

Creating Figures as an Intro to R

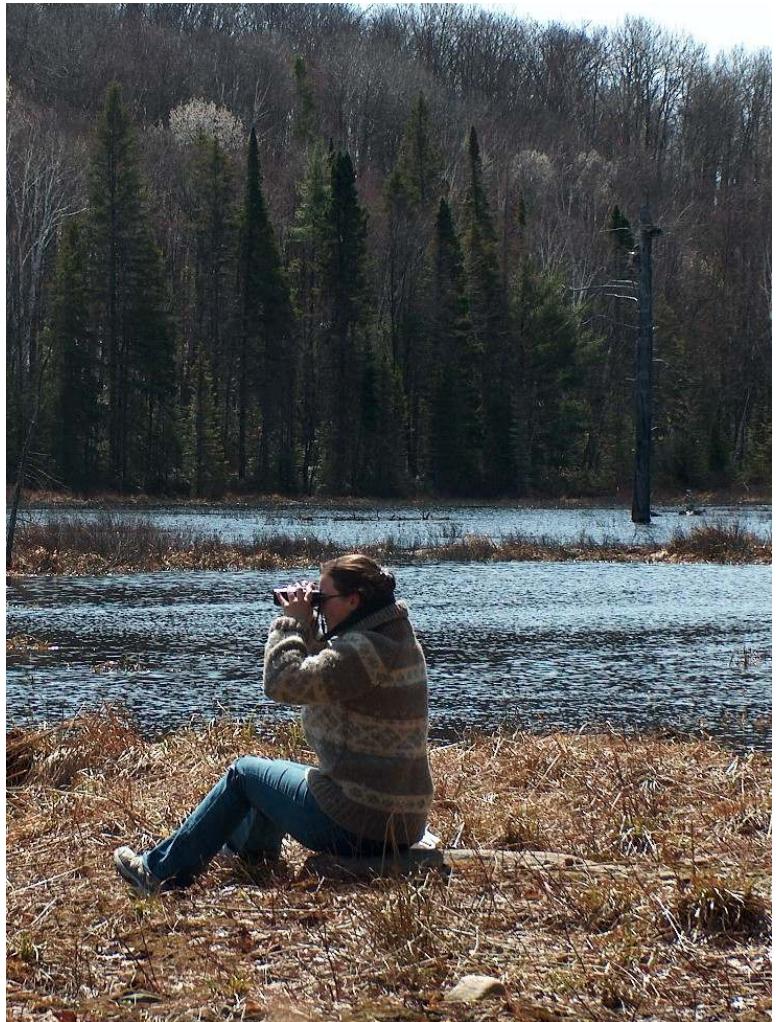
Using the `ggplot2` package



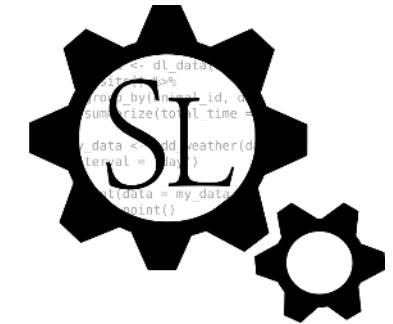
Preamble

Thank you

- Workshop developed by Dr. Steffi Lazerte
- R programmer



Dr. Steffi LaZerte
Analysis and Data Tools for Science



Me and my creatures



What about you?

- Name
- Background (Role, Area of study, etc.)
- Familiarity with R or Programming
- Creatures (furry, feathery, scaley, green or otherwise)?

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!

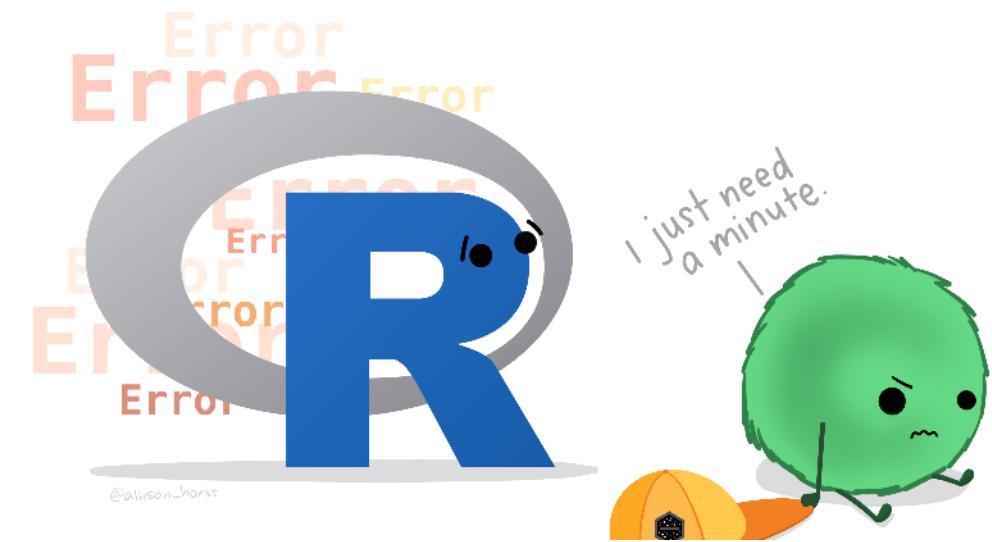
About this Lab/Tutorial

Format

- I will provide you tools and workflow to get started with making figures in R
- We'll have hands-on activities, and demonstrations

R is hard: But have no fear!

- Don't expect to remember everything!
- Copy/Paste is your friend (never apologize for using it!)
- Consider this workshop a resource to return to



What is R?

RStudio vs. R



RStudio



R

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

R is a 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
```

R, save this value for later

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

R, multiply this value by 6

```
alex_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
```

But R is powerful (and reproducible)!

The screenshot shows the R Global Environment window. It has three main sections: Data, Values, and Functions.

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

A green oval highlights the value for `telem_total`, which is 12950046 obs. of 10 variables.

Definitions

Reproducibility

- Given the same data set the analyses can be reproduced

Replicability

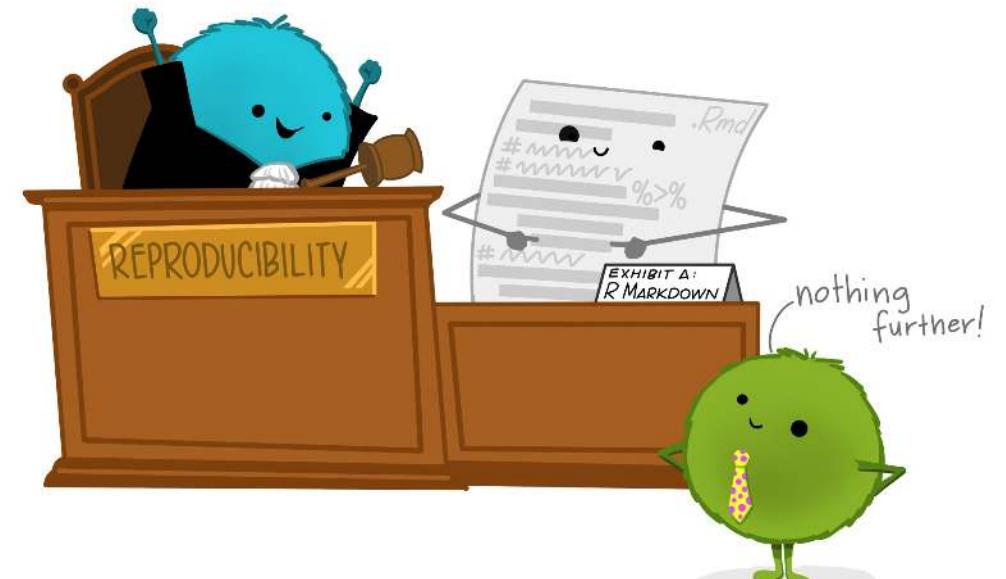
- A separate investigator conducted an independent study and came to the same conclusion as the original study

Reproducibility

- Less about ensuring the correctness of the results
- More about being transparent and understanding exactly what was done
 - This is especially important in large and complex data sets

! Important

A study can be reproducible and still be wrong



Allison Horst

Working with large data sets

Data munging/wrangling

1. Formatting
2. Merging
3. Quality assurance
 - NA's
 - 0's
 - Detection limits
 - Outliers
 - Typos/errors



Allison Horst

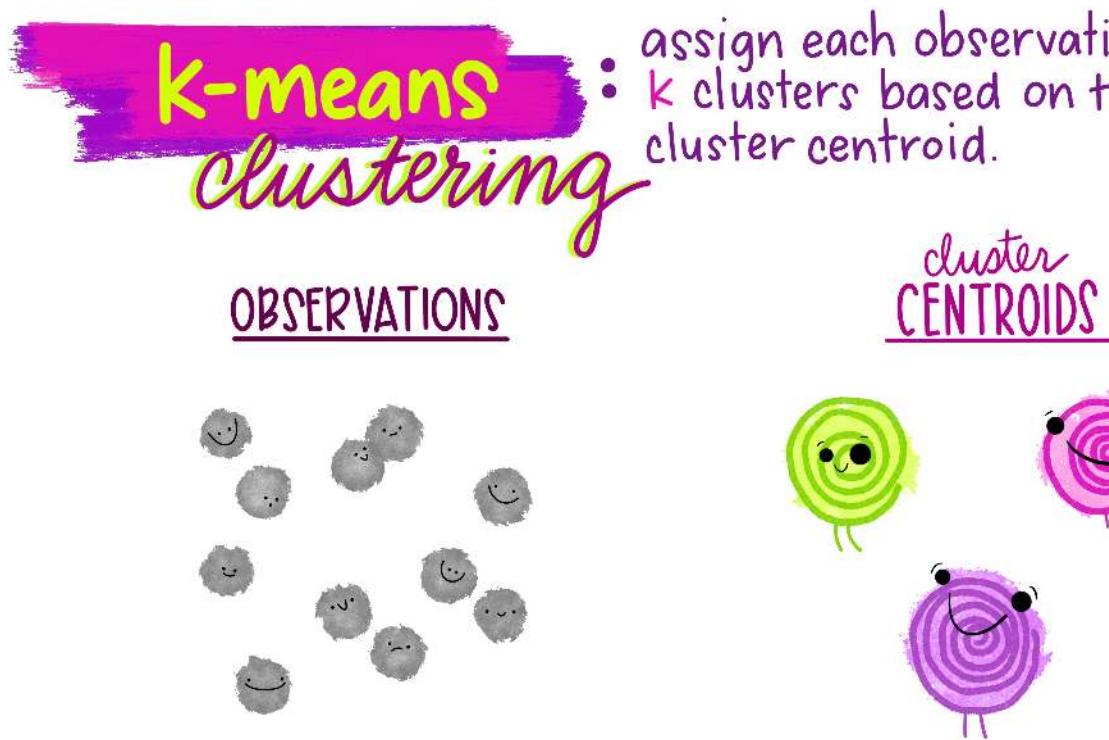
Need to document every change you make

Data analysis

Analysis/figures

- Data used
- Analysis used (trial and error)
- Parameters
- Diagnostics
- Figure creation process
- Software versions

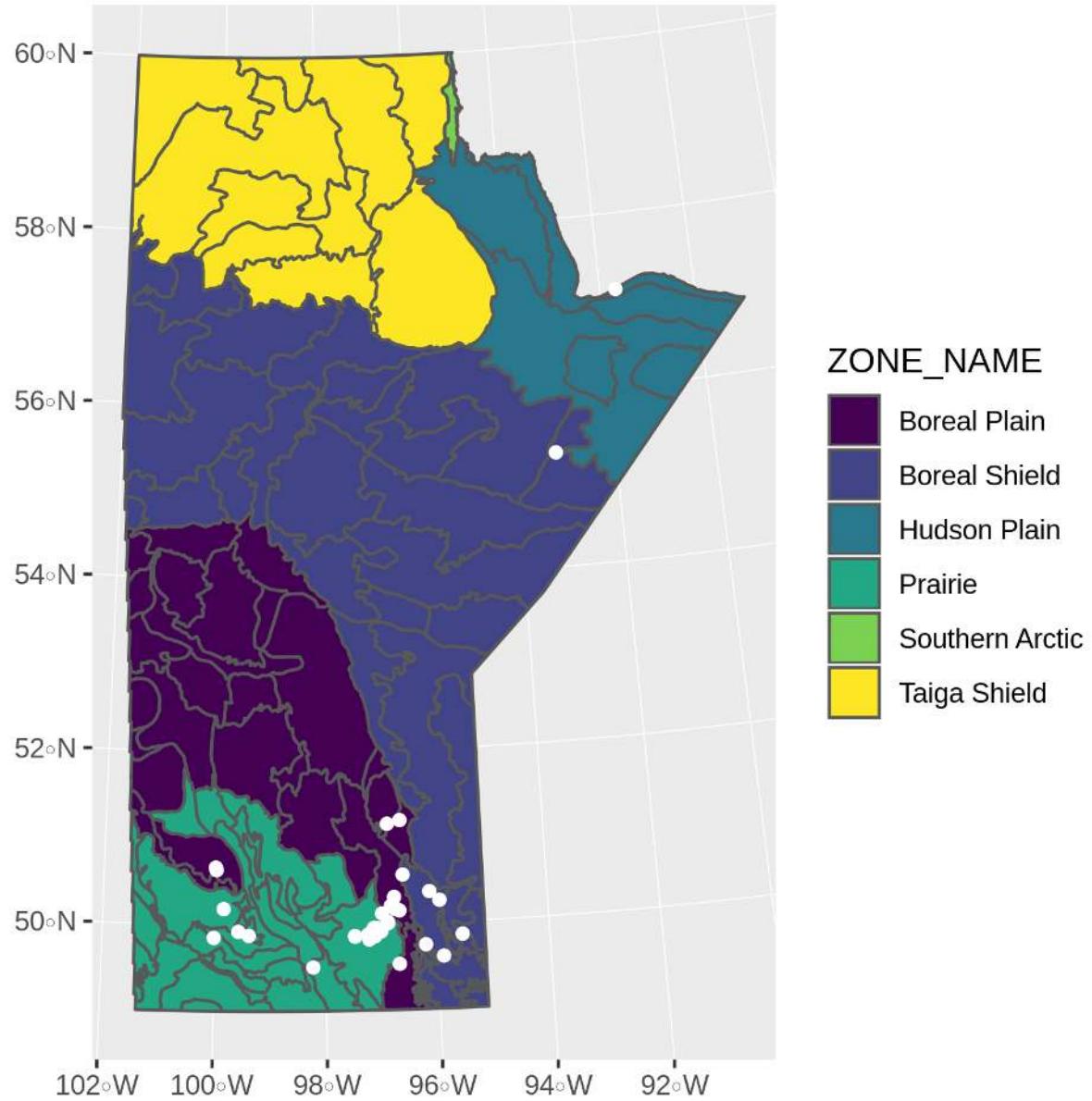
Hard to write papers if you don't keep track of this!



@ausr_horst

Allison Horst

R is also beautiful



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

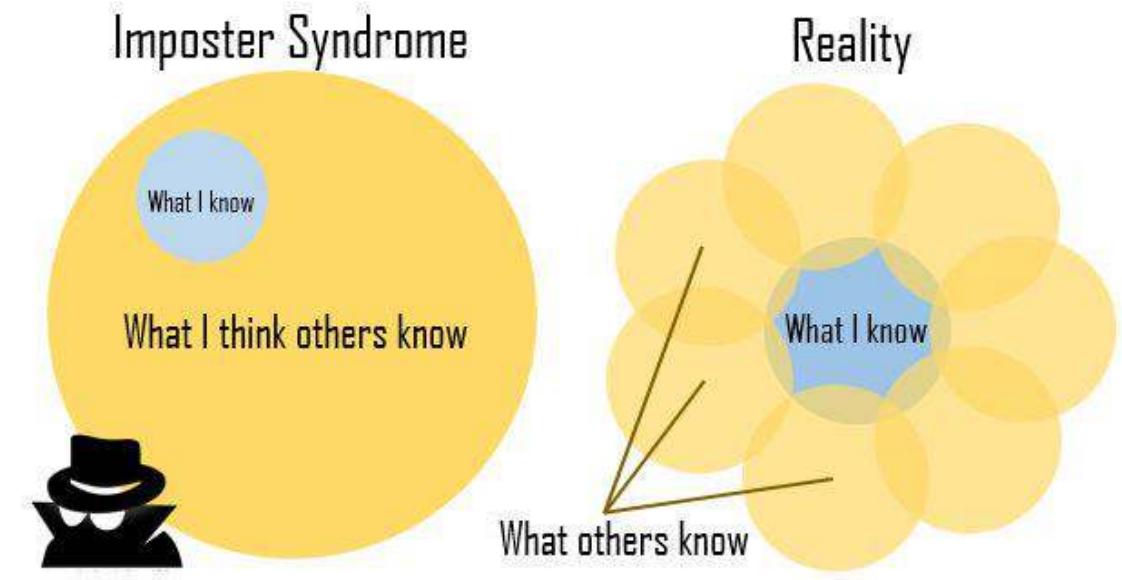
R is available as Free Software under the terms of the [Free Software Foundation's GNU General Public License](#) in source code form. It compiles and runs on a wide variety of UNIX platforms and similar systems (including FreeBSD and Linux), Windows and MacOS.

ImpostR Syndrome

Impost^R
Syndrome

ImpostR Syndrome

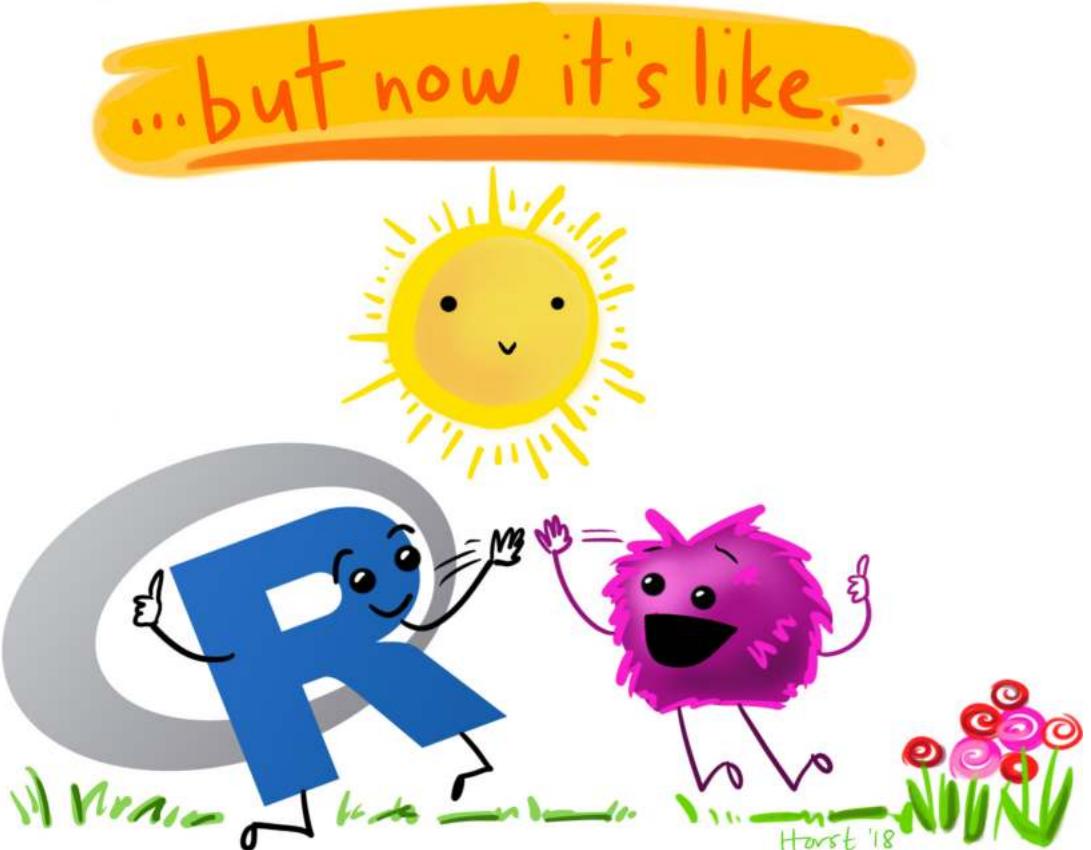
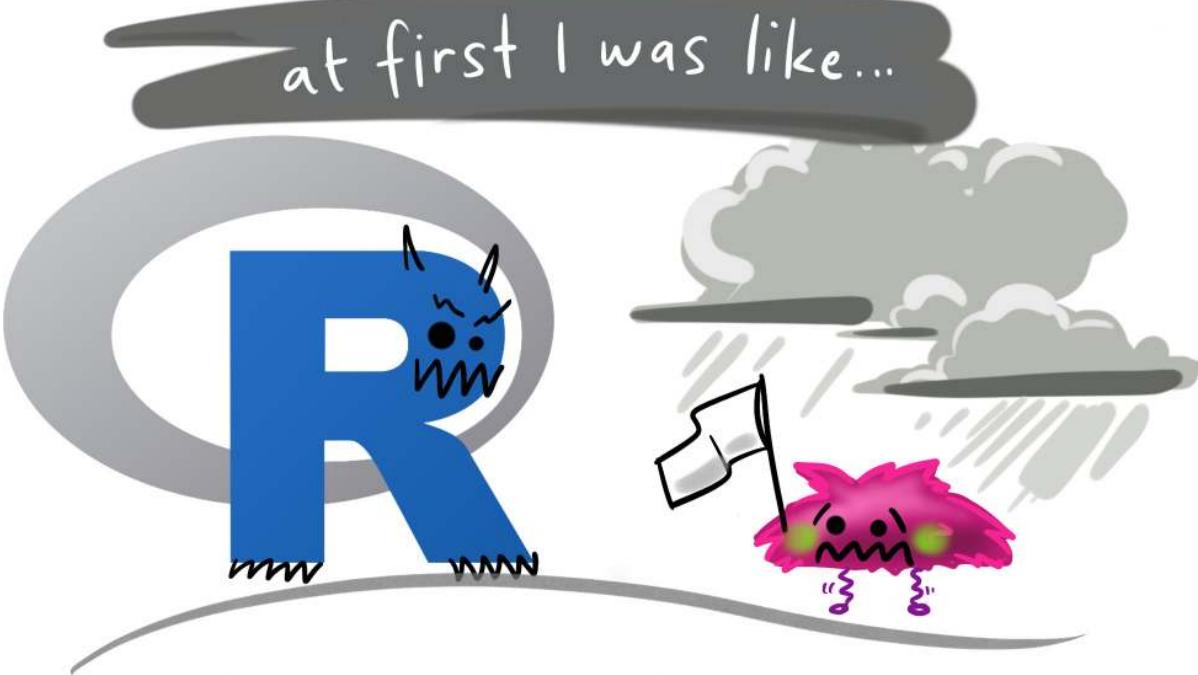
ImpostR Syndrome



Moral of the story?

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

The Goal



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

For example:

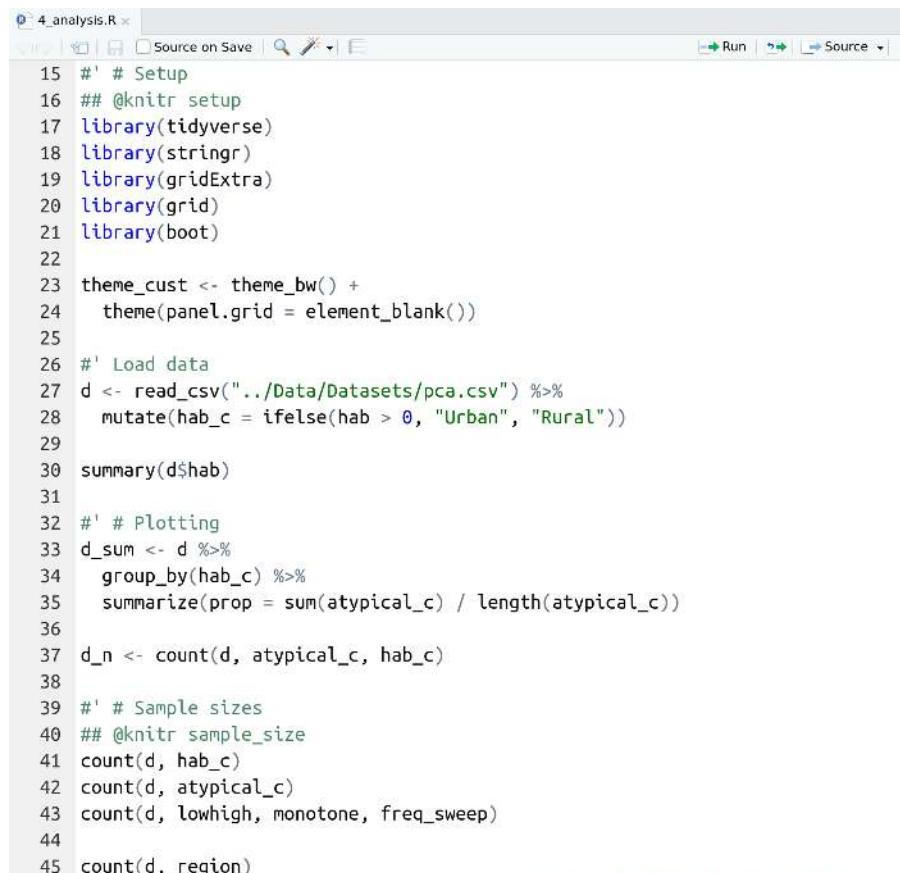
```
mean(c(1, 2, 3, 4))
```

```
[1] 2.5
```

Code

Output

Script



```
4_analysis.R * Source on Save Run Source ▾
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() +
  theme(panel.grid = element_blank())
24
25 #' Load data
26 d <- read_csv("../Data/Datasets/pca.csv") %>%
  mutate(hab_c = ifelse(hab > 0, "Urban", "Rural"))
27
28 summary(d$hab)
29
30 #' # Plotting
31 d_sum <- d %>%
  group_by(hab_c) %>%
  summarize(prop = sum(atypical_c) / length(atypical_c))
32
33 d_n <- count(d, atypical_c, hab_c)
34
35 #' # Sample sizes
36 ## @knitr sample_size
37 count(d, hab_c)
38 count(d, atypical_c)
39 count(d, lowhigh, monotone, freq_sweep)
40 count(d, region)
```

RStudio vs. R



RStudio



R

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

RStudio Features

Projects

- Handles working directories
- Organizes your work

Changing Options: Tools > Global Options

- General > Restore RData into workspace at startup (NO!)
- General > Save workspace to on exit (NEVER!)
- Code > Insert matching parens/quotes (Personal preference)

Let's change some options
in RStudio!

Packages

- Can use the package manager to install packages
- Can use the manager to load them as well, but not recommended

Getting Ready

 Open New File

(make sure you're in the RStudio Project)

 Write `library(tidyverse)` at the top

 Save this new script

(consider names like `intro.R` or `1_getting_started.R`)

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

1 ?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

