NRI 7350

Plots and Loading Data

Artwork by @allison_horst

Check-in

- Everyone getting emails? (e.g., email about these slides?)
- Everyone have access to these slides?
  https://steffilazerte.ca/NRI_7350/slides.html

Data for Assignments 2, 3 and 4

Assignment 2 (first R assignment!) comes next week

You'll need a data set with

- One *continuous* dependent variable (response)
- One *categorical* independent variable with **at least three categories** (explanatory)
- Two *continuous* independent variables (explanatory)

Example:

- response = `frequency`
- categorical explanatory = `site`
- continuous explanatory = `noise` and `mass`

frequency	site	noise	mass
3500	rural	45	11.0
3600	city	65	10.0
3555	town	55	10.5
3650	rural	47	9.5
3300	town	52	10.0

Data for Assignments 2, 3 and 4

Don't have enough variables? You can...

- Create a categorical variable from continuous
  - `noise` in dB = `quiet`, `regular`, `noisy`
  - `mass` in grams = `small`, `medium`, `large`
  - `concentration` in g/mL = `low`, `medium`, `high`
  - `amount` = `none`, `some`, `lots`
- Create a dummy continuous variable
  - `x` = random numbers between 1 and 250

Don't have any data?

- Ask your supervisor for something related to your project
- Ask your fellow students
- Email Nicky and I together with a brief description of your project and its design and we'll figure something out

Getting started (again)

Open RStudio

Open your NRI project

Open a **new** script for today:

File > New File > R Script

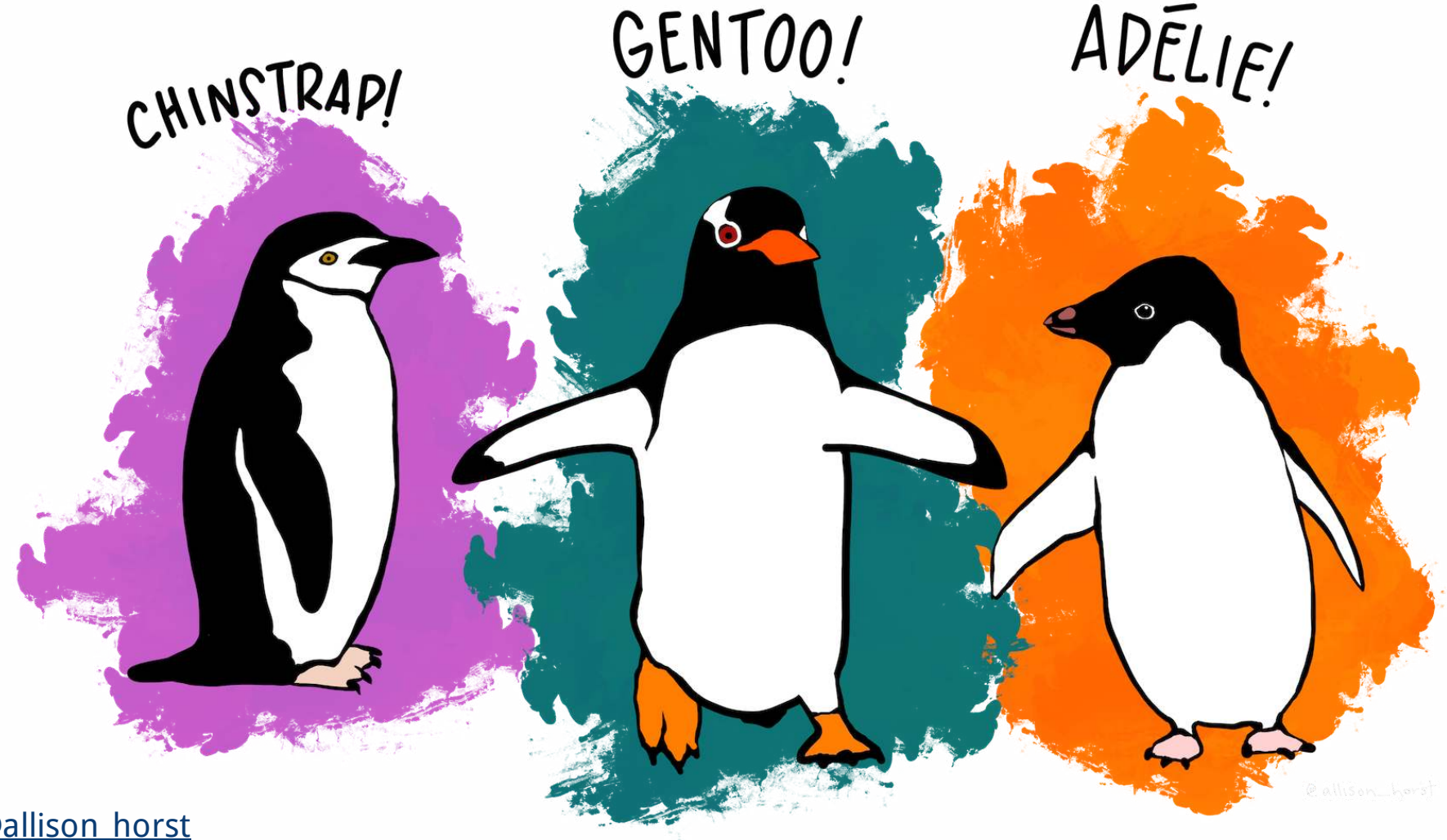
Make sure to load **`tidyverse`** at the top:

