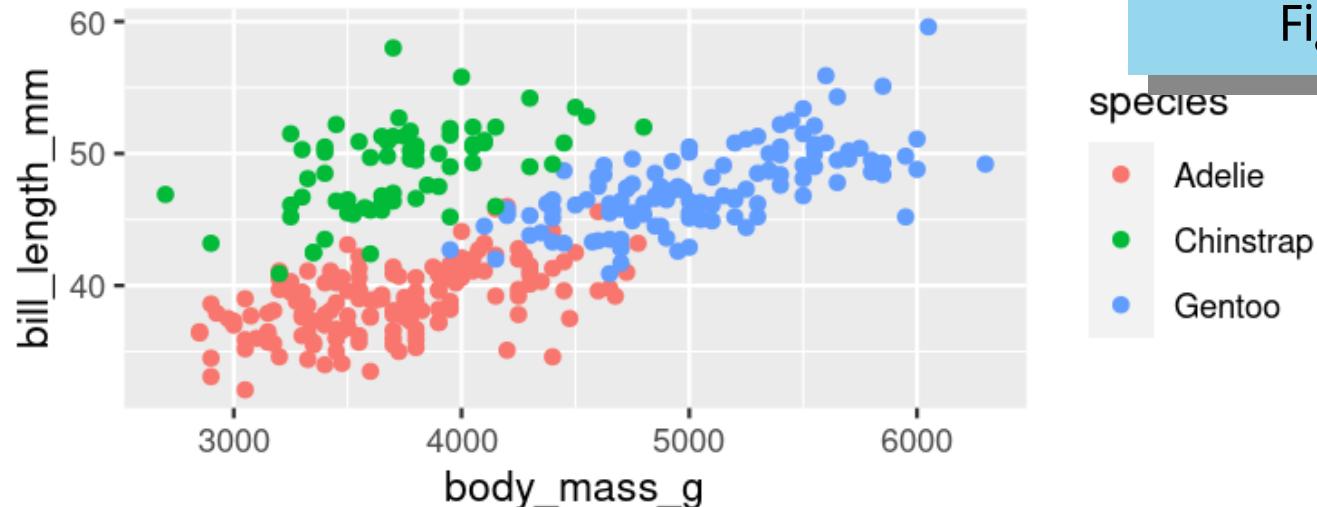
+
(Specific to **ggplot2**)



First Code

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# First load the packages  
library(palmerpenguins)  
library(ggplot2)  
  
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ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point()
```

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



Figure!

species

- Adelie
- Chinstrap
- Gentoo

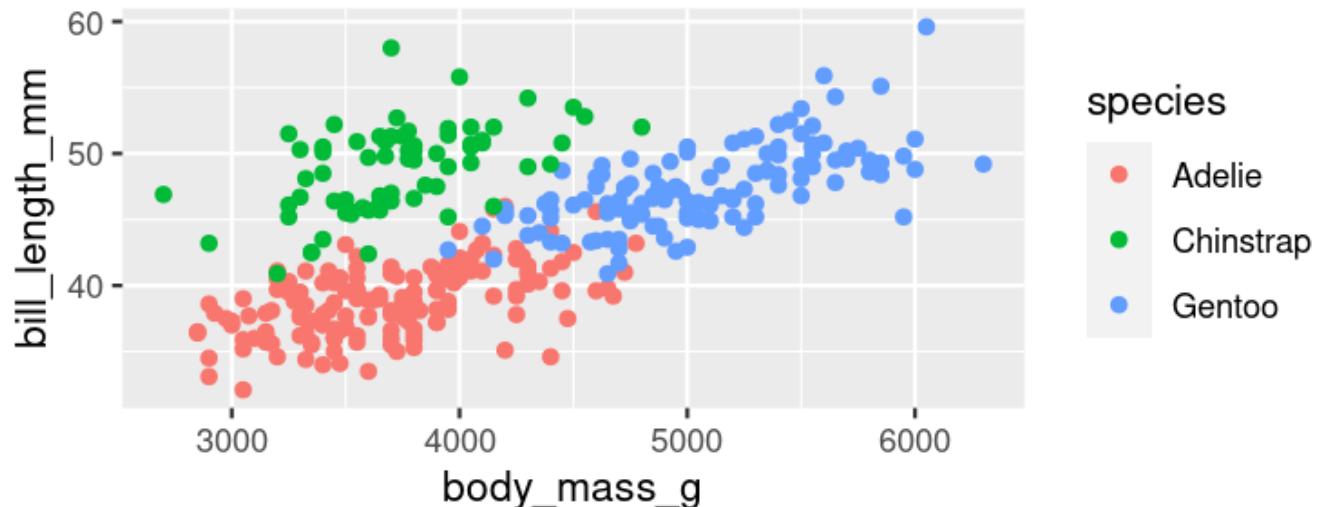
First Code

```
# First load the packages
library(palmerpenguins)
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# Now create the figure
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +
  geom_point()

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

Warning



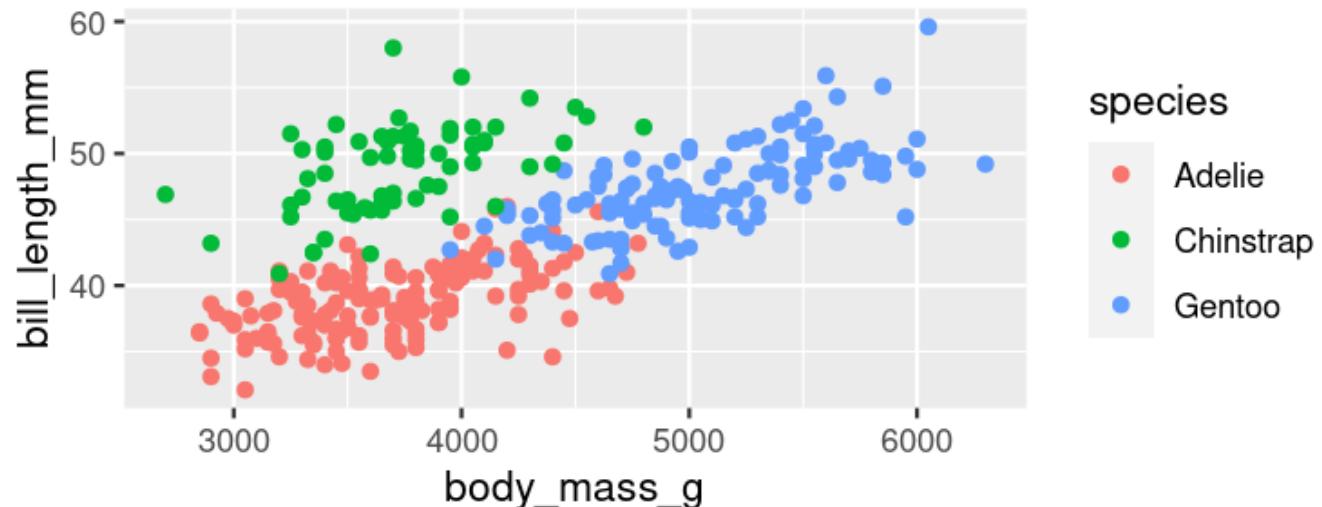
First Code

```
# First load the packages  
library(palmerpenguins)  
library(ggplot2)
```

Comments

```
# Now create the figure  
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point()
```

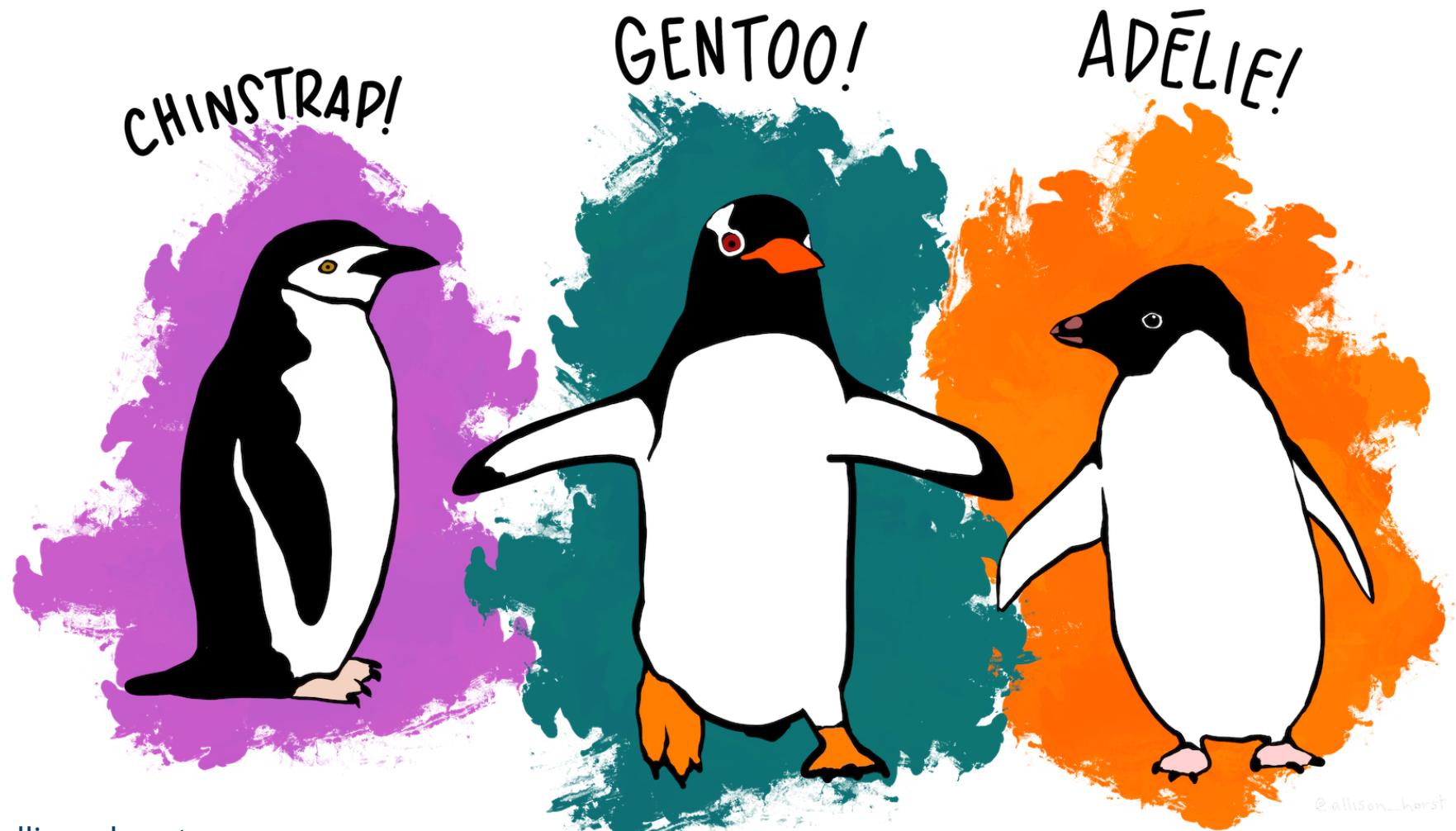
```
## Warning: Removed 2 rows containing missing values (geom_point).
```



Now you know R!

Let's get started

Our data set: Palmer Penguins!



Artwork by [@allison_horst](#)

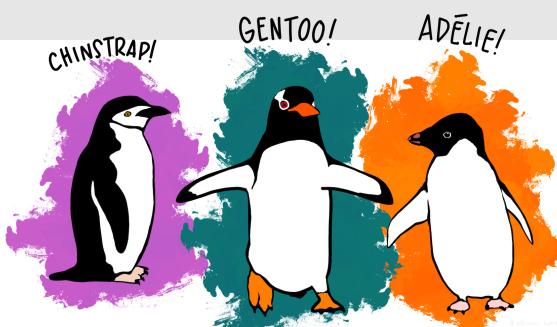
@allison_horst

Our data set: Palmer Penguins!



```
library(palmerpenguins)  
penguins
```

```
## # A tibble: 344 x 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  
## 9 Adelie  Torgersen     34.1             18.1              193       3475 <NA> 2007  
## 10 Adelie Torgersen      42               20.2              190       4250 <NA> 2007  
## # ... with 334 more rows
```



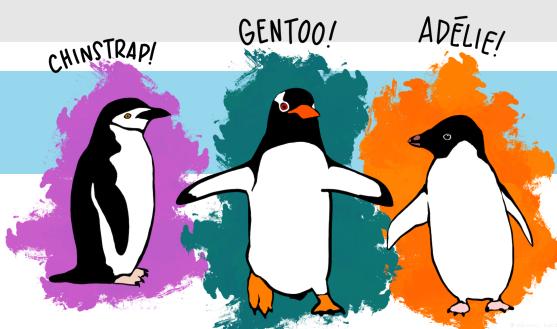


Our data set: Palmer Penguins!

```
library(palmerpenguins)  
penguins
```

```
## # A tibble: 344 x 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  
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## # ... with 334 more rows
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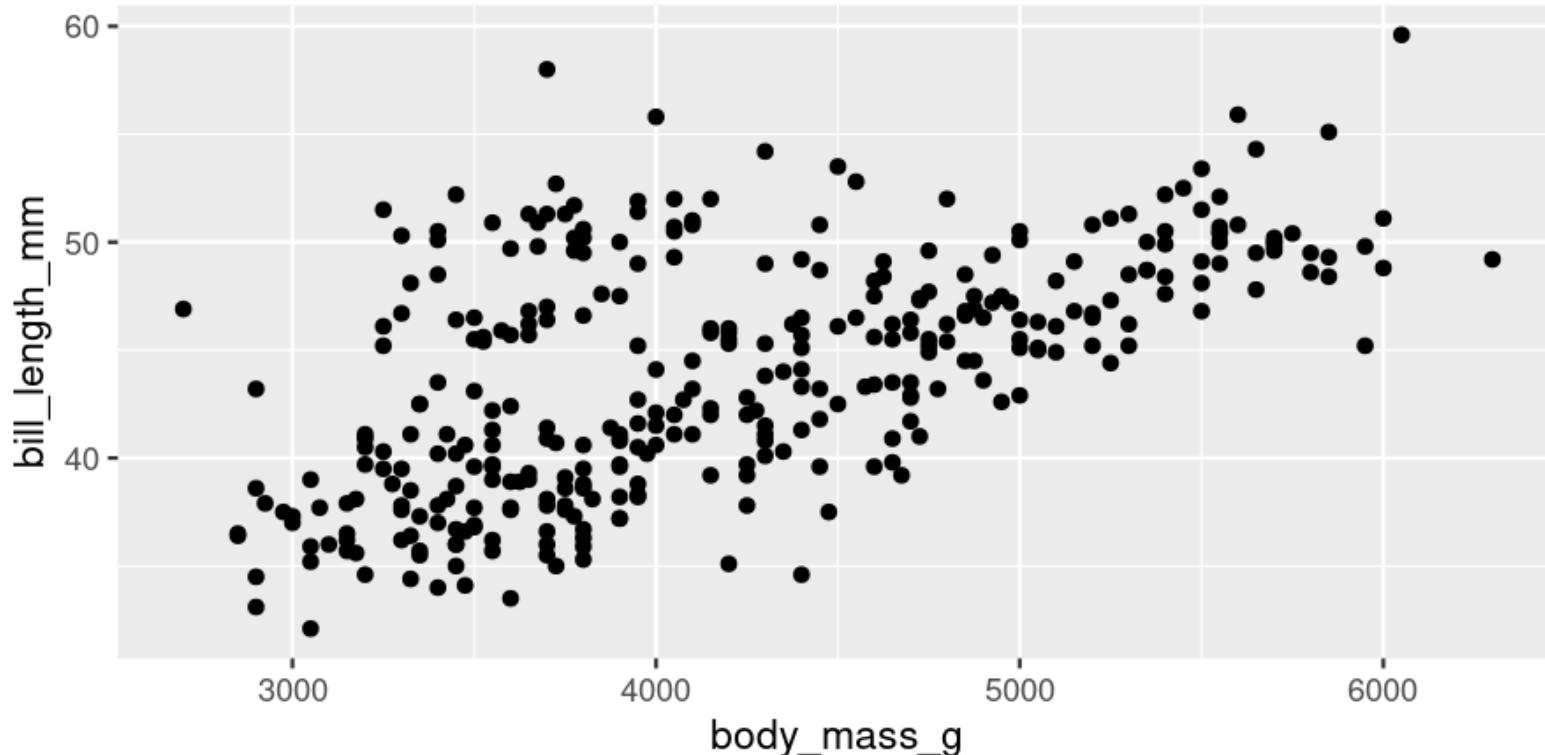
Your turn! Run this code and look at the output in the console



A basic plot

```
library(palmerpenguins)
library(ggplot2)

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



Break it down

```
library(palmerpenguins)
library(ggplot2)

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(ggplot2)

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

library(ggplot2)

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

Break it down

```
library(palmerpenguins)
library(ggplot2)

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(ggplot2)

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

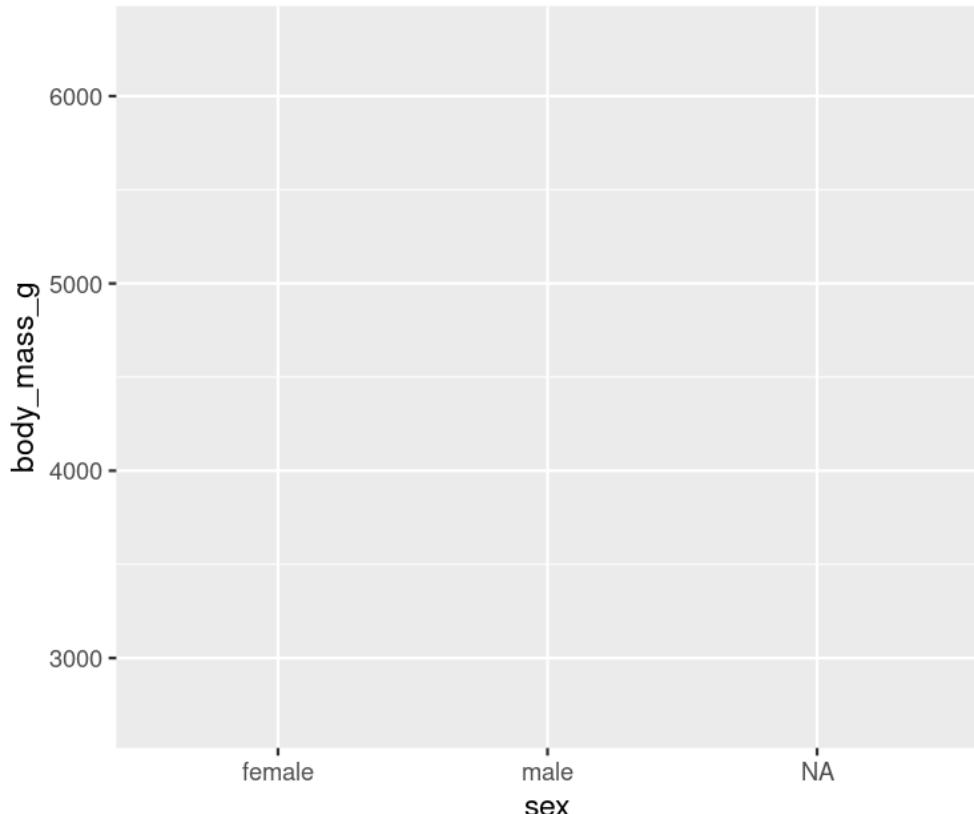
geom_point()

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

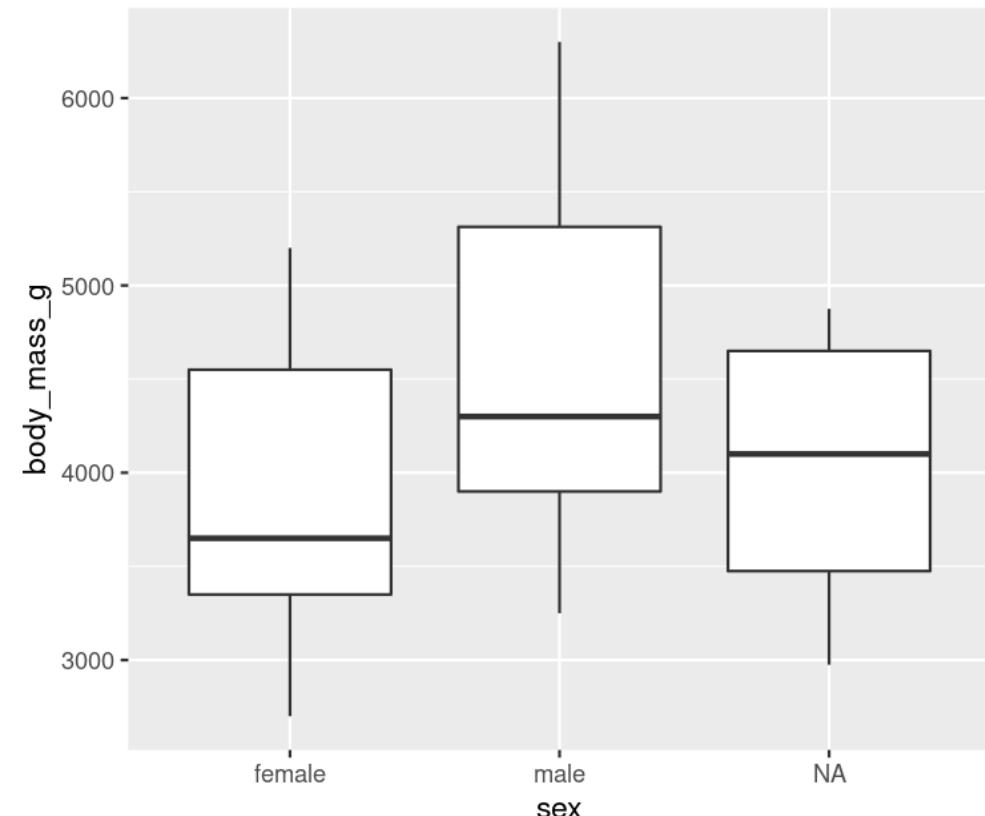
ggplots are essentially layered objects, starting with a call to **ggplot()**