```
1 # First load the packages
2 library(palmerpenguins)
3 library(ggplot2)
4
5 # Now create the figure
6 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +
7   geom_point()
```

1. Copy/paste or type this into the **script** window in RStudio

- You may have to go to File > New File > R Script

2. Click on the **first line of code**

3. Run the code

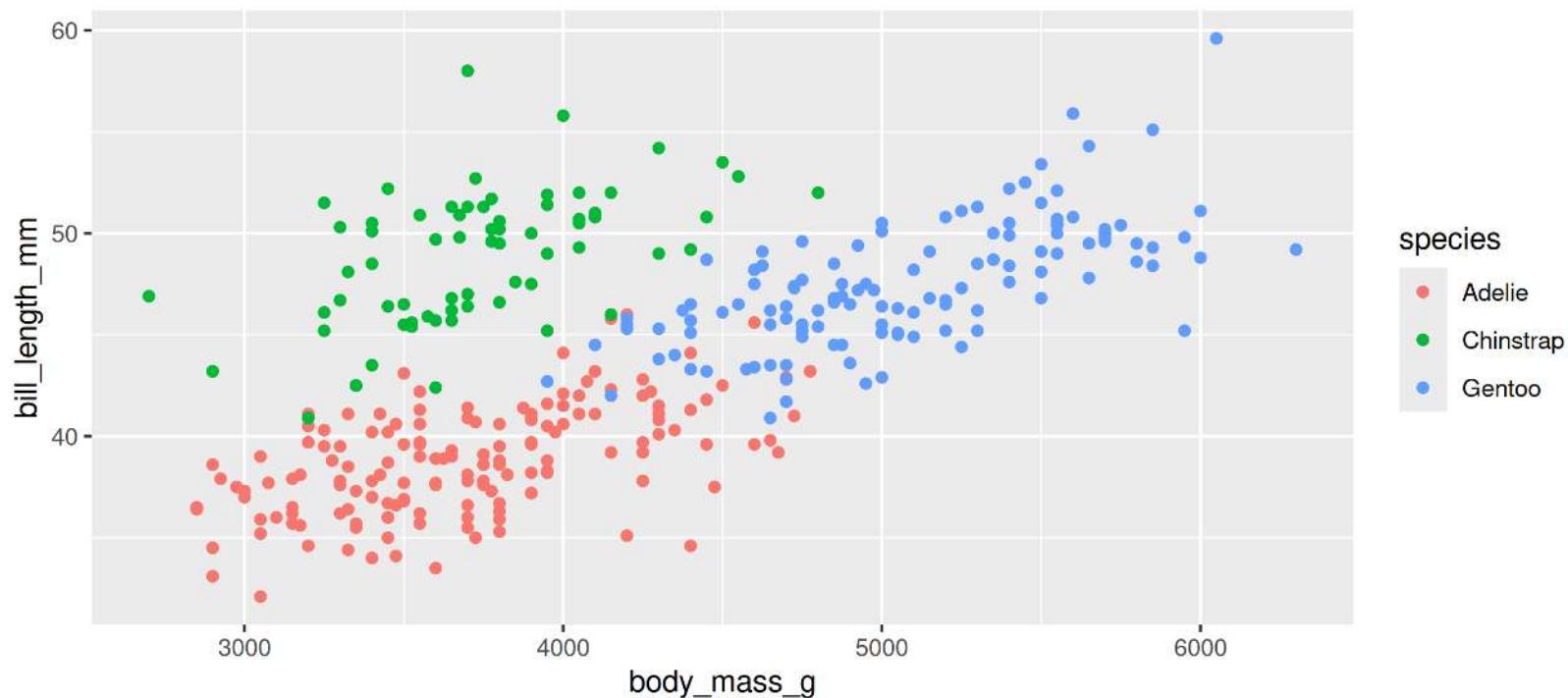
- Click ‘Run’ button (upper right) **or**
- Use the short-cut **Ctrl-Enter**

4. Repeat until all the code has run

First Code

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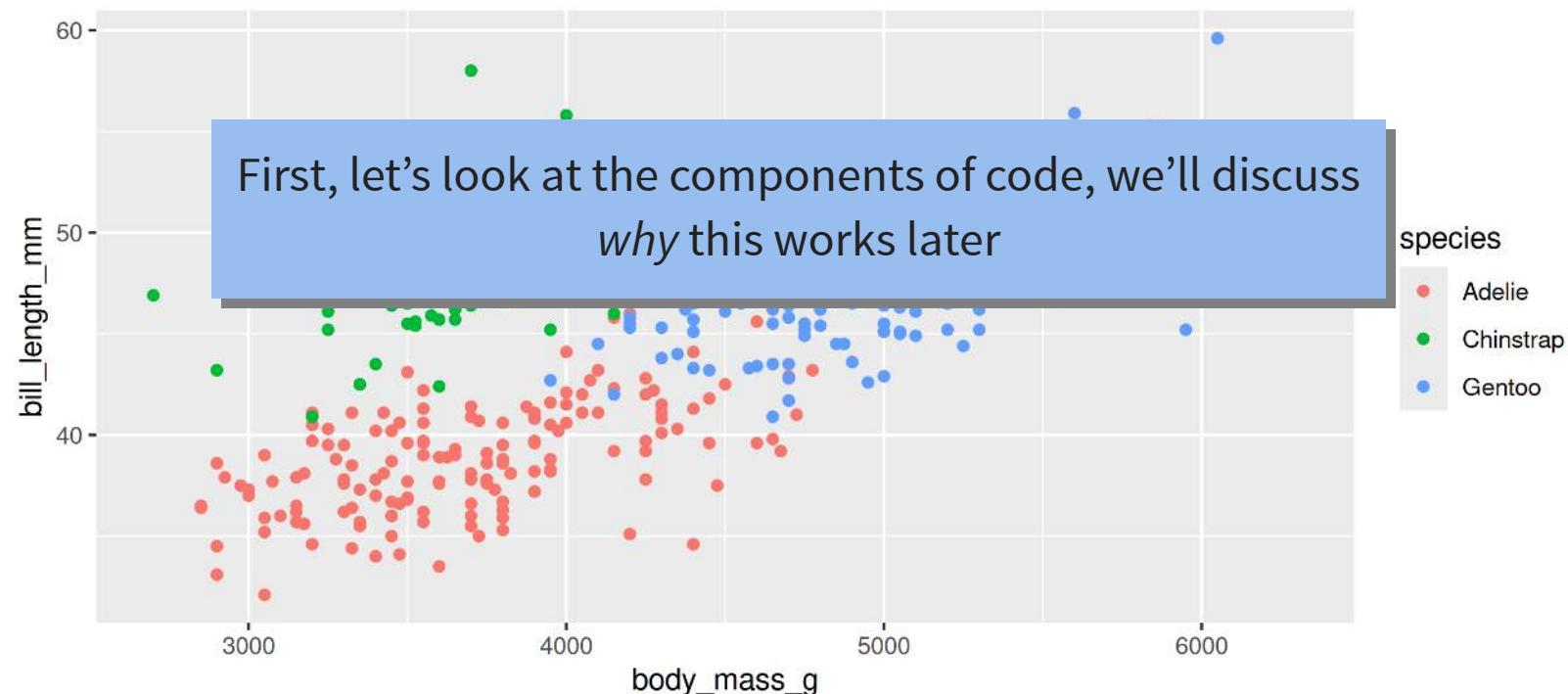
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).



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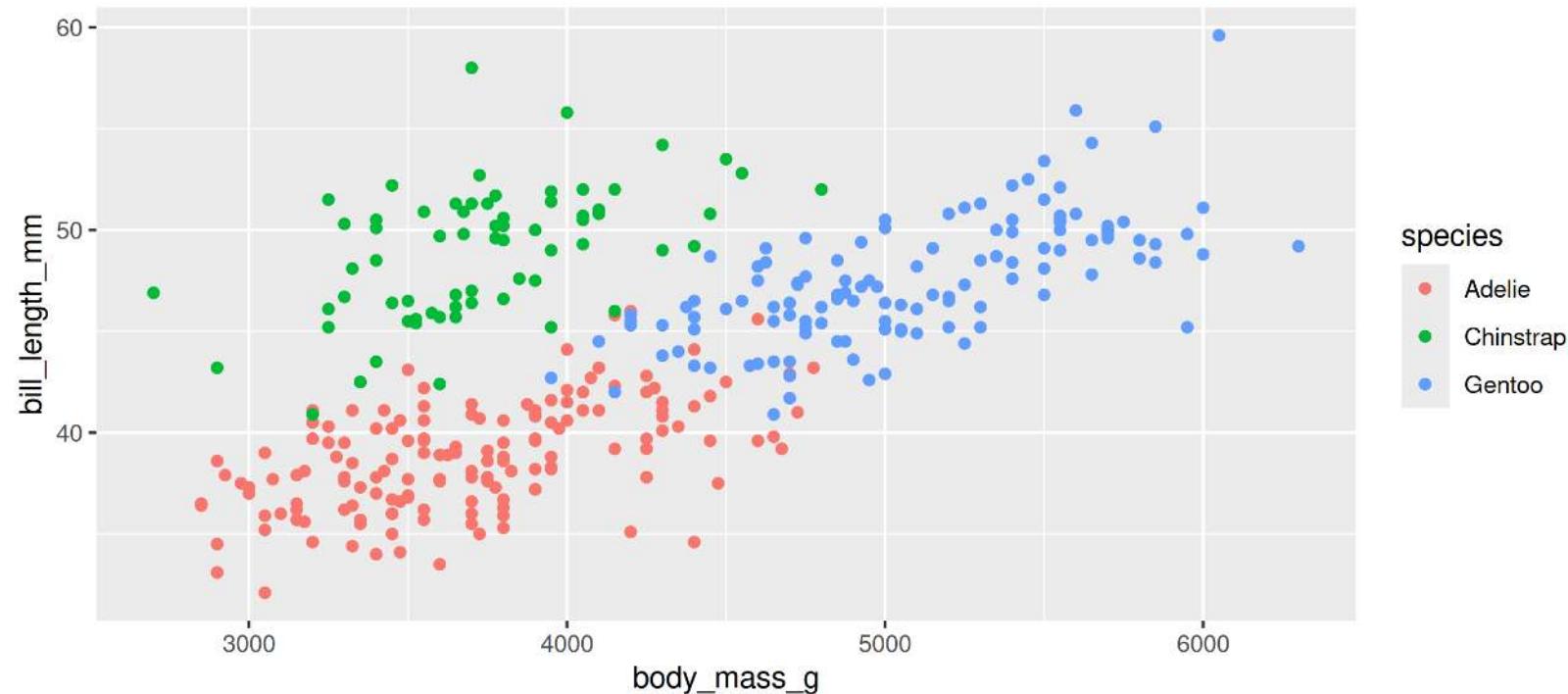


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Packages ggplot2 and palmerpenguins



species

- Adelie
- Chinstrap
- Gentoo

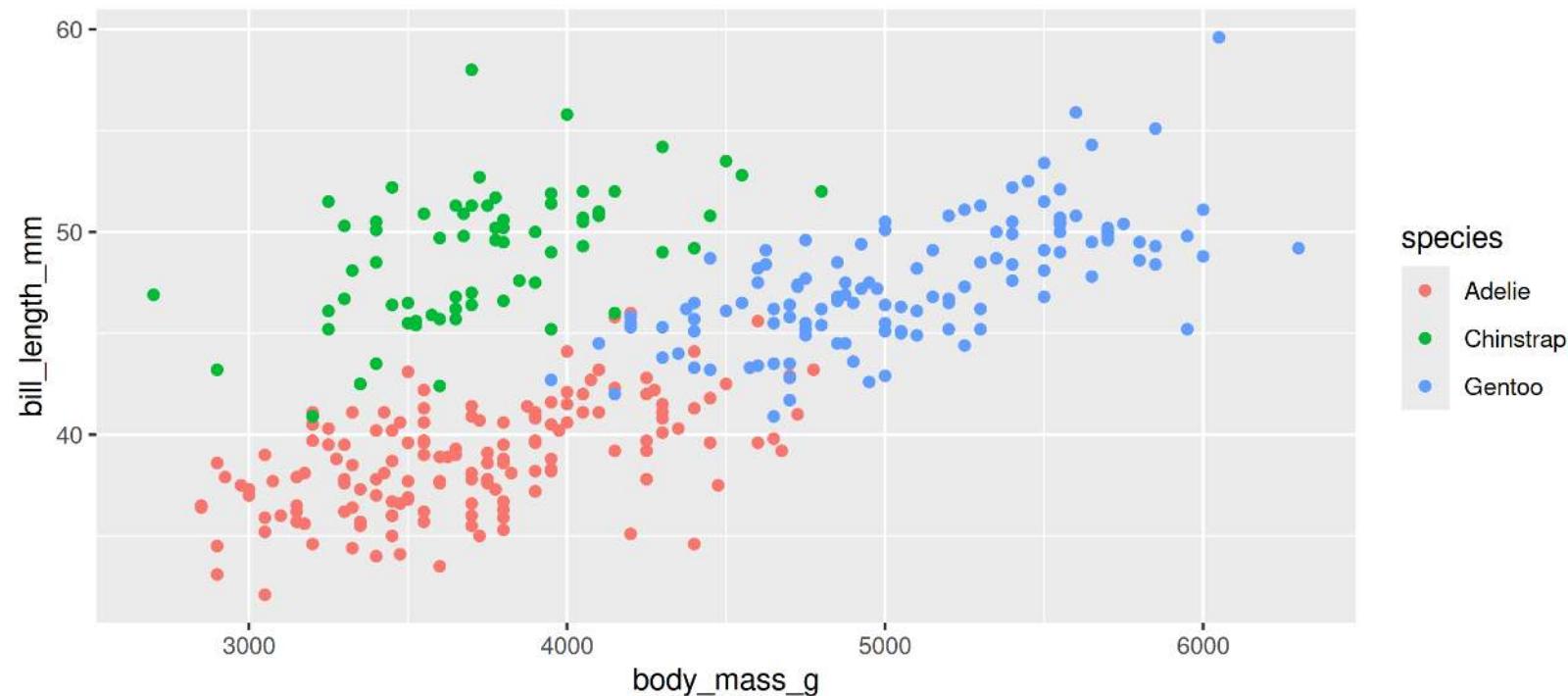
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7   geom_point()
```

Functions

library(), ggplot(), aes(), geom_point()

Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).



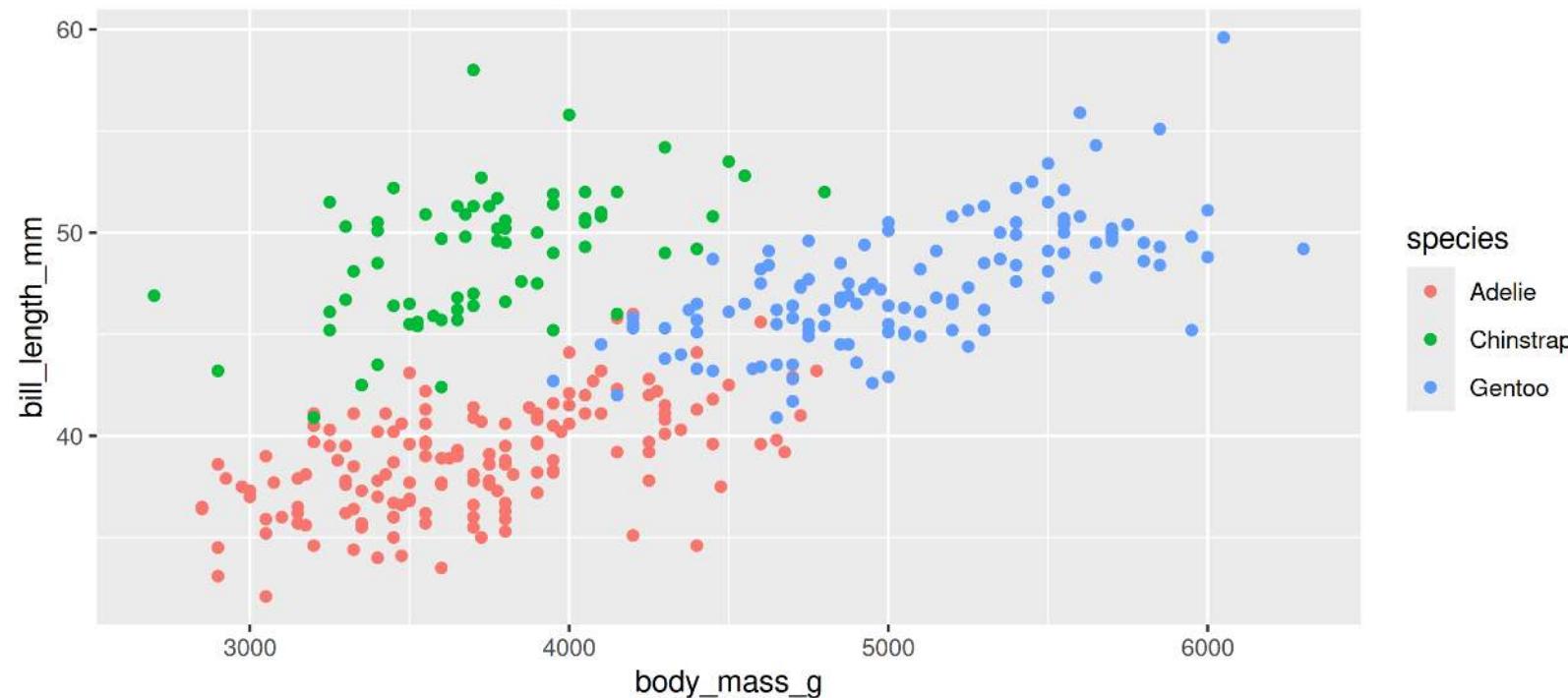
First Code

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7   geom_point()
```

+

(Specific to ggplot)

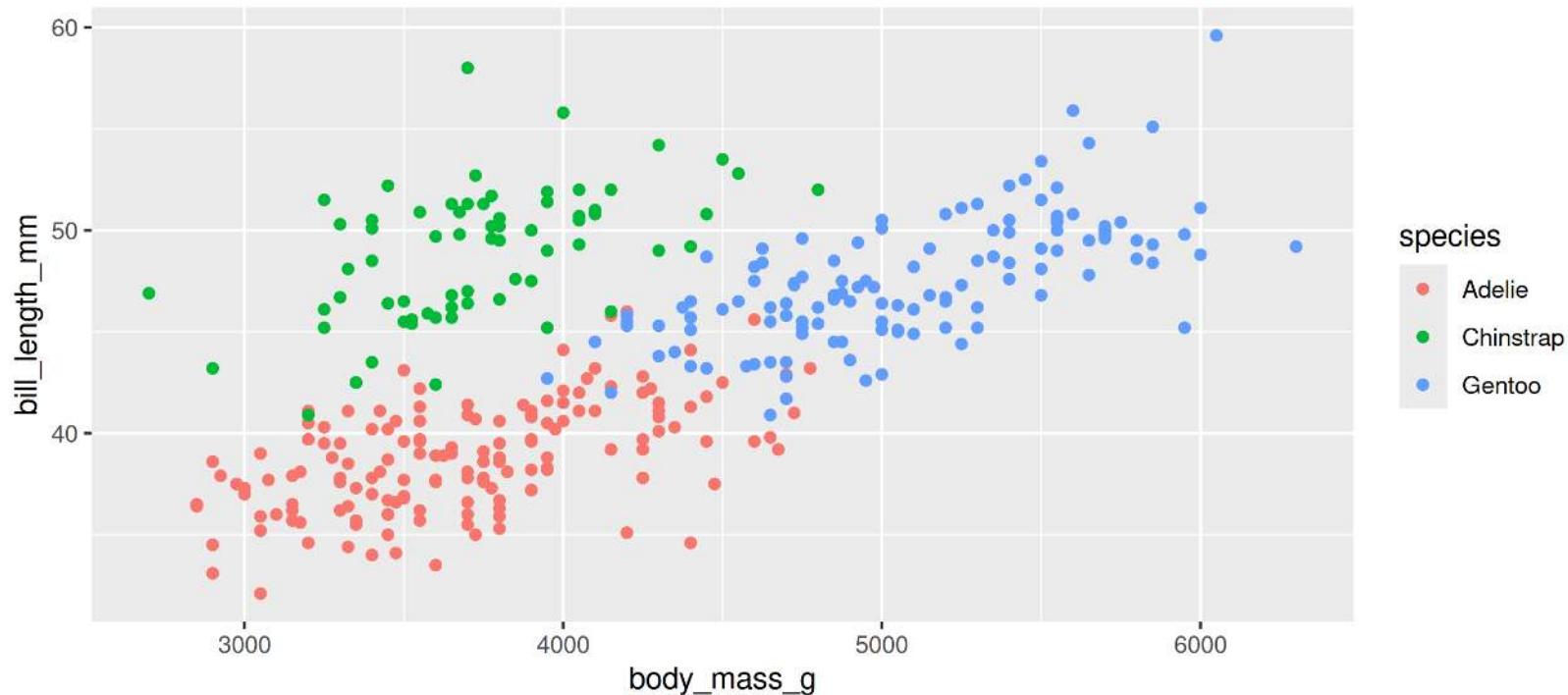
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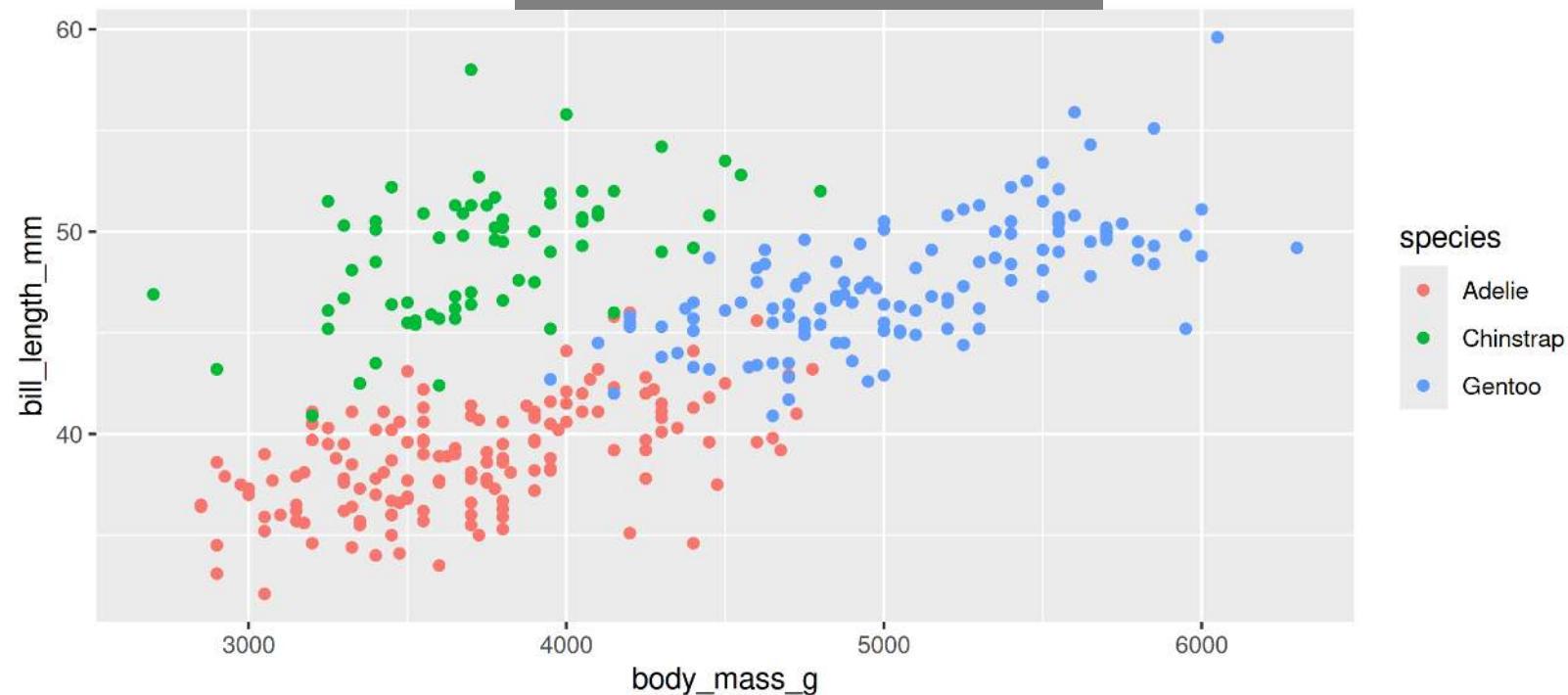


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Warning

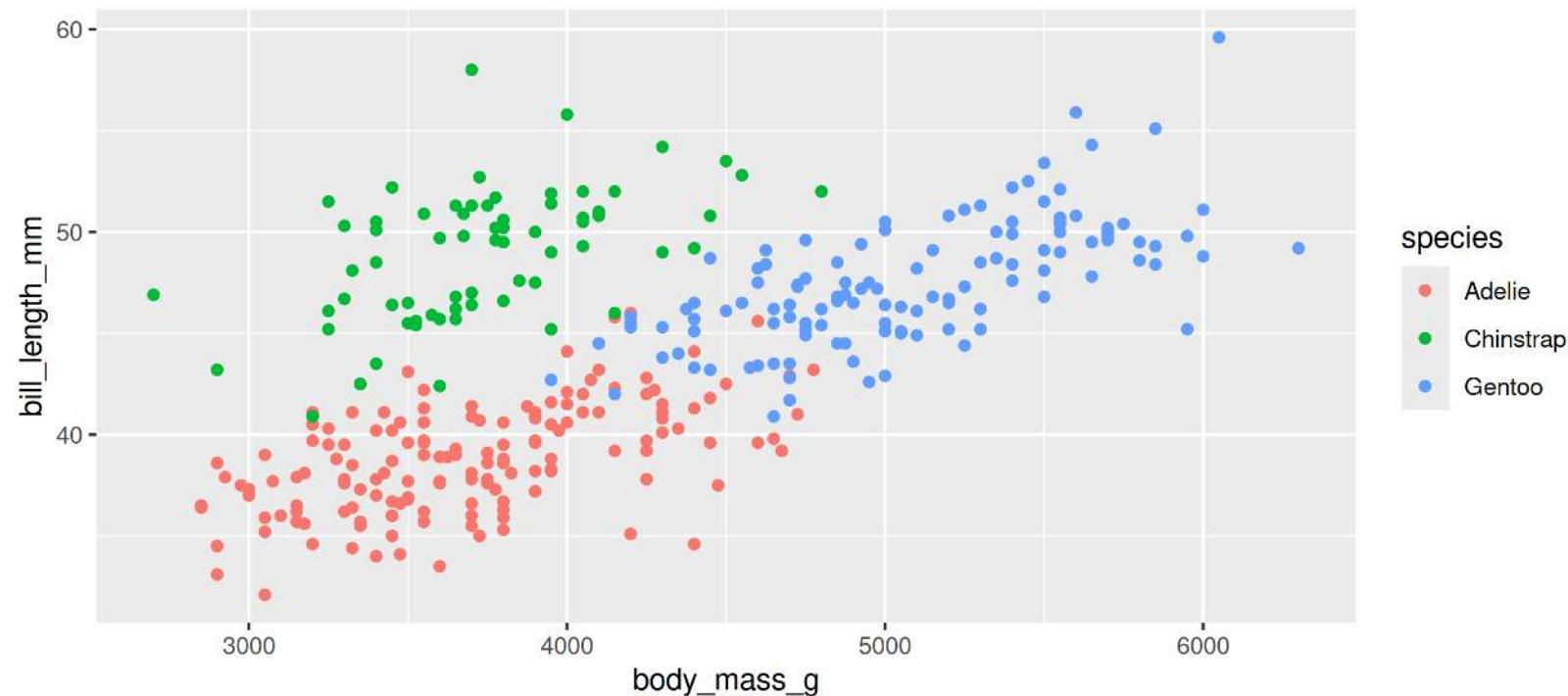


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7   geom_point()
```

Comments

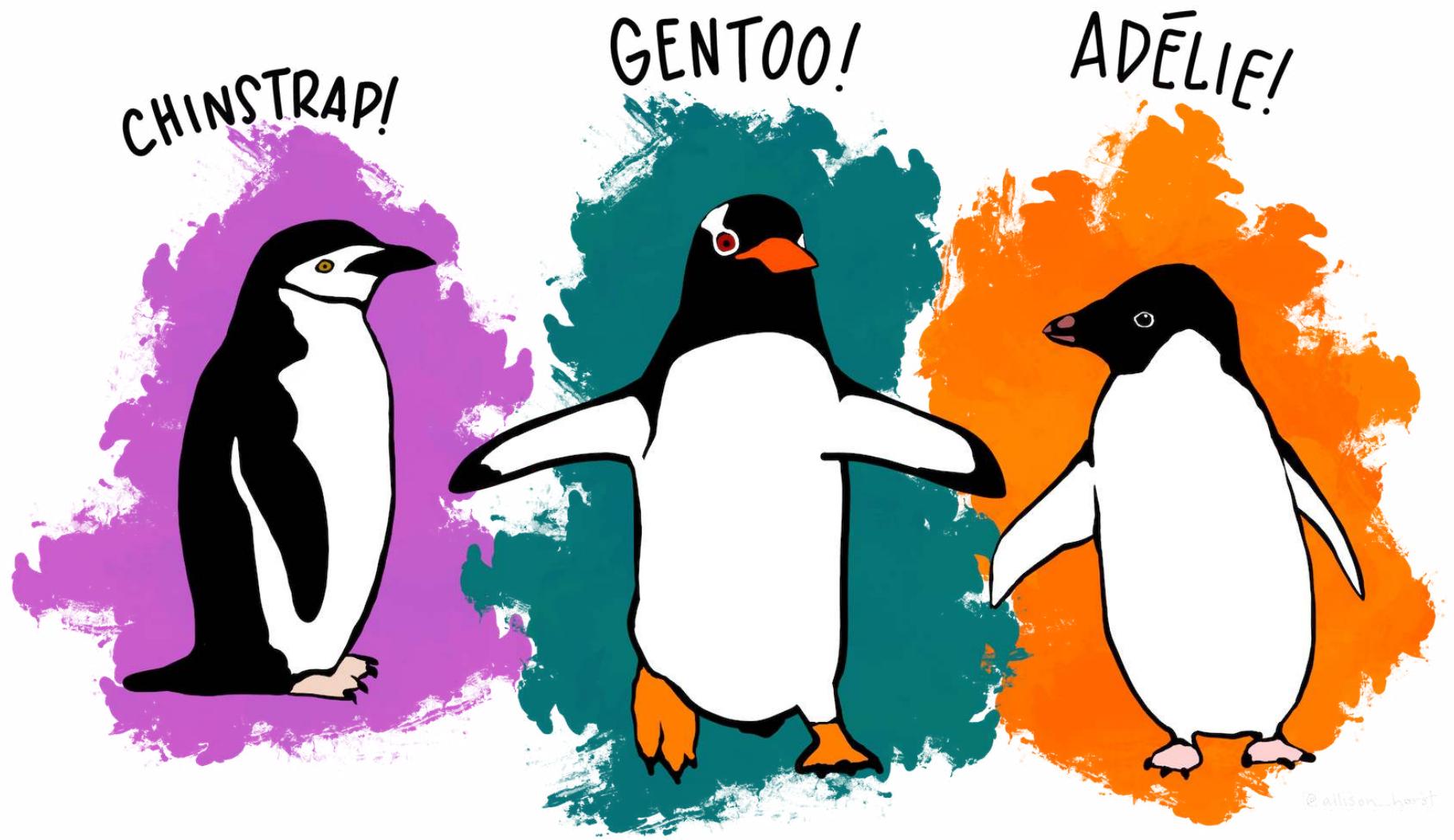
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).



Now you have the vocabulary!

Let's get started

Our data set: Palmer Penguins!



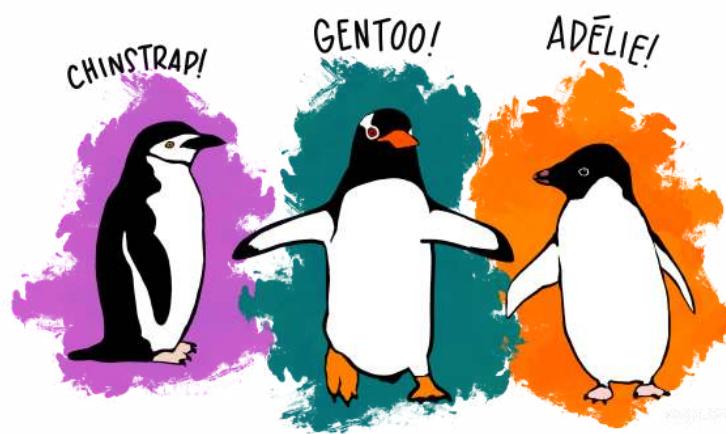
@allison_horst

Our data set: Palmer Penguins!

```
1 library(palmerpenguins)
2 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
9 Adelie  Torgersen     34.1           18.1            193       3475 <NA>   2007
10 Adelie Torgersen      42             20.2            190      4250 <NA>   2007
# i 334 more rows
```



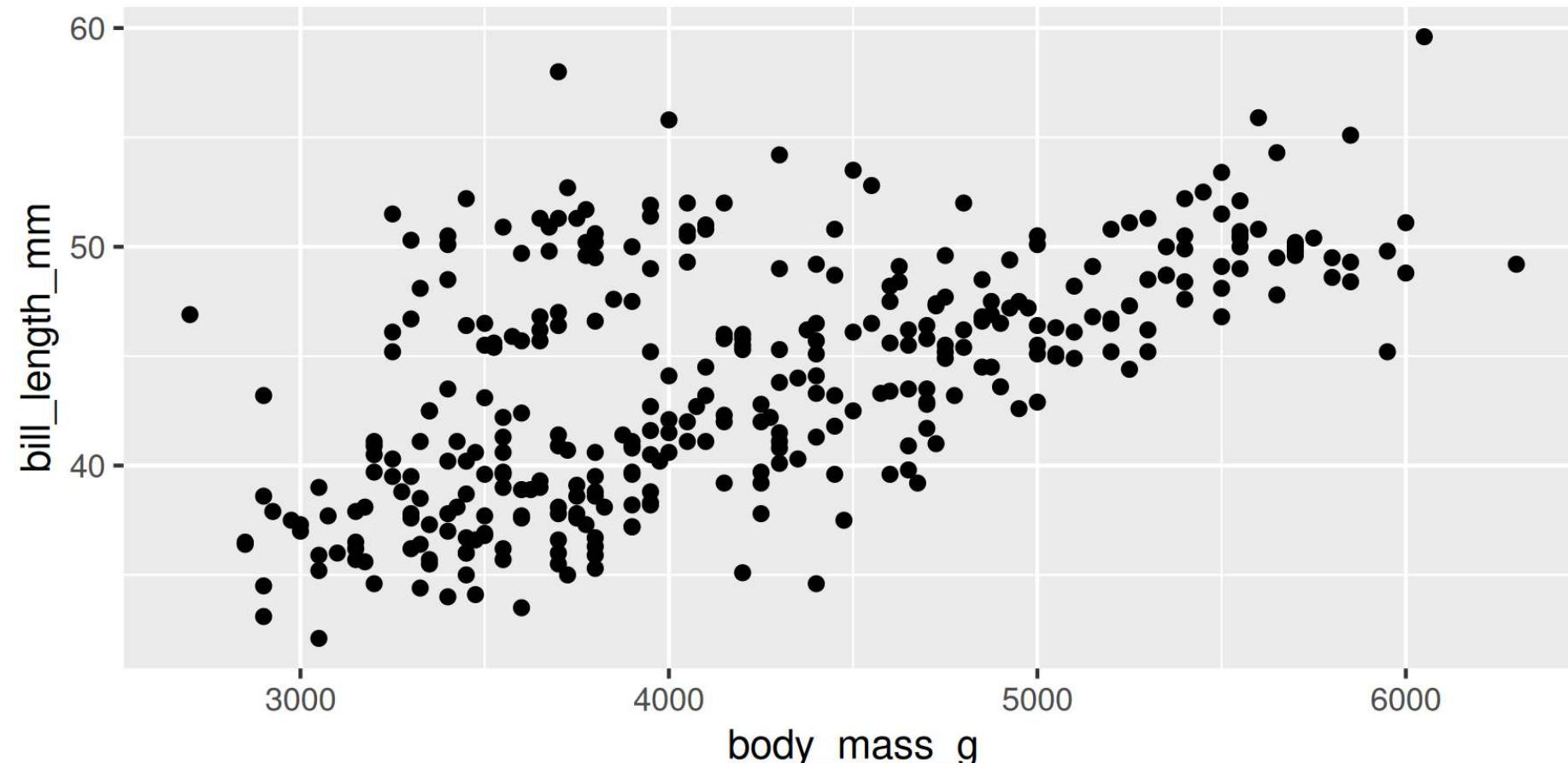


Your turn!