`library(tidyverse)`

Creating Figures

Artwork by @allison_horst

Our data set: Palmer Penguins!

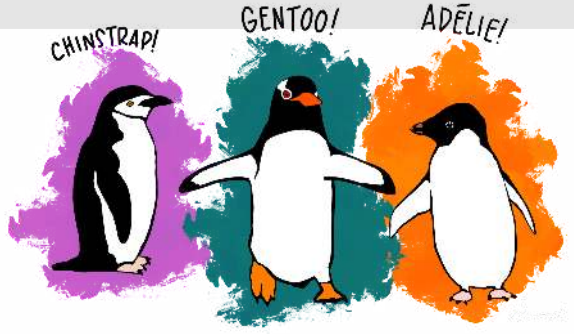


Artwork by @allison_horst

Our data set: Palmer Penguins!

```
library(palmerpenguins)
penguins
```

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



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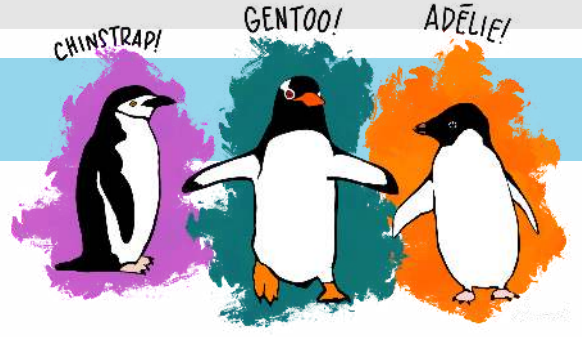
Our data set: Palmer Penguins!

```
library(palmerpenguins)
penguins
```