Plots are layered

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

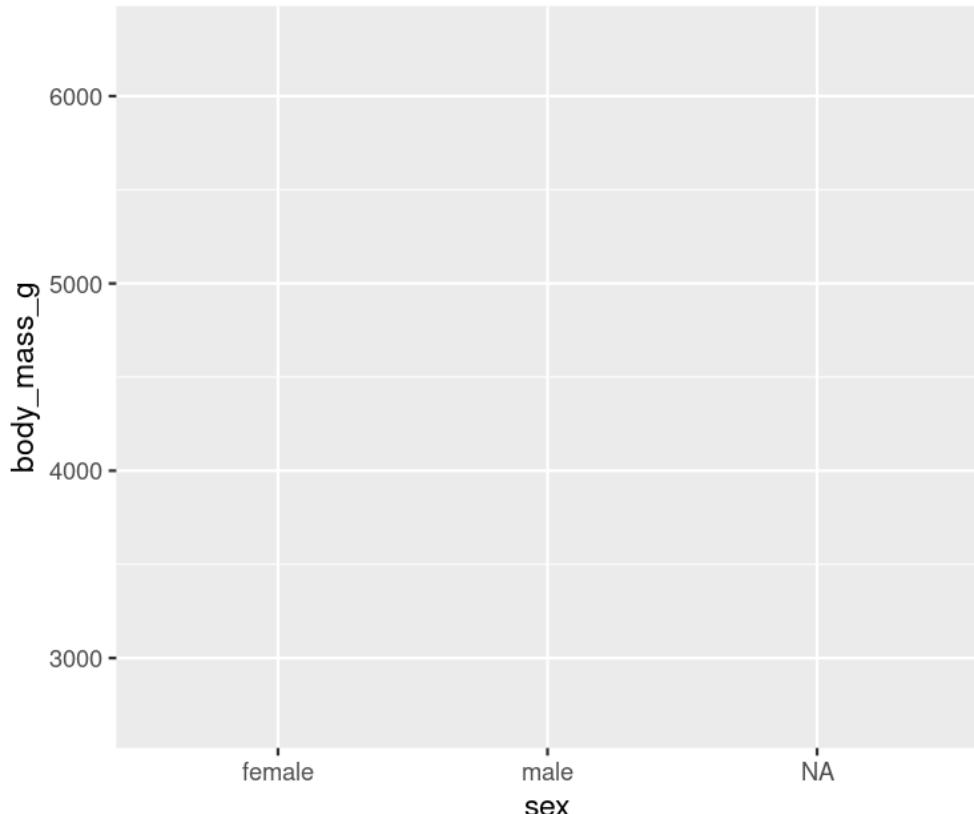


```
ggplot(data = penguins, aes(x = sex, y =  
body_mass_g)) +  
  geom_boxplot()
```

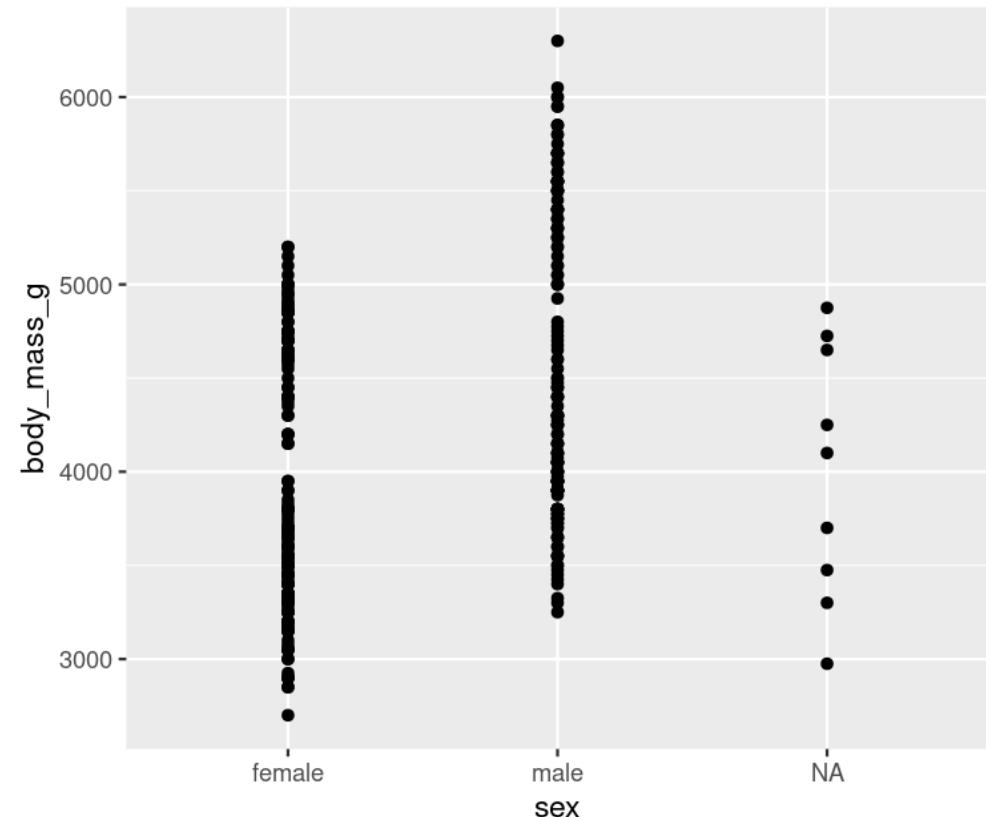


Plots are layered

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

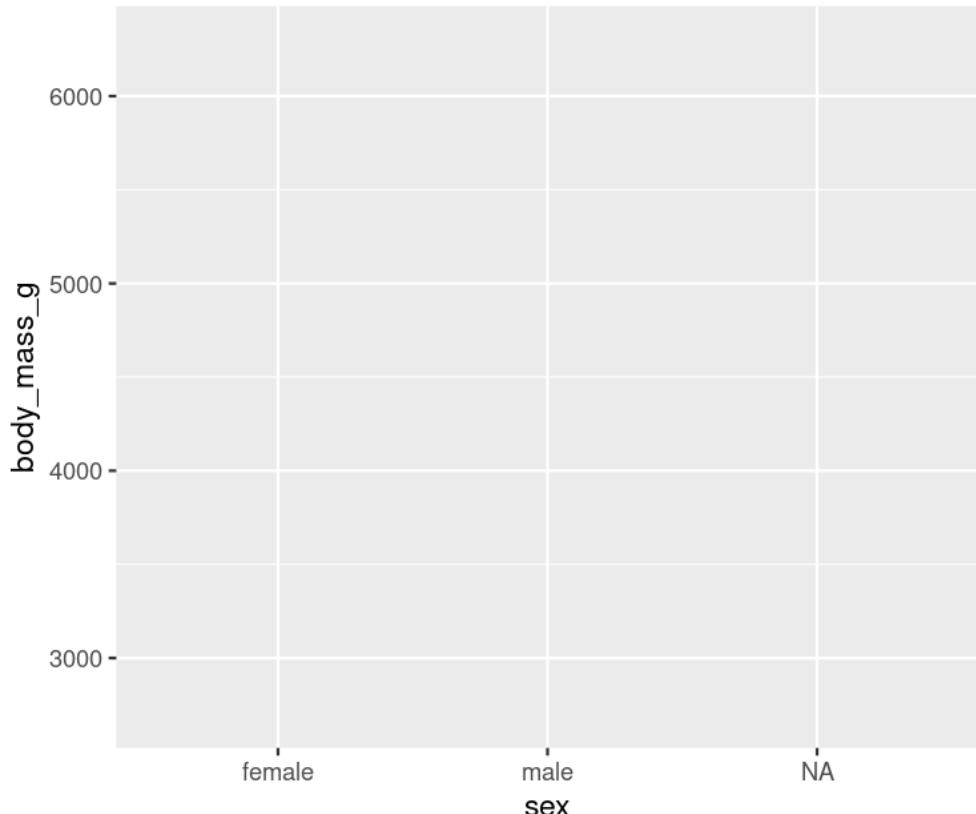


```
ggplot(data = penguins, aes(x = sex, y =  
body_mass_g)) +  
  geom_point()
```

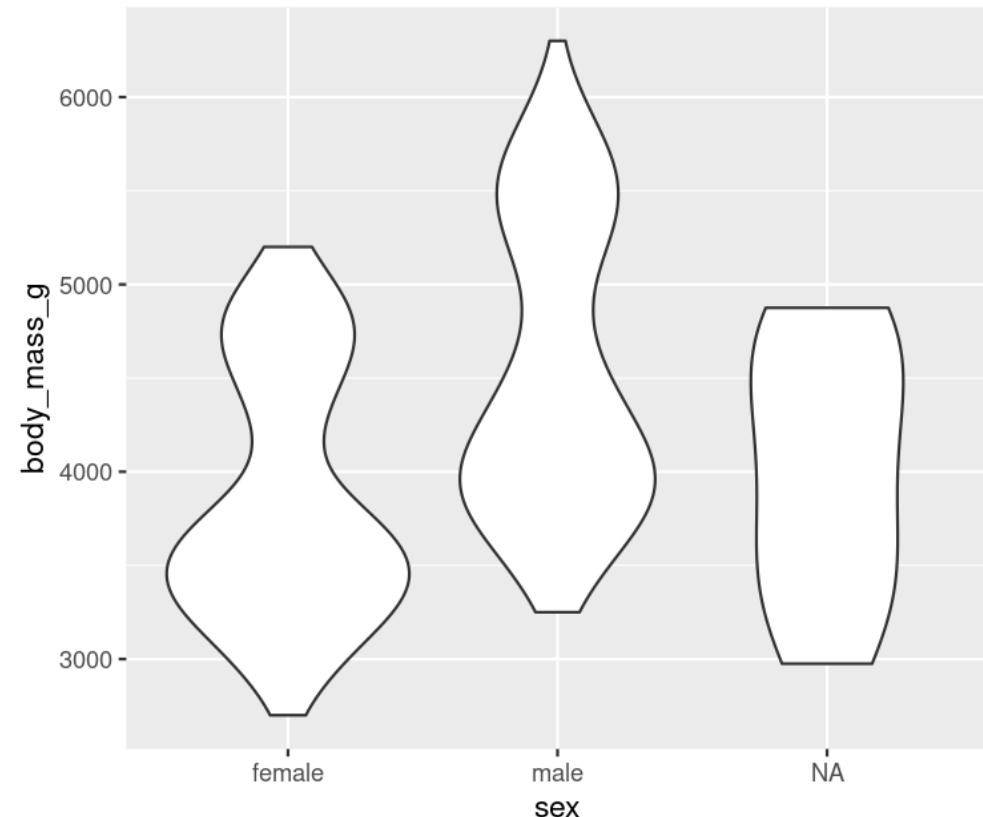


Plots are layered

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



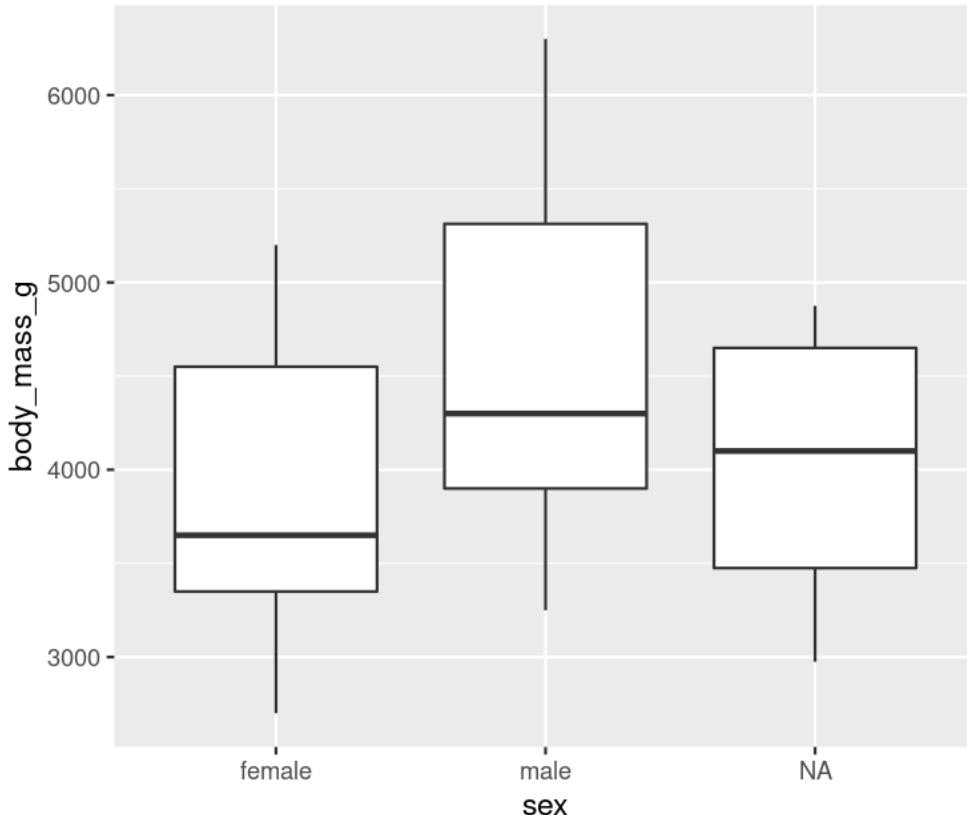
```
ggplot(data = penguins, aes(x = sex, y =  
body_mass_g)) +  
  geom_violin()
```



Plots are layered

You can add multiple layers

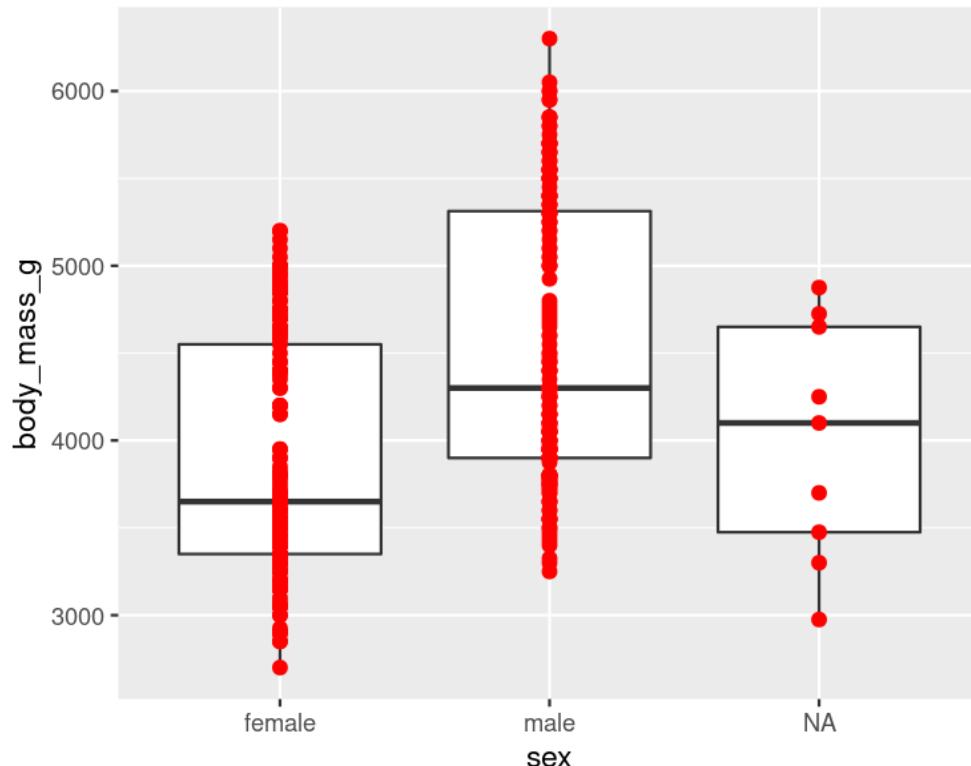
```
ggplot(data = penguins, aes(x = sex, y =  
body_mass_g)) +  
  geom_boxplot()
```



Plots are layered

You can add multiple layers

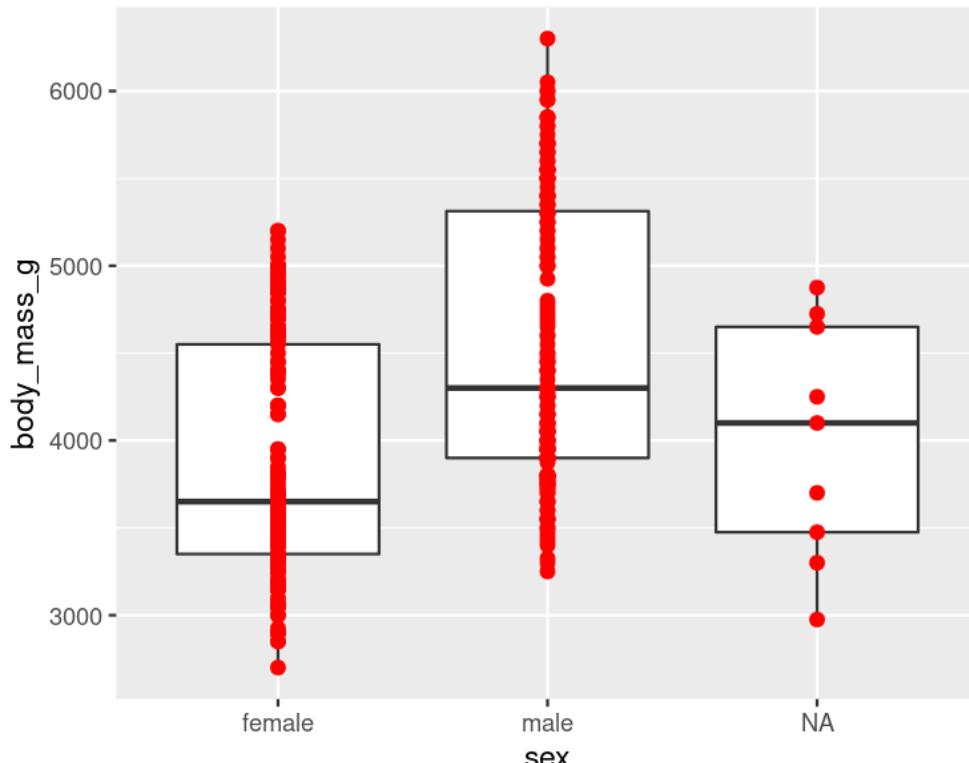
```
ggplot(data = penguins, aes(x = sex, y =  
body_mass_g)) +  
  geom_boxplot() +  
  geom_point(size = 2, colour = "red")
```



Plots are layered

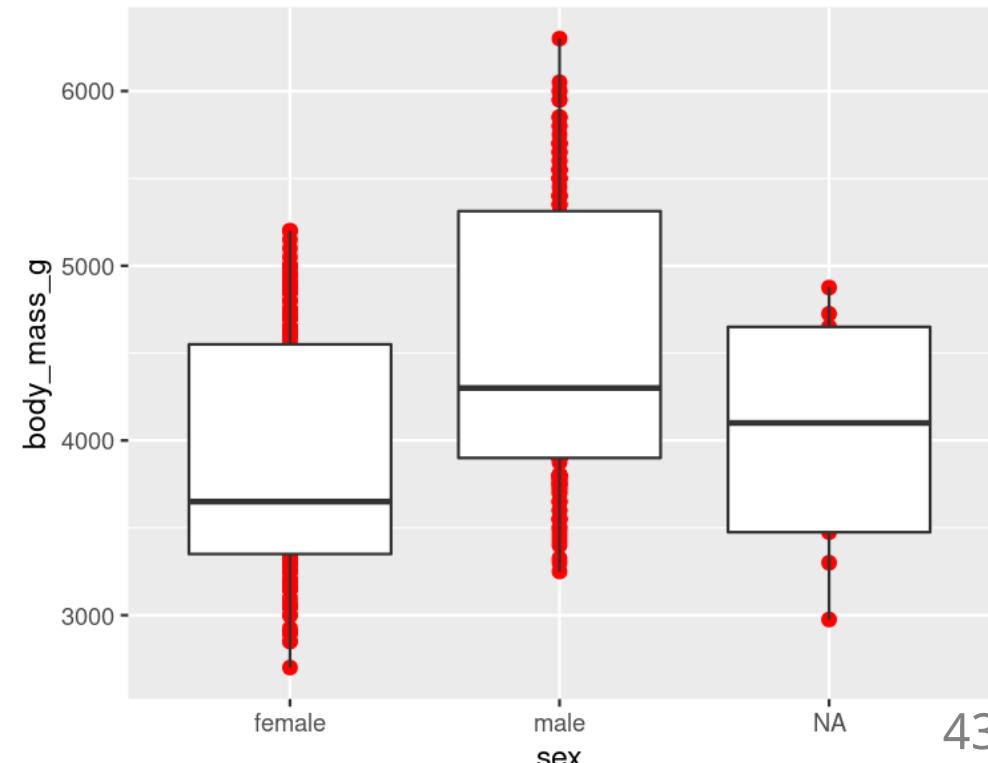
You can add multiple layers

```
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

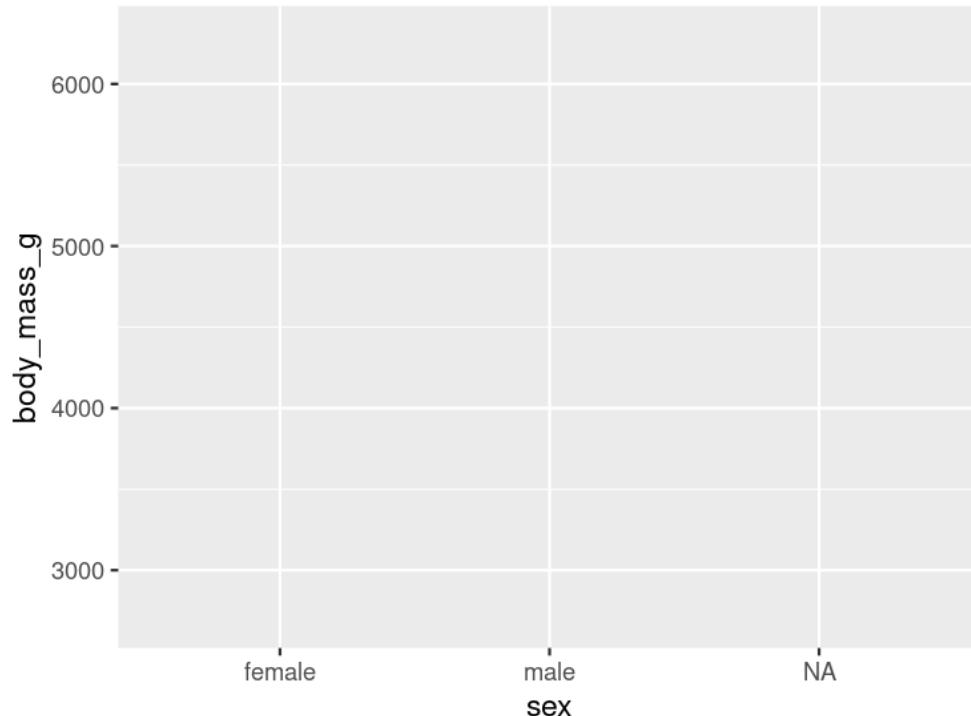
```
g <- ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