Run this code and look at the output in the console

A basic plot

```
1 library(palmerpenguins)
2 library(ggplot2)
3
4 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +
5   geom_point()
```



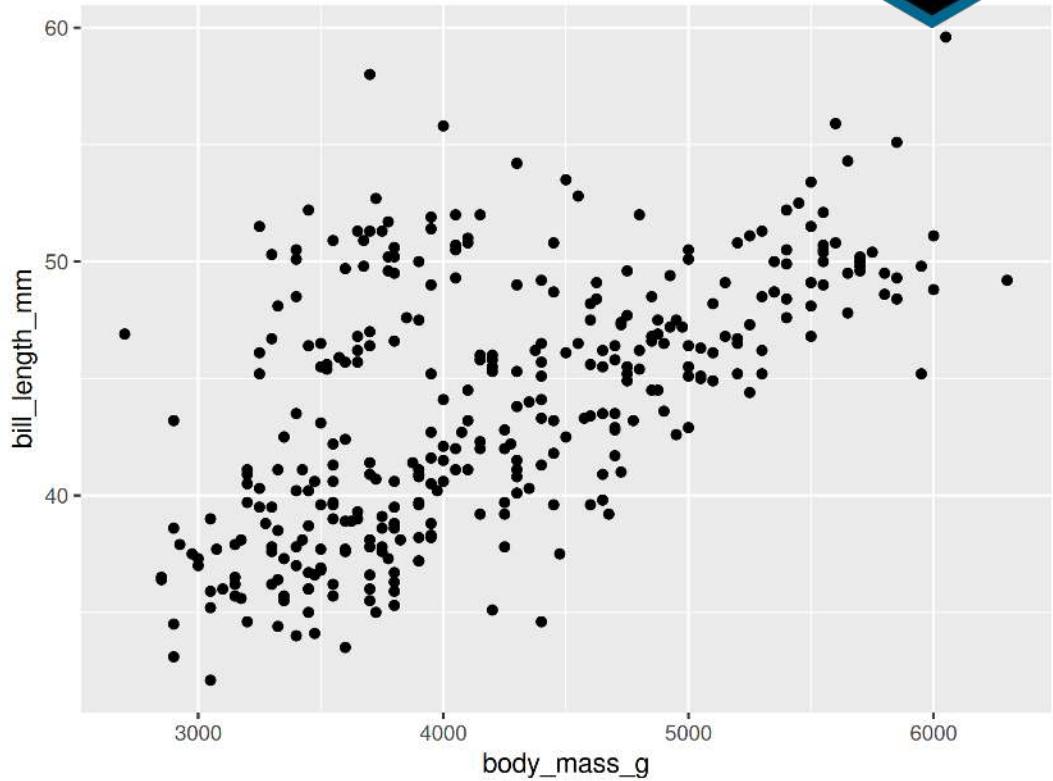
Break it down

```
1 library(palmerpenguins)
2 library(ggplot2)
3
4 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +
5   geom_point()
```



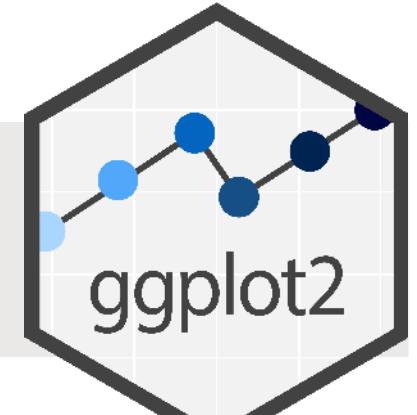
library(palmerpenguins)

- Load the `palmerpenguins` package
- Now we have access to `penguins` data



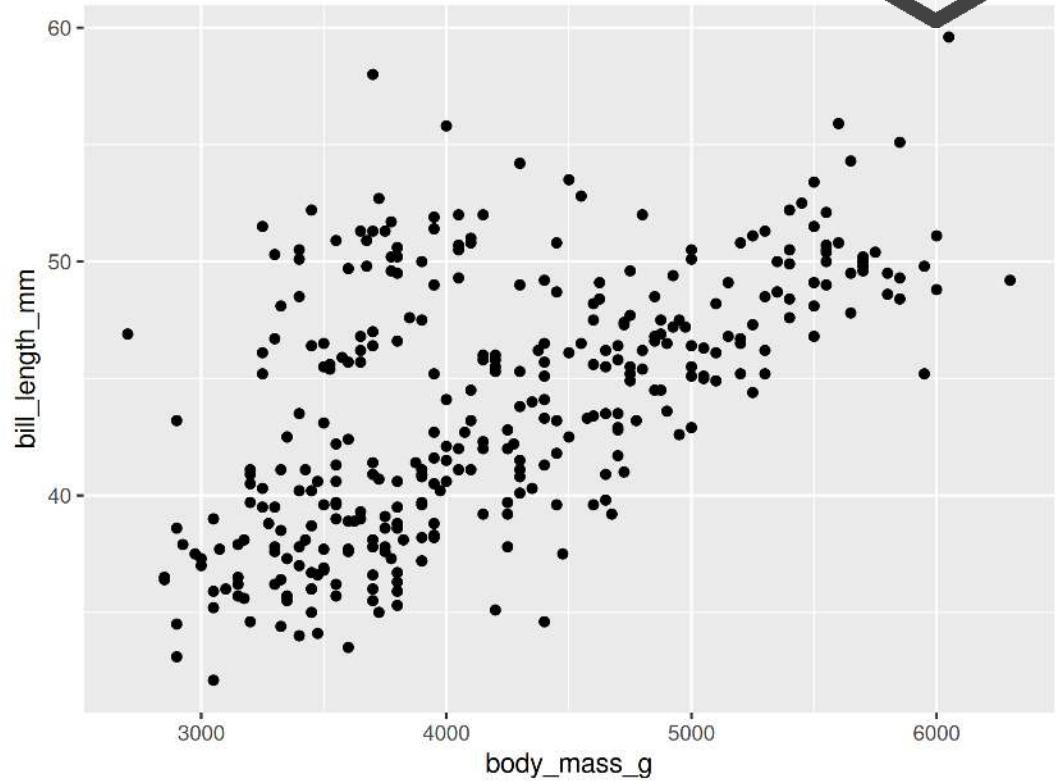
Break it down

```
1 library(palmerpenguins)
2 library(ggplot2)
3
4 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +
5   geom_point()
```



library(ggplot2)

- Load the `ggplot2` package
- Now we have access to the `ggplot()` function
 - (and `aes()` and `geom_point()` etc.)

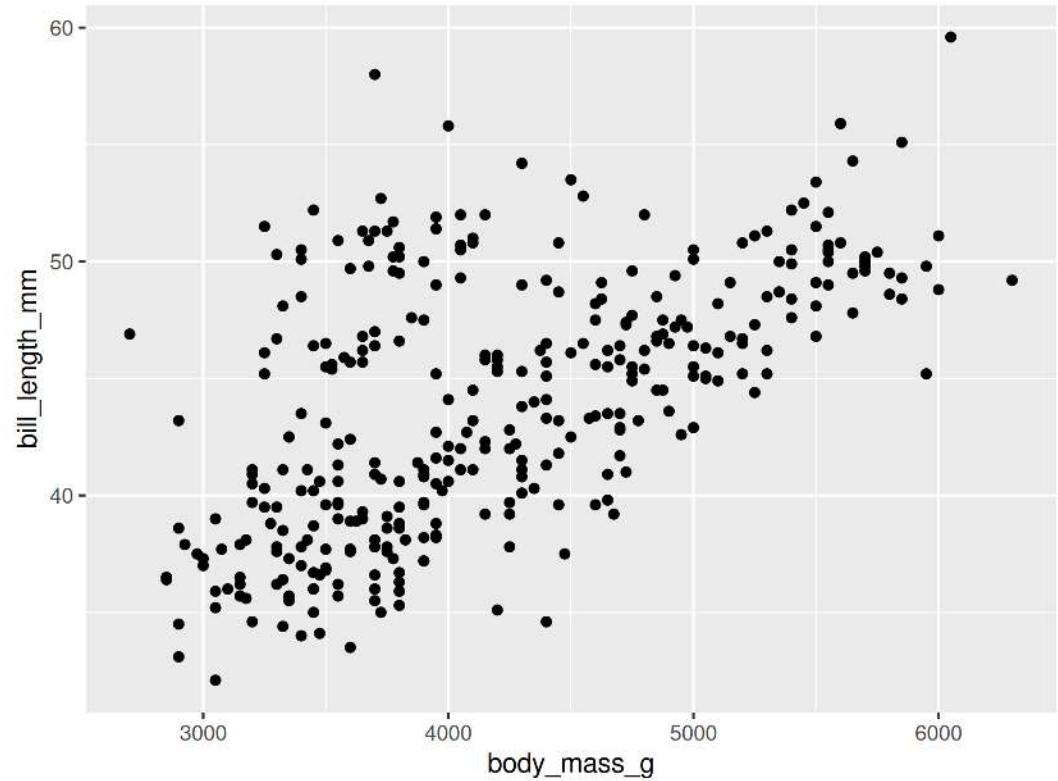


Break it down

```
1 library(palmerpenguins)
2 library(ggplot2)
3
4 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +
5   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



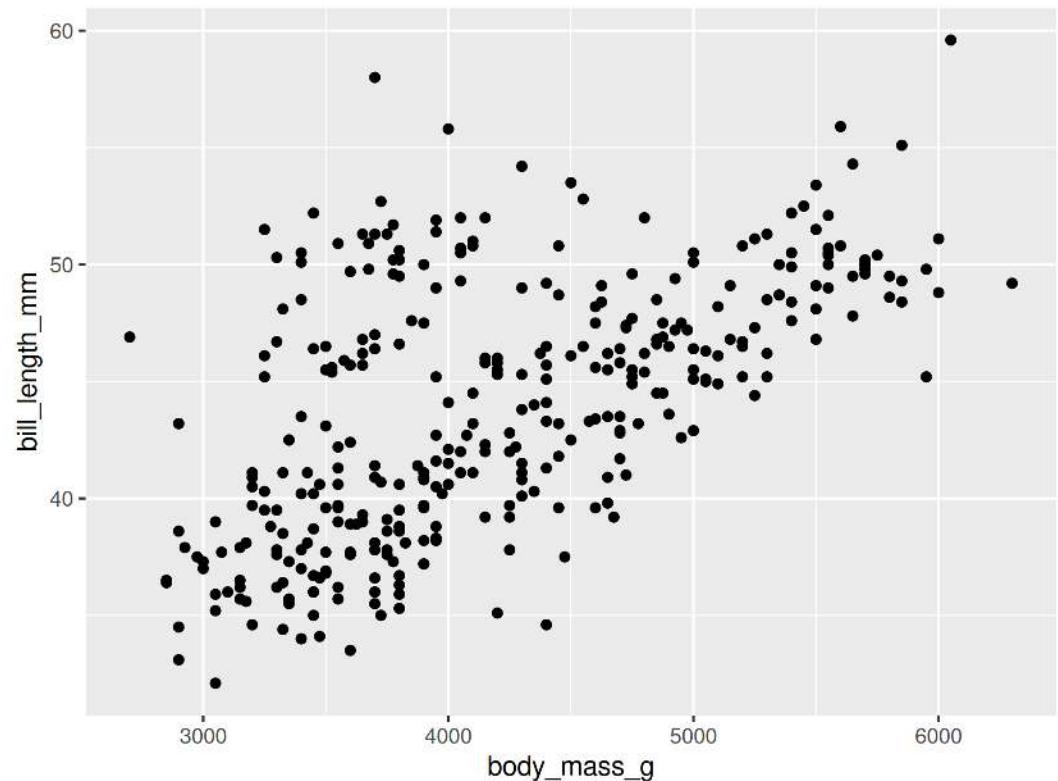
Break it down

```
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3
4 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +
5   geom_point()
```

geom_point()

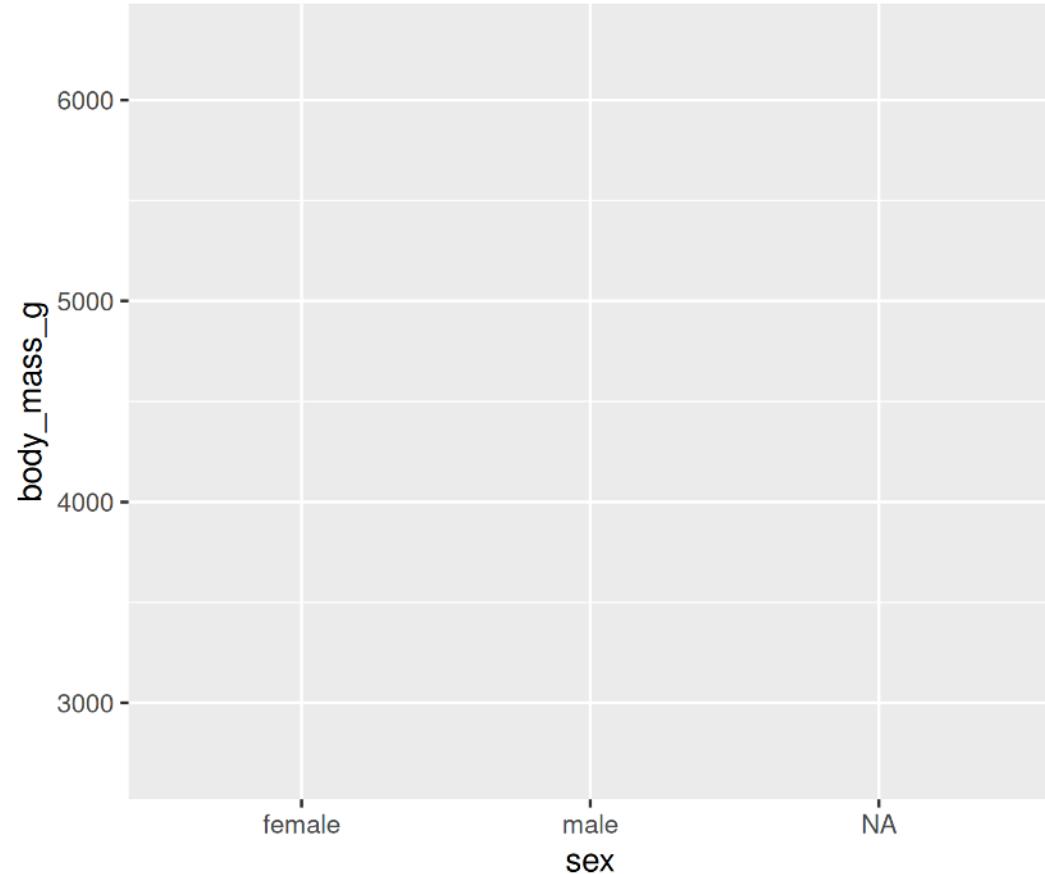
- Choose a `geom` function to display the data
- Always *added* to a `ggplot()` call with `+`

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

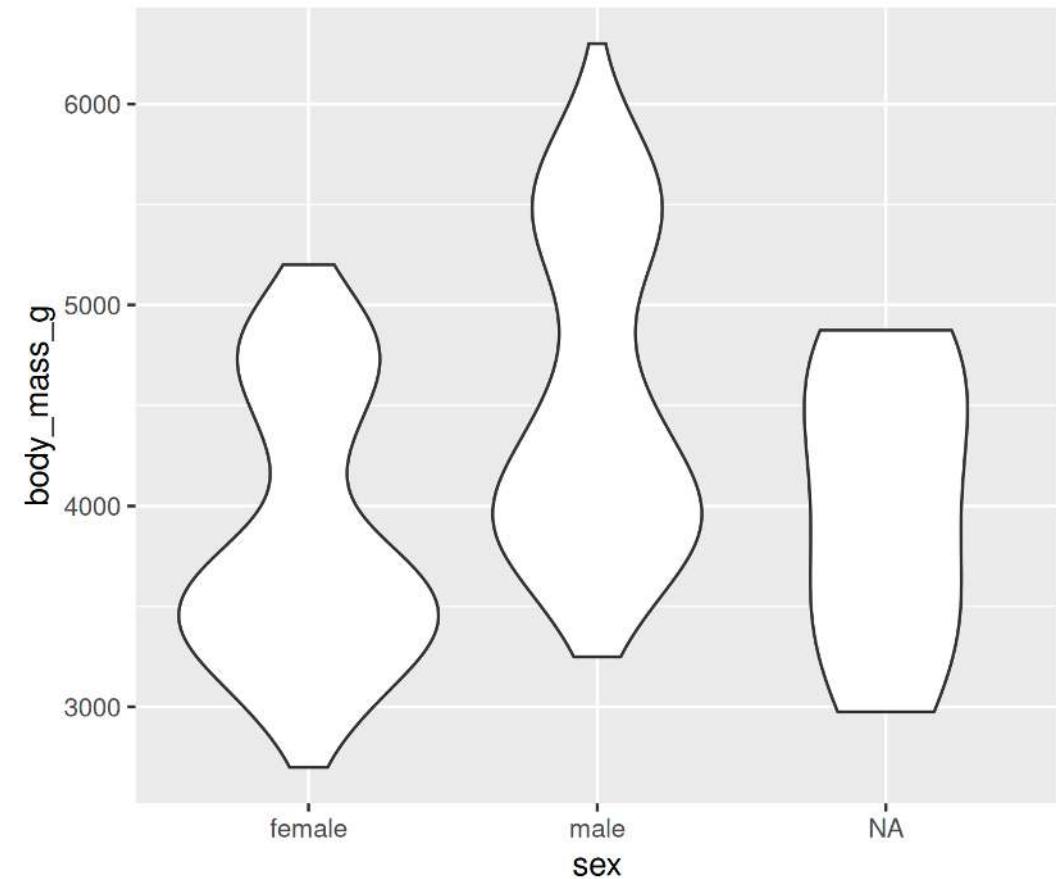


Plots are layered

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



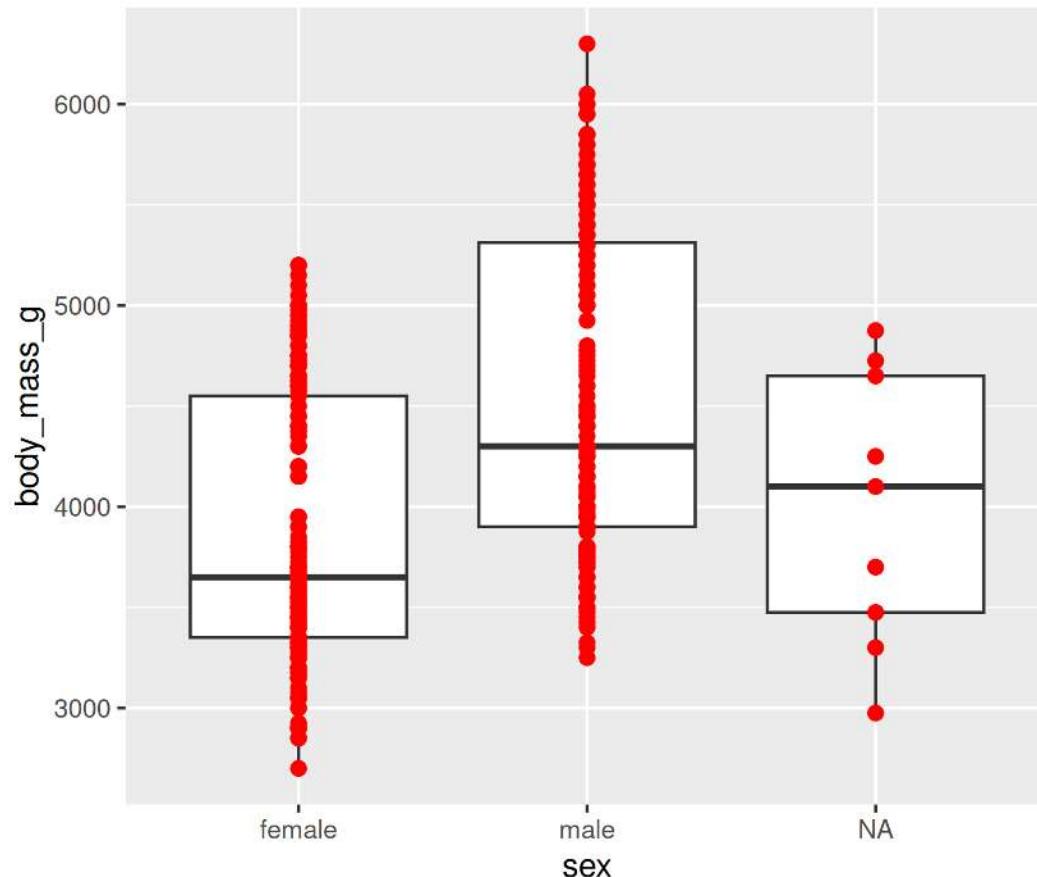
```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2   geom_violin()
```



Plots are layered

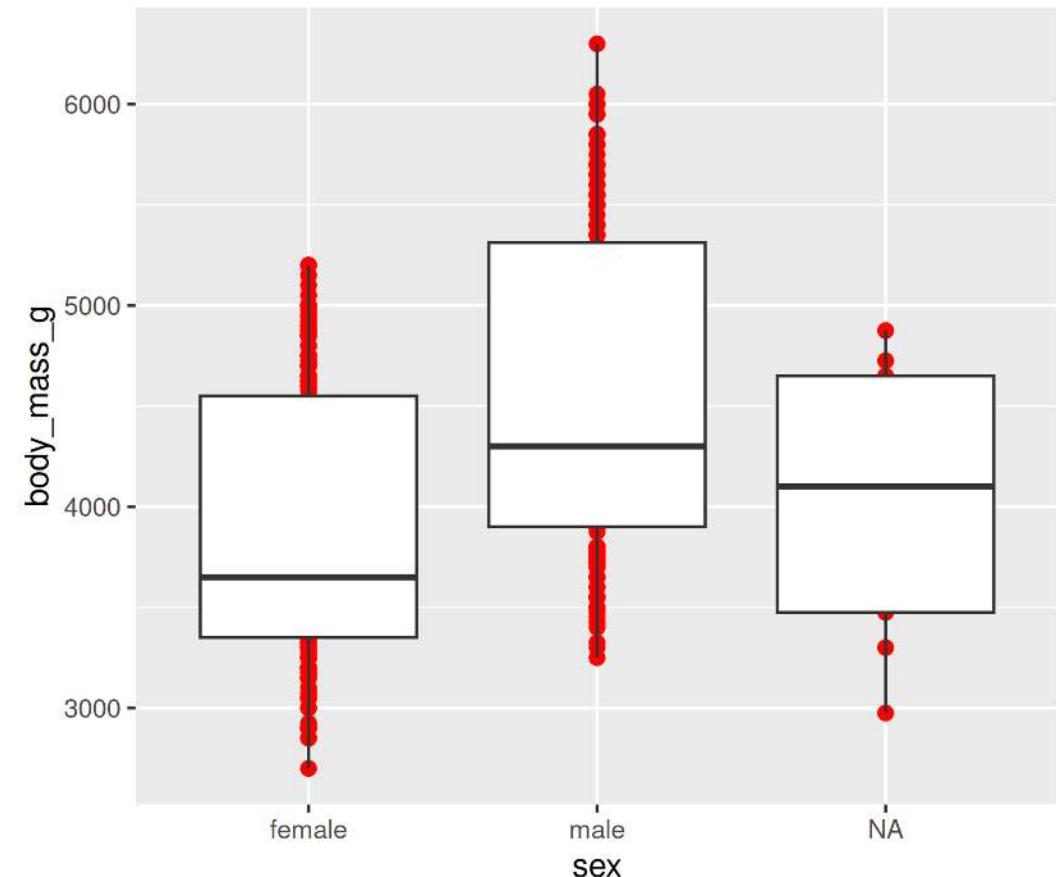
You can add multiple layers

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



Order matters

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

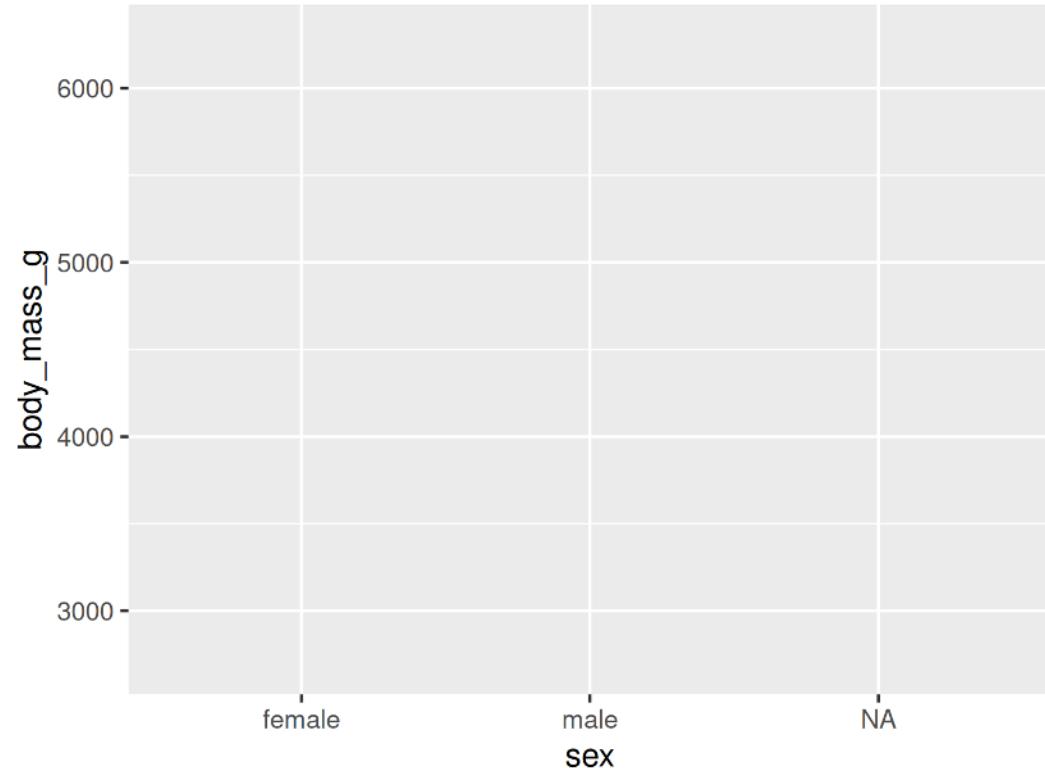


Plots are objects

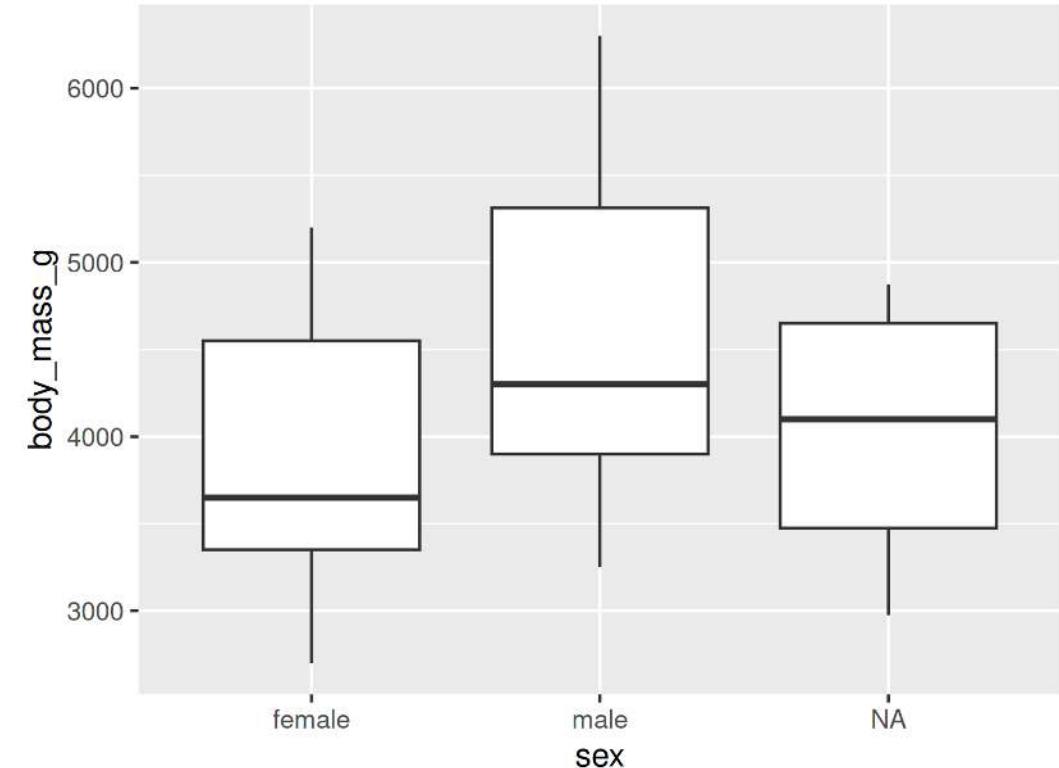
Any ggplot can be saved as an object

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