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

Your turn! Run this code and look at the output in the console

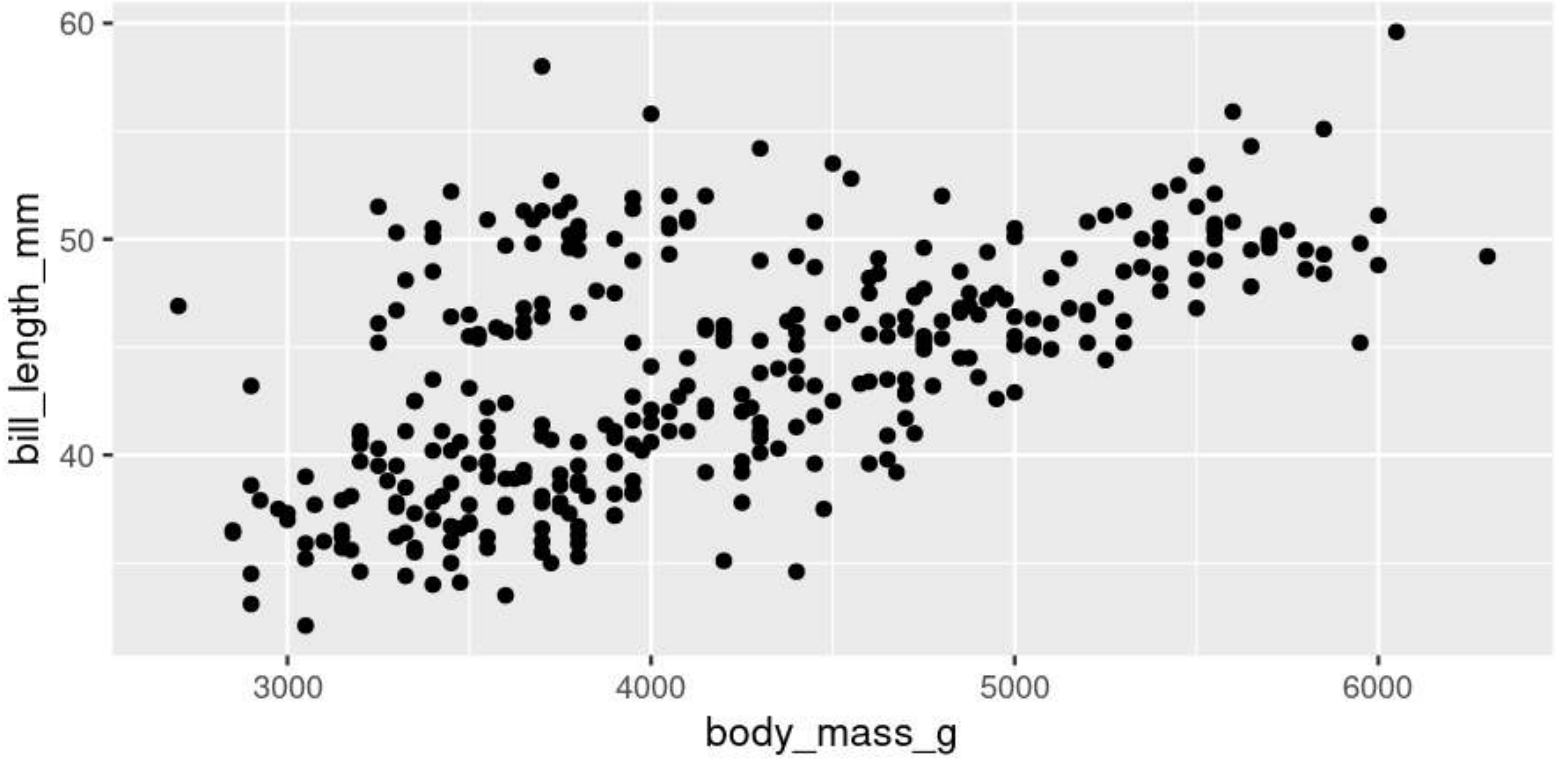


Artwork by @allison_horst

A basic plot

```
library(palmerpenguins)
library(tidyverse)

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



Break it down

```
library(palmerpenguins)
library(tidyverse)

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

`library(palmerpenguins)`

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

Break it down

```
library(palmerpenguins)
library(tidyverse)

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

`library(tidyverse)`

- Load the **`tidyverse`** package (which loads the **`ggplot2`** package)

Break it down

```
library(palmerpenguins)
library(tidyverse)