Plots are objects

Any ggplot can be saved as an object

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

```
g
```

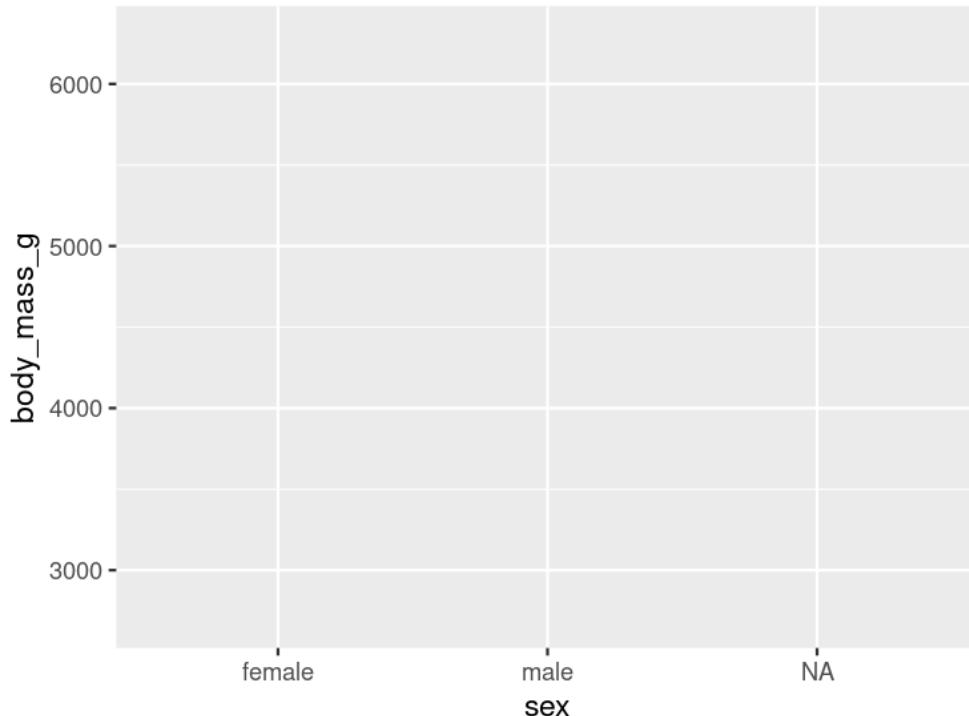


Plots are objects

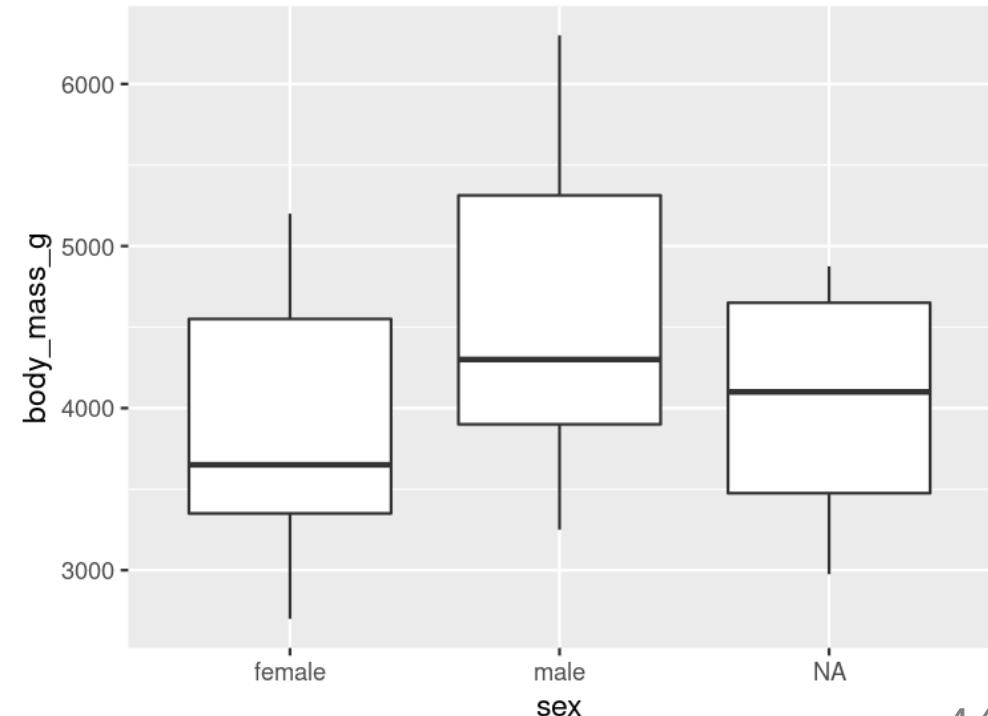
Any ggplot can be saved as an object

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

```
g
```



```
g + geom_boxplot()
```

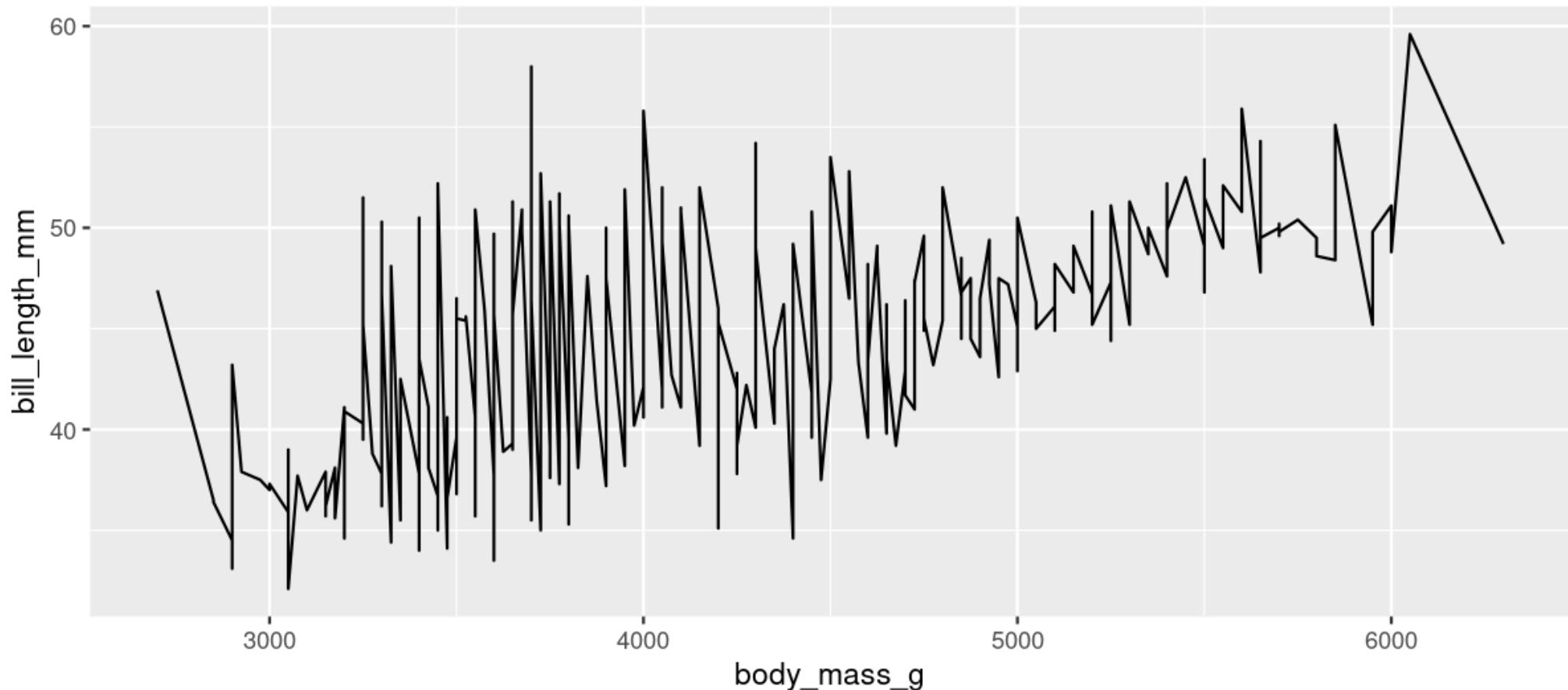


More Geoms

(Plot types)

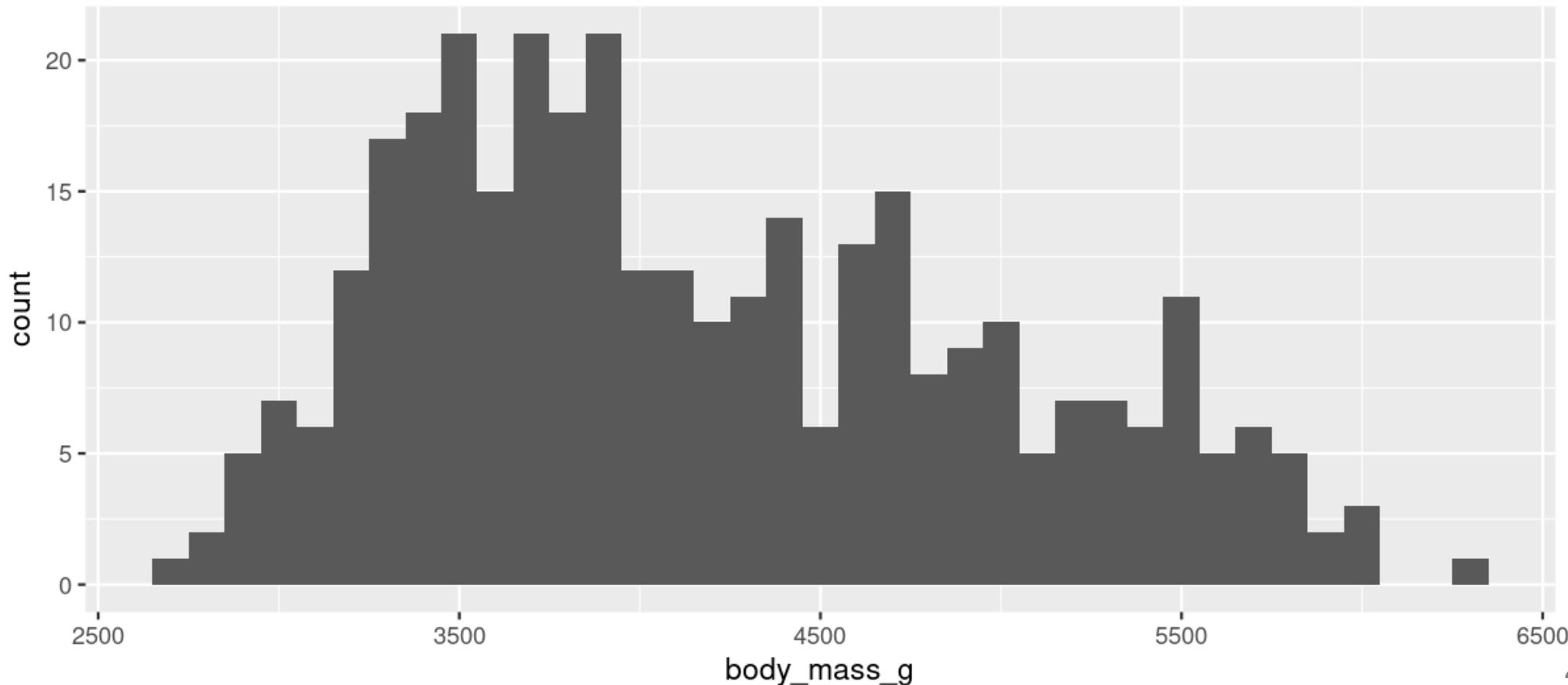
Geoms: Lines

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



Geoms: Histogram

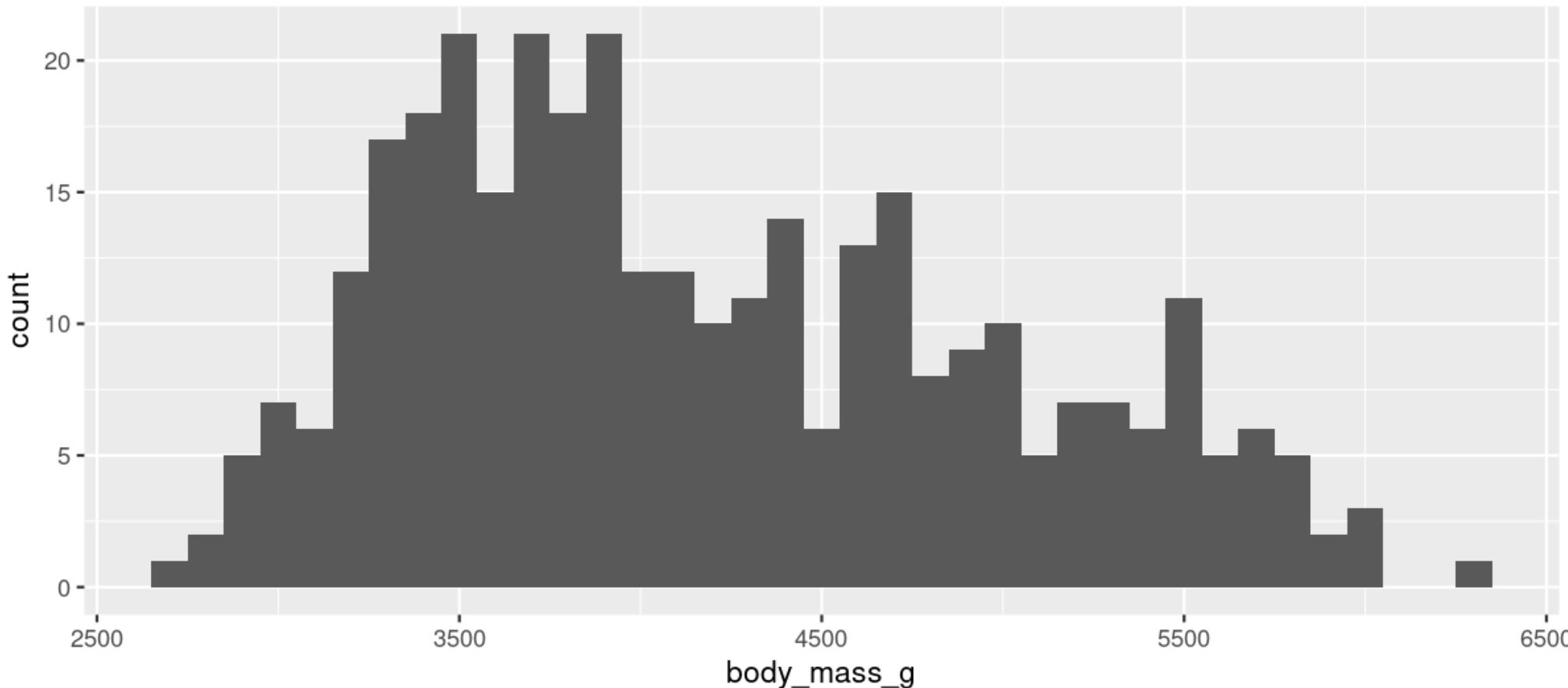
```
ggplot(data = penguins, aes(x = body_mass_g)) +  
  geom_histogram(binwidth = 100)
```



Geoms: Histogram

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

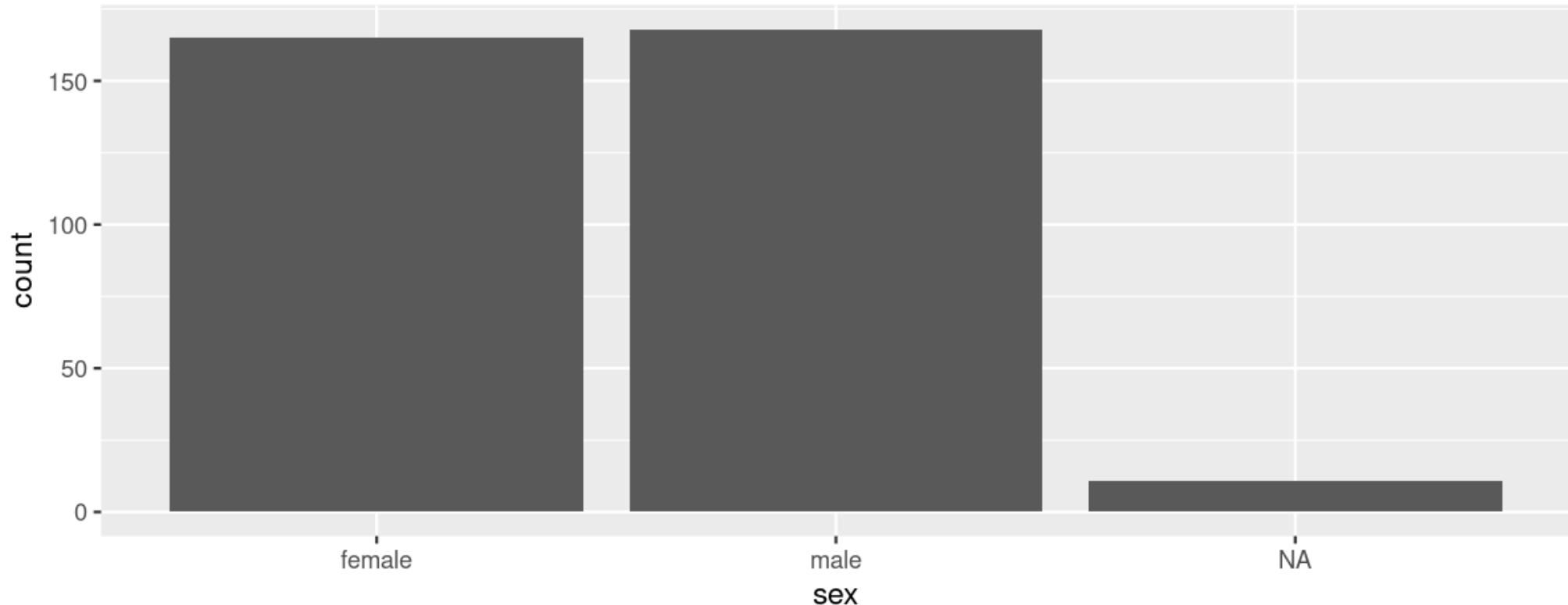
Note: We only need 1 aesthetic here (x)



Geoms: Barplots

Let **ggplot** count your data

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

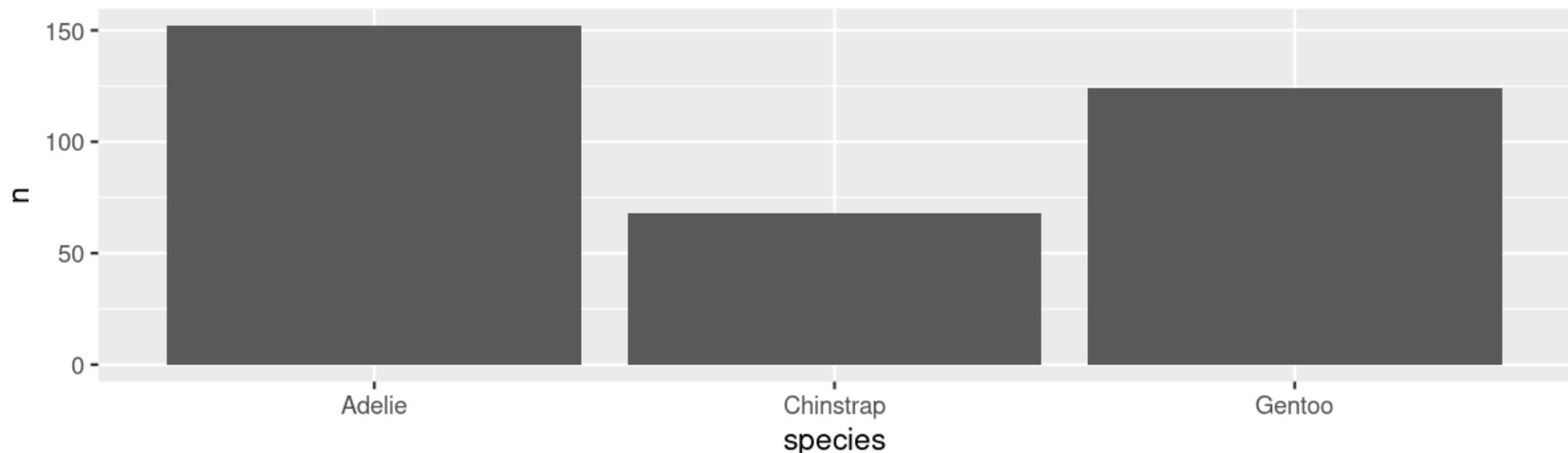


Geoms: Barplots

You can also provide the counts

```
# Create our own data frame
species <- data.frame(species = c("Adelie", "Chinstrap", "Gentoo"),
                      n = c(152, 68, 124))

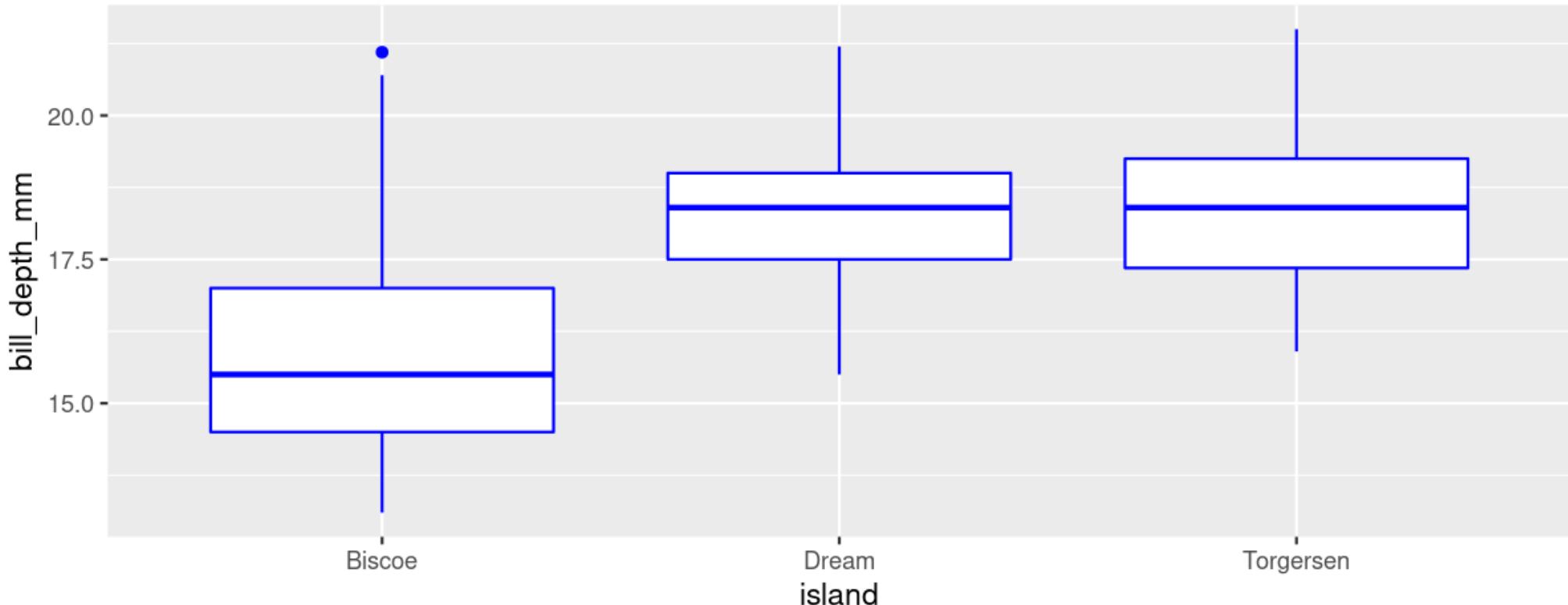
ggplot(data = species, aes(x = species, y = n)) +
  geom_bar(stat = "identity")
```