```
1 g
```



```
1 g + geom_boxplot()
```

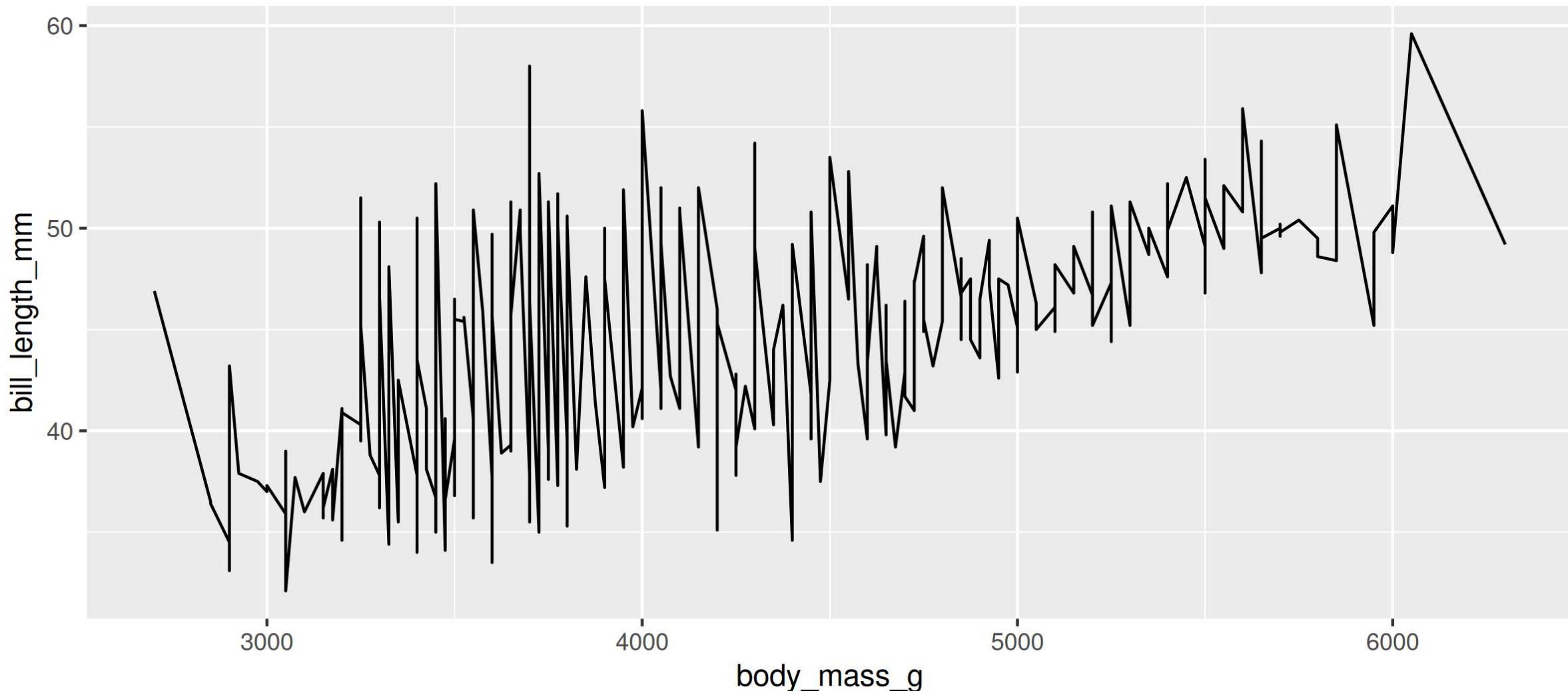


More Geoms

(Plot types)

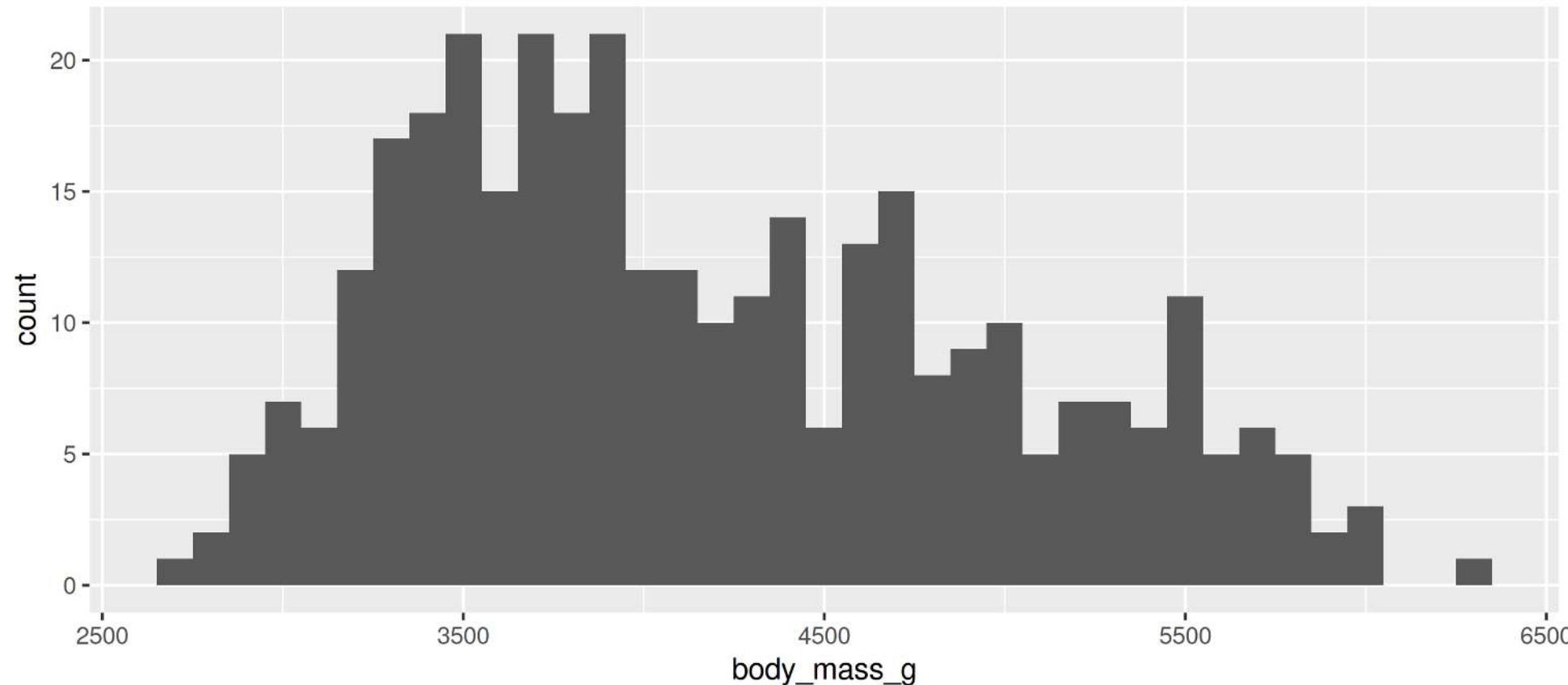
Geoms: Lines

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



Geoms: Histogram

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

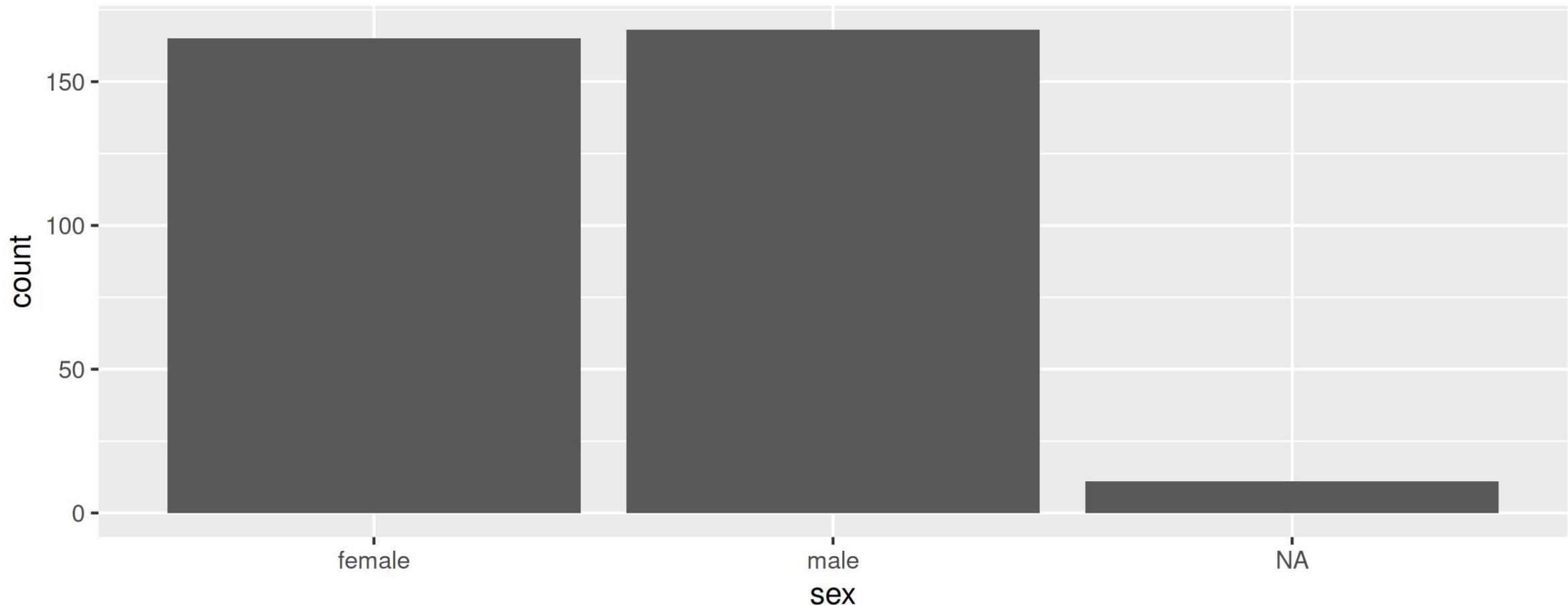


Note: We only need 1 aesthetic here

Geoms: Barplots

Let `ggplot` count your data

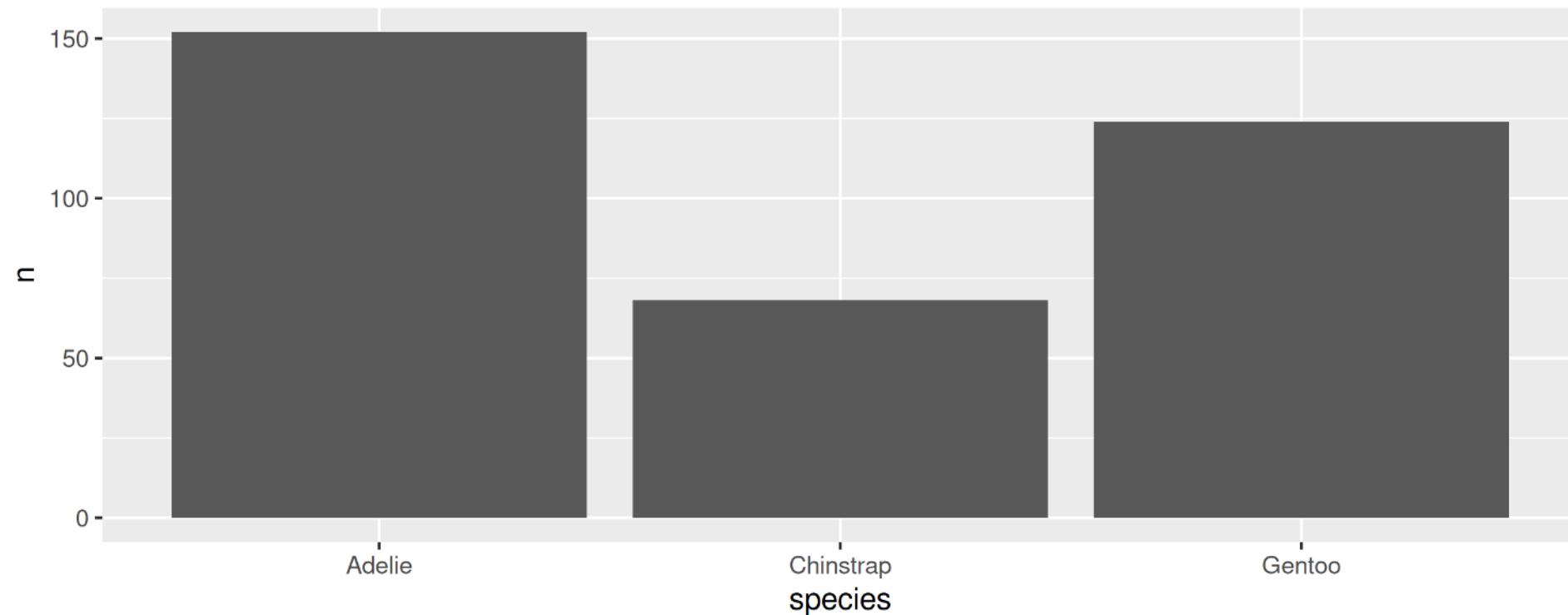
```
1 ggplot(data = penguins, aes(x = sex)) +  
2   geom_bar()
```



Geoms: Barplots

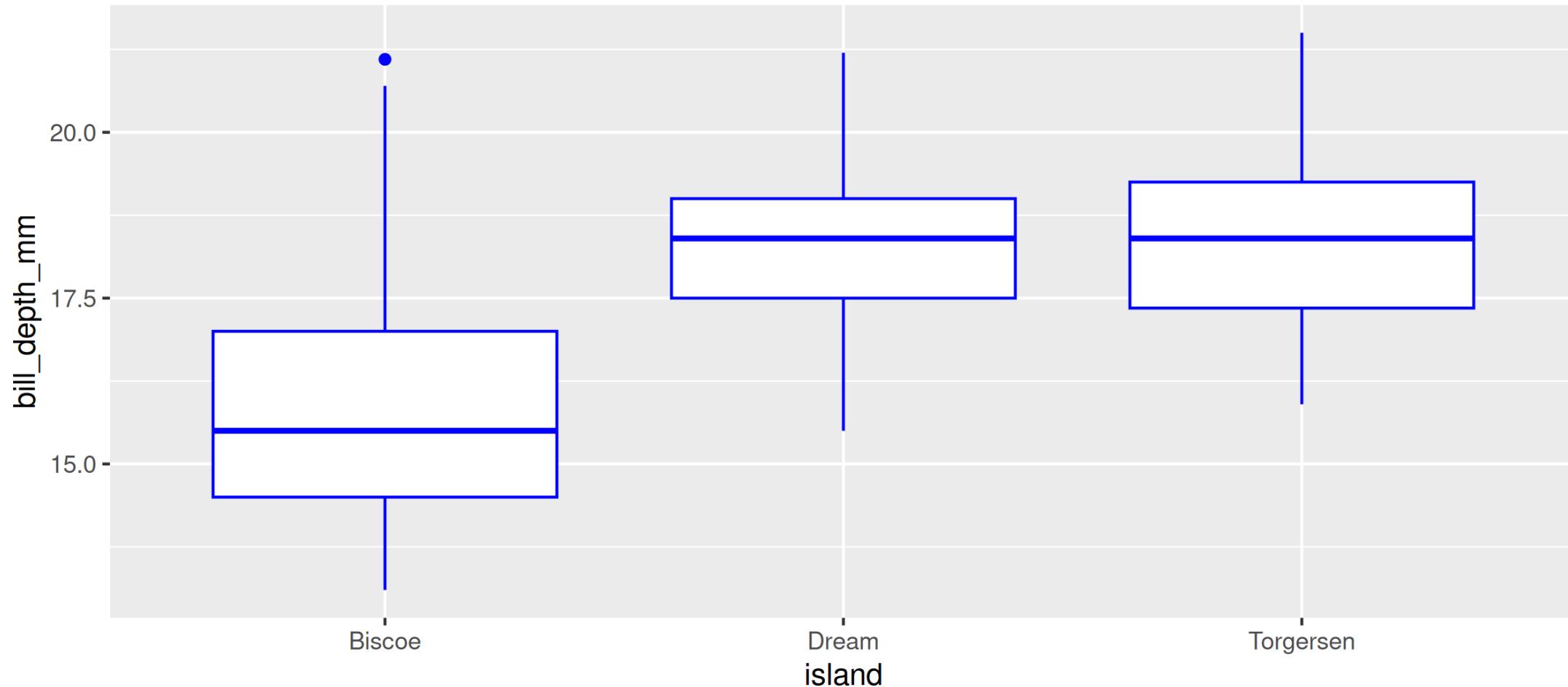
You can also provide the counts

```
1 # Create our own data frame
2 species_counts <- data.frame(species = c("Adelie", "Chinstrap", "Gentoo"),
3                                n = c(152, 68, 124))
4
5 ggplot(data = species_counts, aes(x = species, y = n)) +
6   geom_bar(stat = "identity")
```



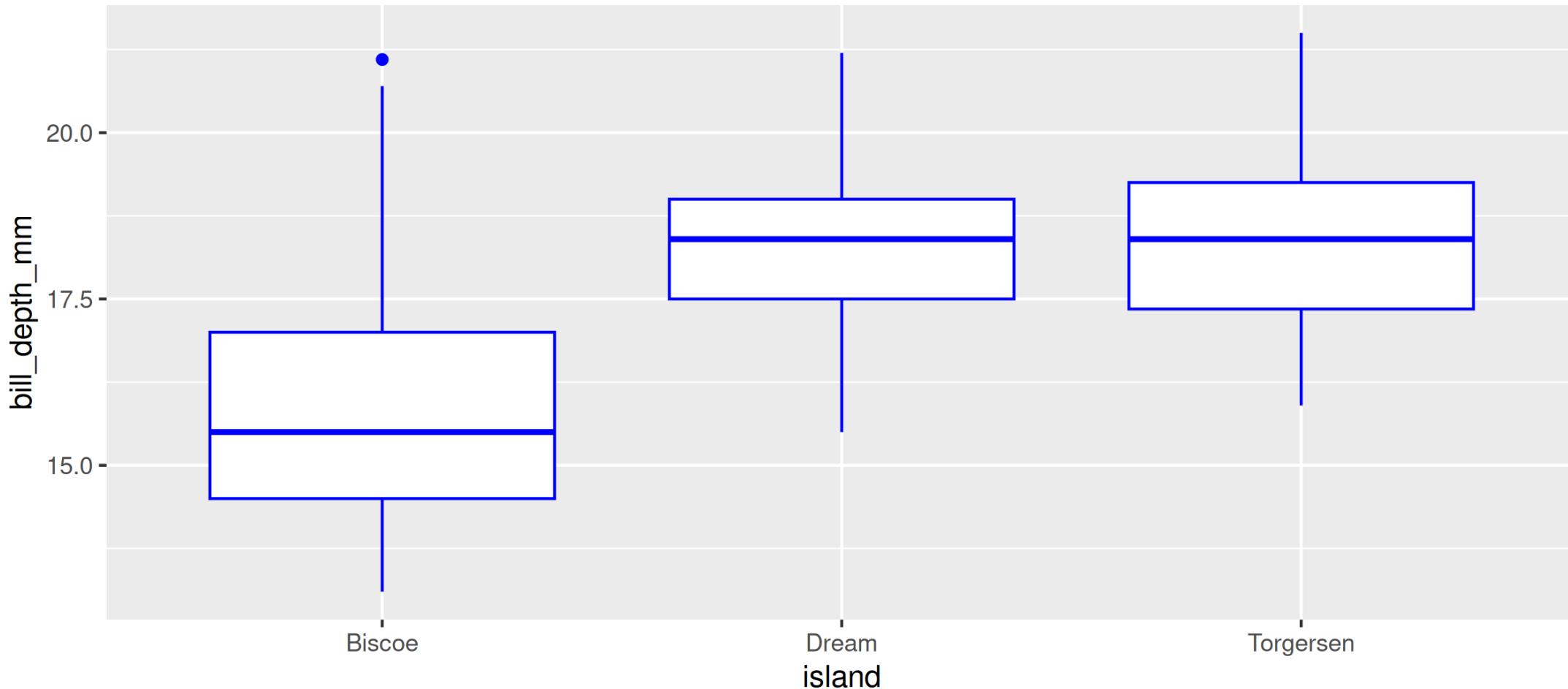
Your Turn: Create this plot

```
1 library(ggplot2)  
2  
3 ggplot(data = ___, aes(x = ___, y = ___)) +  
4   geom___(____)
```



Your Turn: Create this plot

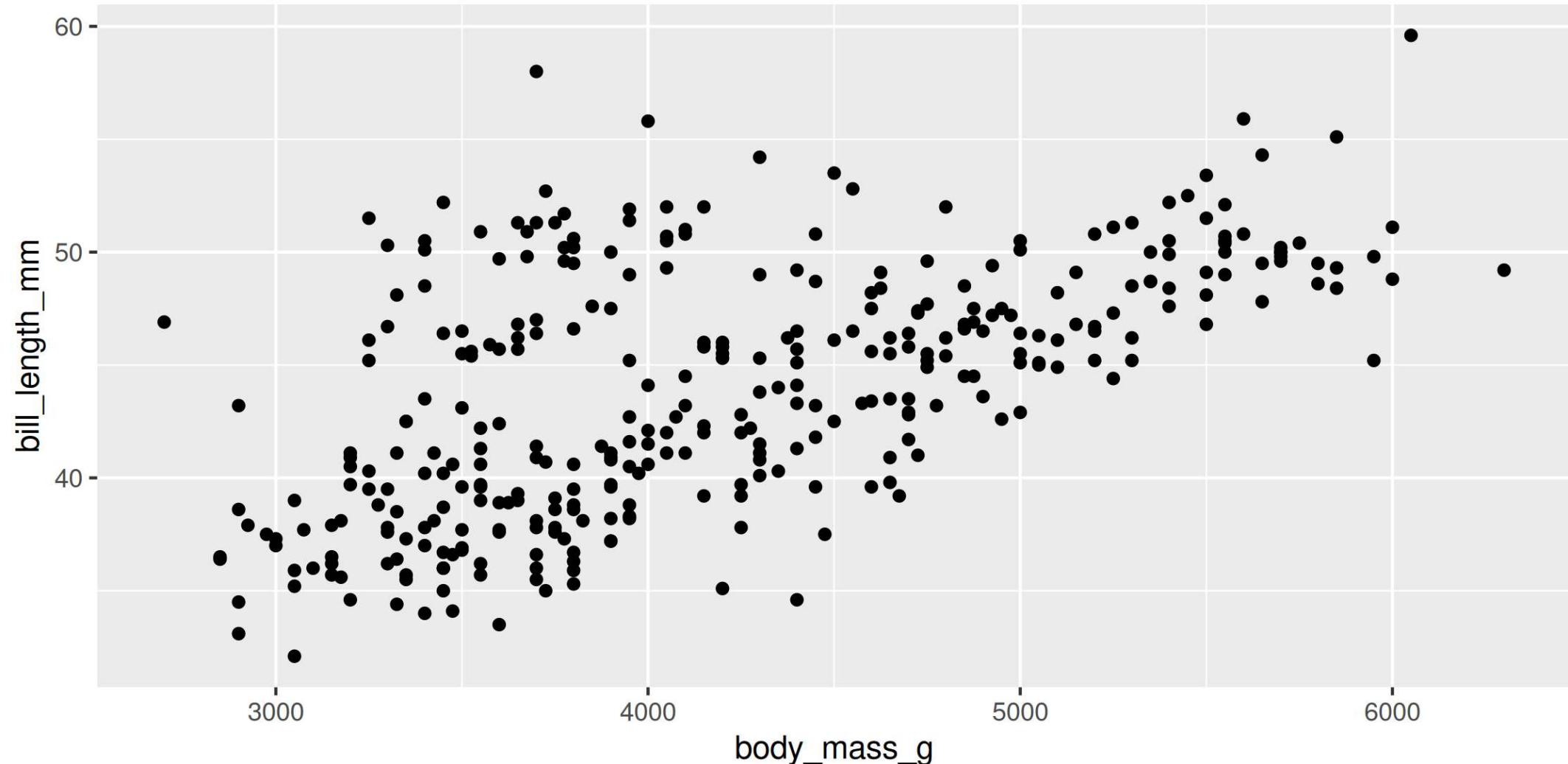
```
1 library(ggplot2)
2
3 ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +
4   geom_boxplot(colour = "blue")
```



Showing** data by group**

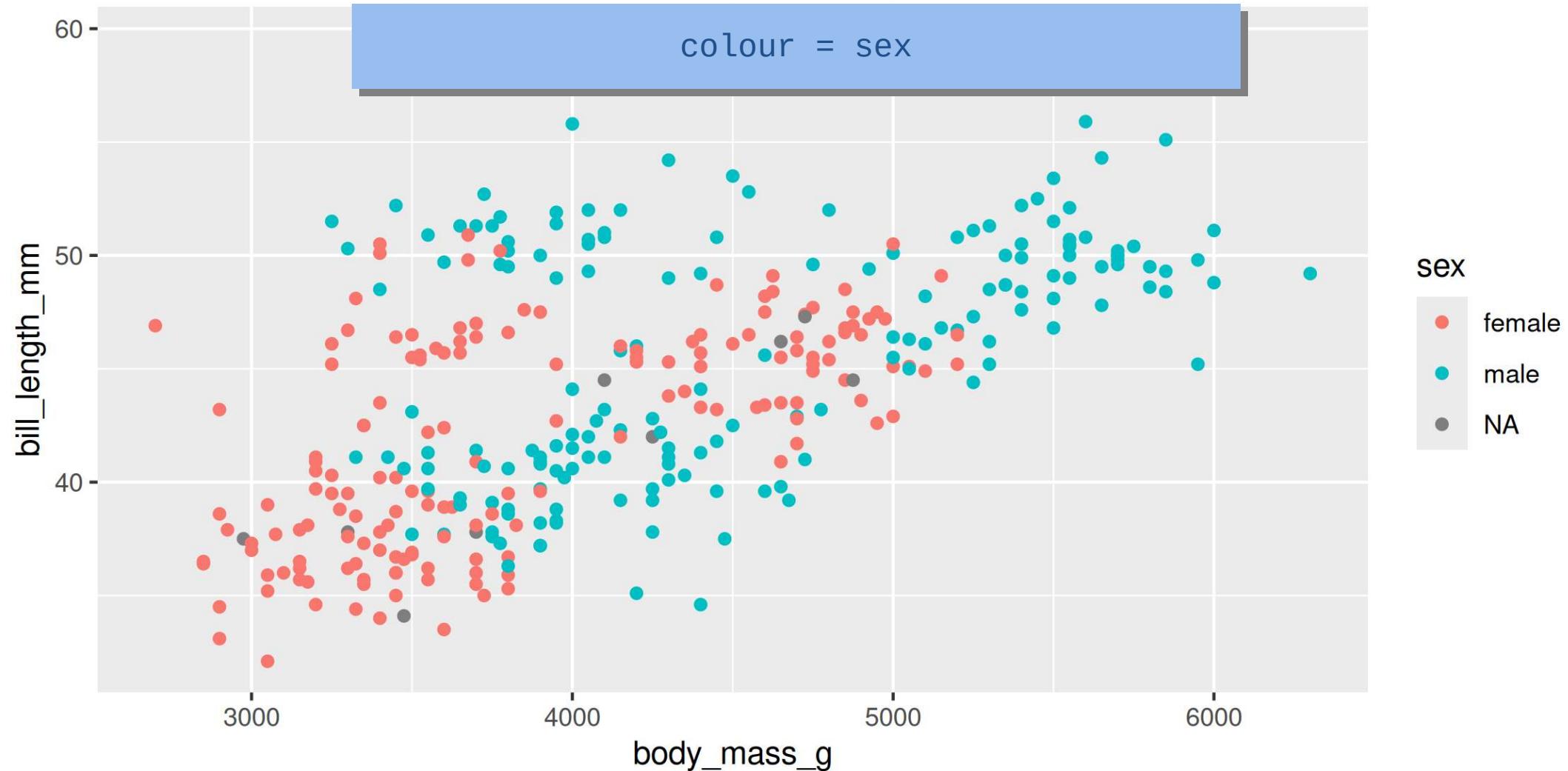
Mapping aesthetics

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



Mapping aesthetics

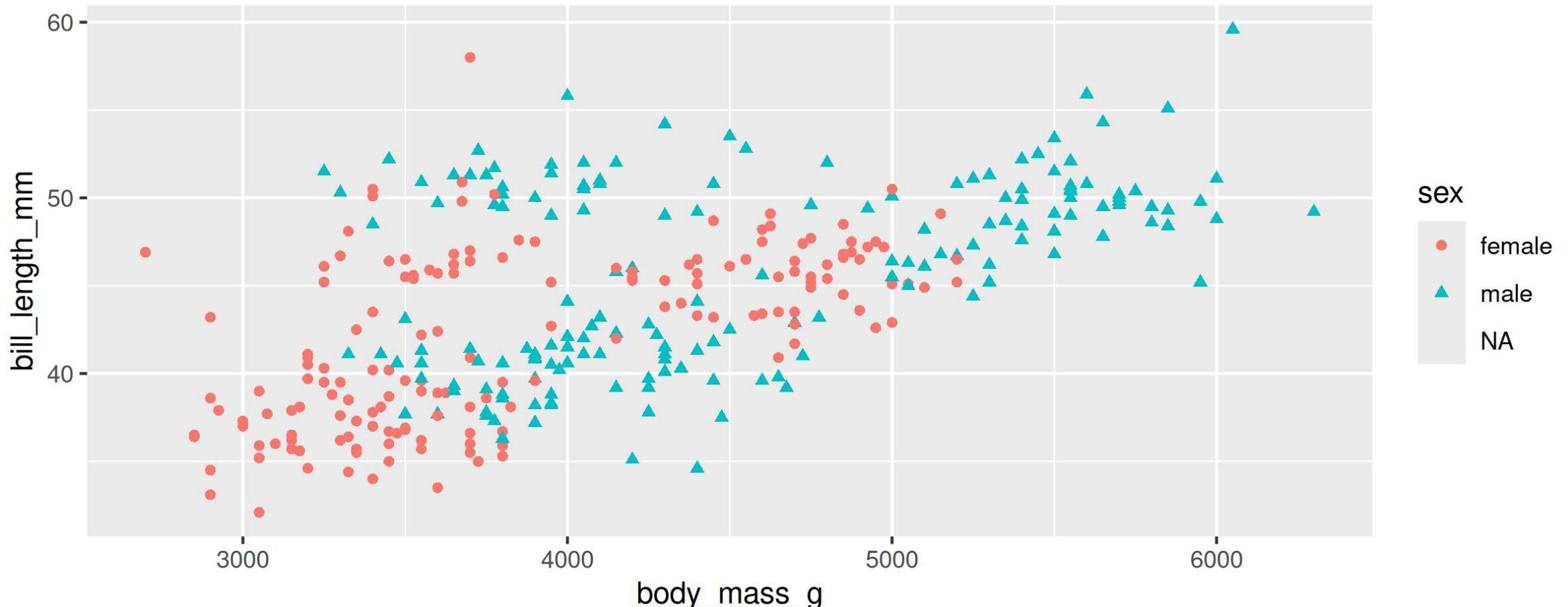
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
2   geom_point()
```



Mapping aesthetics

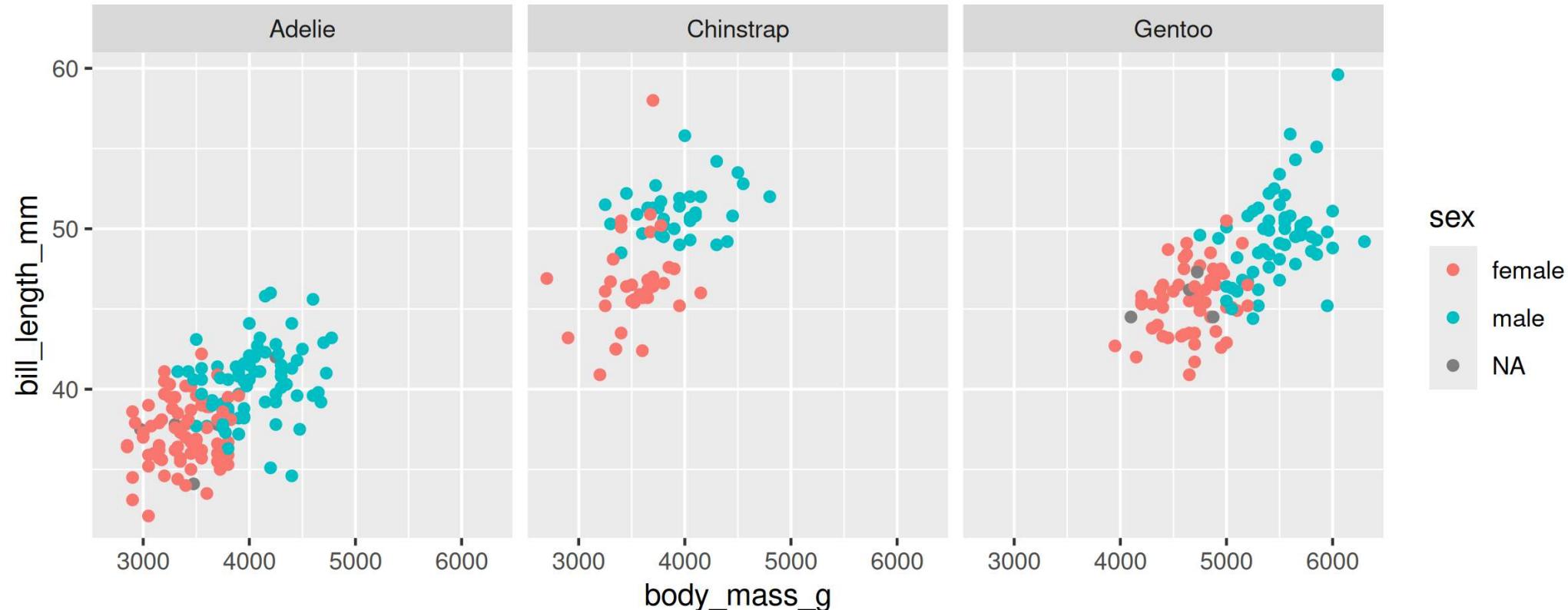
ggplot automatically populates the legends (combining where it can)