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

`ggplot()`

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

Break it down

```
library(palmerpenguins)
library(tidyverse)

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

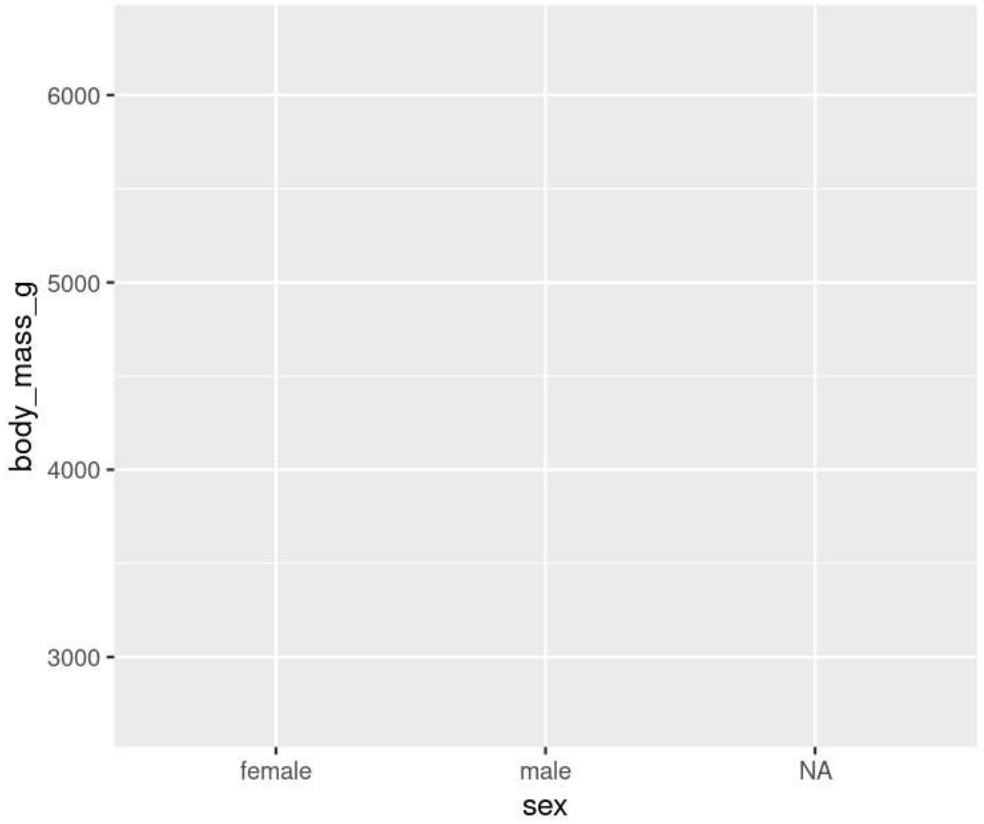
`geom_point()`