Your Turn: Create this plot

```
library(ggplot2)

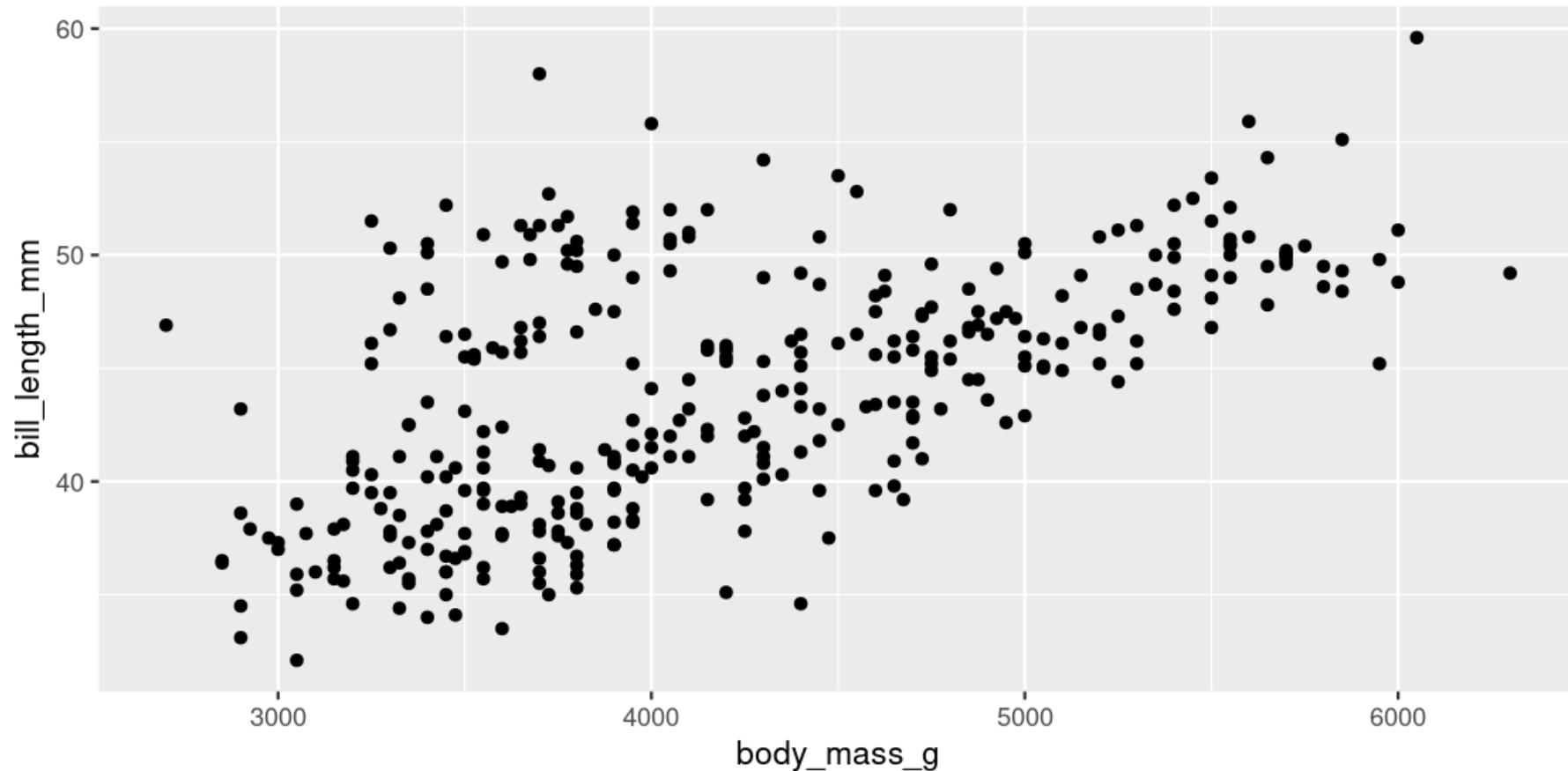
ggplot(data = [REDACTED], aes(x = [REDACTED], y = [REDACTED])) +
  geom_[REDACTED]([REDACTED])
```



Showing data by group

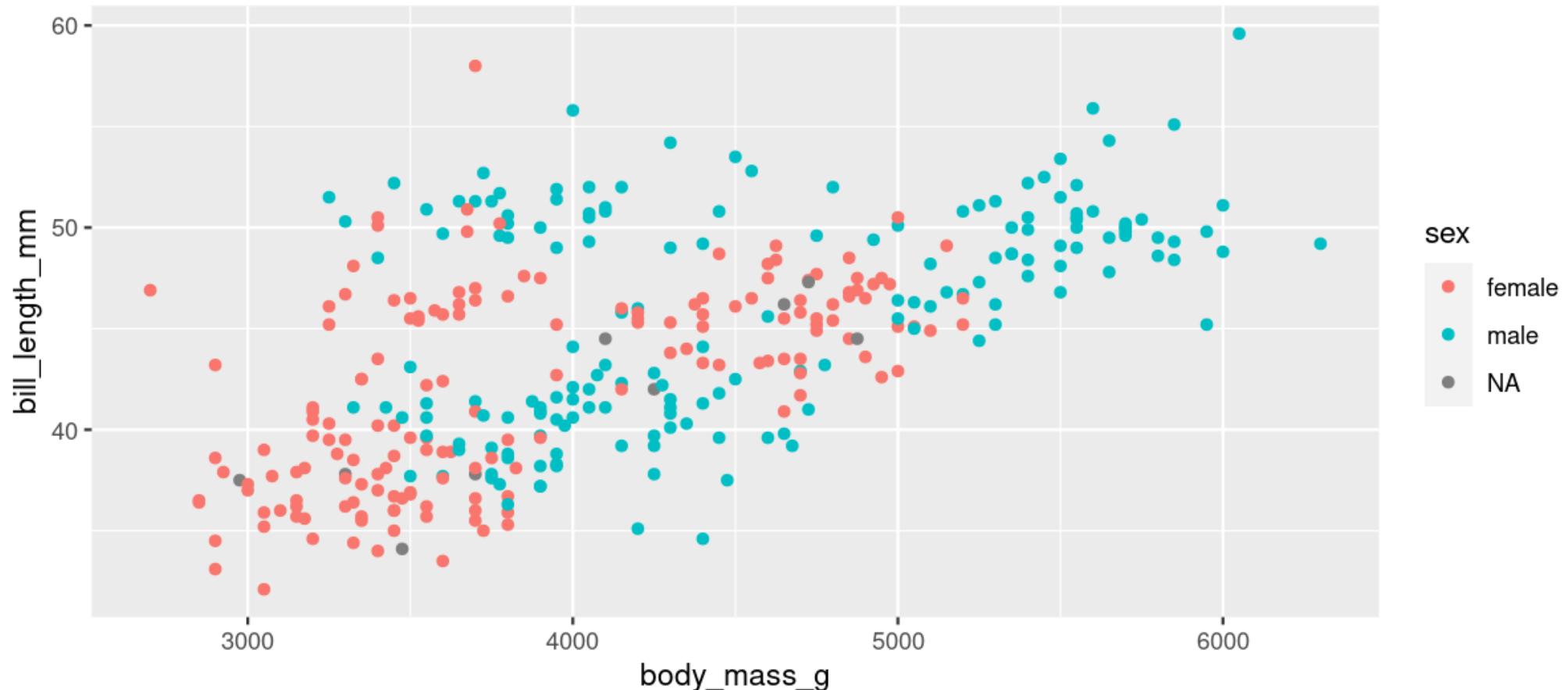
Mapping aesthetics

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



Mapping aesthetics

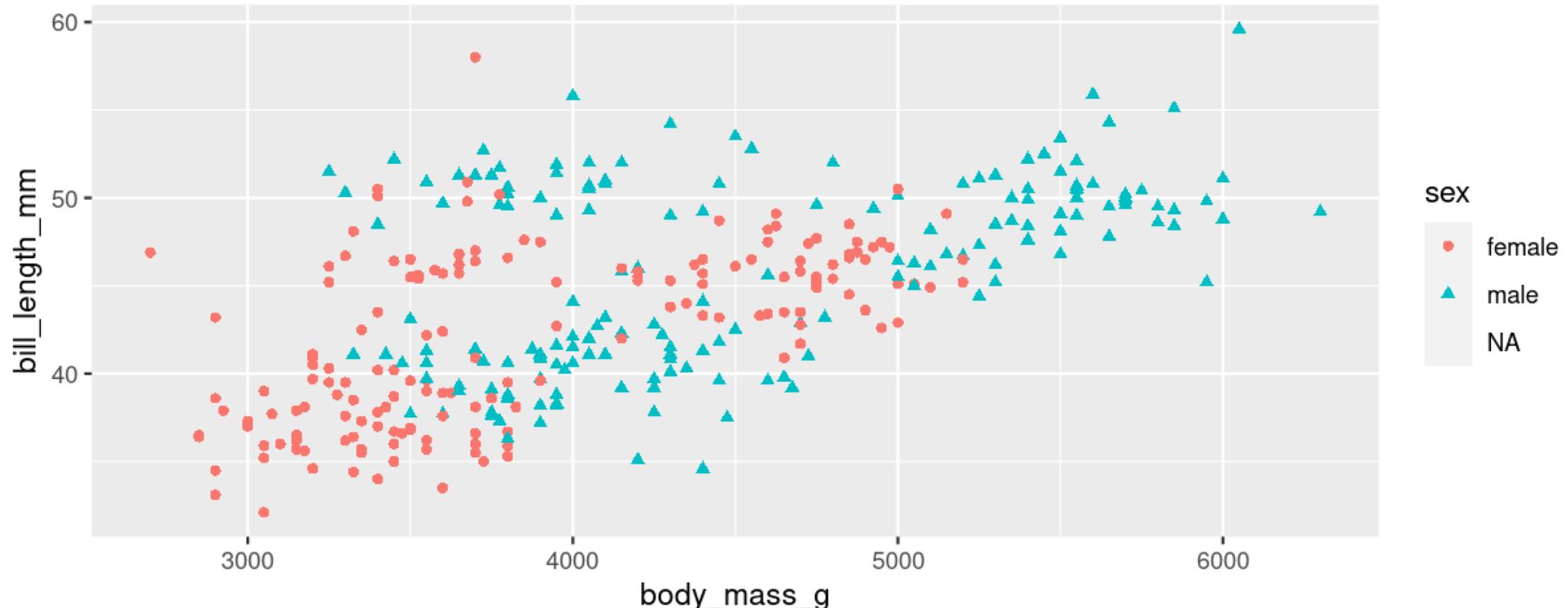
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
  geom_point()
```



Mapping aesthetics

ggplot automatically populates the legends (combining where it can)

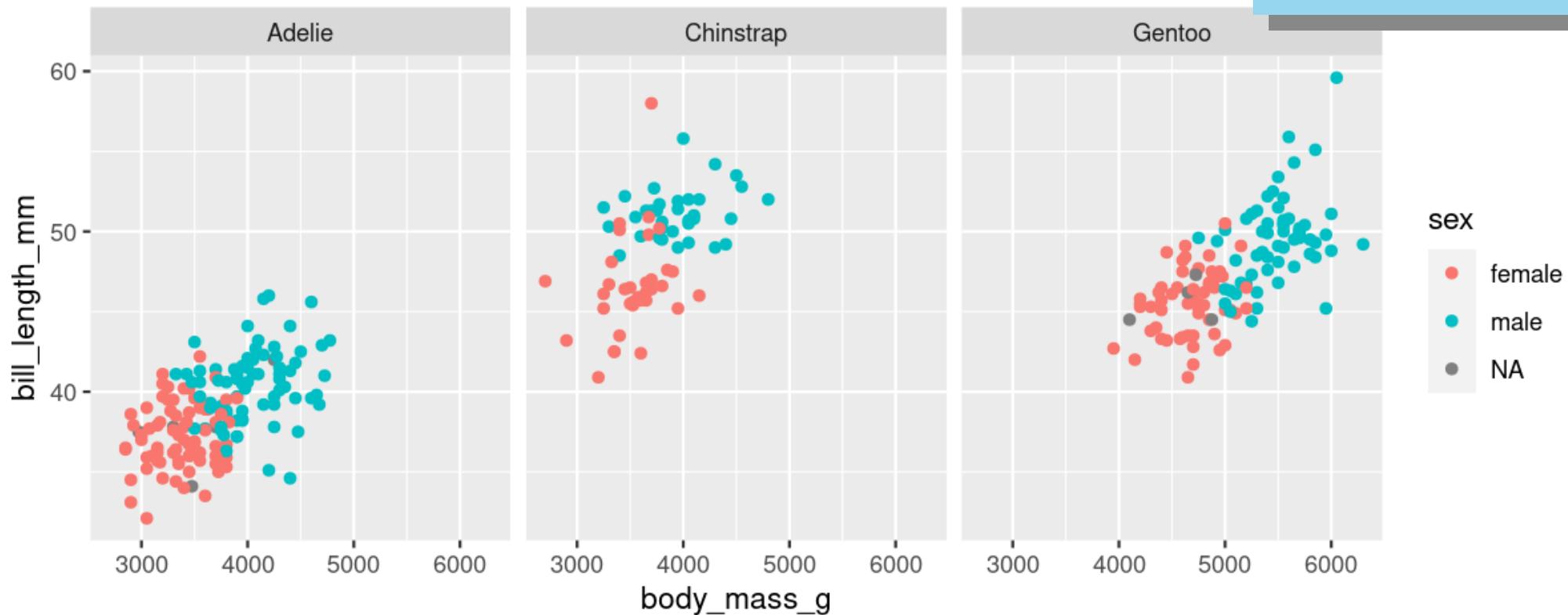
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex, shape = sex)) +  
  geom_point()
```



Faceting: `facet_wrap()`

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

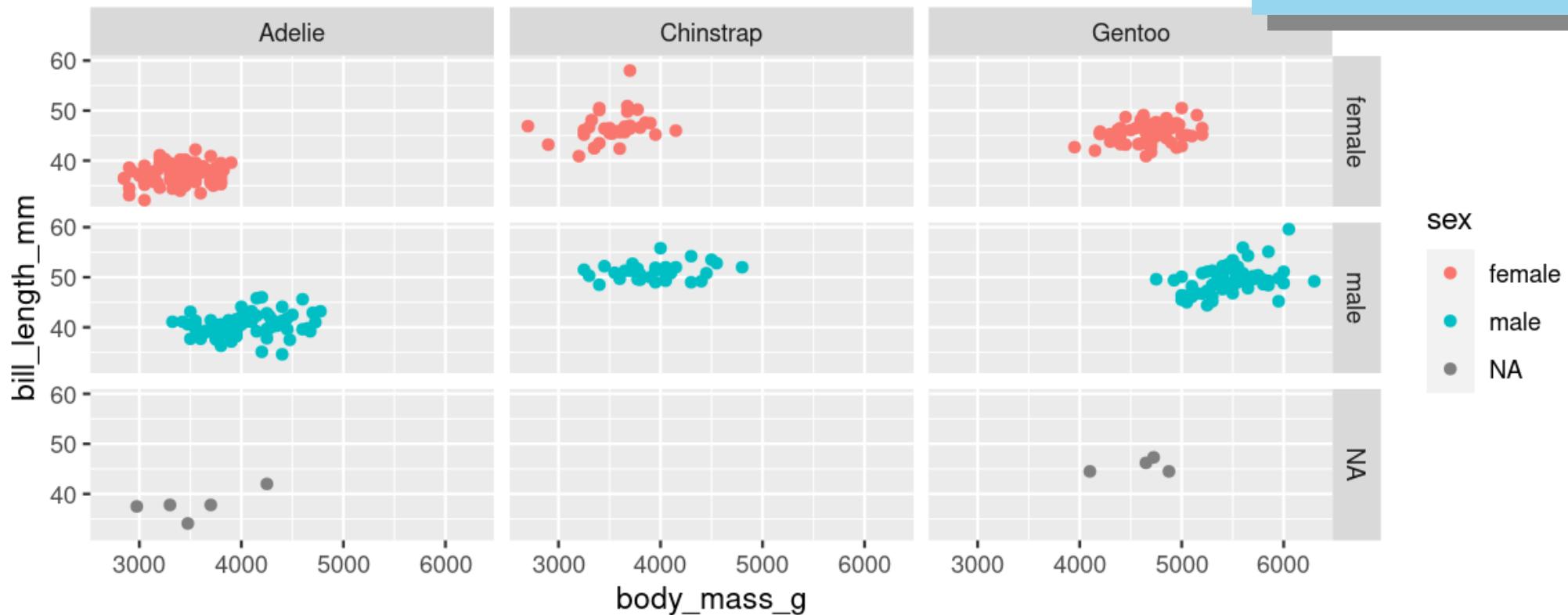
Split plots by **one** grouping variable



Faceting: `facet_grid()`

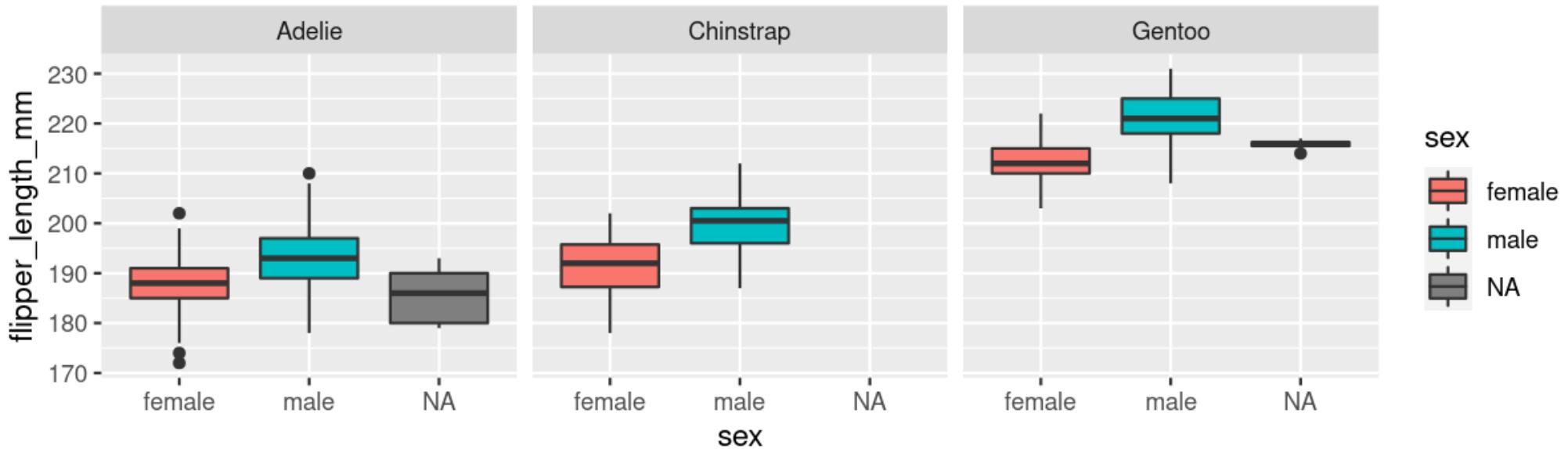
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
  geom_point() +  
  facet_grid(sex ~ species)
```

Split plots by **two** grouping variables



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

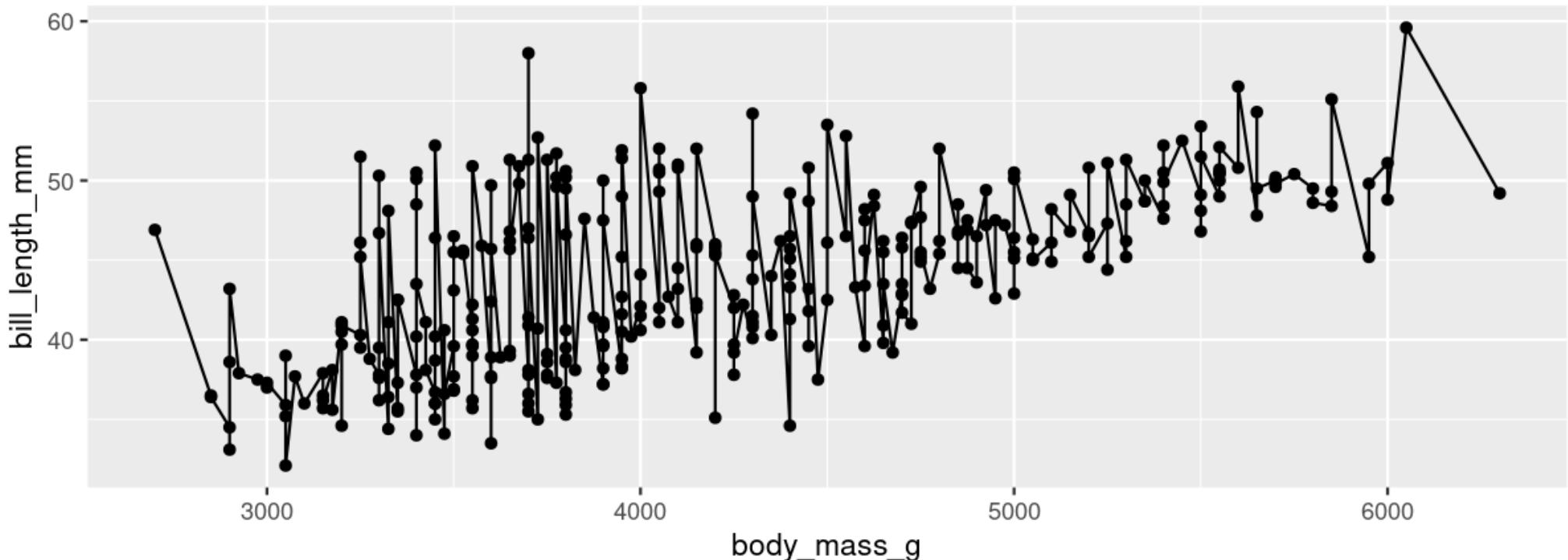
Too Easy? Split boxplots by sex **and** island

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()
```