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



Faceting: facet_wrap()

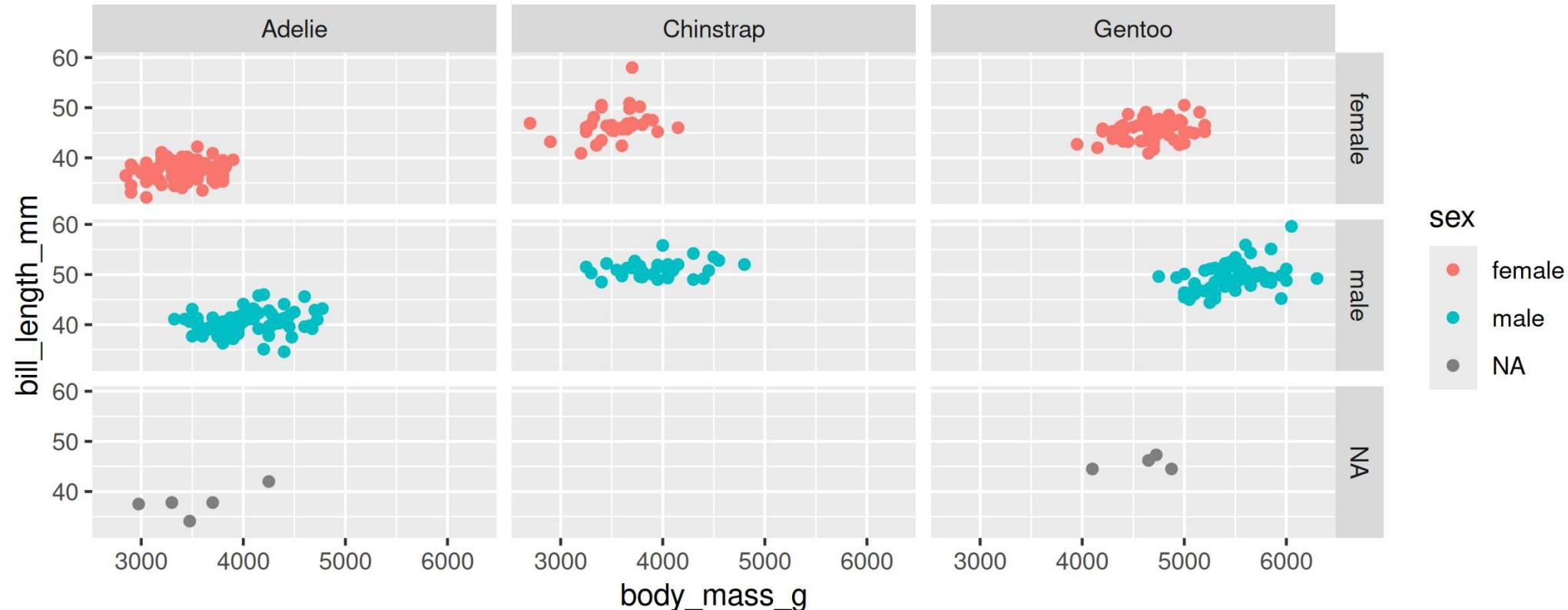
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
2   geom_point() +  
3   facet_wrap(~ species)
```



Split plots by **one** grouping variable

Faceting: facet_grid()

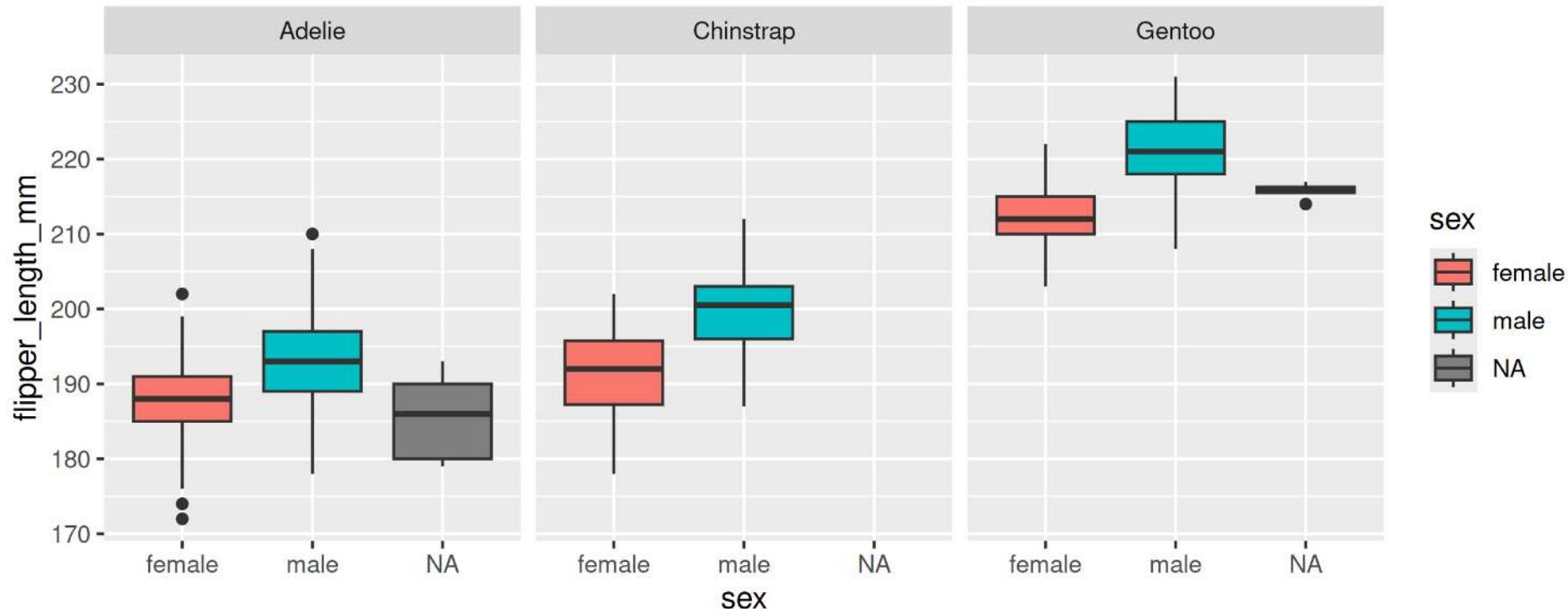
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
2   geom_point() +  
3   facet_grid(species ~ sex)
```



Split plots by **two** grouping variables

Your Turn: Create this plot

```
1 ggplot(data = ___, aes(____)) +  
2   _____ +  
3   _____
```

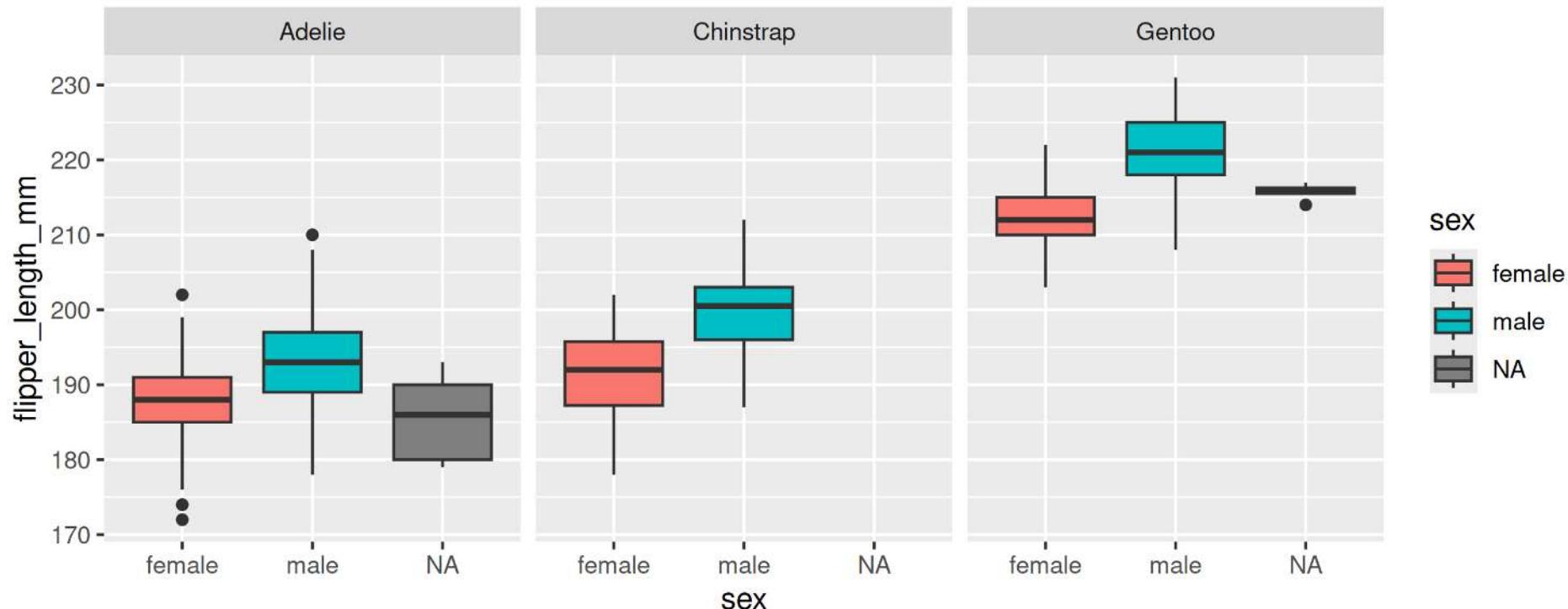


Hint: `colour` is for outlining with a colour, `fill` is for ‘filling’ with a colour

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

Your Turn: Create this plot

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



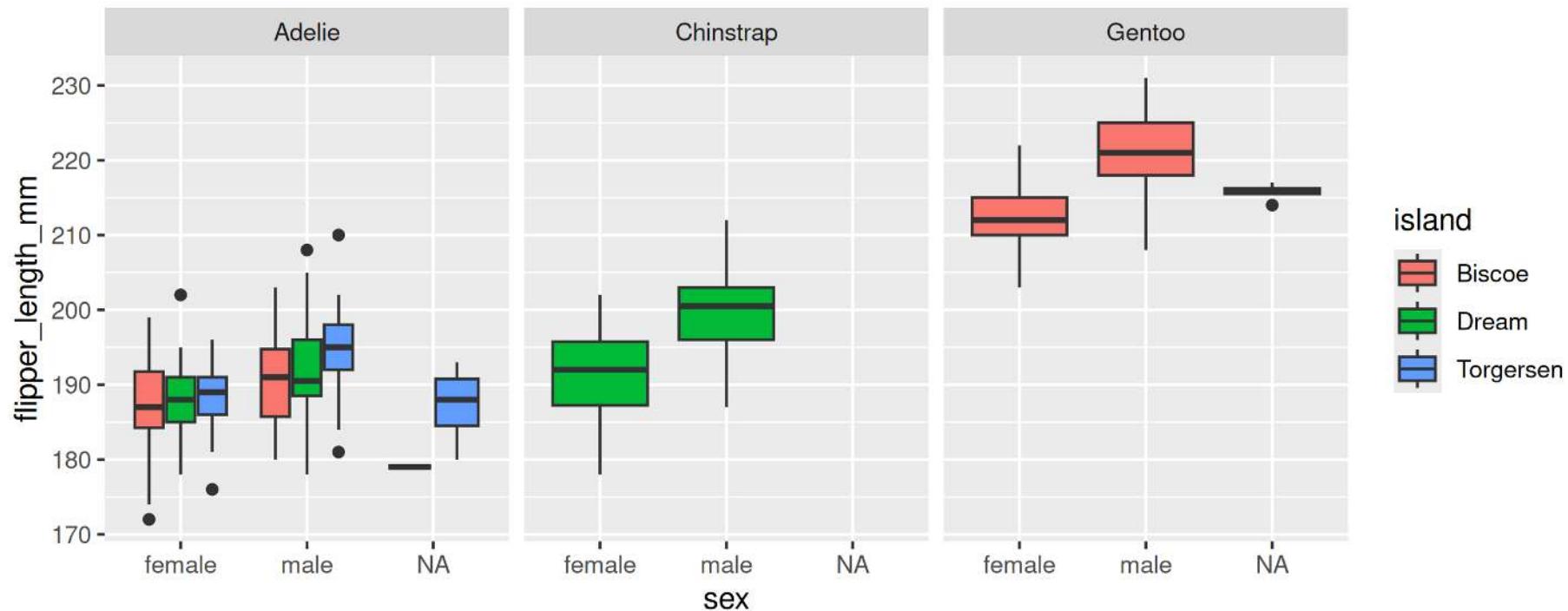
Hint: `colour` is for outlining with a colour, `fill` is for ‘filling’ with a colour

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

Your Turn: Create this plot

Too Easy?

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



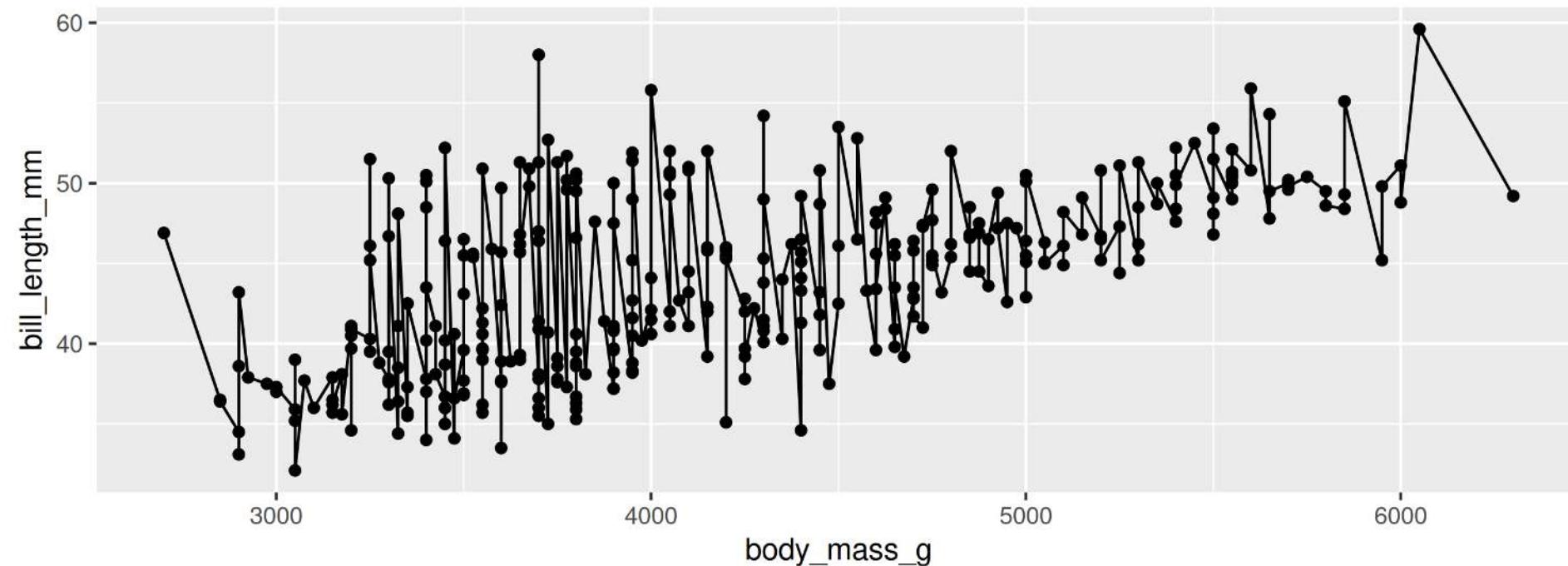
Small change (`fill = sex` to `fill = island`) results in completely different plot

Trendlines / Regression Lines

Trendlines / Regression lines

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

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



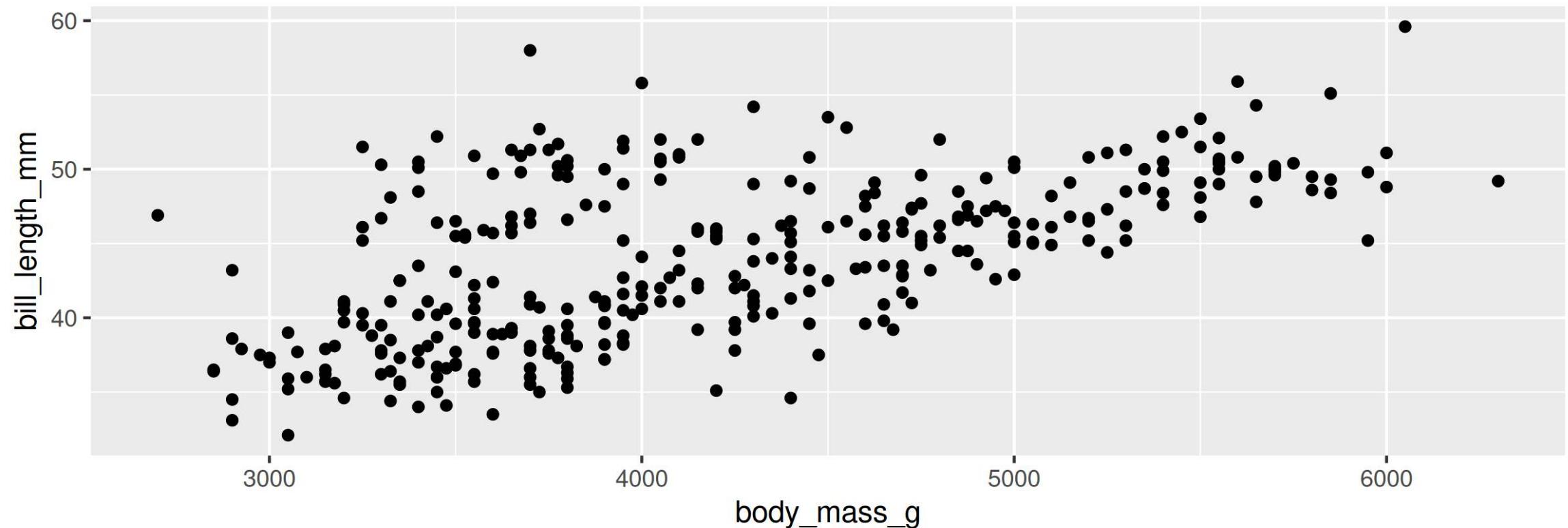
Not what we're looking for

Trendlines / Regression lines

Let's add a trend line properly

Start with basic plot:

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

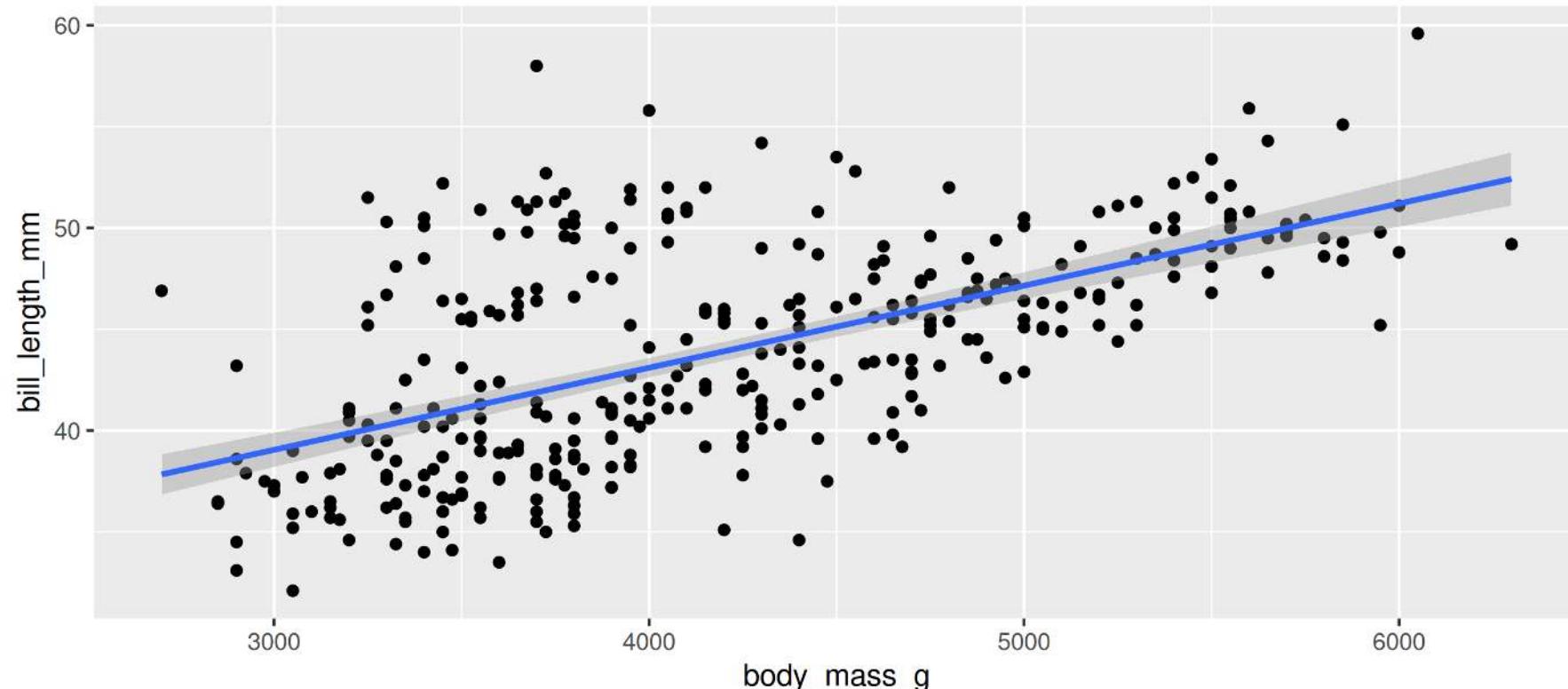


Trendlines / Regression lines

Add the `stat_smooth()`

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

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

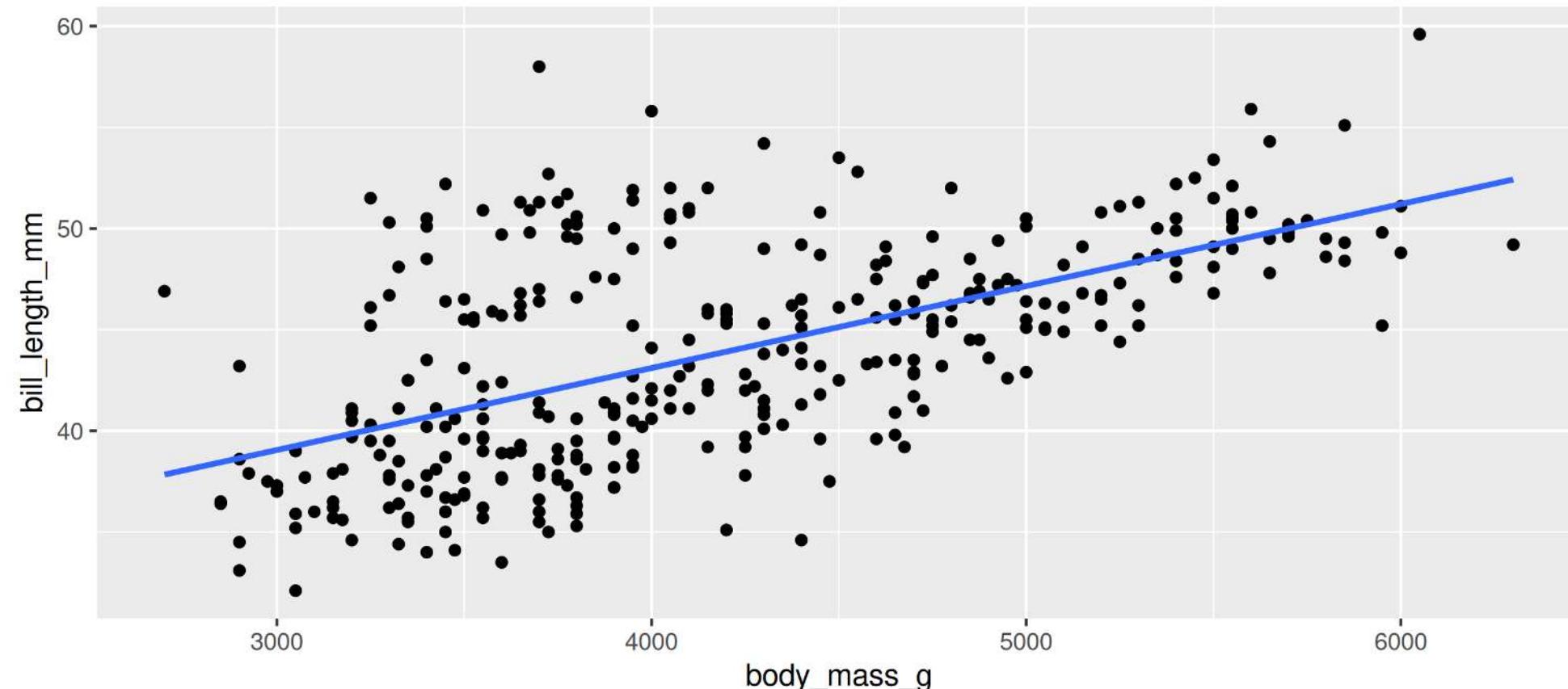


Trendlines / Regression lines

Add the `stat_smooth()`

- remove the grey ribbon `se = FALSE`

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

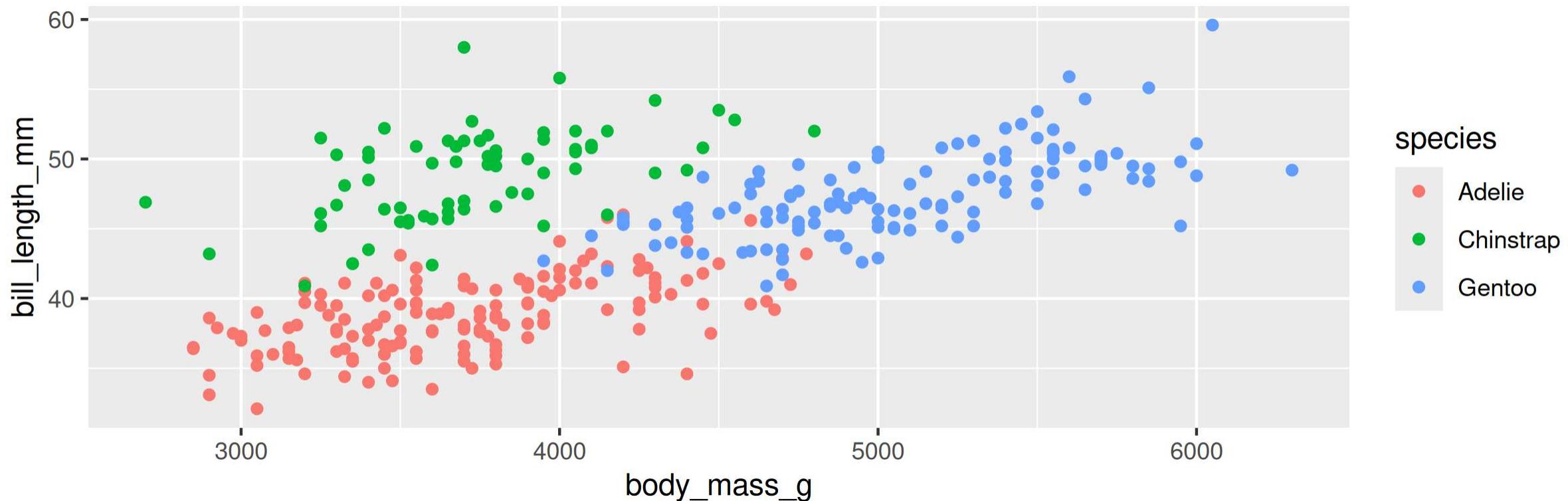


Trendlines / Regression lines

A line for each group

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

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

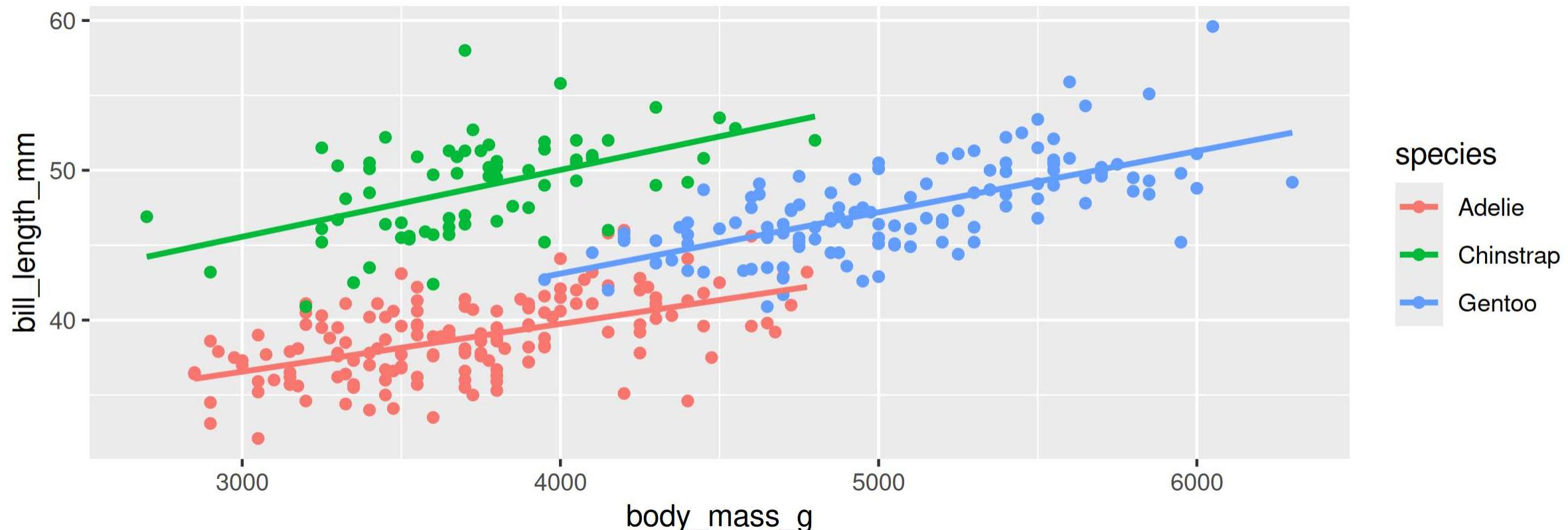


Trendlines / Regression lines

A line for each group

- `stat_smooth()` automatically uses the same grouping

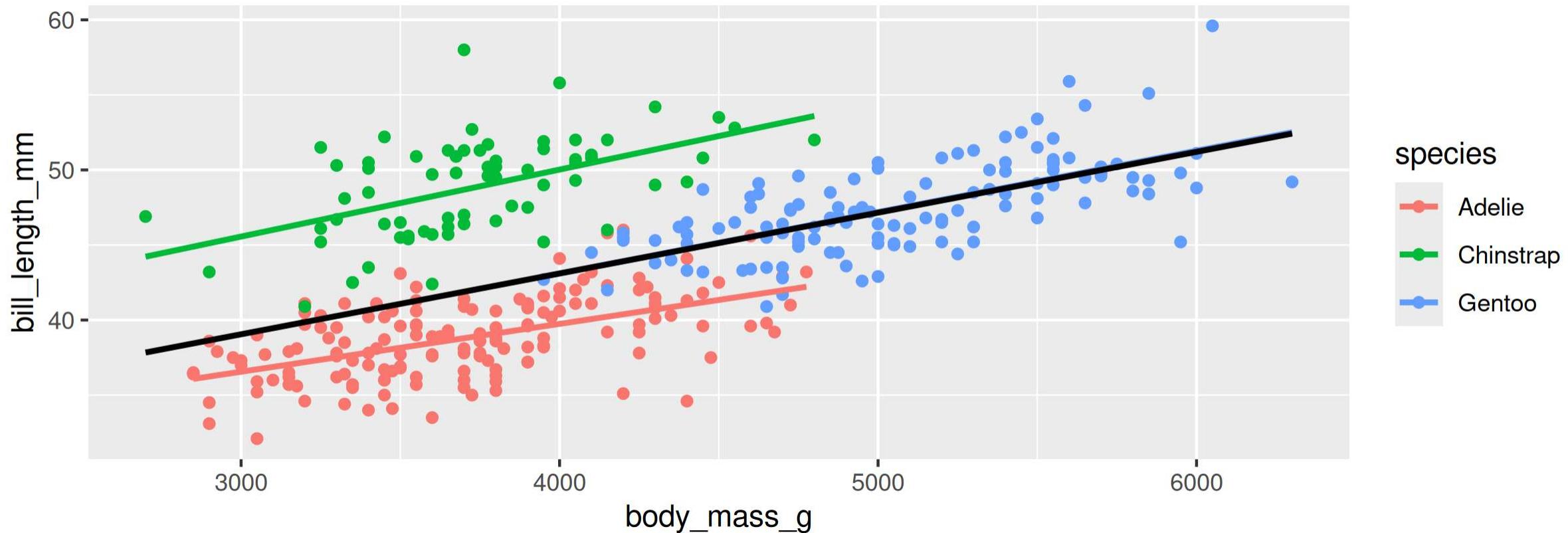
```
1 g + stat_smooth(method = "lm", se = FALSE)
```