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

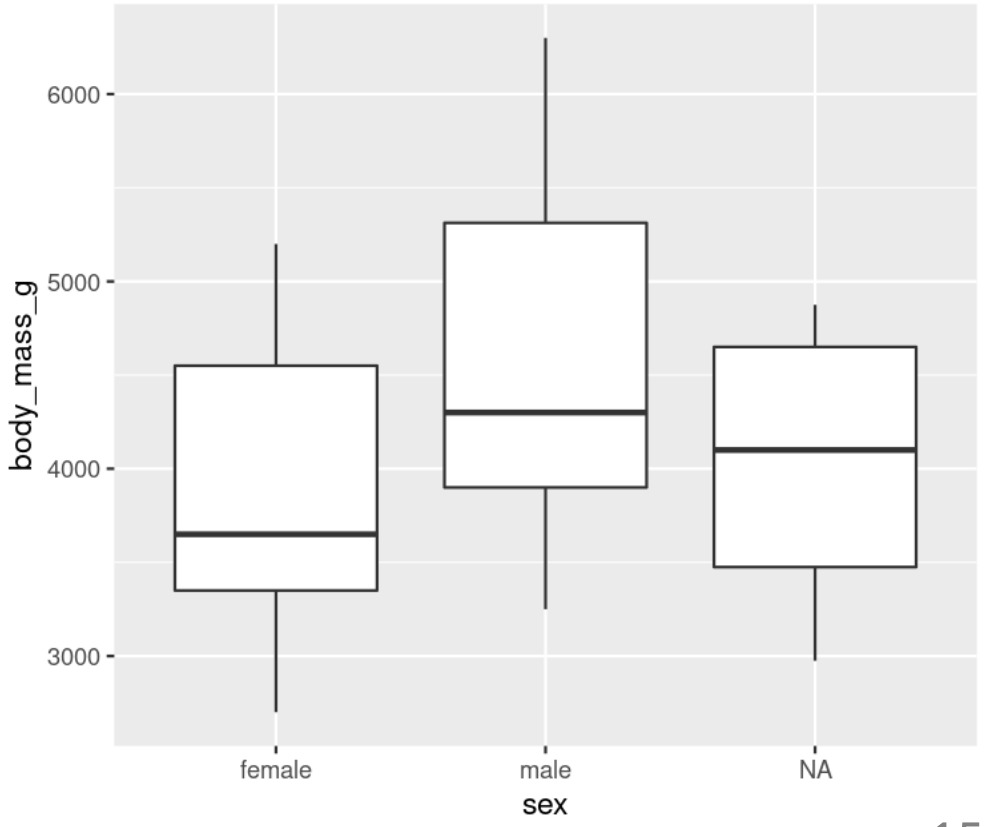
> ggplots are essentially layered objects, starting with a call to **`ggplot()`**

Plots are layered

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

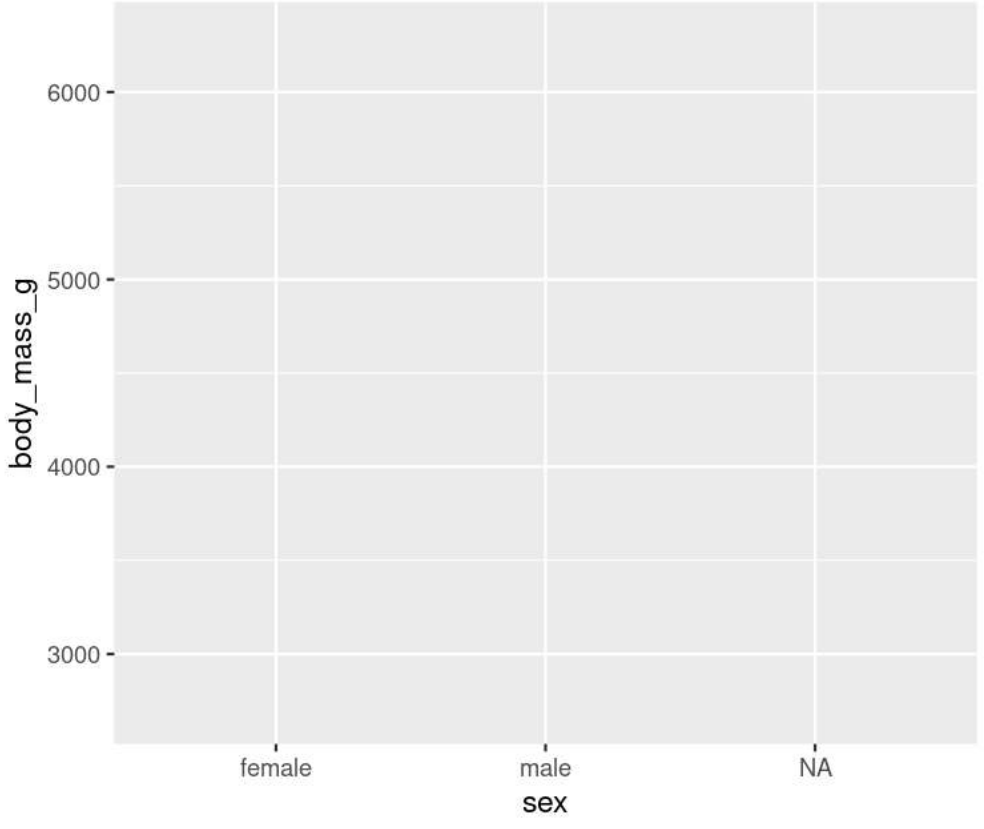