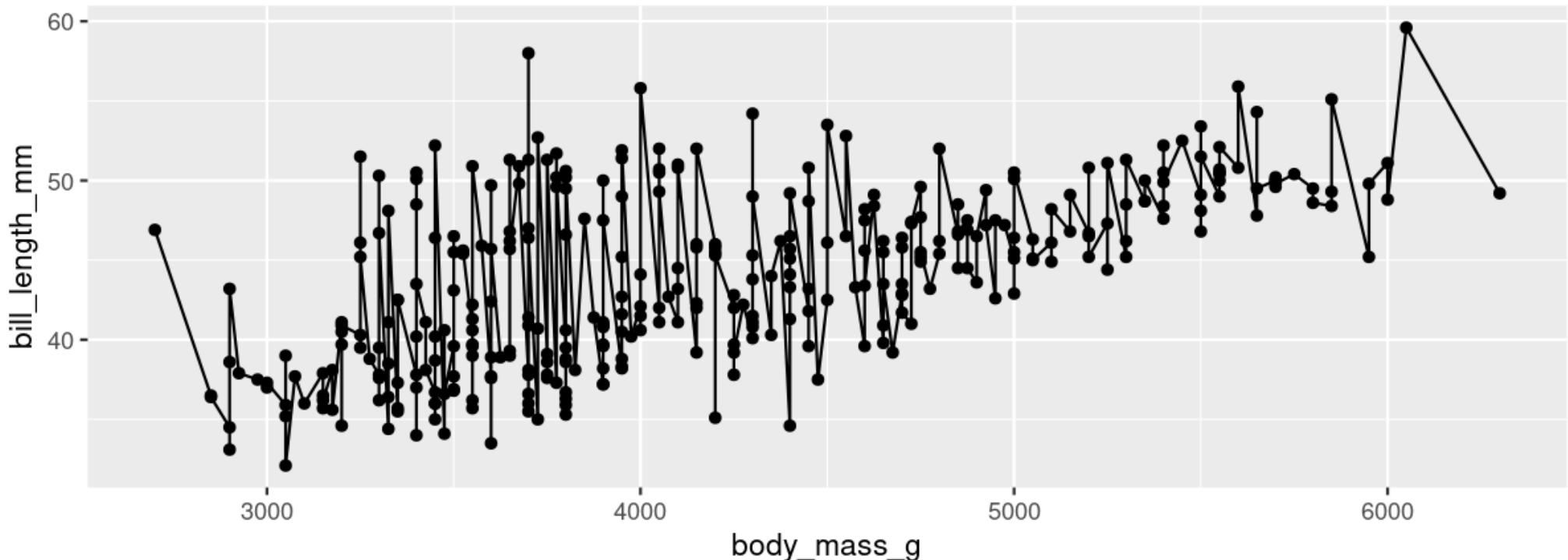


Trendlines / Regression lines

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

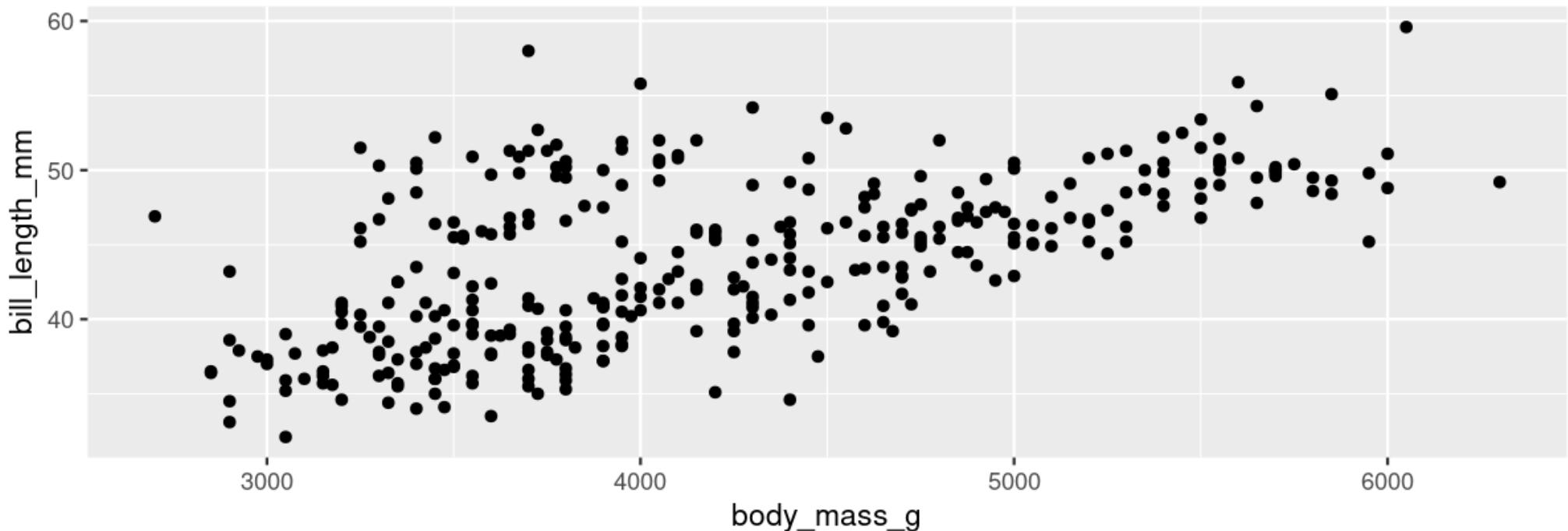


Trendlines / Regression lines

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
```

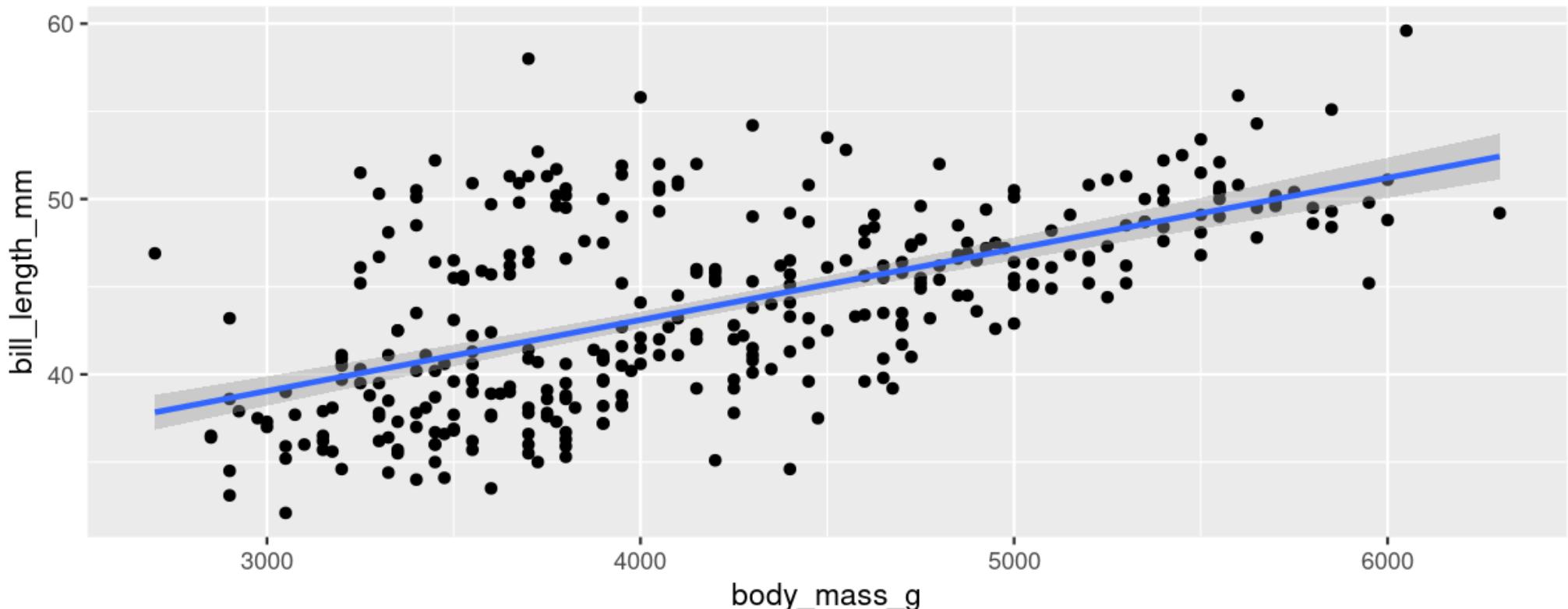


Trendlines / Regression lines

Add the `stat_smooth()`

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

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

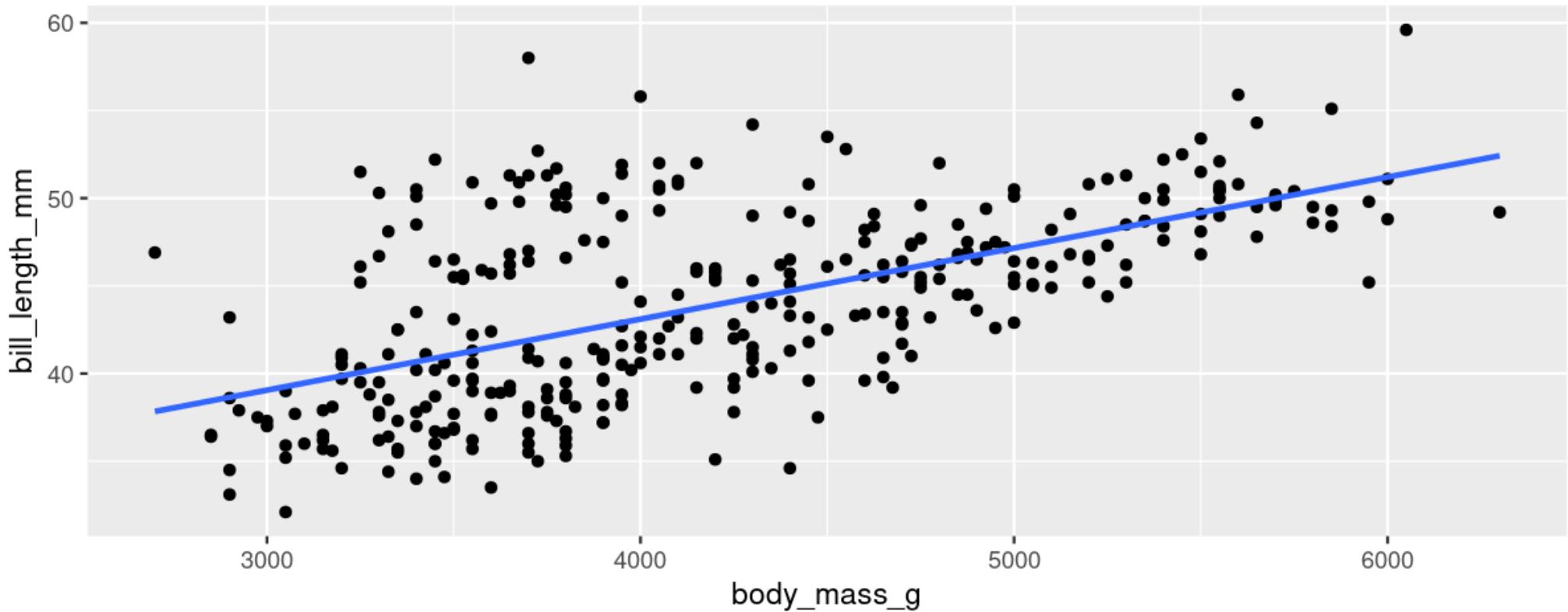


Trendlines / Regression lines

Add the `stat_smooth()`

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

- remove the grey ribbon `se = FALSE`

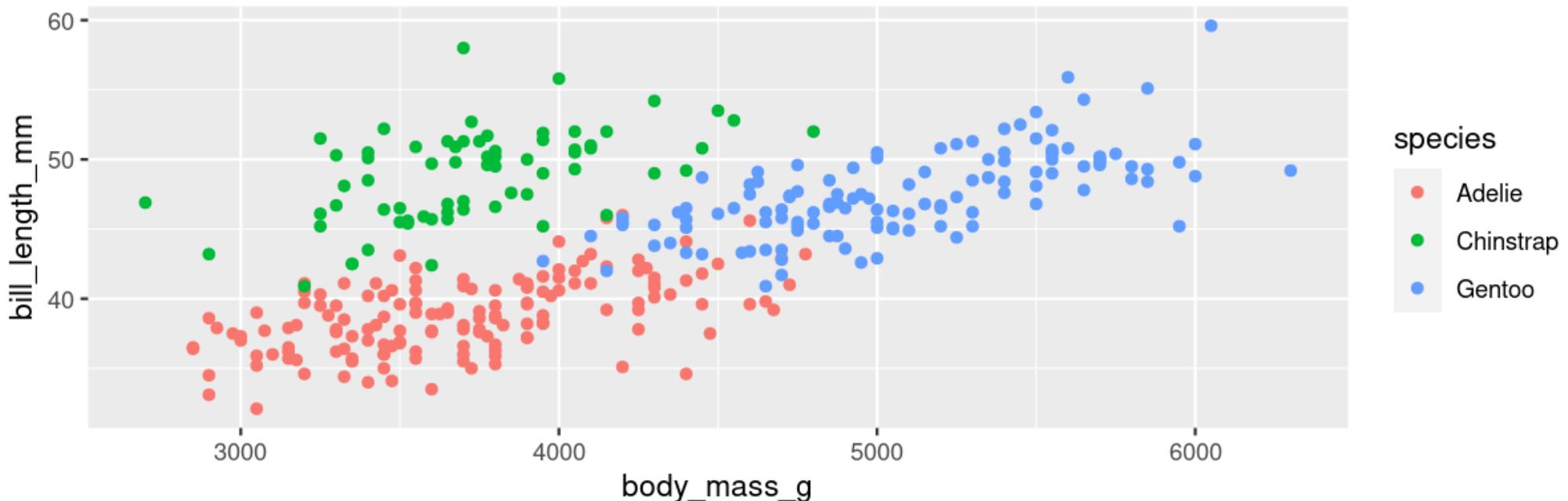


Trendlines / Regression lines

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
```

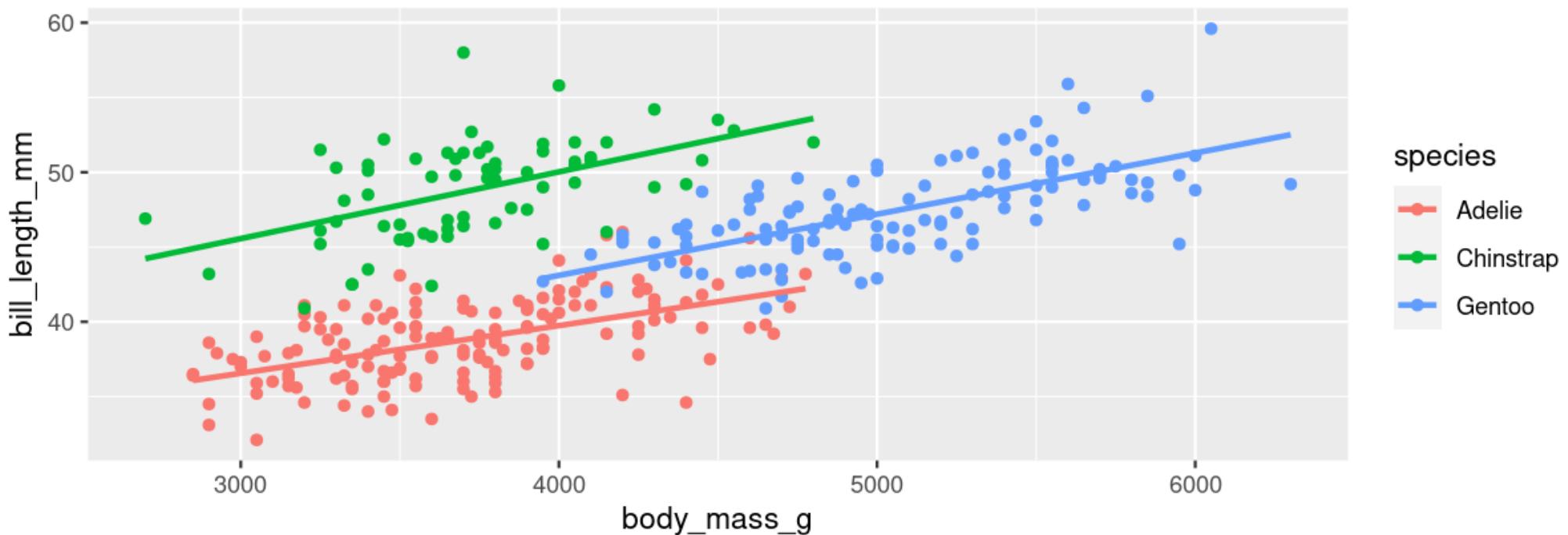


Trendlines / Regression lines

A line for each group

- `stat_smooth()` automatically uses the same grouping

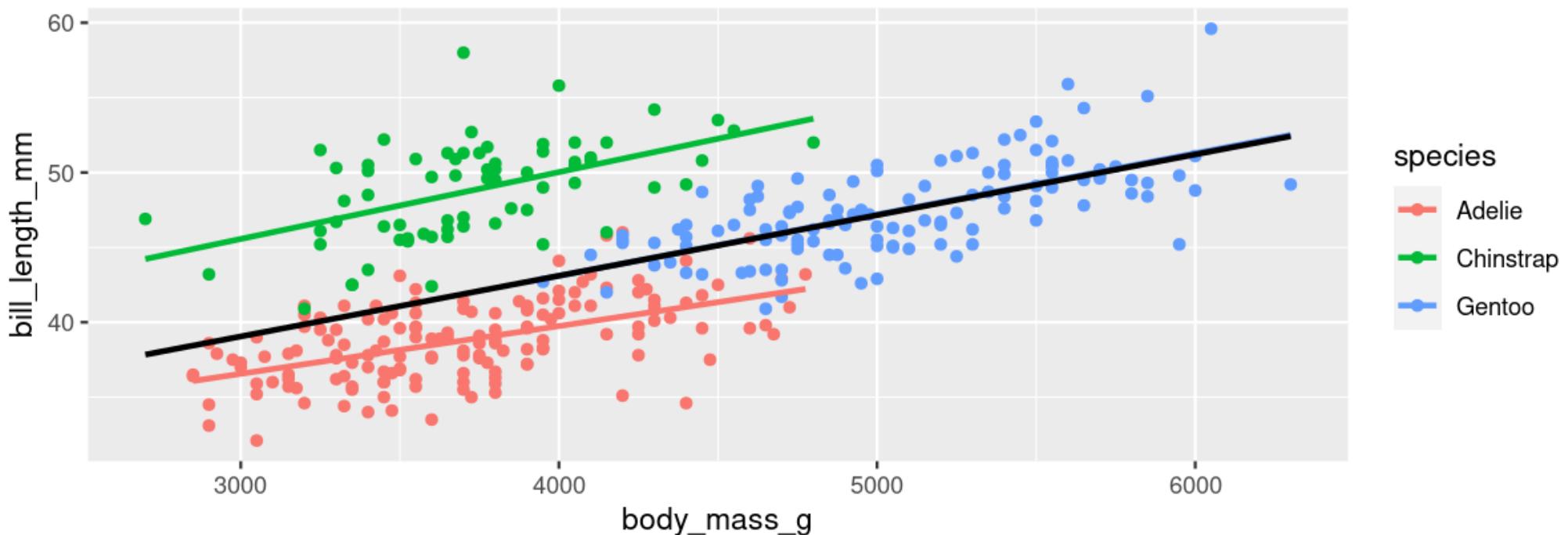
```
g + stat_smooth(method = "lm", se = FALSE)
```



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*

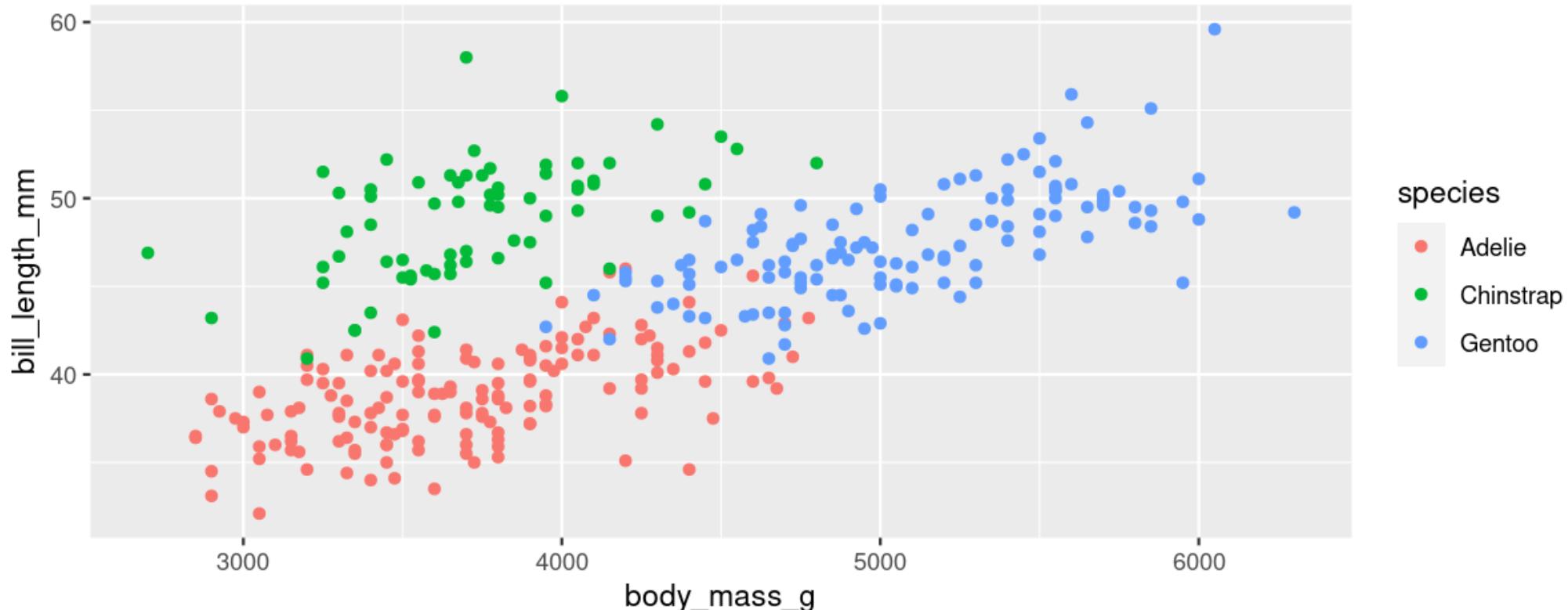
Too Easy? Create a separate plot for each sex as well