Trendlines / Regression lines

A line for each group AND overall

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



Your Turn: Create this plot

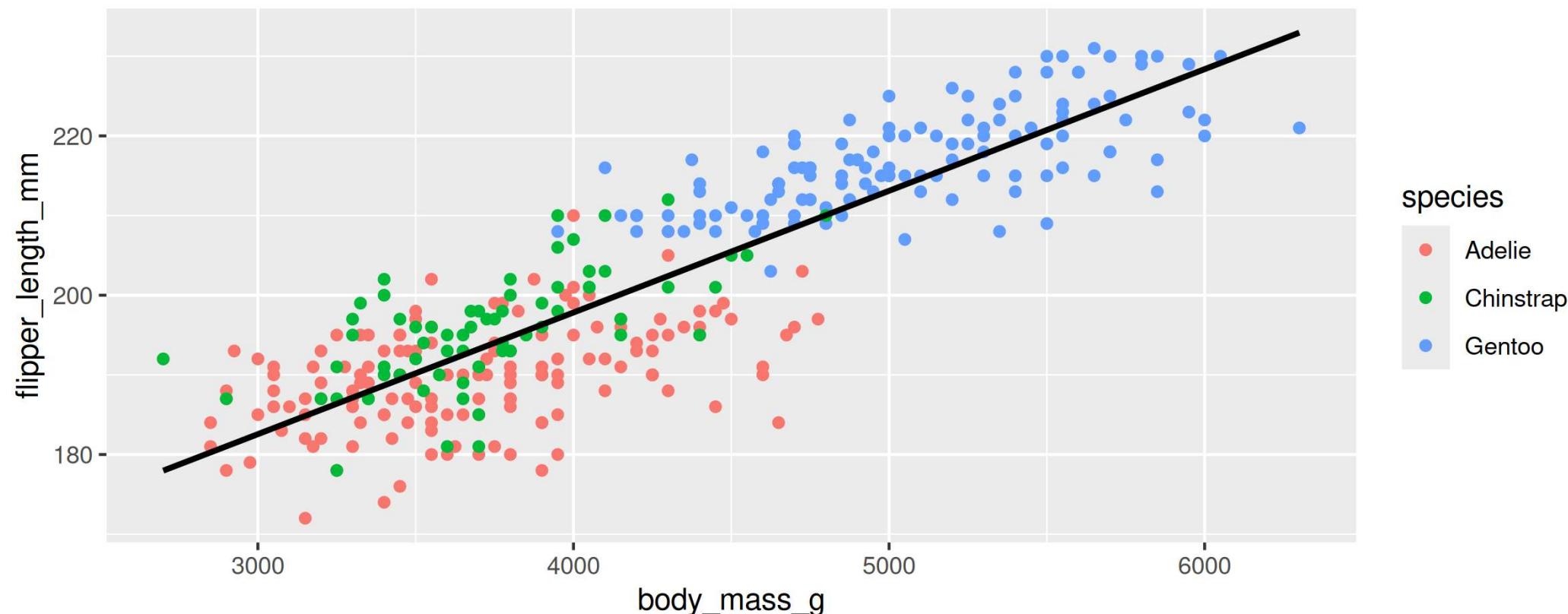
- A scatter plot: Flipper Length by Body Mass grouped by Species
- With *a single regression line for the overall trend*

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

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*

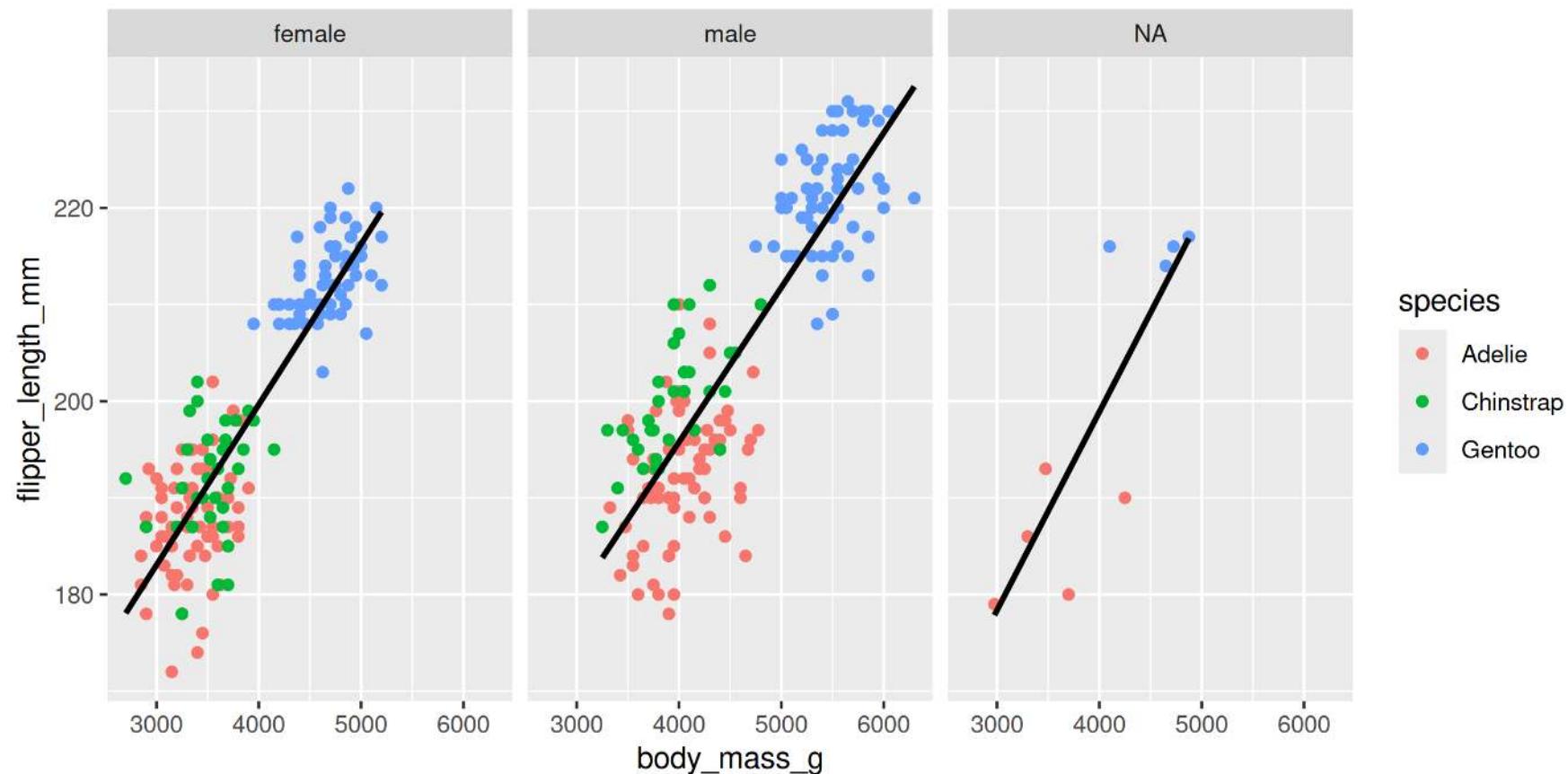
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
2   geom_point() +  
3   stat_smooth(se = FALSE, colour = "black", method = "lm")
```



Your Turn: Create this plot

Too Easy?

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

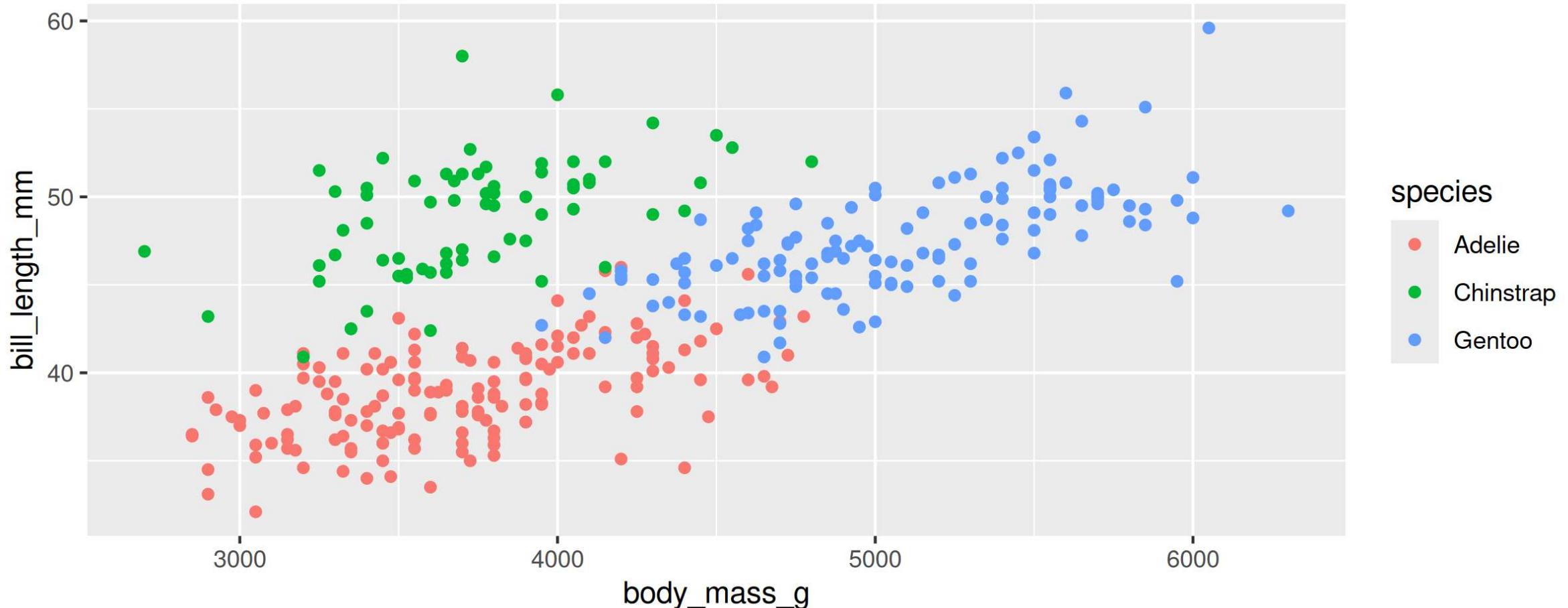


Customizing plots

Customizing: Starting plot

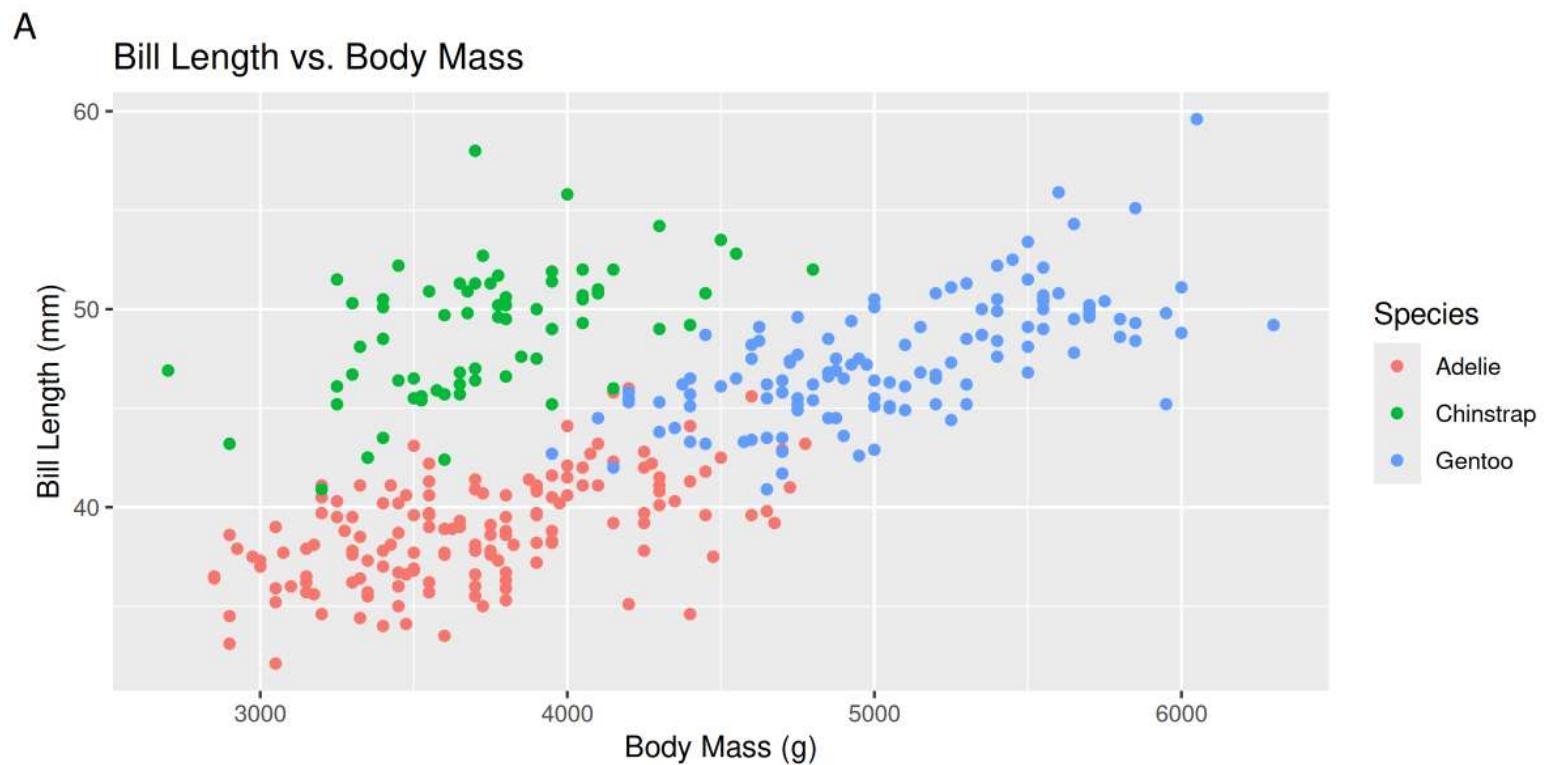
Let's work with this plot

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



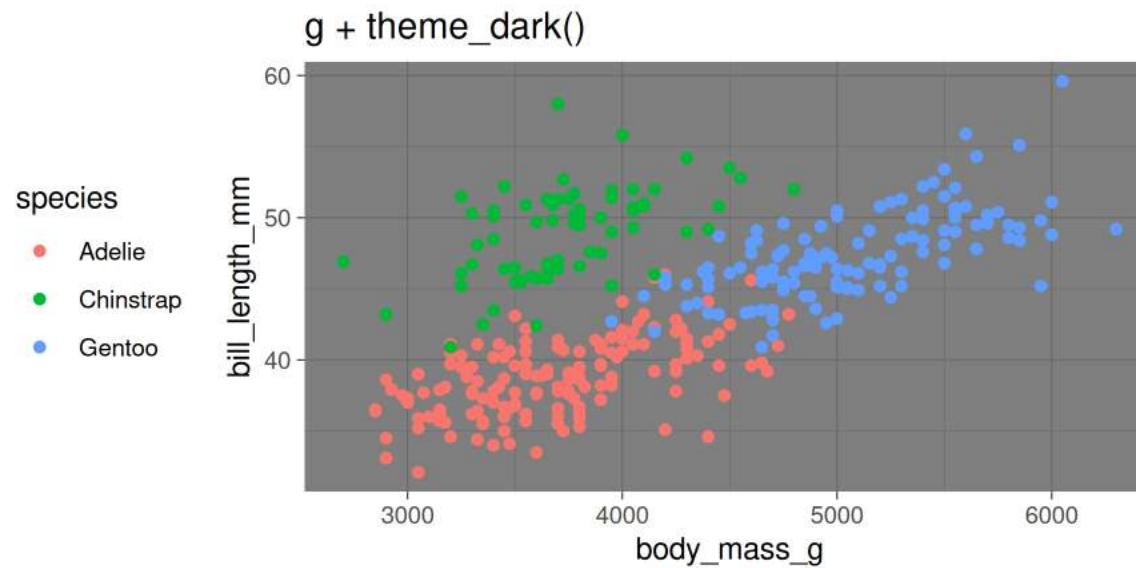
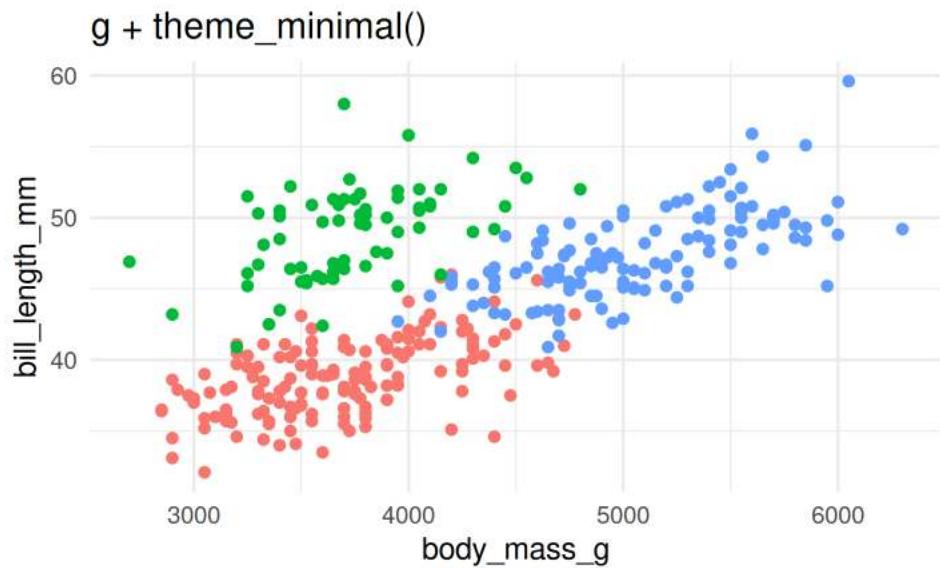
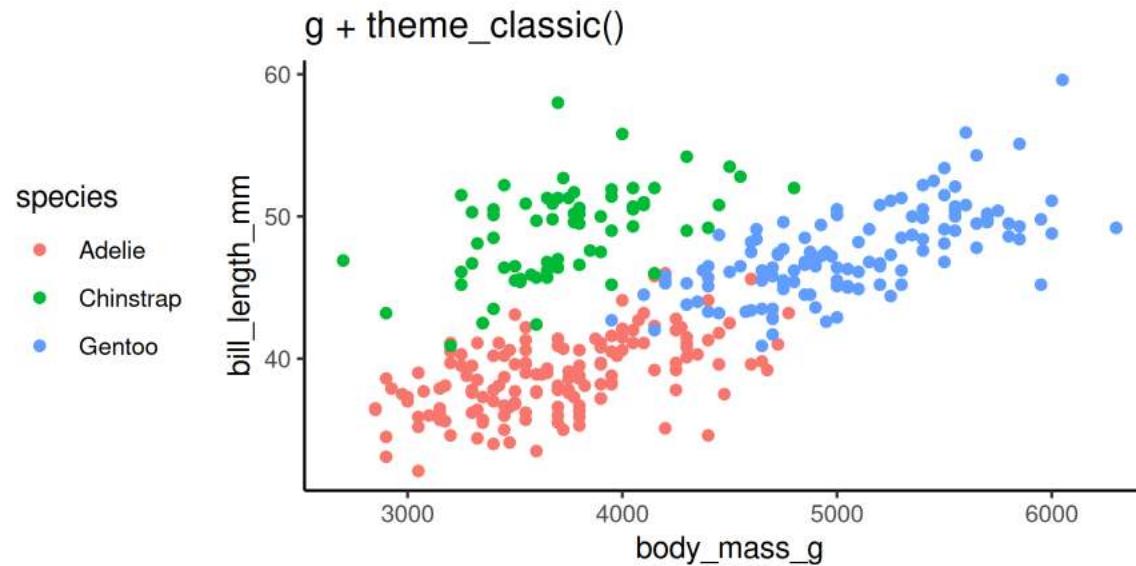
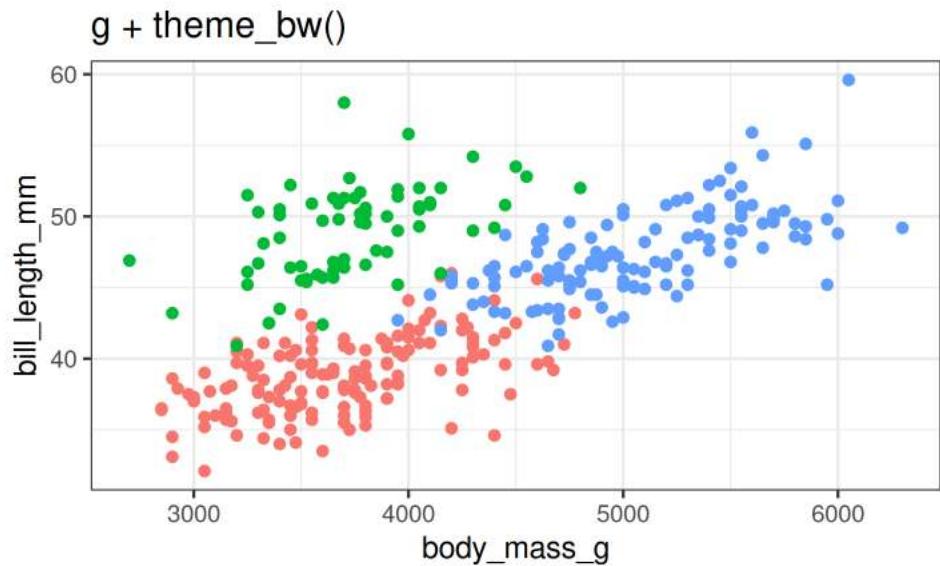
Customizing: Labels

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



Practice for later: Add proper labels to some 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.

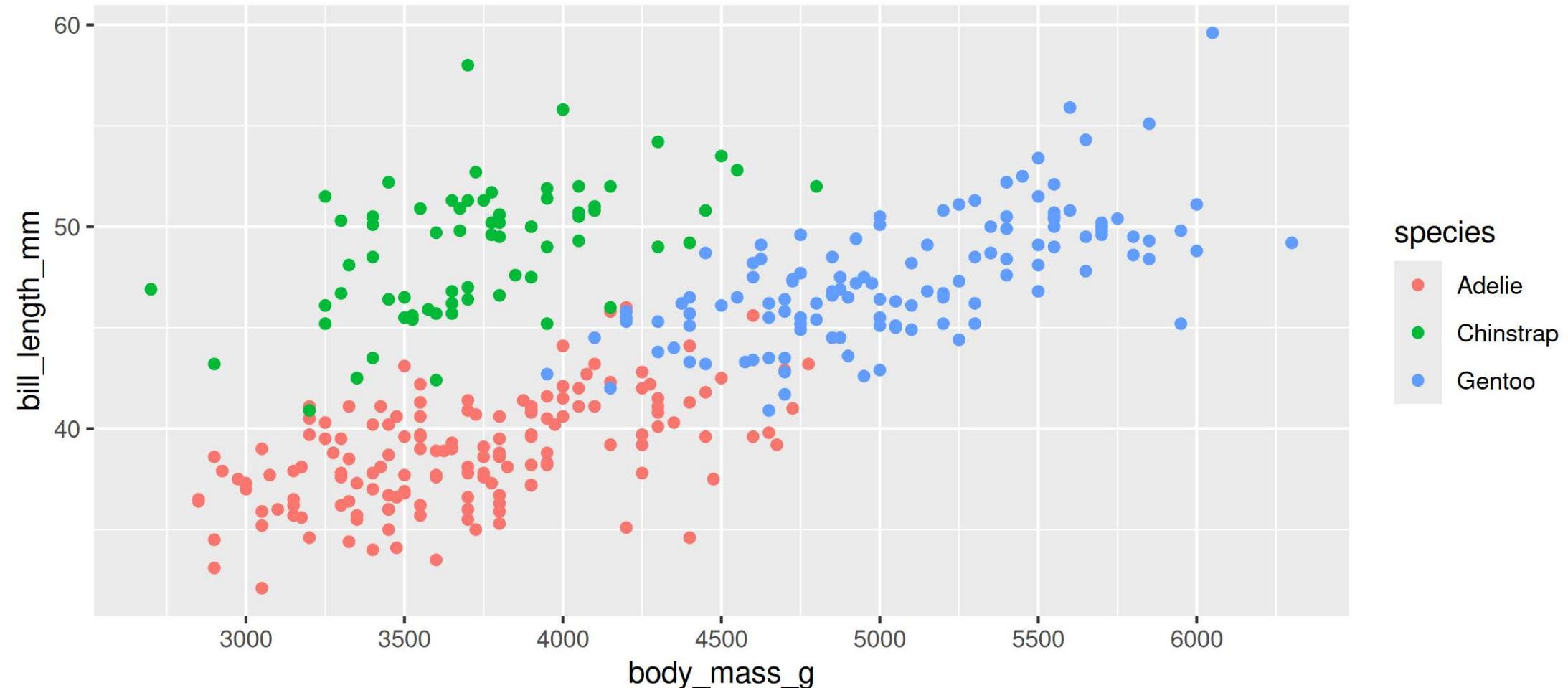
Common arguments

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

Customizing: Axes

Breaks

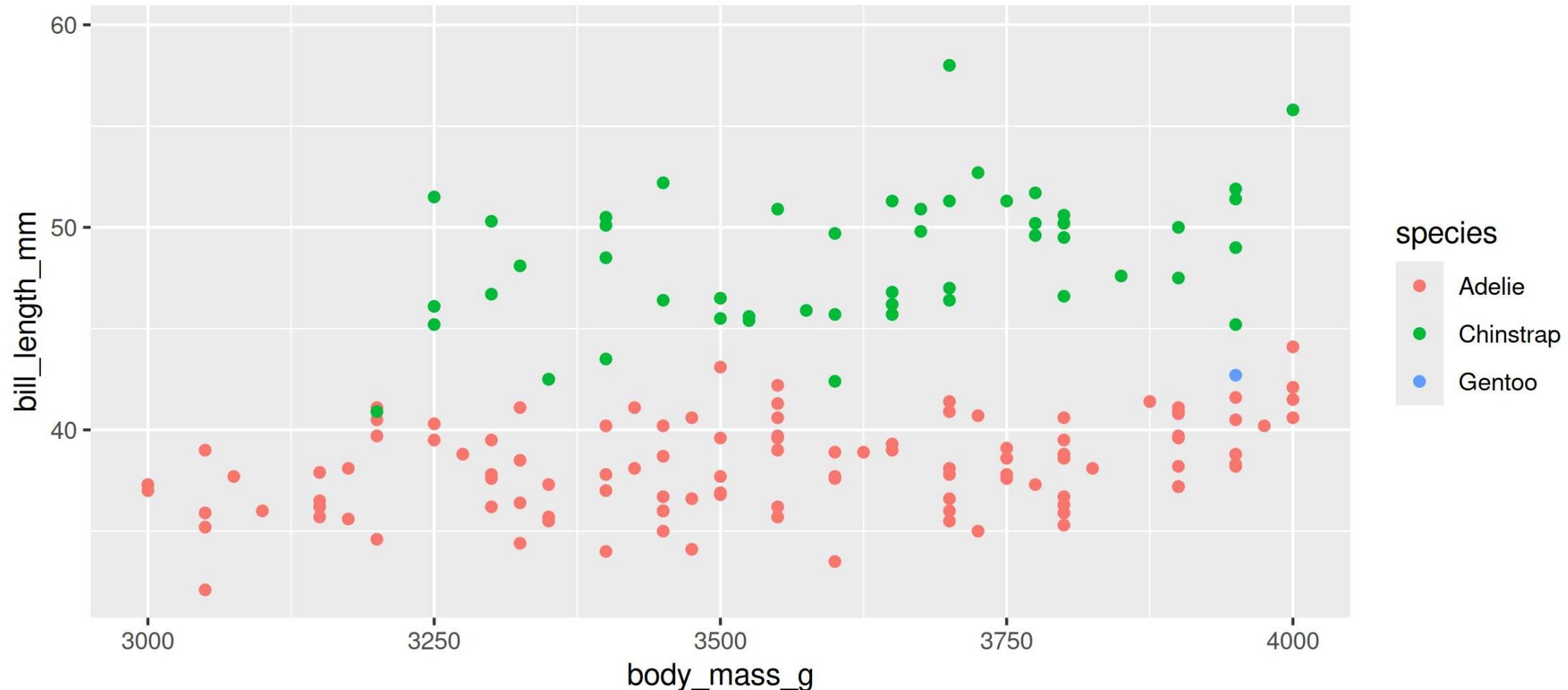
```
1 g + scale_x_continuous(breaks = seq(2500, 6500, 500))
```



Customizing: Axes

Limits

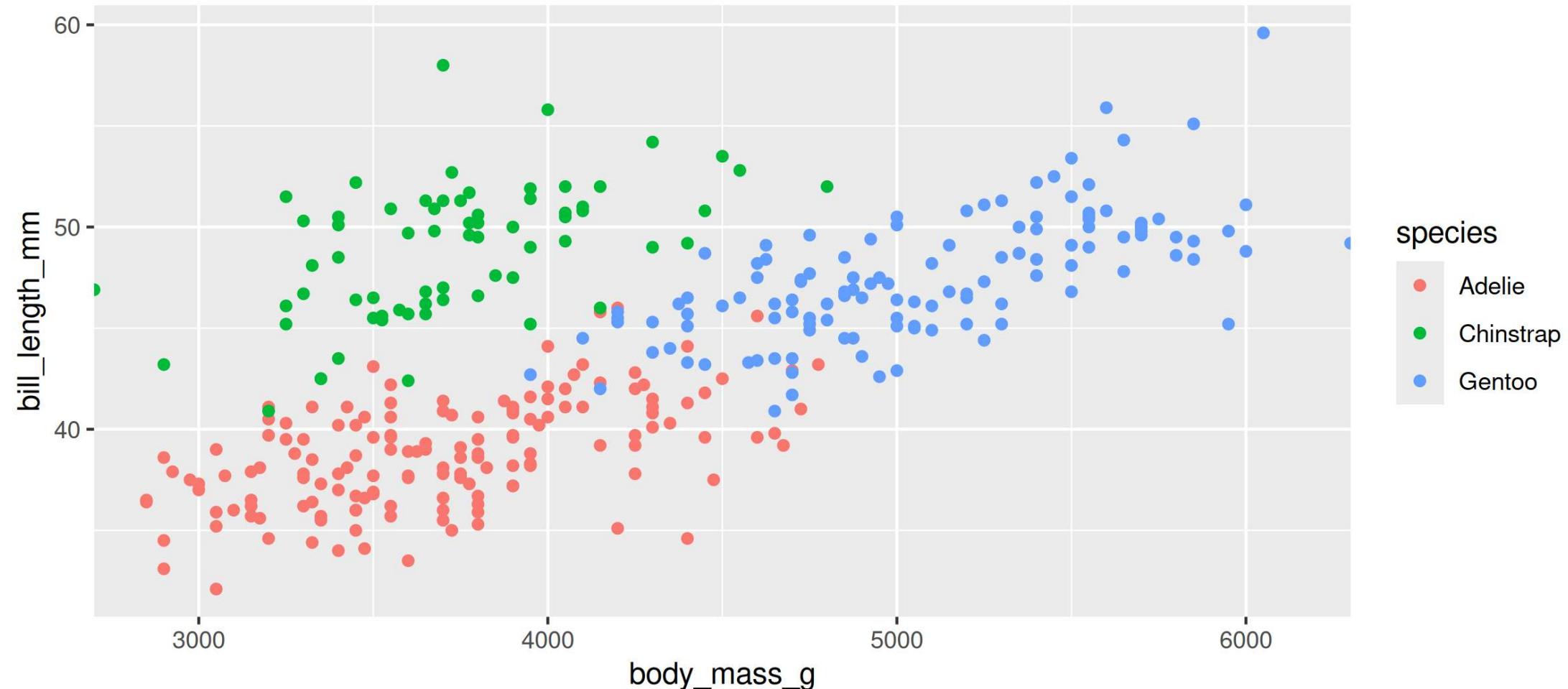
```
1 g + scale_x_continuous(limits = c(3000, 4000))
```



Customizing: Axes

Space between origin and axis start

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

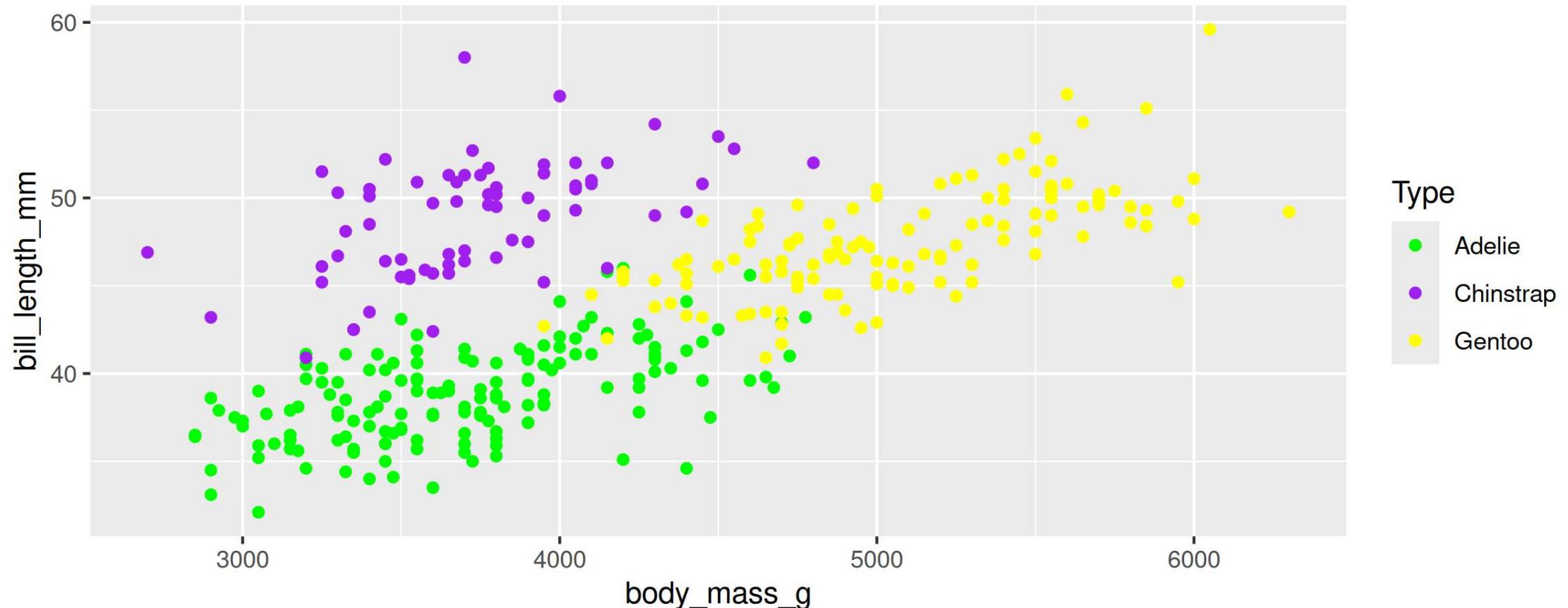


Customizing: Aesthetics

Using scales

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

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

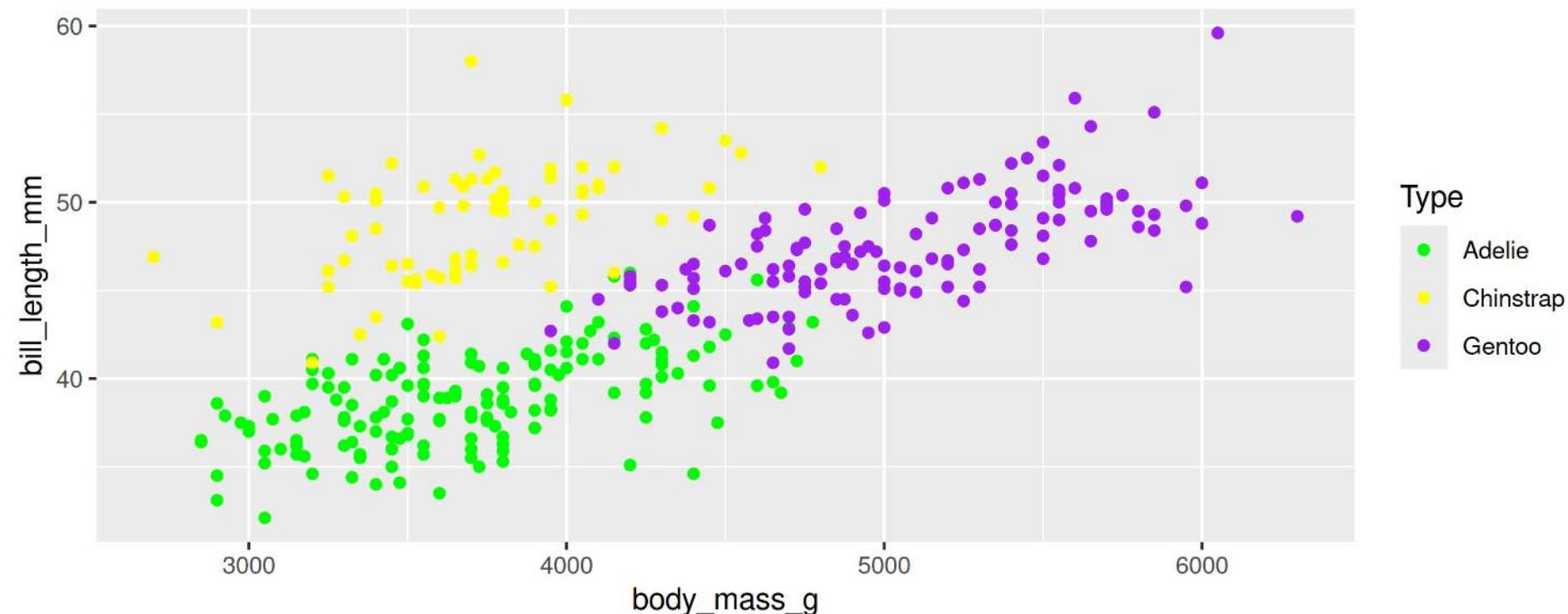


Customizing: Aesthetics

Using scales

Or be very explicit:

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

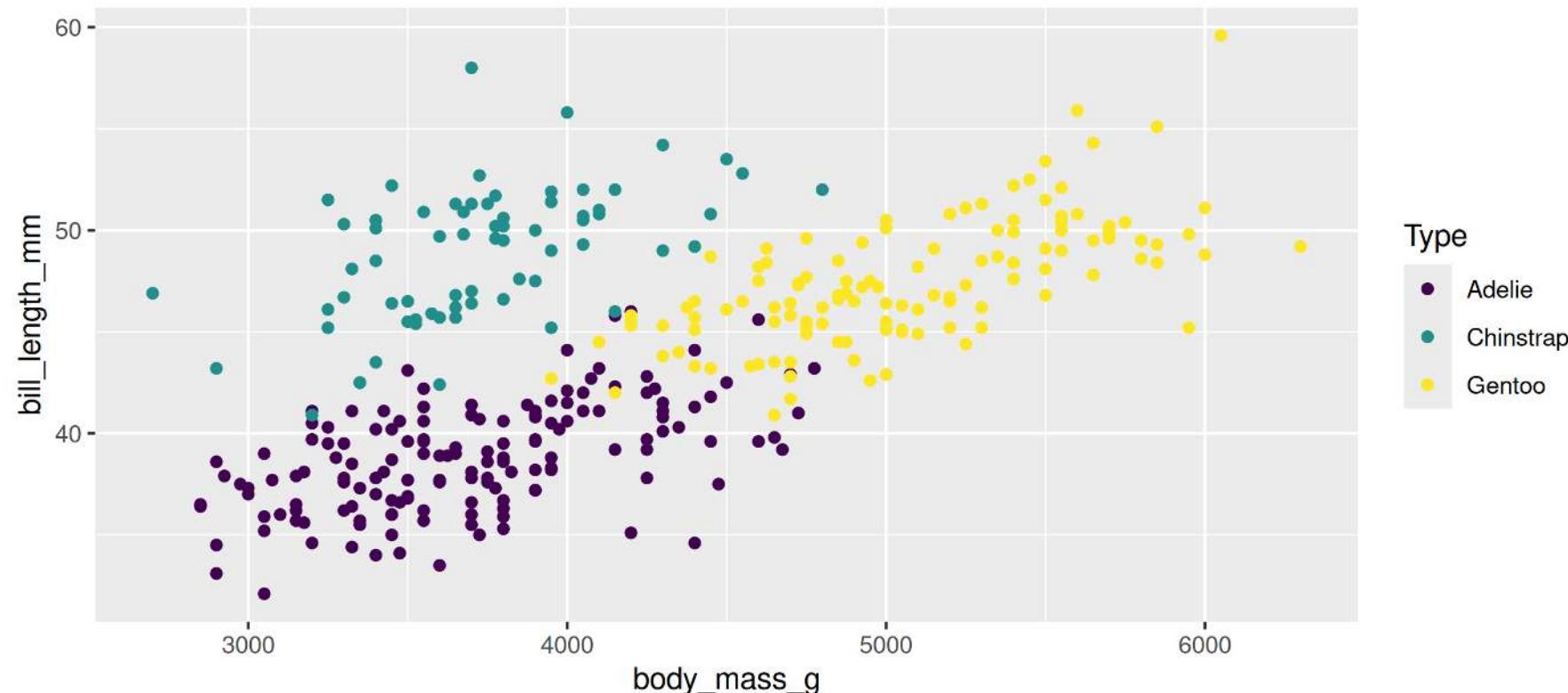


Customizing: Aesthetics

For colours, consider colour-blind-friendly scale

`viridis_d` for “discrete” data

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

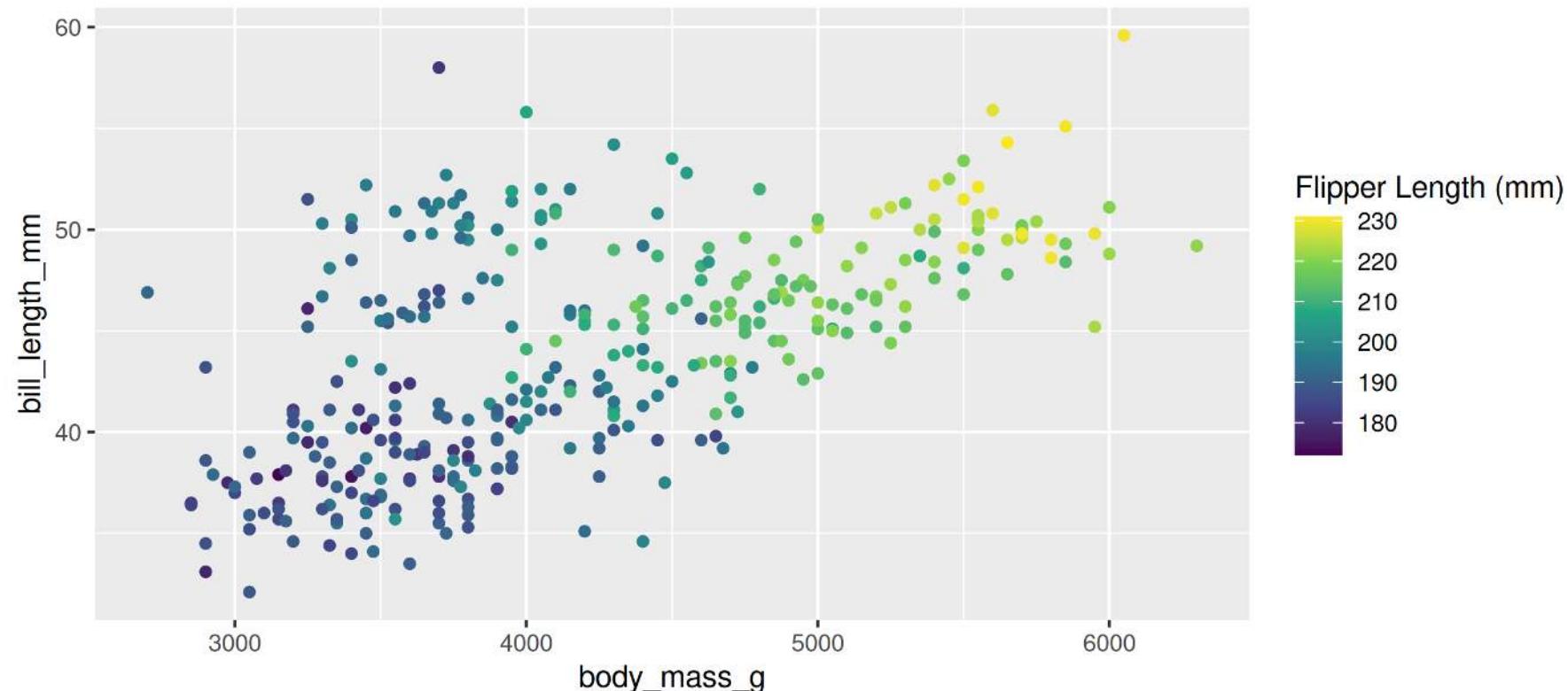


Customizing: Aesthetics

For colours, consider colour-blind-friendly scale

`viridis_c` for “continuous” data