```
ggplot(data = penguins, aes(x = sex, y =
body_mass_g)) +
  geom_boxplot()
```

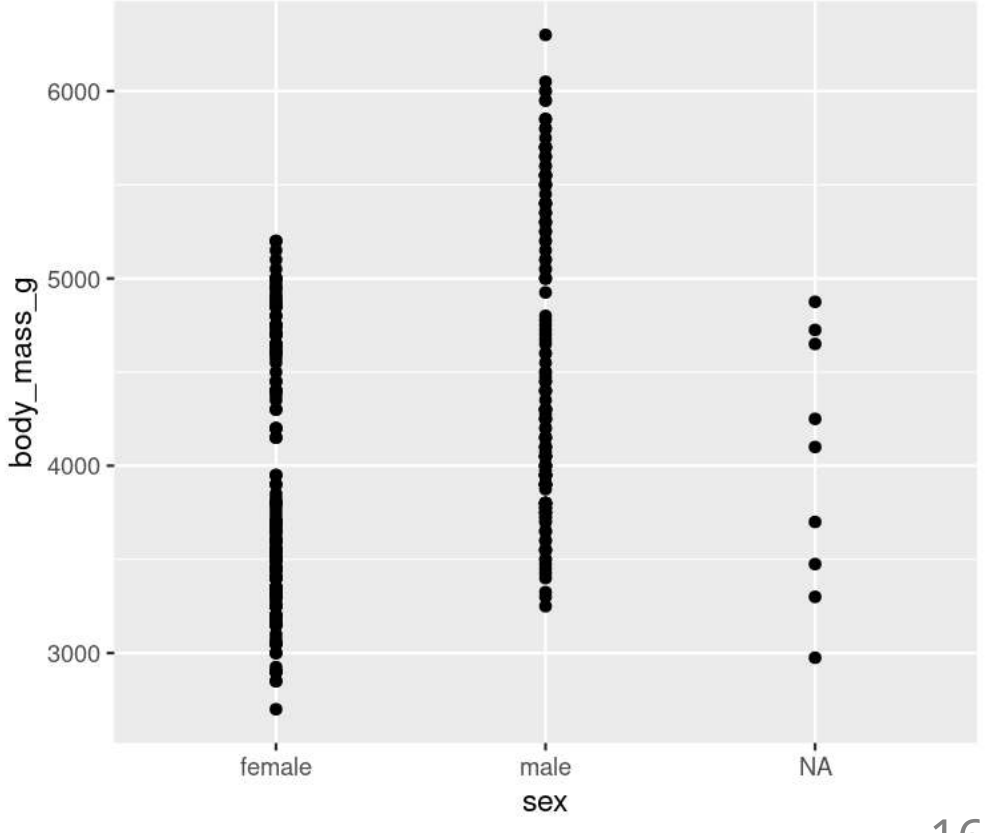


Plots are layered

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




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



Plots are layered

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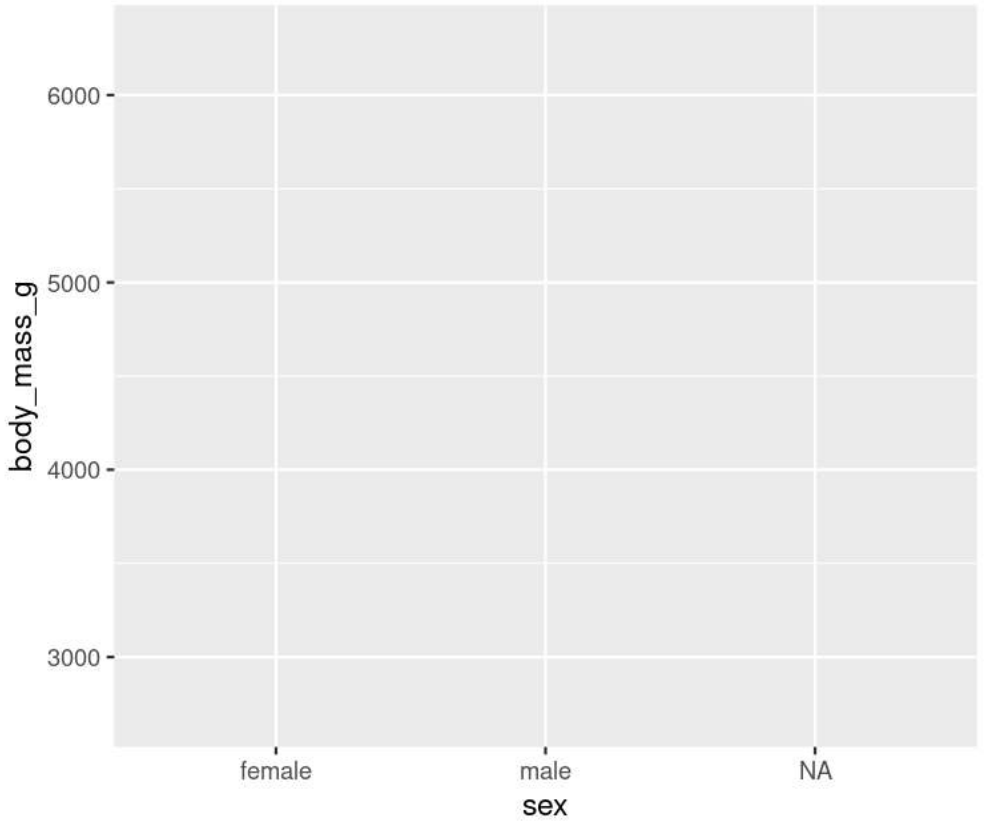
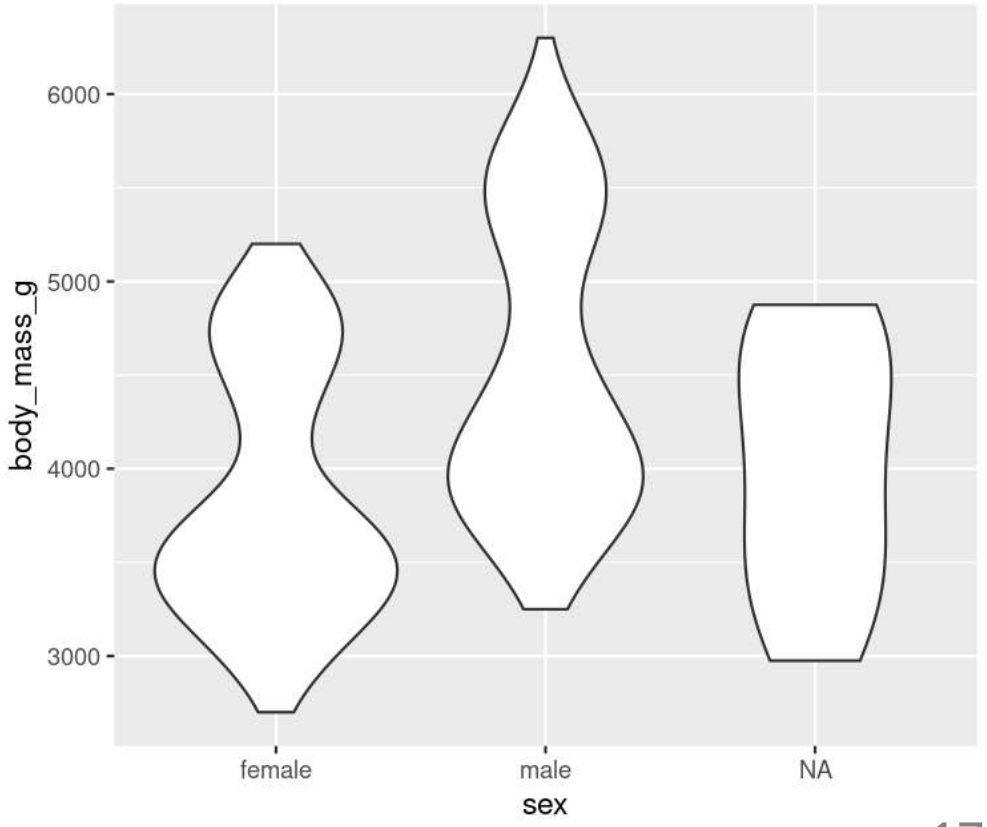
```