Customizing plots

Customizing: Starting plot

Let's work with this plot

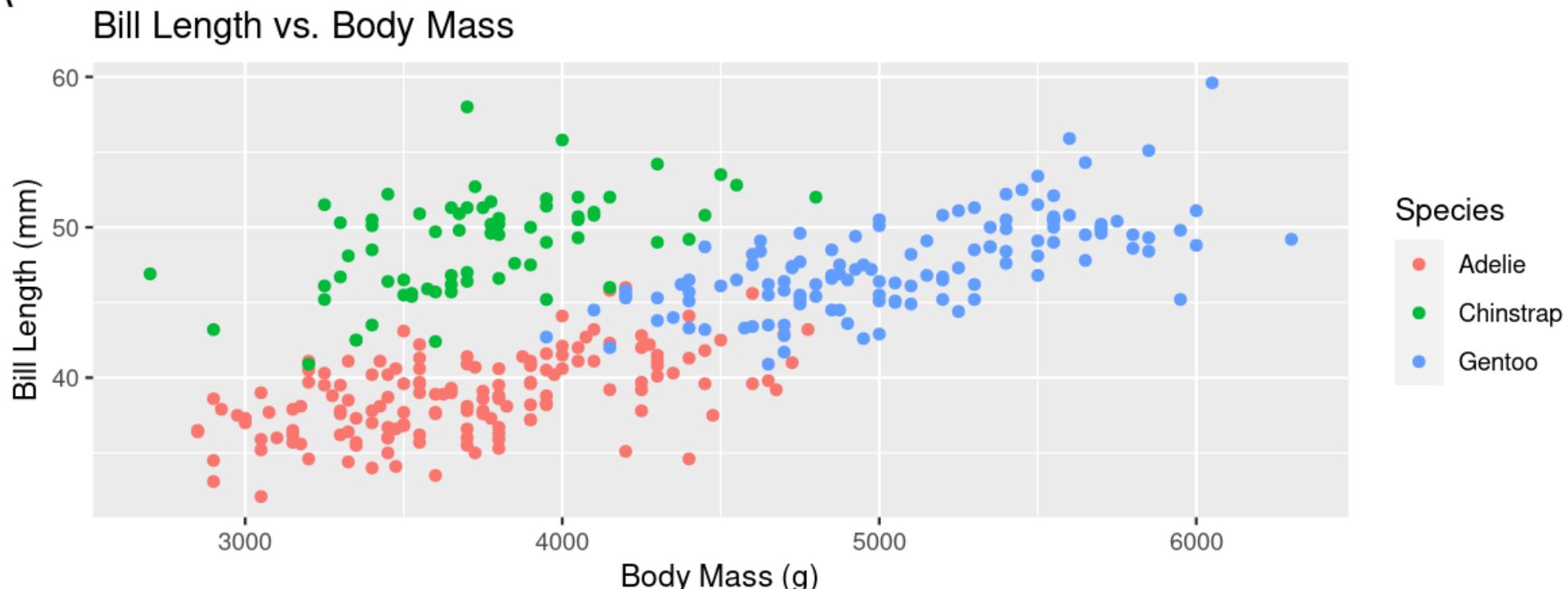
```
g <- ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point()
```



Customizing: Labels

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

A



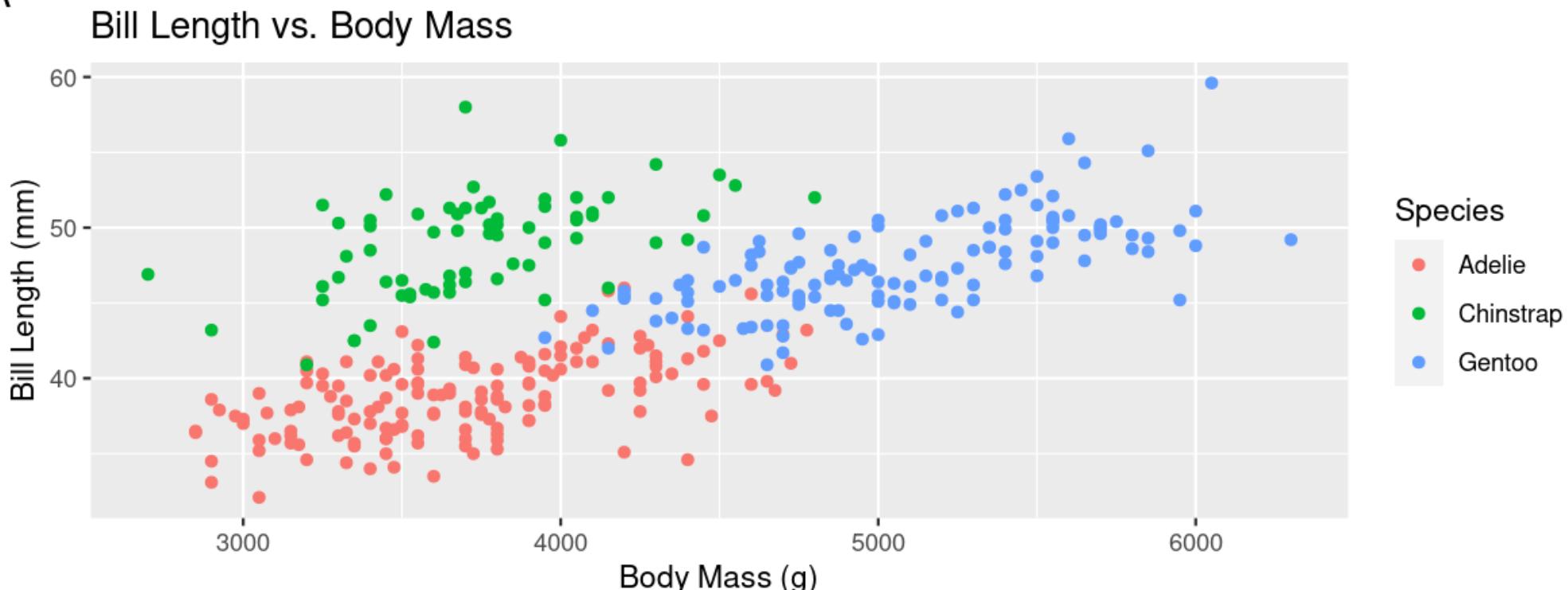
Customizing: Labels

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

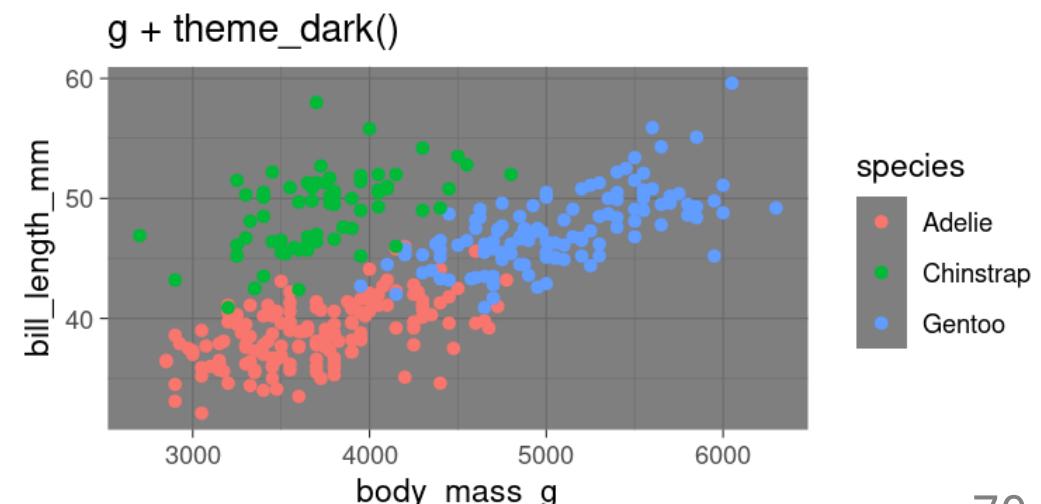
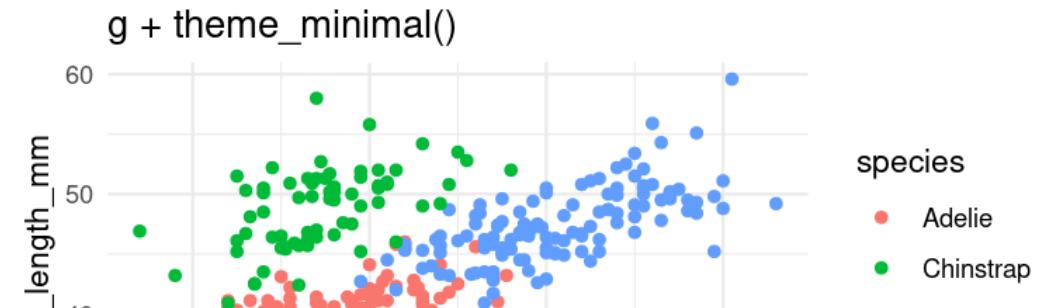
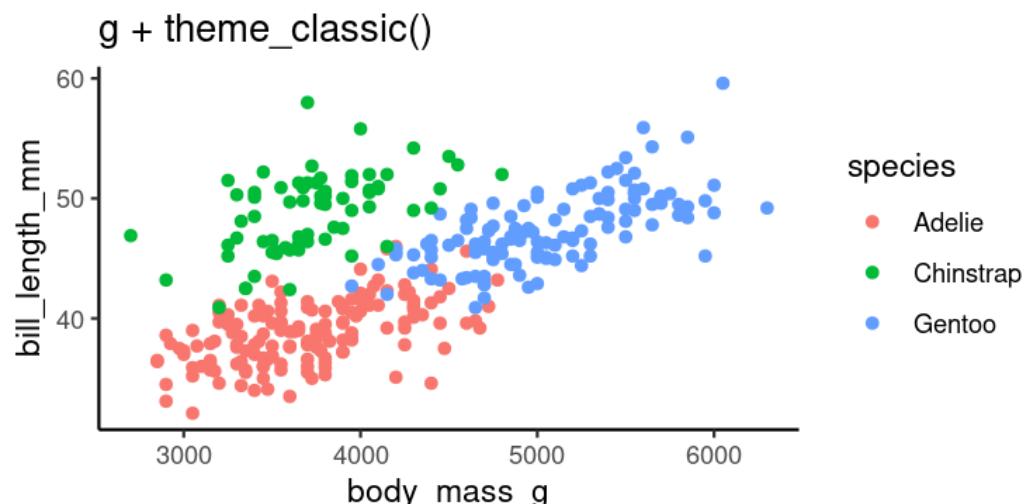
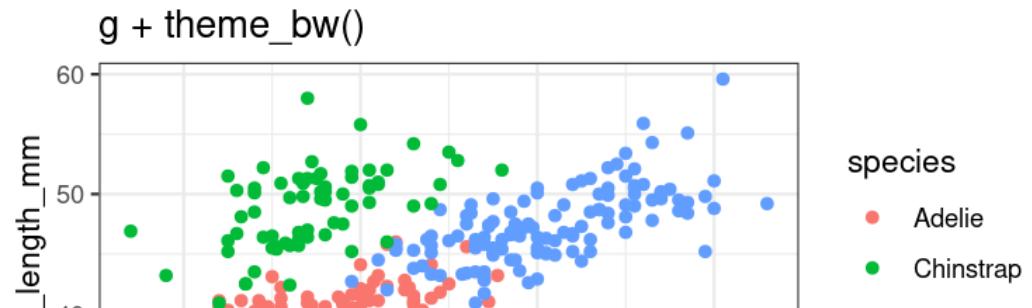
Practice for later

Add proper labels to some of your previous plots

A



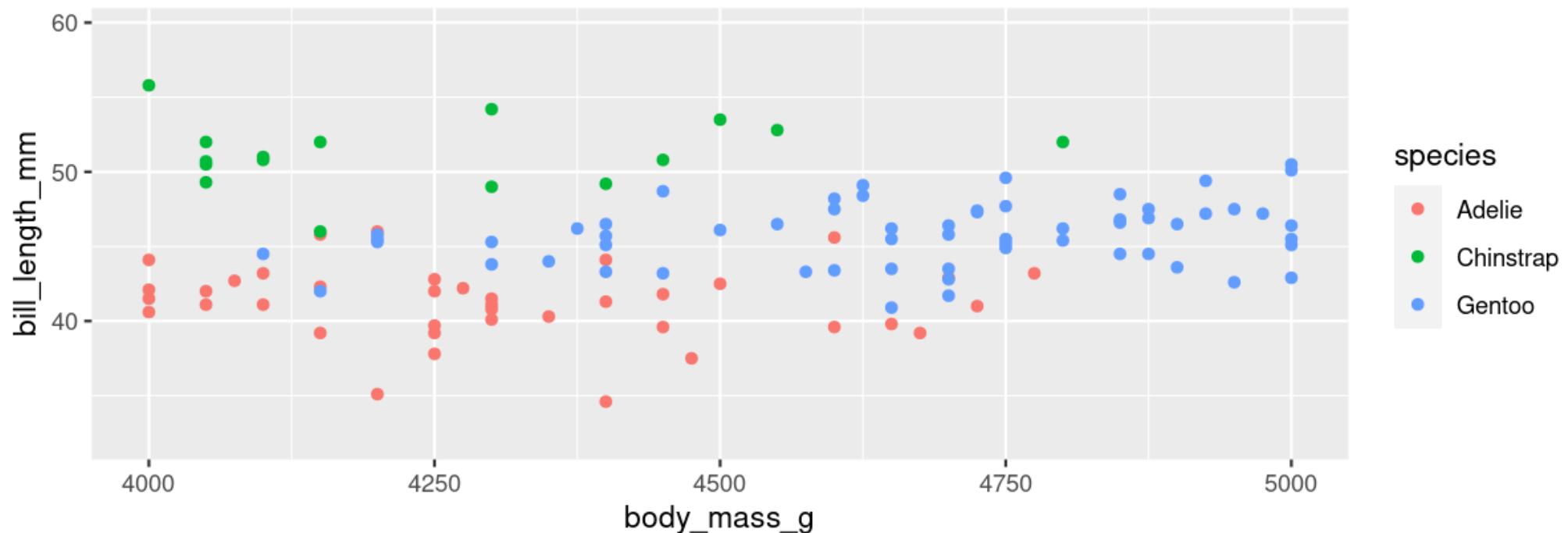
Customizing: Built-in themes



Customizing: Data range

Limit the data (exclude data)

```
g + xlim(c(4000, 5000))
```



```
## Warning: Removed 228 rows containing missing values (geom_point).
```

Customizing: Axes

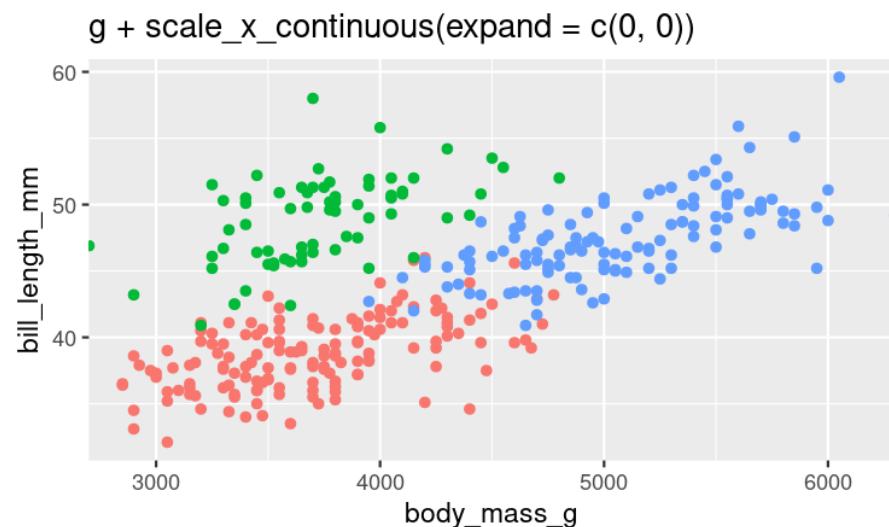
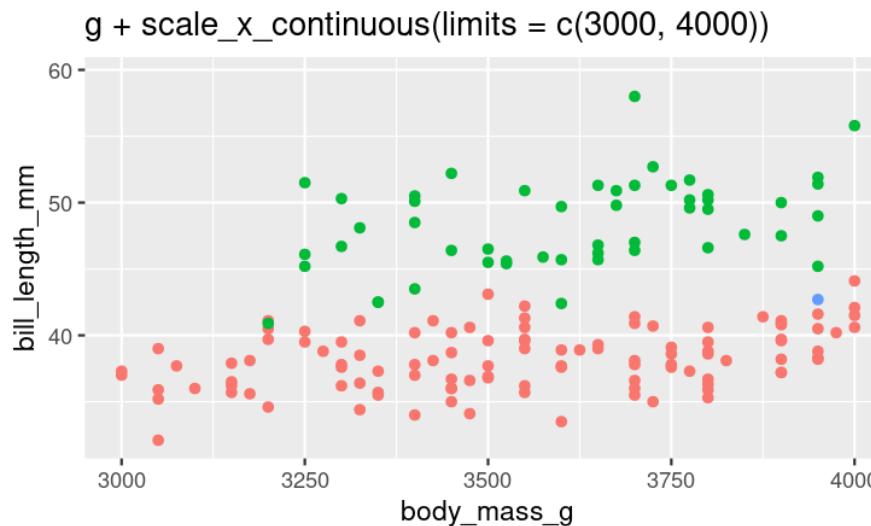
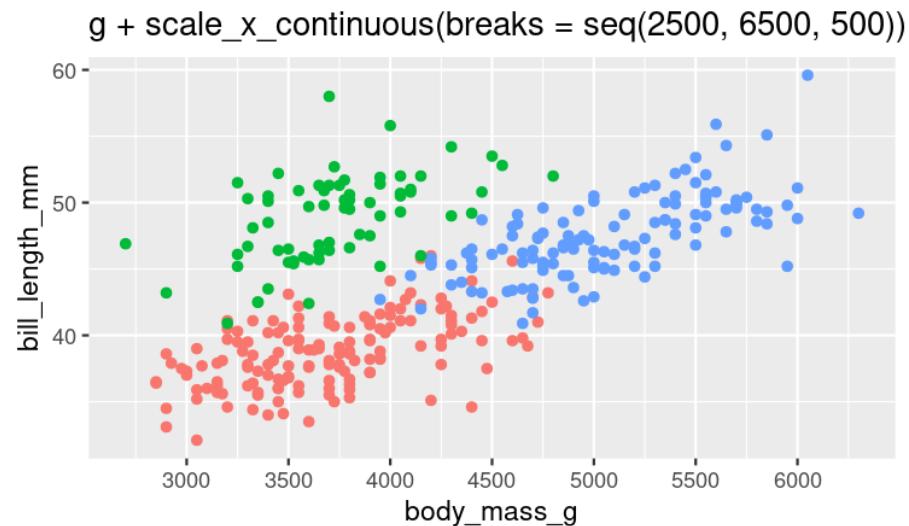
scale_ + (x or y) + type (**continuous**, **discrete**, **date**, **datetime**)

- **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

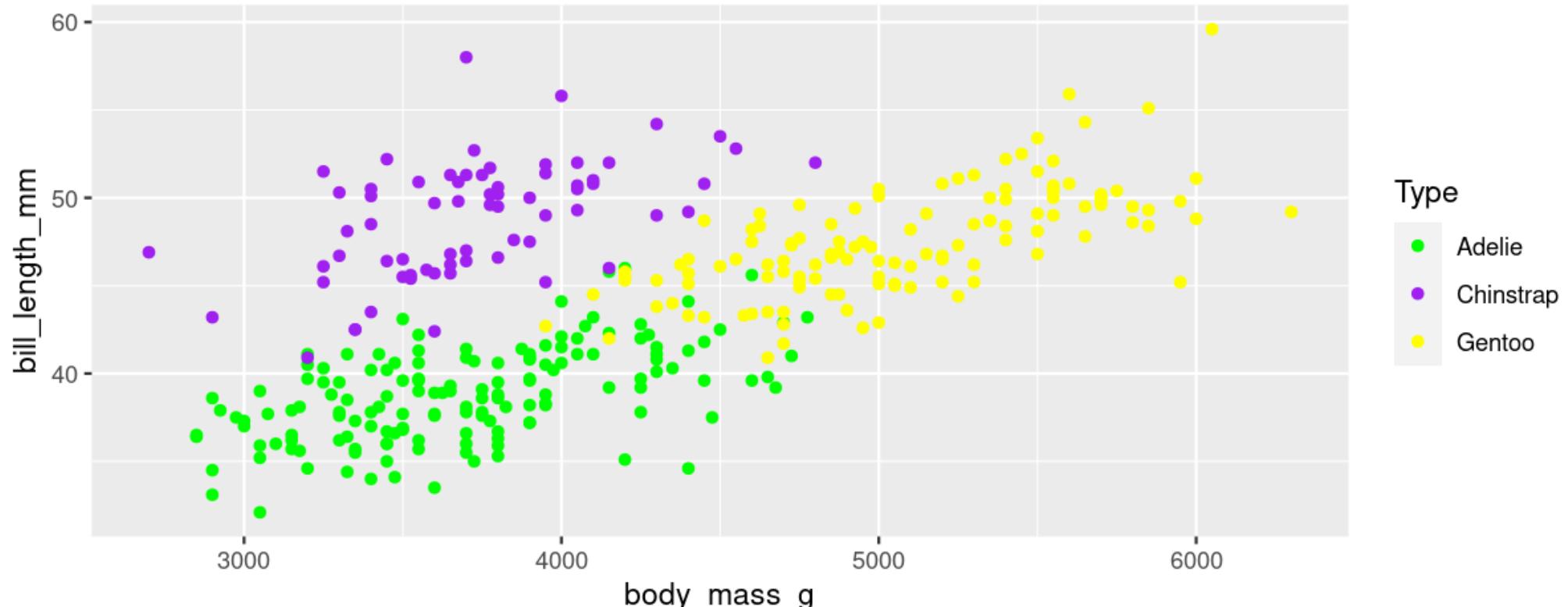


Customizing: Aesthetics

Using scales

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

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

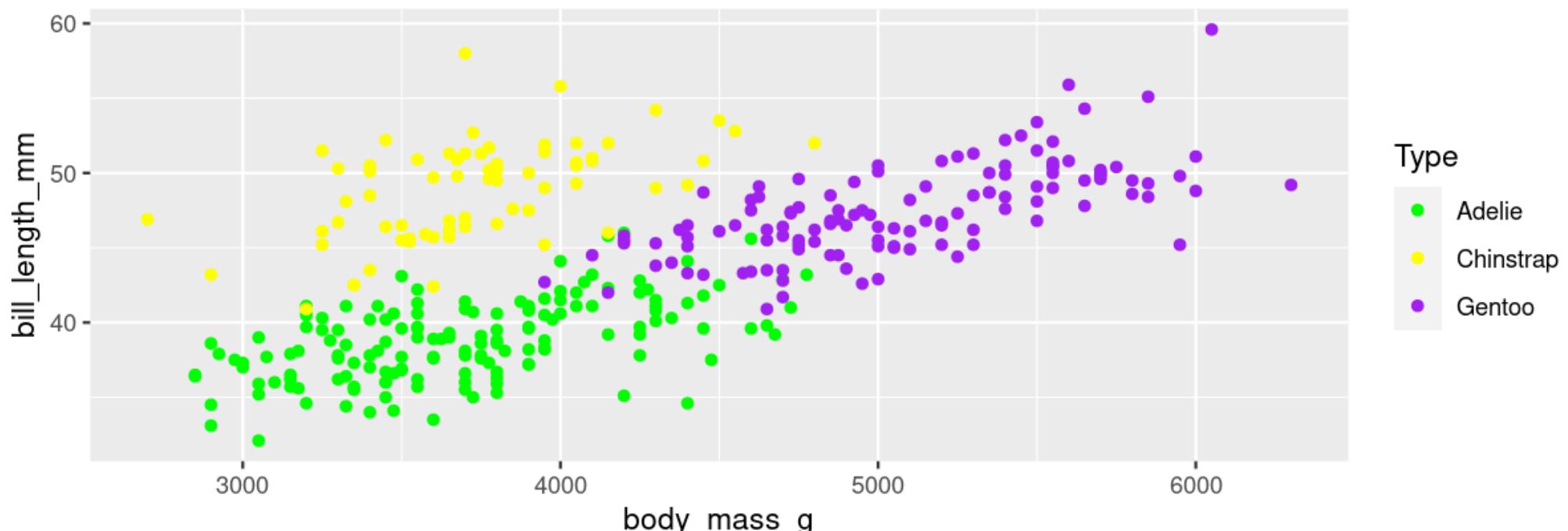


Customizing: Aesthetics

Using scales

Or be very explicit:

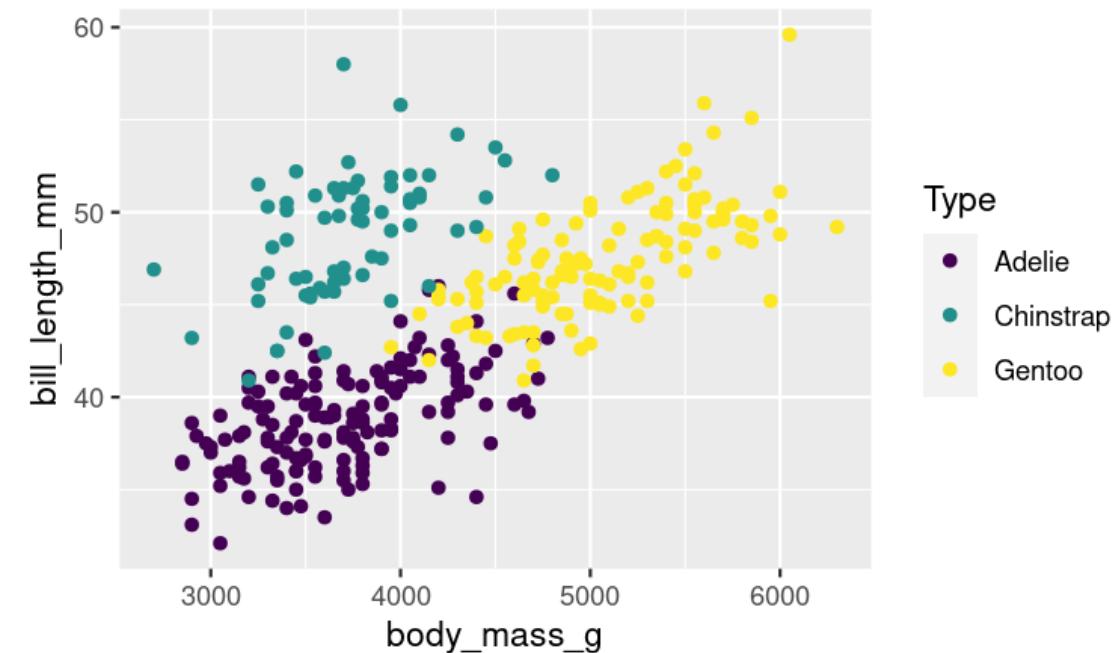
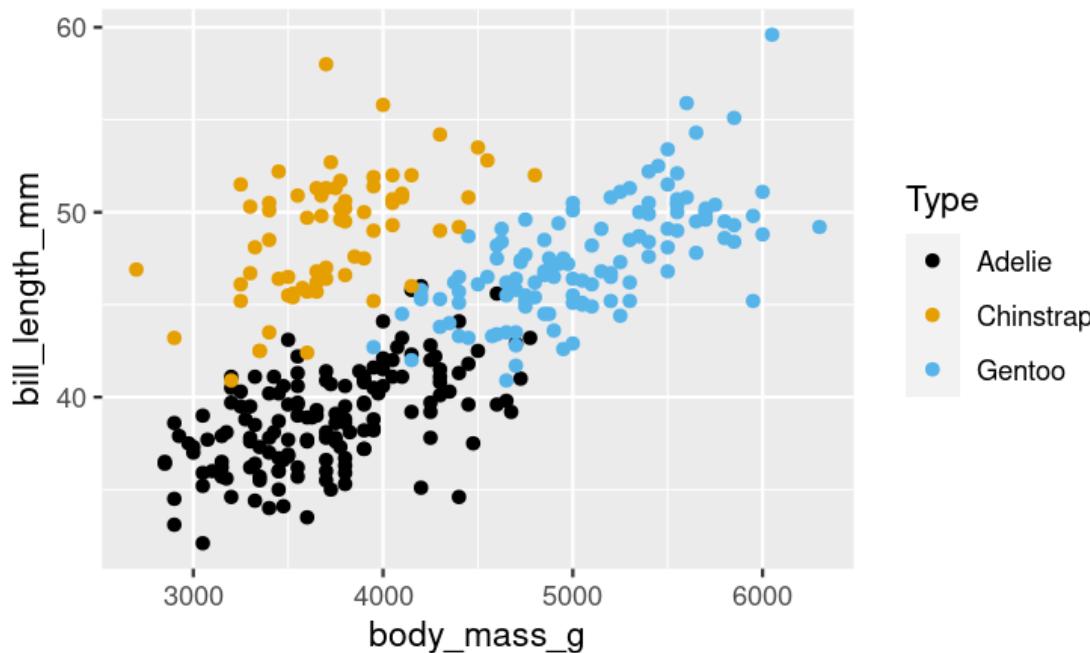
```
g + scale_colour_manual(name = "Type",
                         values = c("Adelie" = "green", "Gentoo" = "purple", "Chinstrap" = "yellow"),
                         na.value = "black")
```



Customizing: Aesthetics

For colours, consider colour-blind-friendly scales

```
library(ggthemes)
g + scale_colour_colorblind(name = "Type")
g + scale_colour_viridis_d(name = "Type")
```