```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = flipper_length_mm)) +  
2   geom_point() +  
3   scale_colour_viridis_c(name = "Flipper Length (mm)")
```

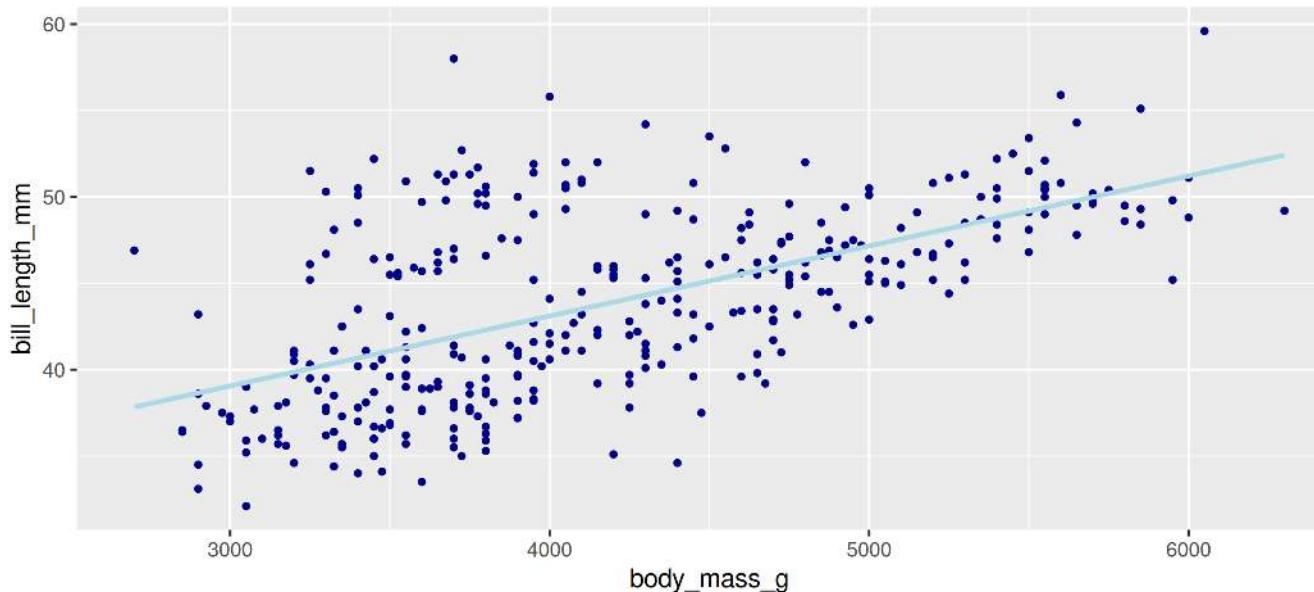


Customizing: Aesthetics

Forcing

Remove the association between a variable and an aesthetic

```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
2   geom_point(colour = "darkblue", size = 1) +  
3   stat_smooth(method = "lm", se = FALSE, colour = "lightblue")
```

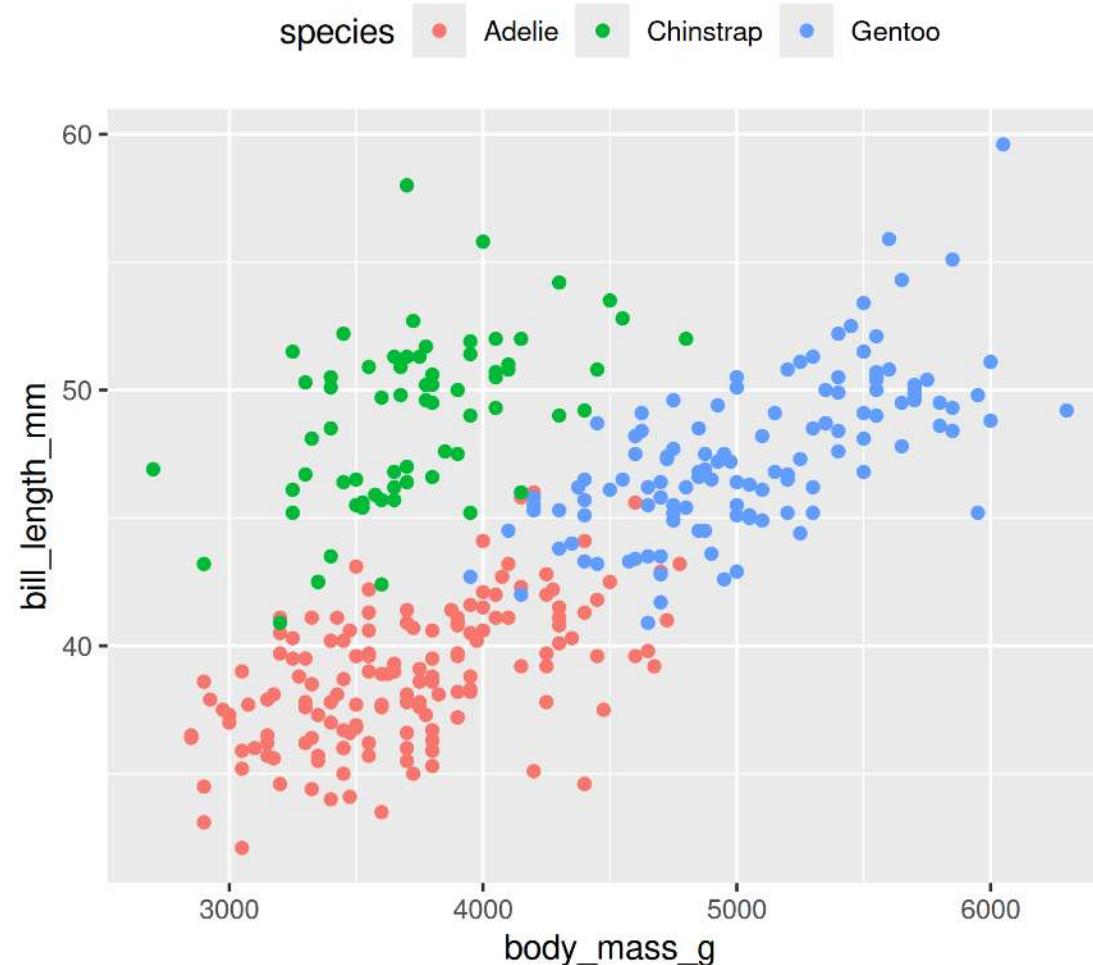


Note: When forcing, aesthetic is not inside aes()

Customizing: Legends placement

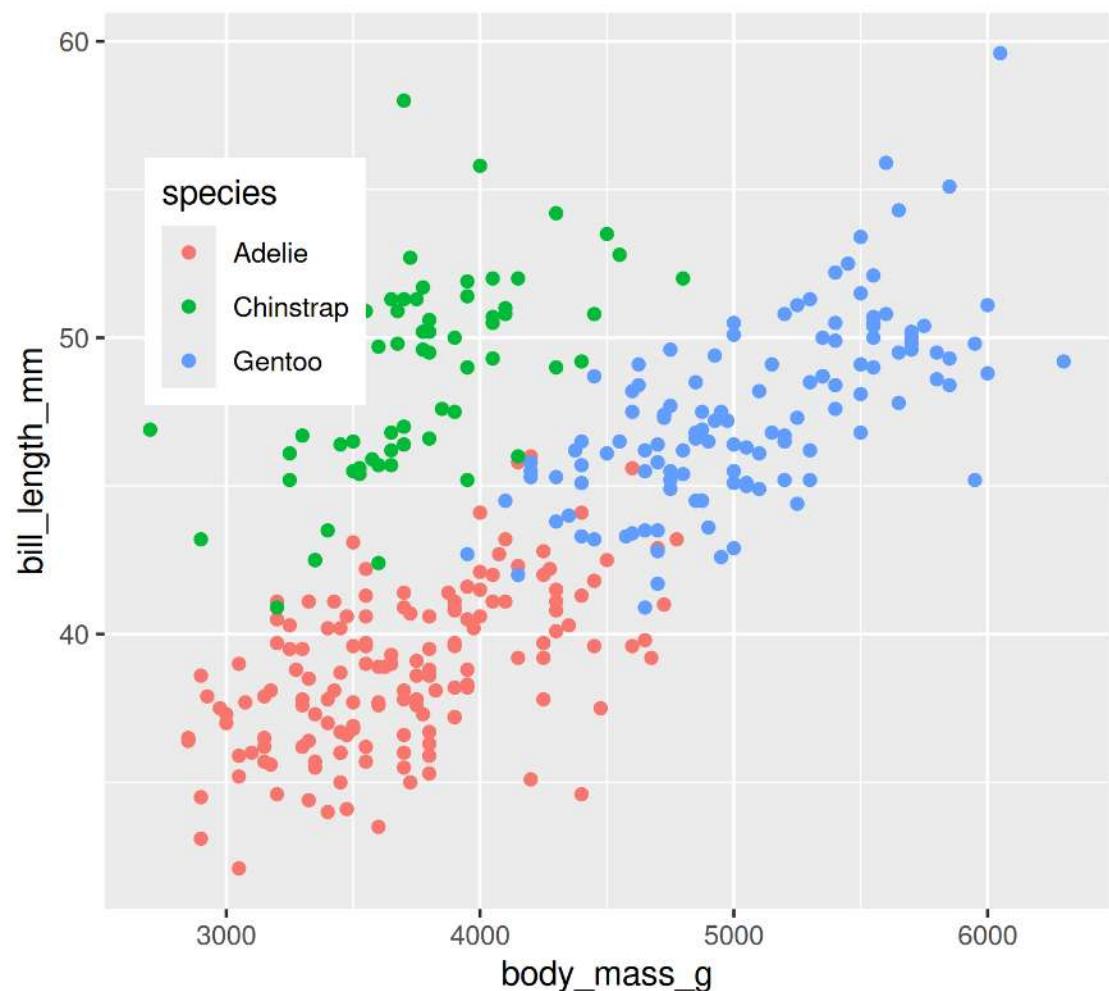
At the: top, bottom, left, right

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



Exactly here

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



Combining plots

Combining plots with patchwork

Setup

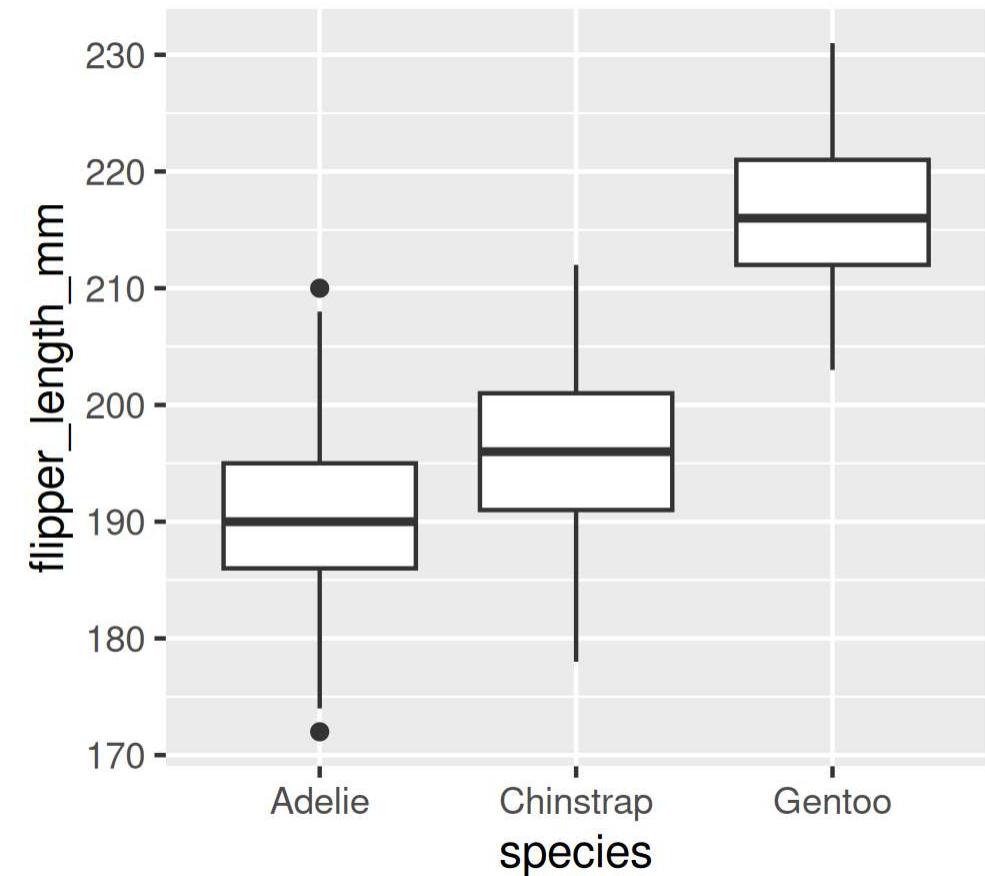
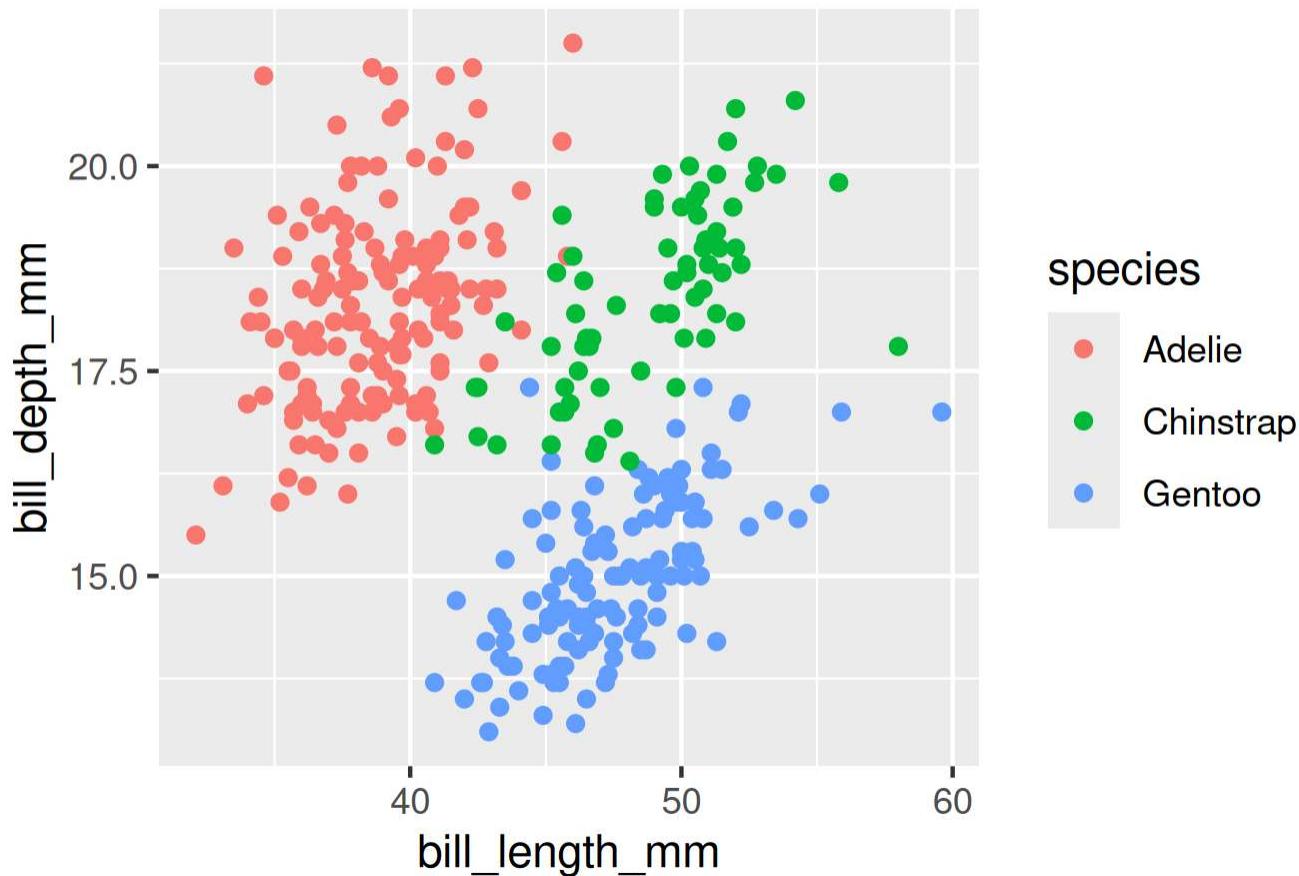
- Load [patchwork](#)
- Create a couple of different plots