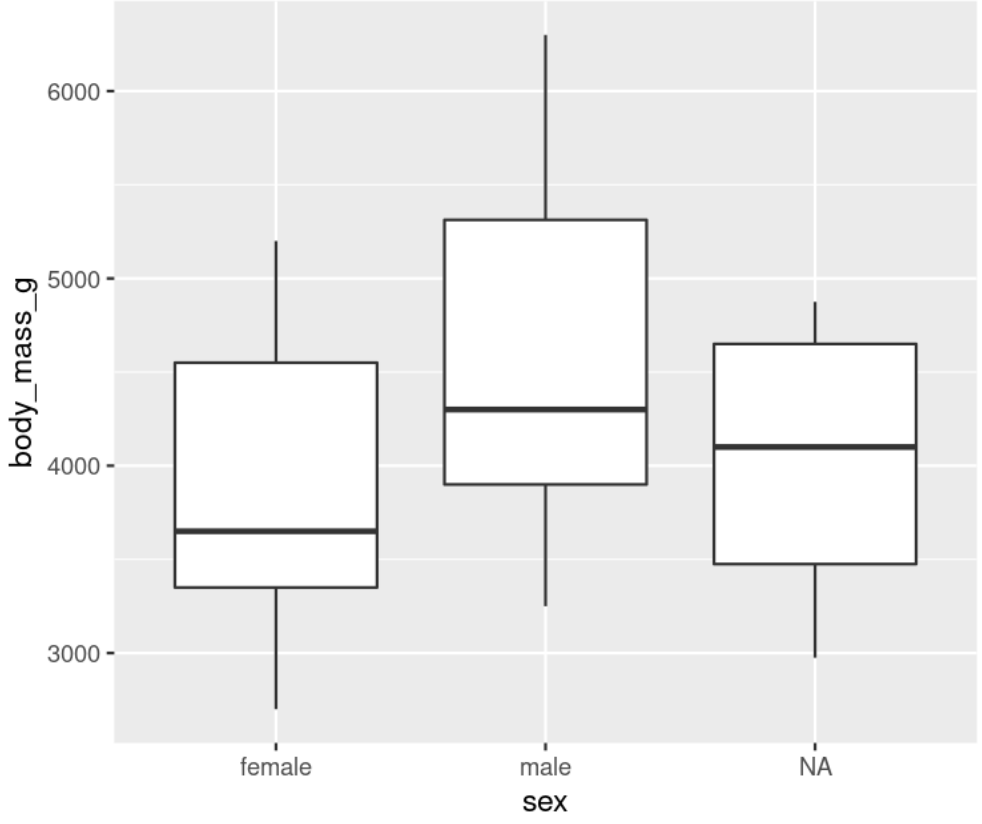

```
ggplot(data = penguins, aes(x = sex, y =
body_mass_g)) +
  geom_violin()
```