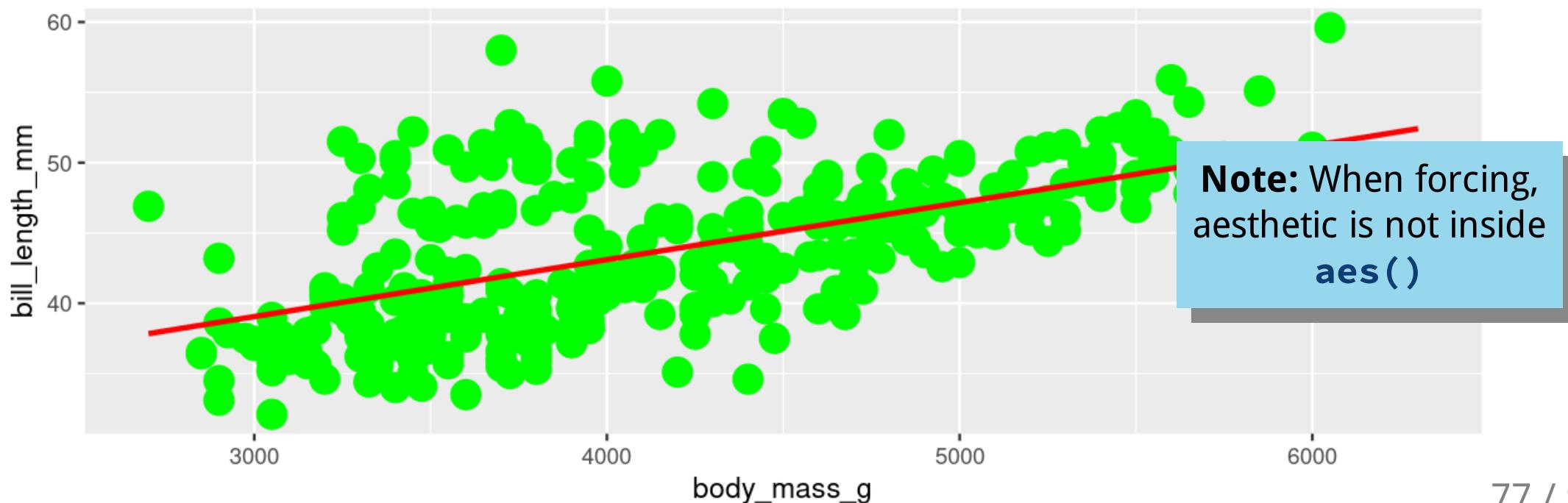


Customizing: Aesthetics

Forcing

Remove the association between a variable and an aesthetic

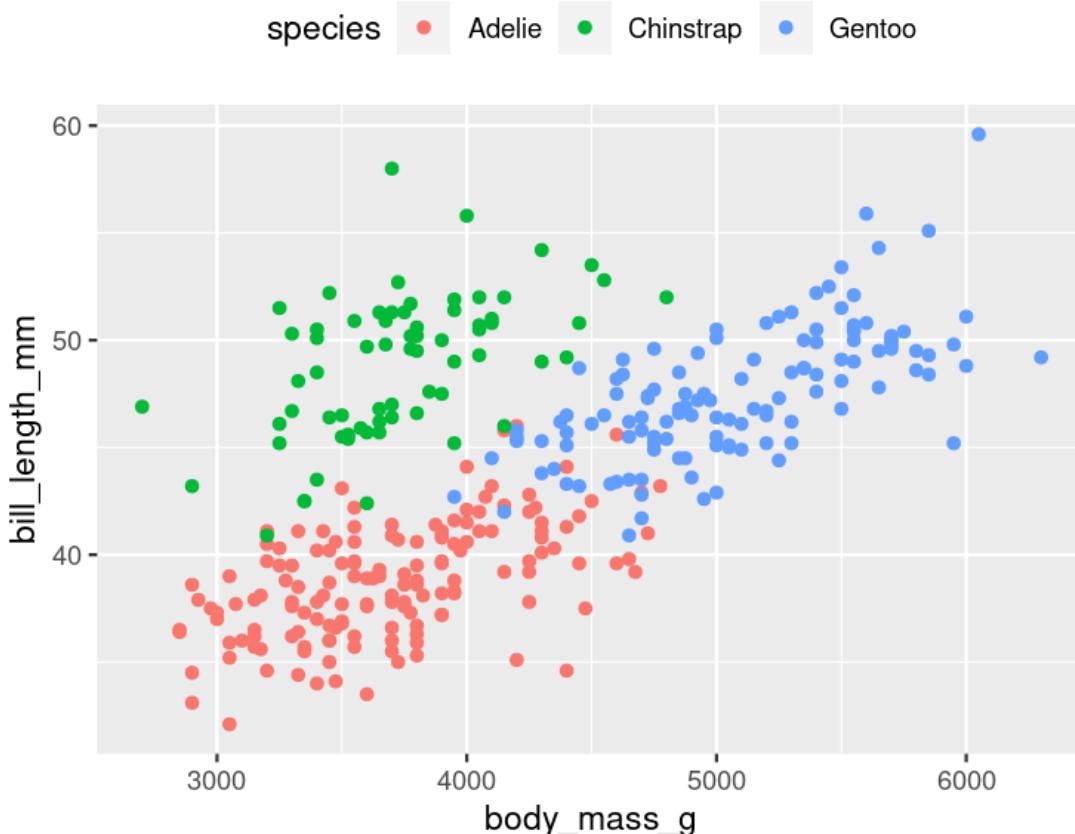
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
  geom_point(colour = "green", size = 5) +  
  stat_smooth(method = "lm", se = FALSE, colour = "red")
```



Customizing: Legends placement

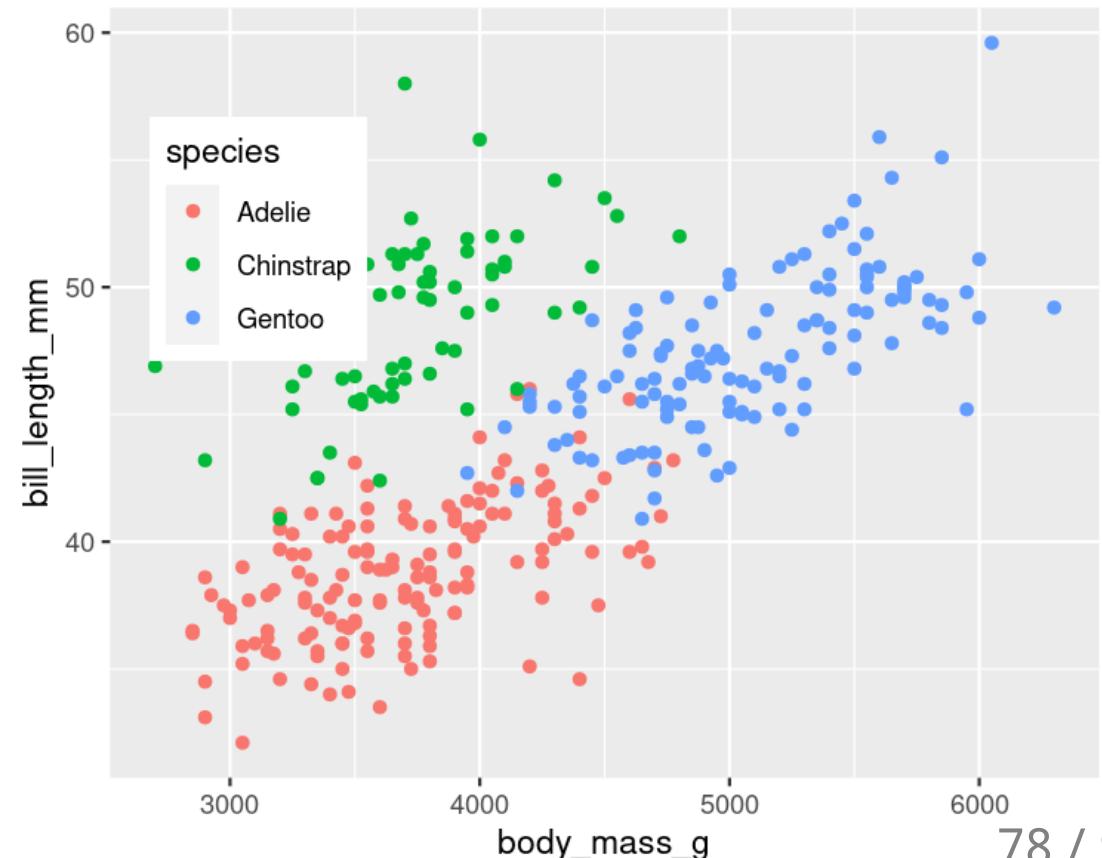
At the: top, bottom, left, right

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



Exactly here

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



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()

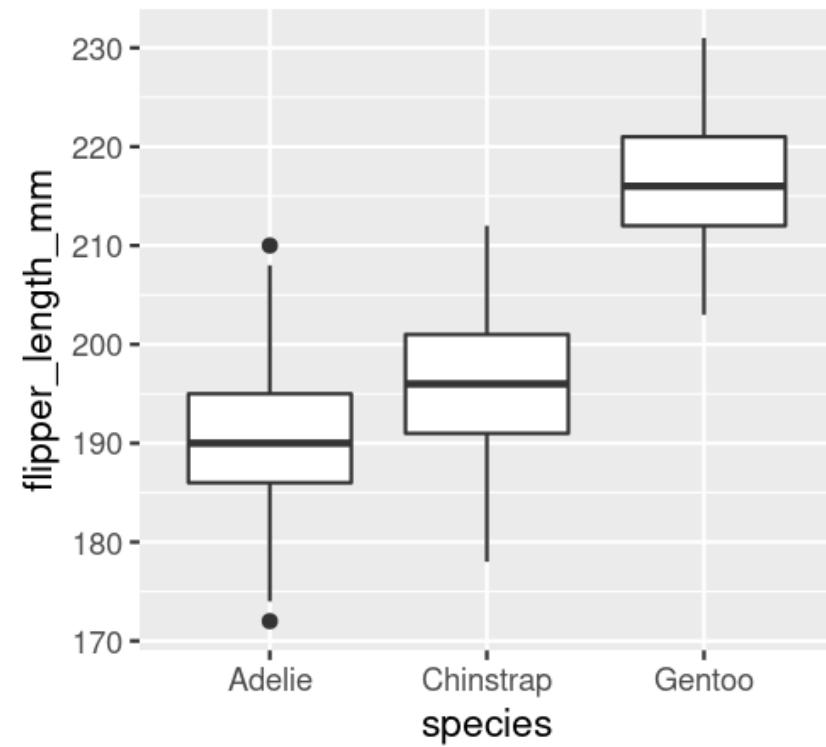
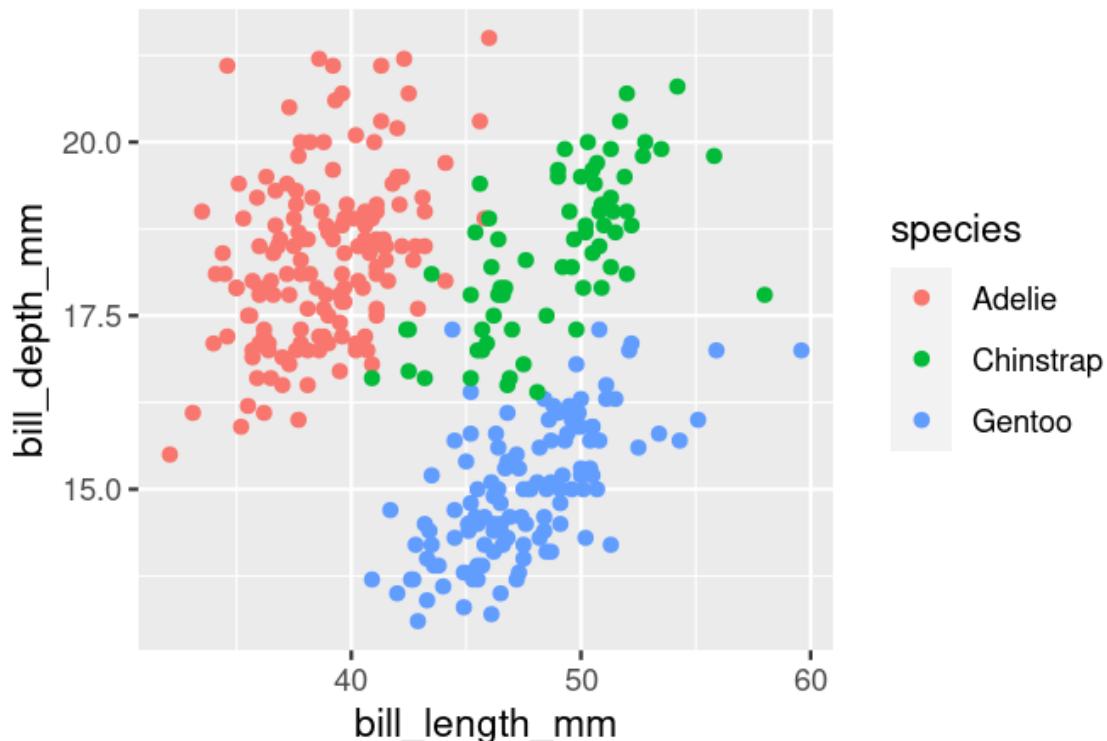
g2 <- ggplot(data = penguins, aes(x = species, y = flipper_length_mm)) +
  geom_boxplot()

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

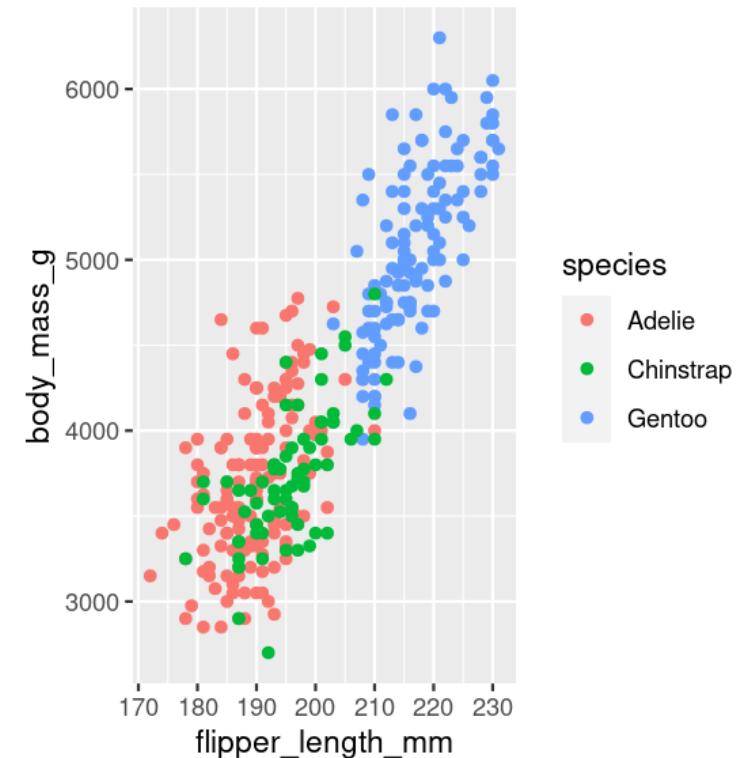
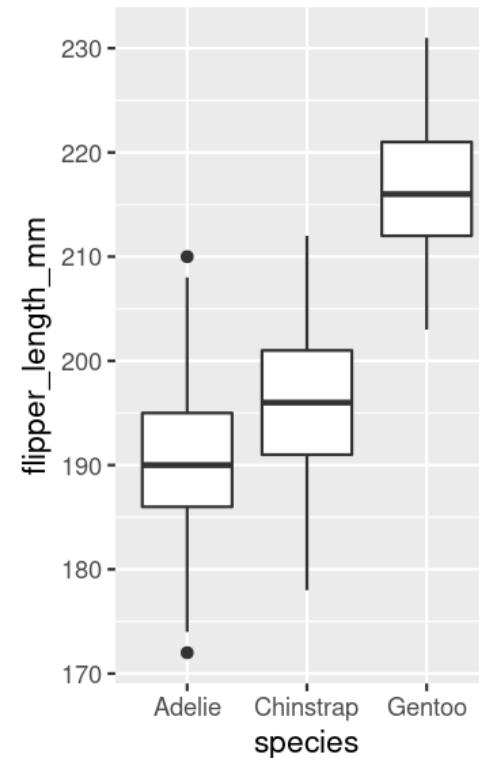
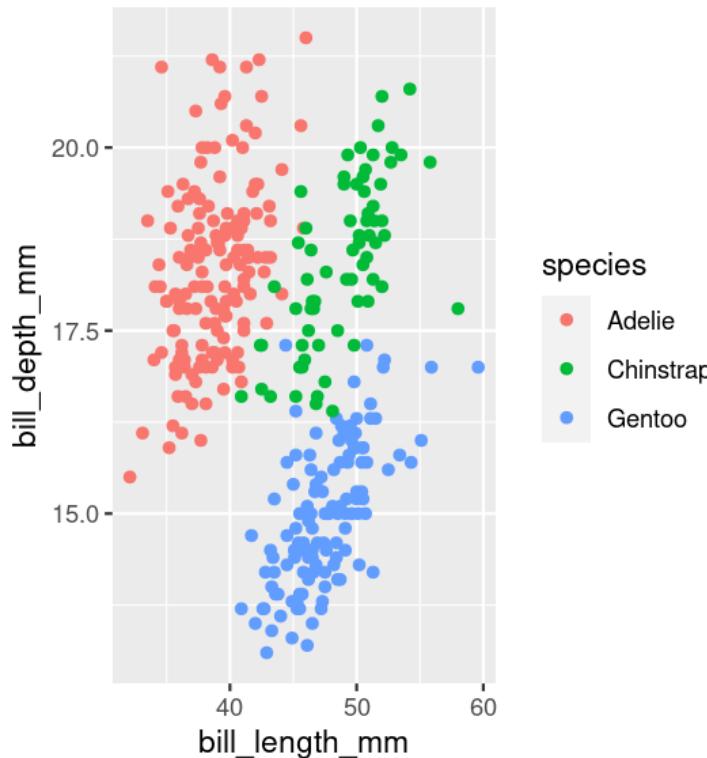
`g1 + g2`



Combining plots with **patchwork**

Side-by-Side 3 plots

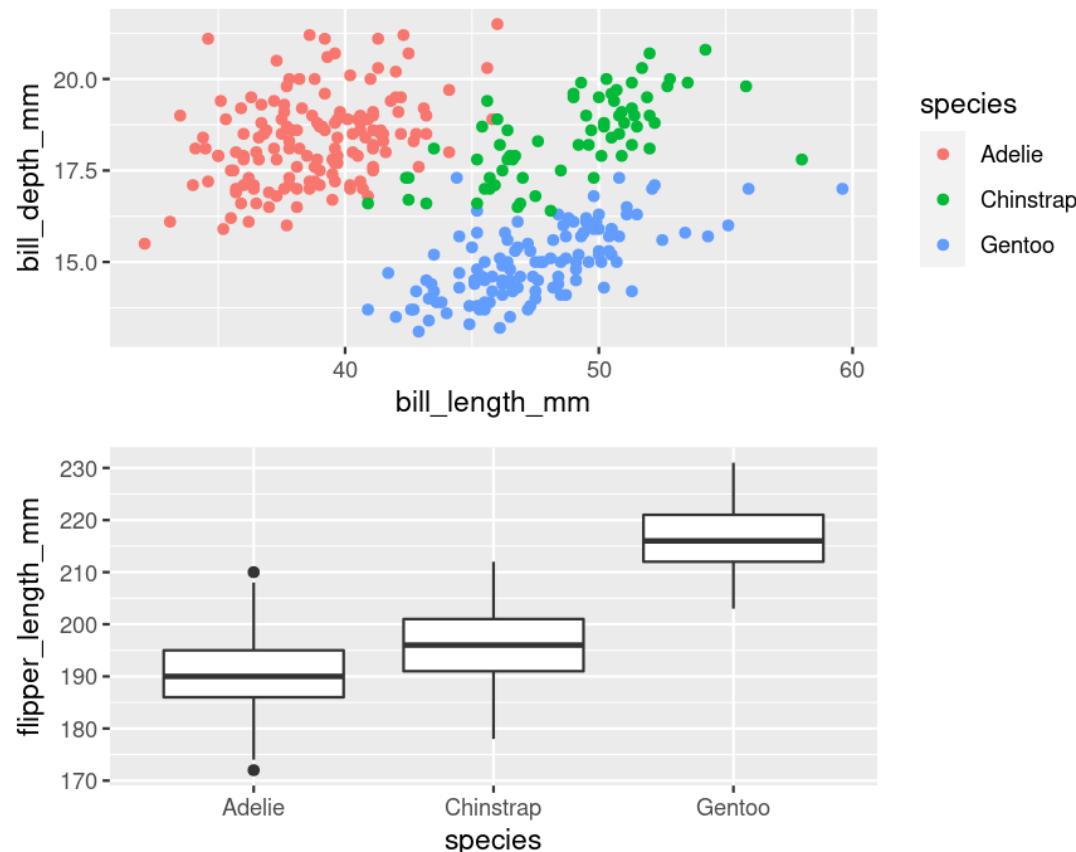
g1 + g2 + g3



Combining plots with **patchwork**

Stacked 2 plots

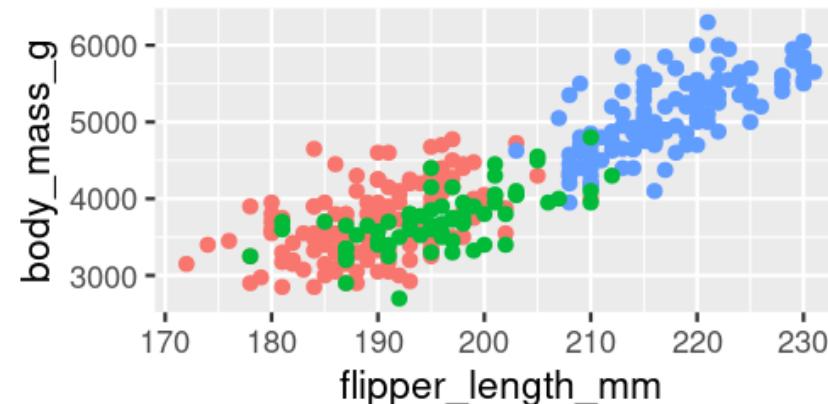
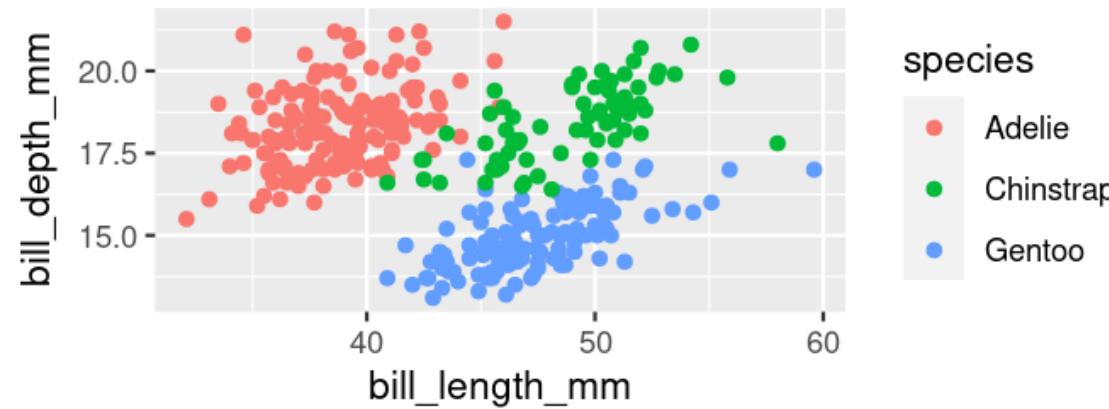
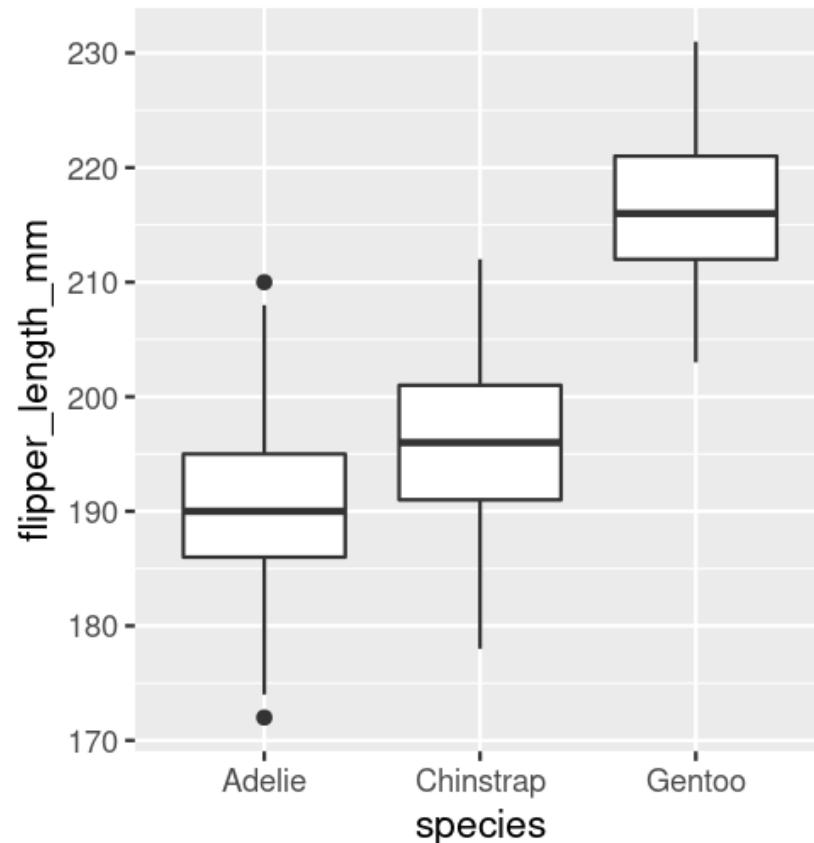
g1 / g2



Combining plots with **patchwork**

More complex arrangements

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



species

- Adelie
- Chinstrap
- Gentoo

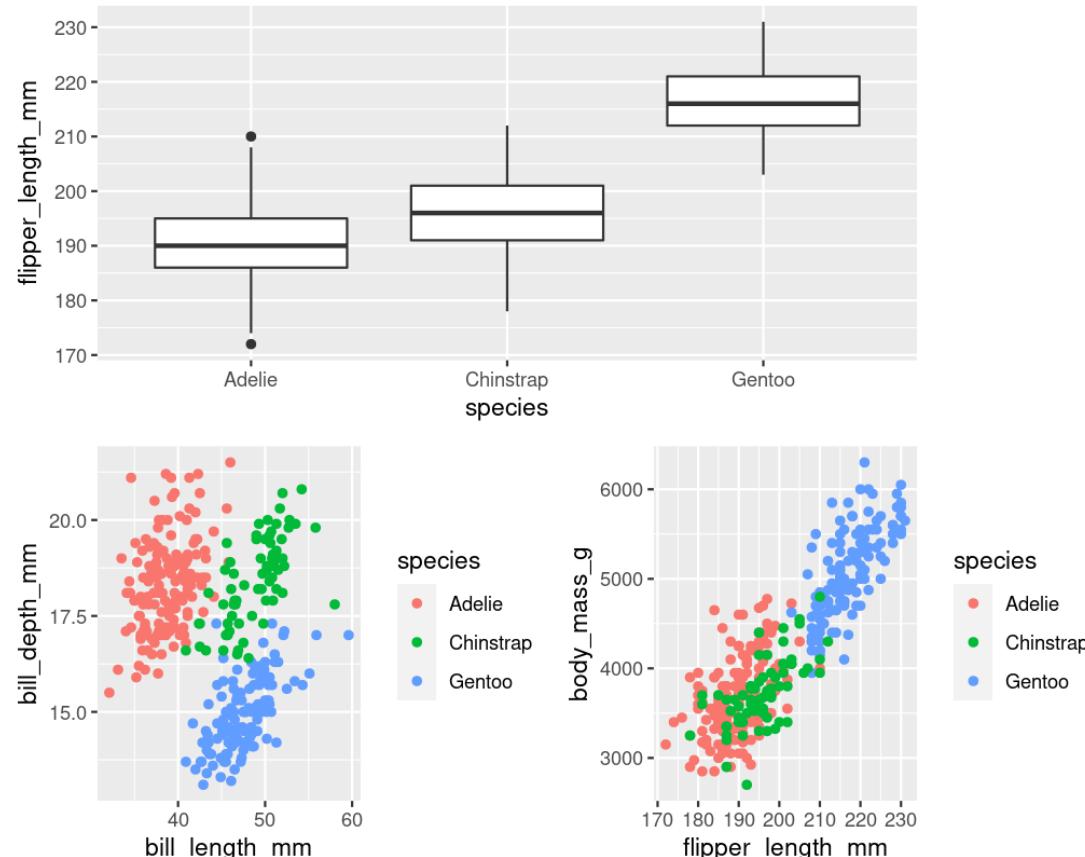
species

- Adelie
- Chinstrap
- Gentoo

Combining plots with patchwork

More complex arrangements

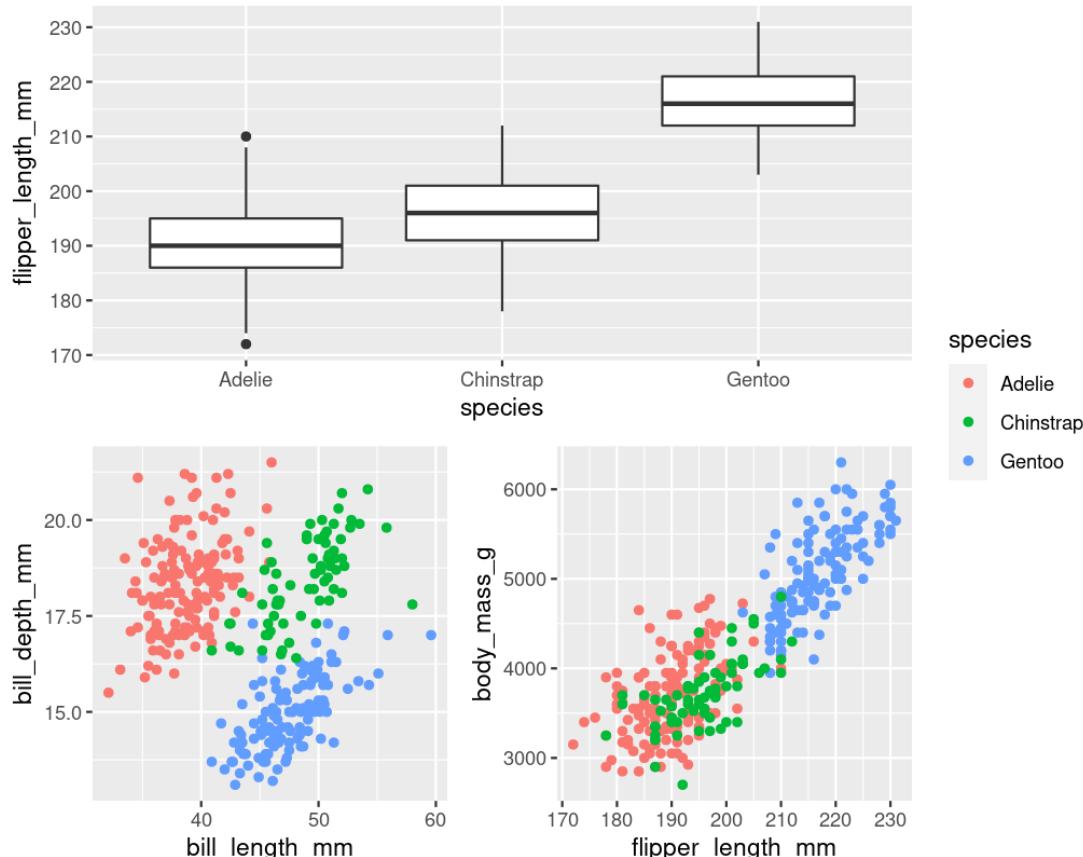
```
g2 / (g1 + g3)
```



Combining plots with patchwork

"collect" common legends

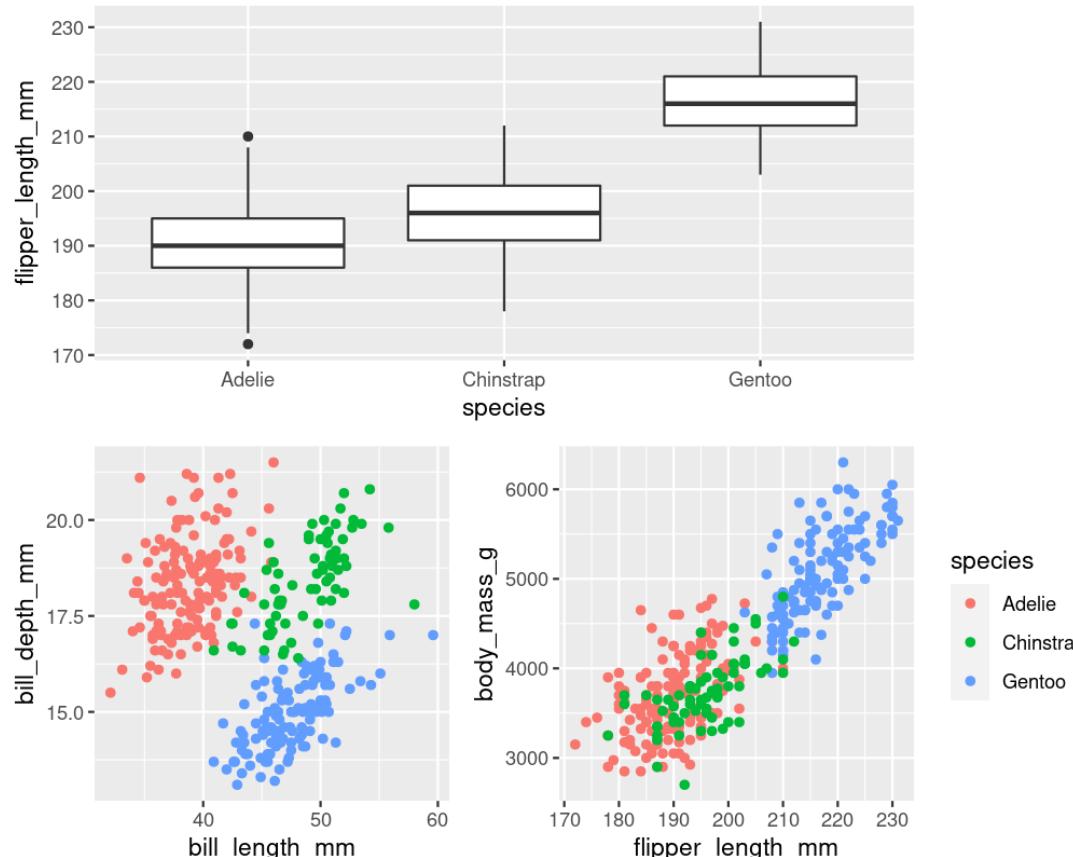
```
g2 / (g1 + g3) + plot_layout(guides = "collect")
```



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

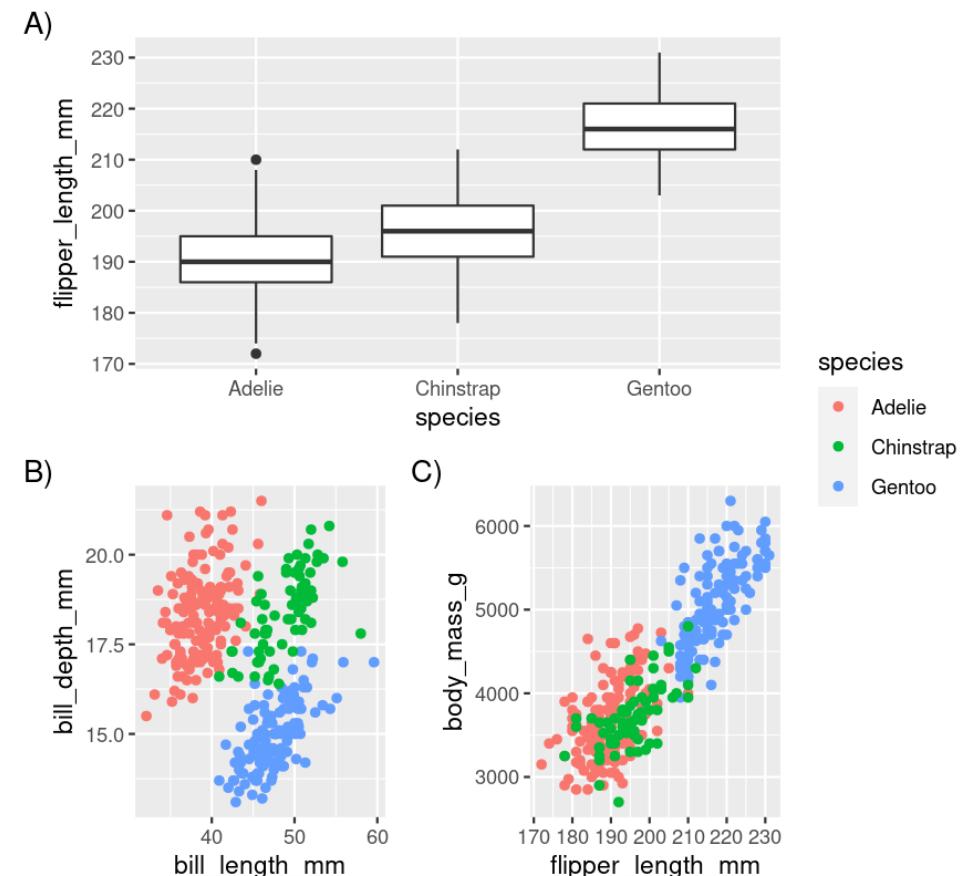


Fig 1. Penguins Data Summary

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 8 x 3.6 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: Further reading (all **Free!**)

- RStudio > Help > Cheatsheets > Data Visualization with ggplot2
- [ggplot2 book v3](#)
 - By Hadley Wickham, Danielle Navarro, and Thomas Lin Pedersen
- [Cookbook for R](#) - by Winston Chang
 - See also R Graphics Cookbook by Winston Chang
- [R for Data Science](#)
 - [Data Visualization](#)

Your Turn!

Create a figure with...

- Custom colour mapping (i.e. `scales_....`)
- Clear, human-readable labels
- More than one graph, each one tagged (e.g., A) or B))
- With more than one geom type
- At least one scatterplot with regression line

:D

OR... Load your own data and create a figure of your own!