```
1 library(patchwork)
2
3 g1 <- ggplot(data = penguins, aes(x = bill_length_mm, y = bill_depth_mm, colour = species)) +
4   geom_point()
5
6 g2 <- ggplot(data = penguins, aes(x = species, y = flipper_length_mm)) +
7   geom_boxplot()
8
9 g3 <- ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g, colour = species)) +
10  geom_point()
```

Combining plots with patchwork

Side-by-Side 2 plots

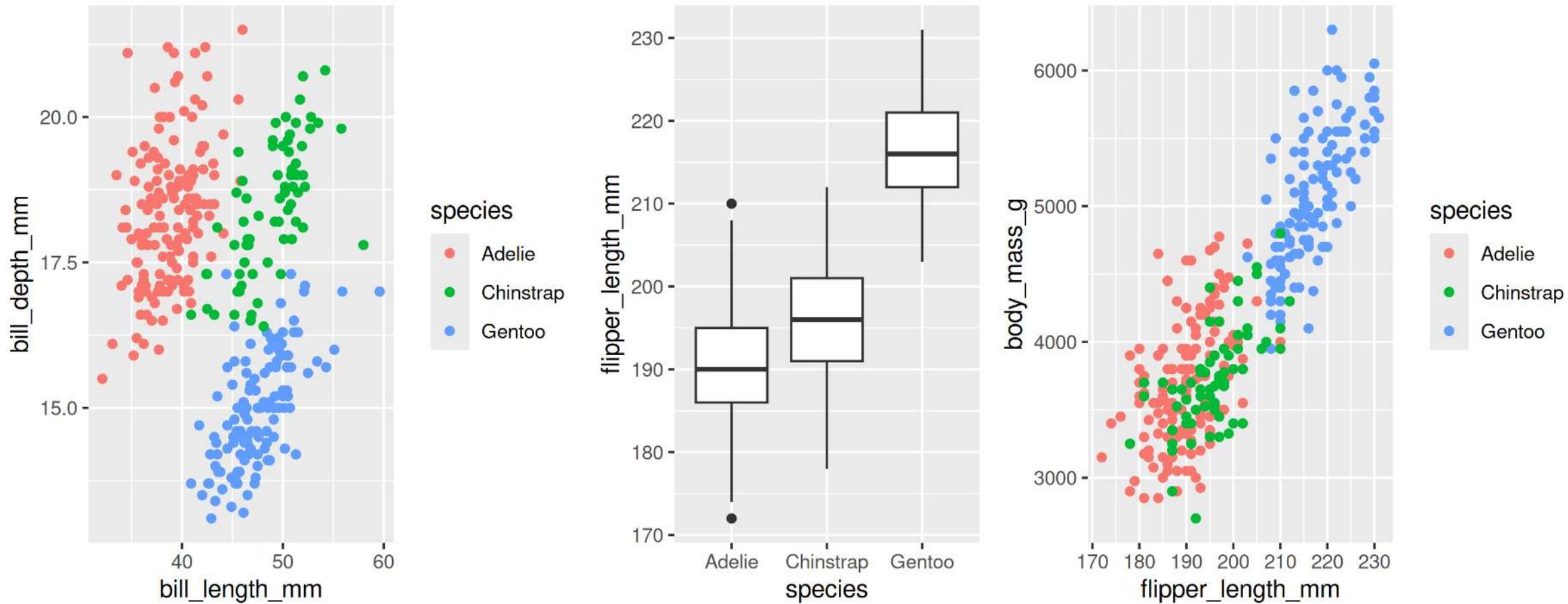
```
1 g1 + g2
```



Combining plots with patchwork

Side-by-Side 3 plots

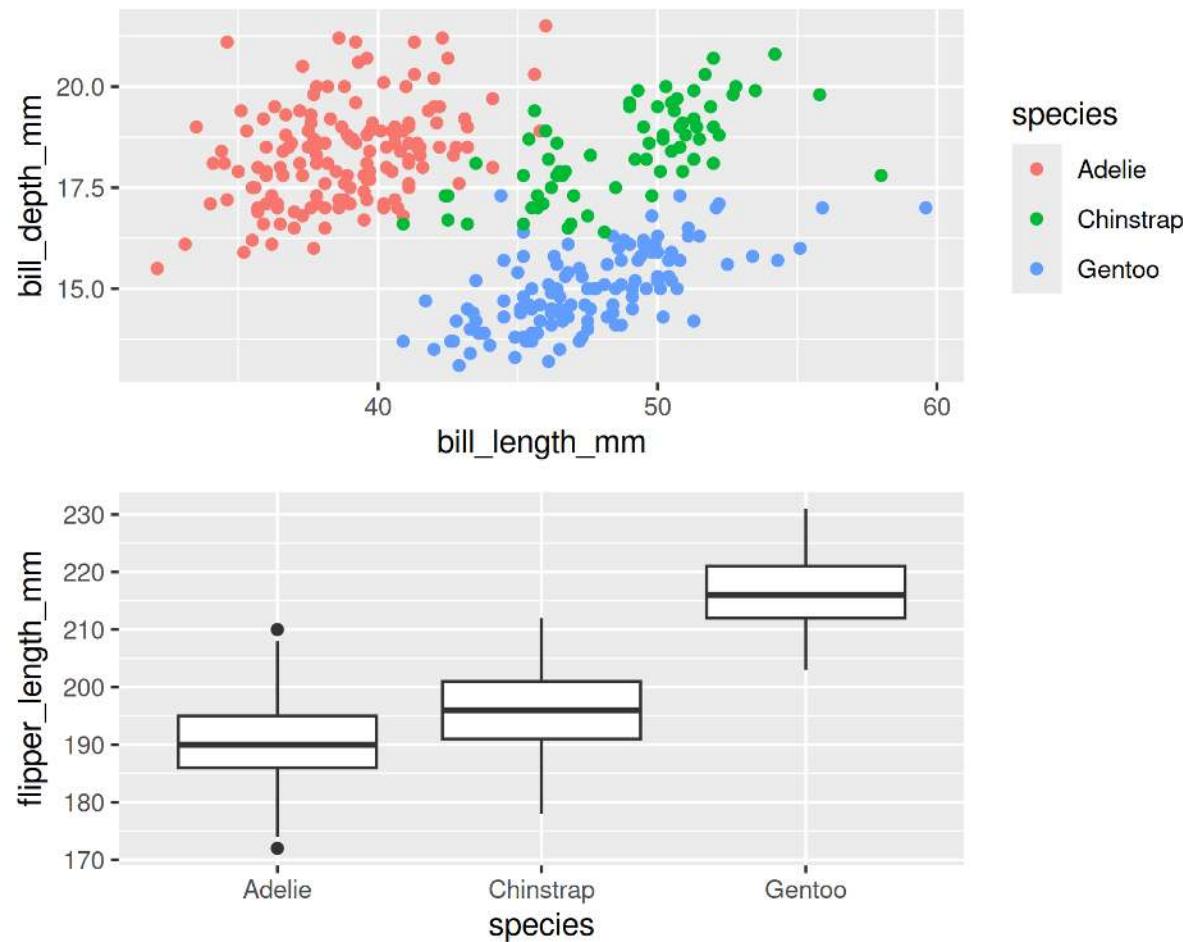
```
1 g1 + g2 + g3
```



Combining plots with patchwork

Stacked 2 plots

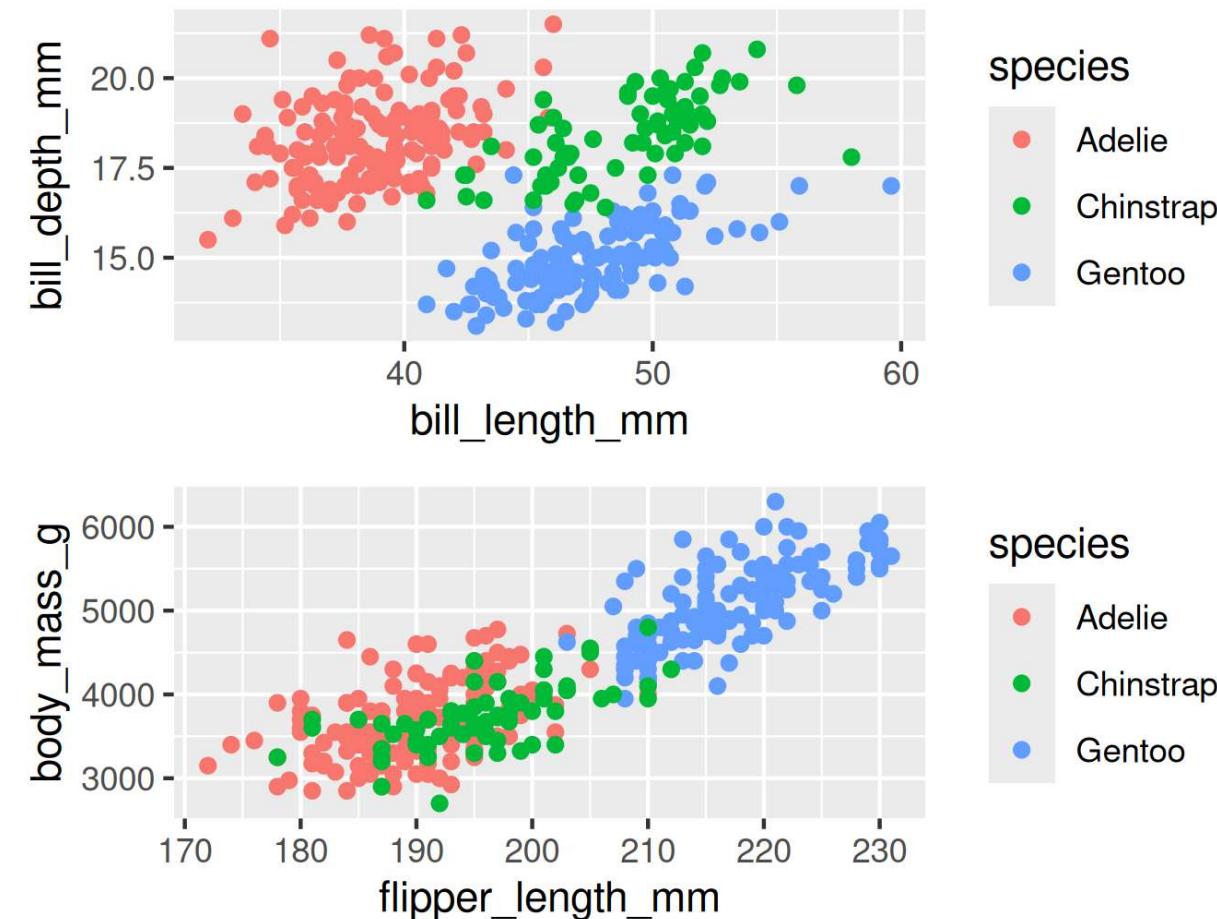
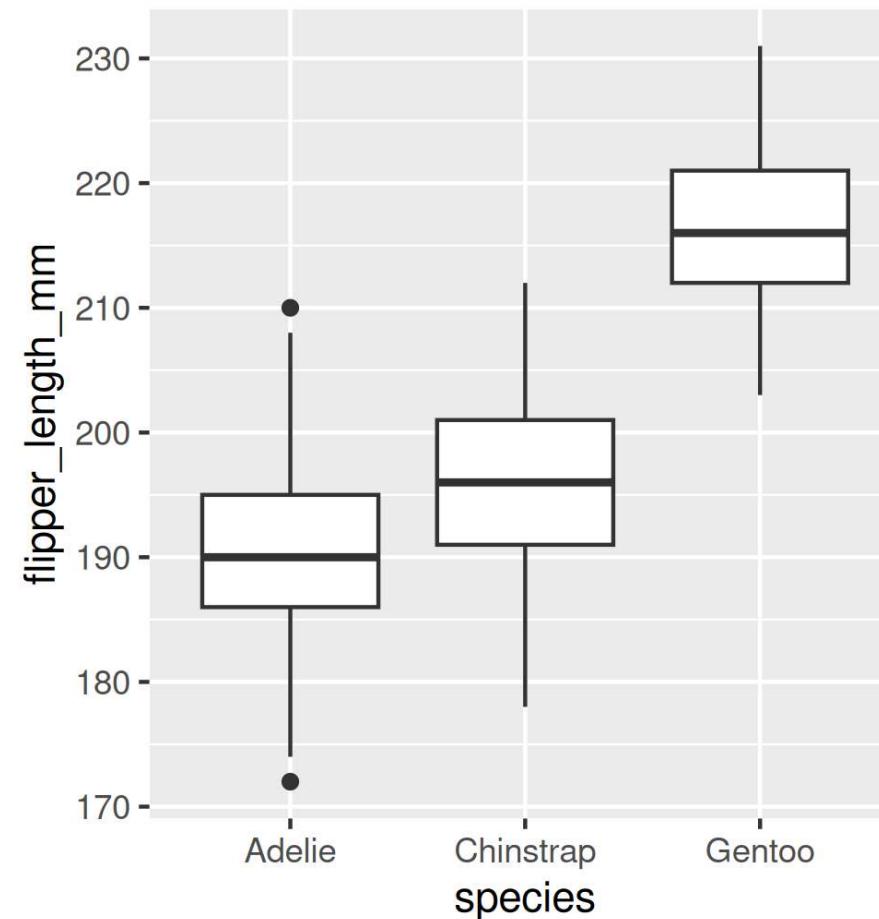
```
1 g1 / g2
```



Combining plots with patchwork

More complex arrangements

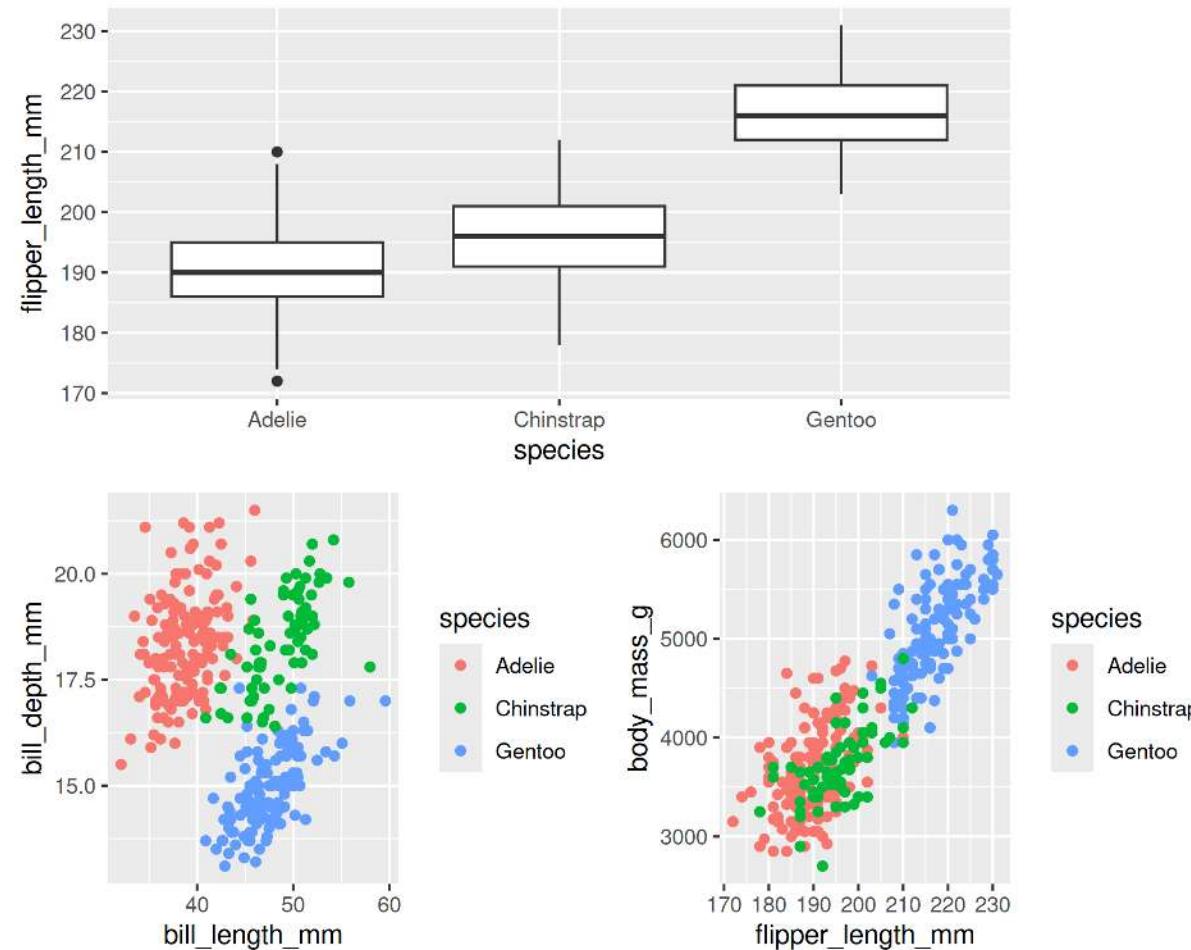
```
1 g2 + (g1 / g3)
```



Combining plots with patchwork

More complex arrangements

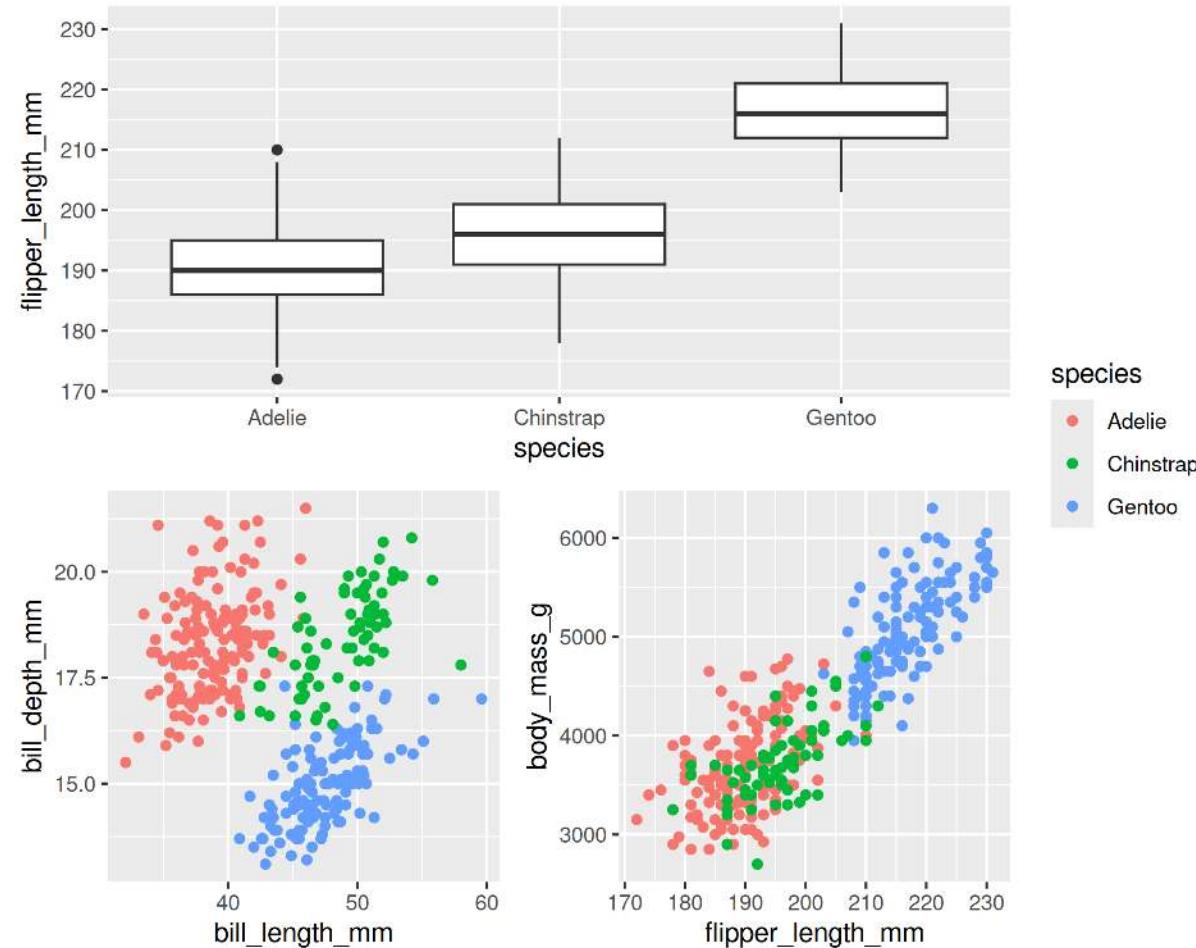
```
1 g2 / (g1 + g3)
```



Combining plots with patchwork

“collect” common legends

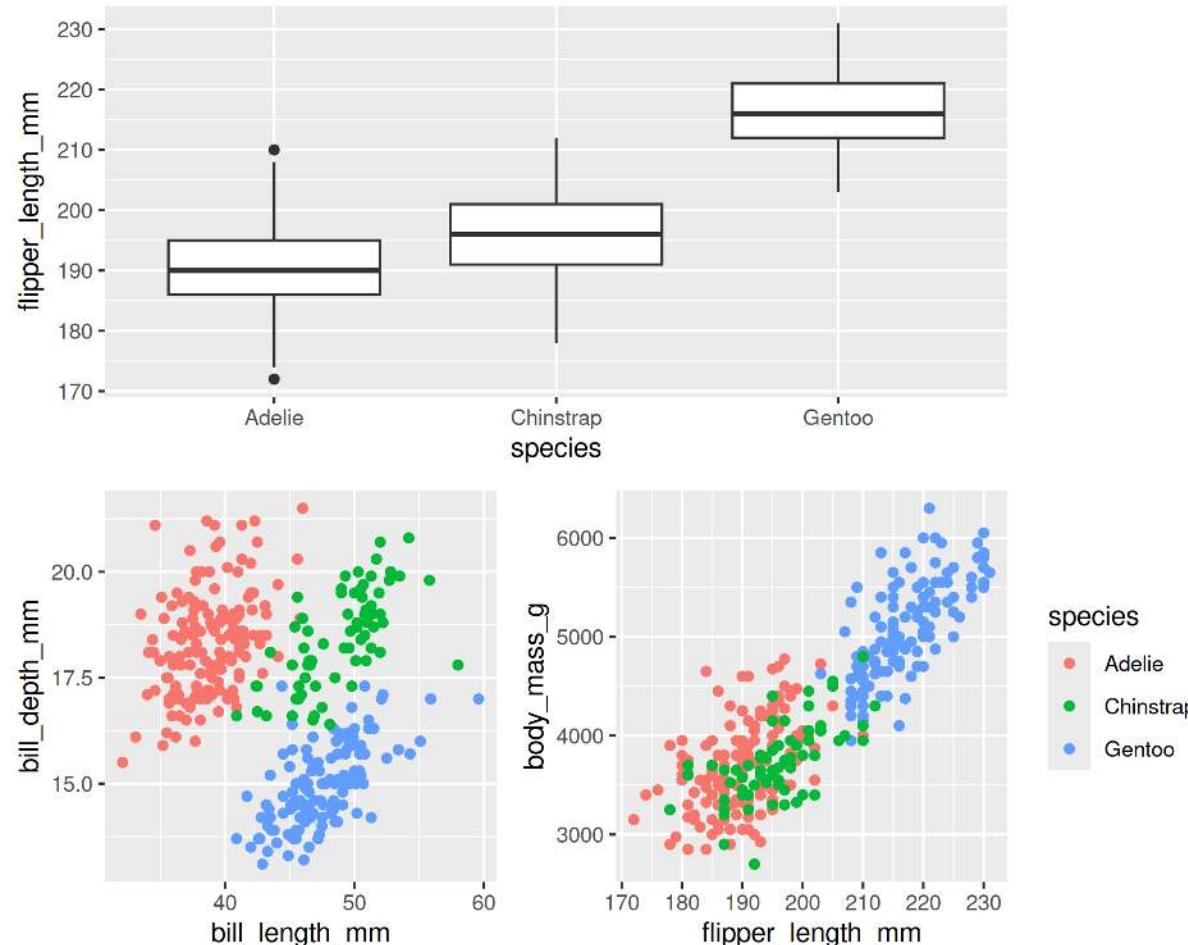
```
1 g2 / (g1 + g3) + plot_layout(guides = "collect")
```



Combining plots with patchwork

“collect” common legends

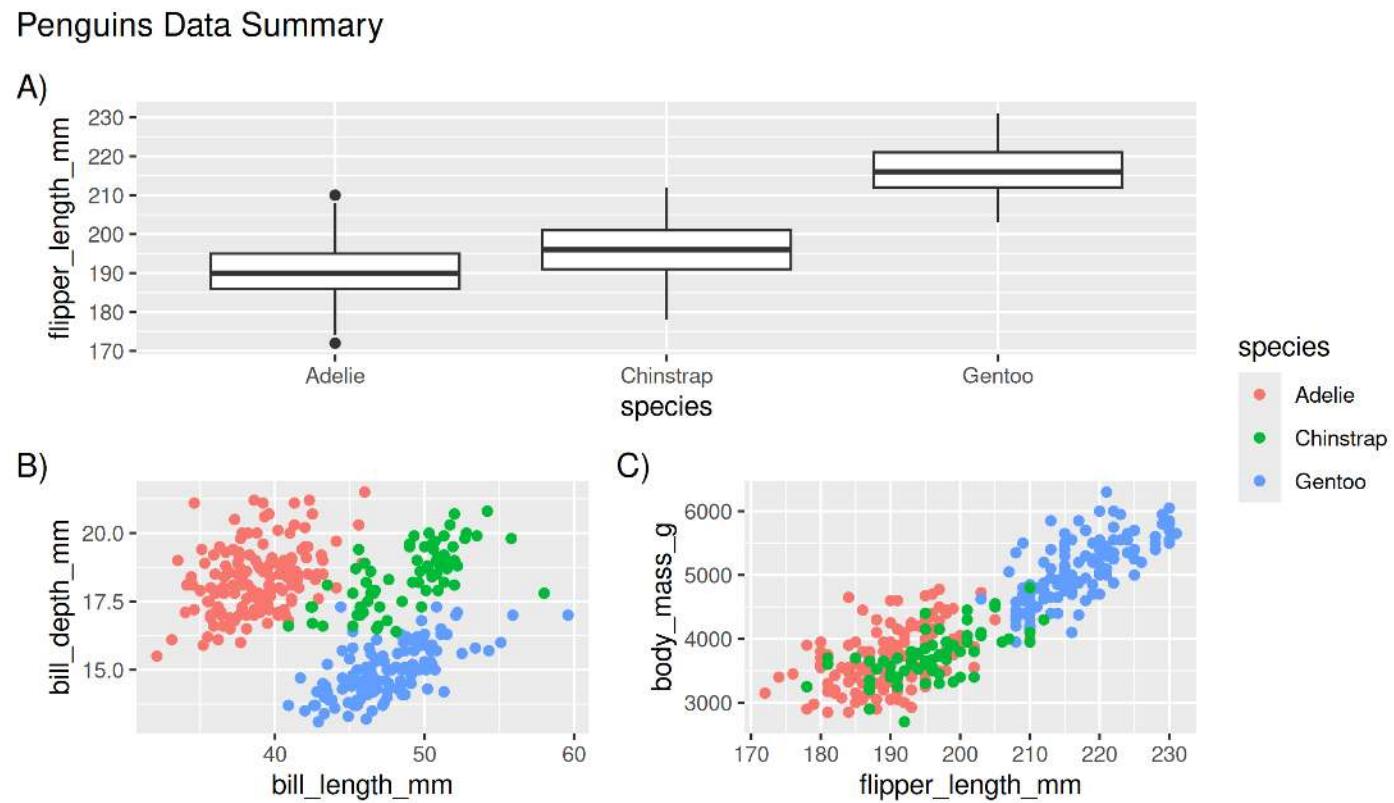
```
1 g2 / (g1 + g3 + plot_layout(guides = "collect"))
```



Combining plots with patchwork

Annotate

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



Saving plots

Saving plots

RStudio Export

Demo

ggsave()

```
1 g <- ggplot(penguins, aes(x = sex, y = bill_length_mm, fill = year)) +  
2   geom_boxplot()  
3  
4 ggsave(filename = "penguins_mass.png", plot = g)
```

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

```
1 g <- ggplot(penguins, aes(x = sex, y = body_mass_g)) +  
2   geom_boxplot() +  
3   labs(x = "Sex", y = "Body Mass (g)") +  
4   theme(axis.text.x = element_text(angle = 45, hjust = 1))  
5  
6 ggsave(filename = "penguins_mass.pdf", plot = g, dpi = 300,  
7         height = 80, width = 129, units = "mm")
```

Wrapping up

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()`
 - e.g. `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](#) (Hadley Wickham, Danielle Navarro, and Thomas Lin Pedersen)
- [patchwork website](#)
- [Cookbook for R](#) (Winston Chang)
- [R for Data Science](#) (Hadley Wickham & Garrett Grolemund)
 - Chp 3 Data Visualization
- [Data Visualization: A practical introduction](#) (Kieran Healy)
- [Using Special Symbols](#) (Steffi LaZerte)

Thank you!

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Extra

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



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