Plots are layered

You can add multiple layers

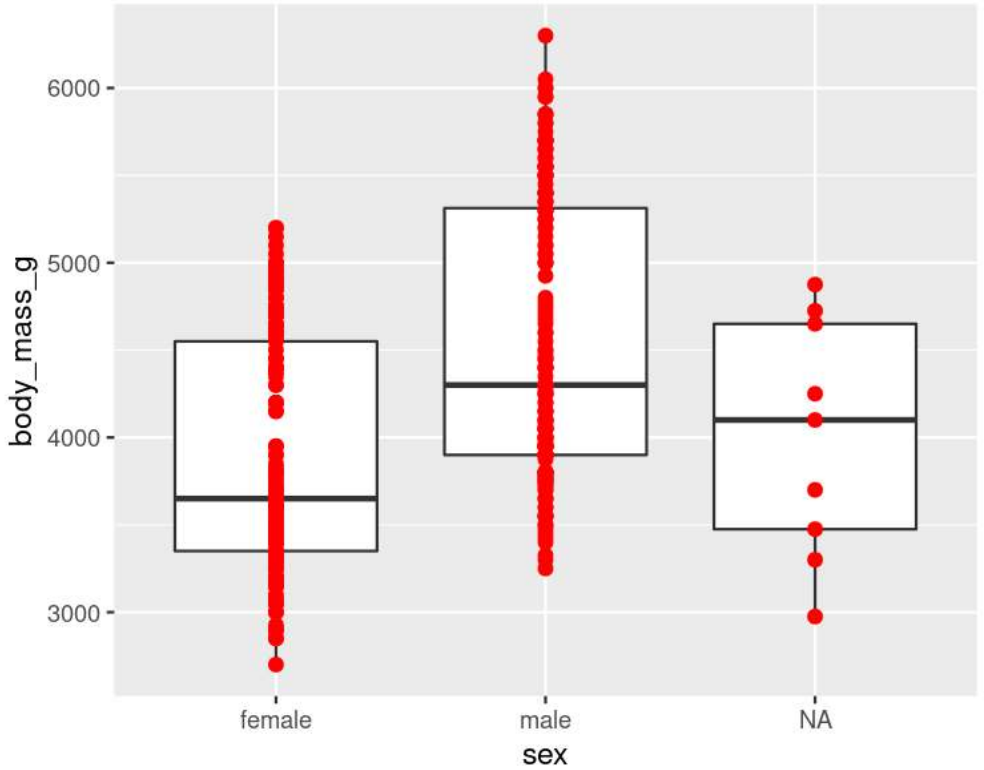
```
ggplot(data = penguins, aes(x = sex, y =
body_mass_g)) +
  geom_boxplot()
```



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 =
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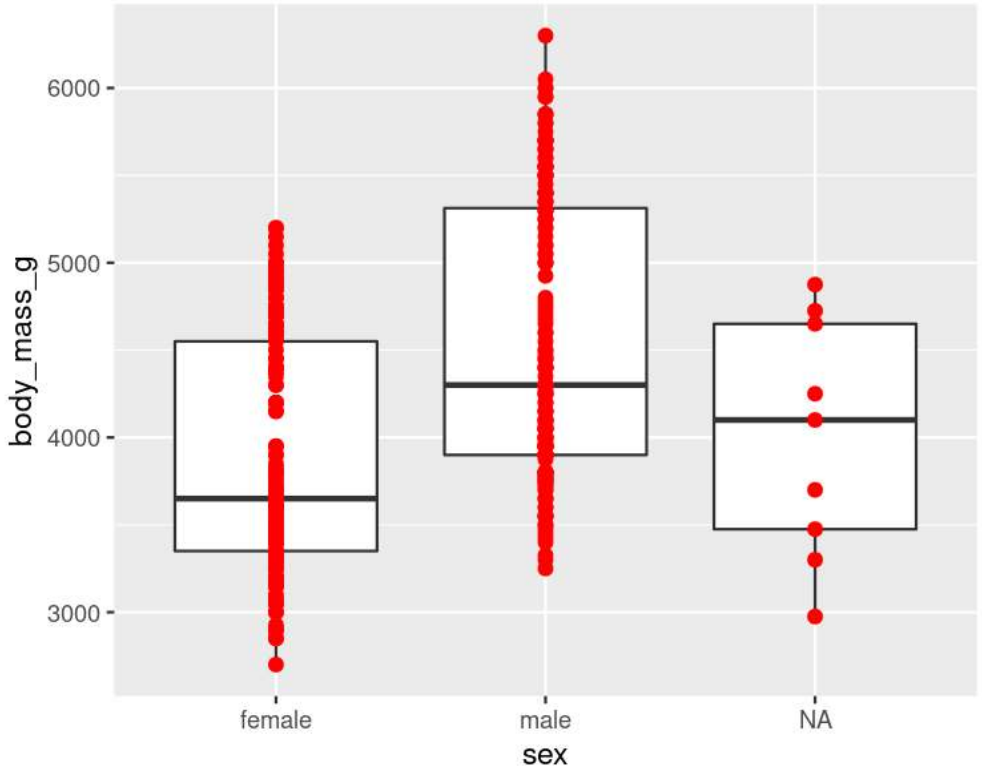
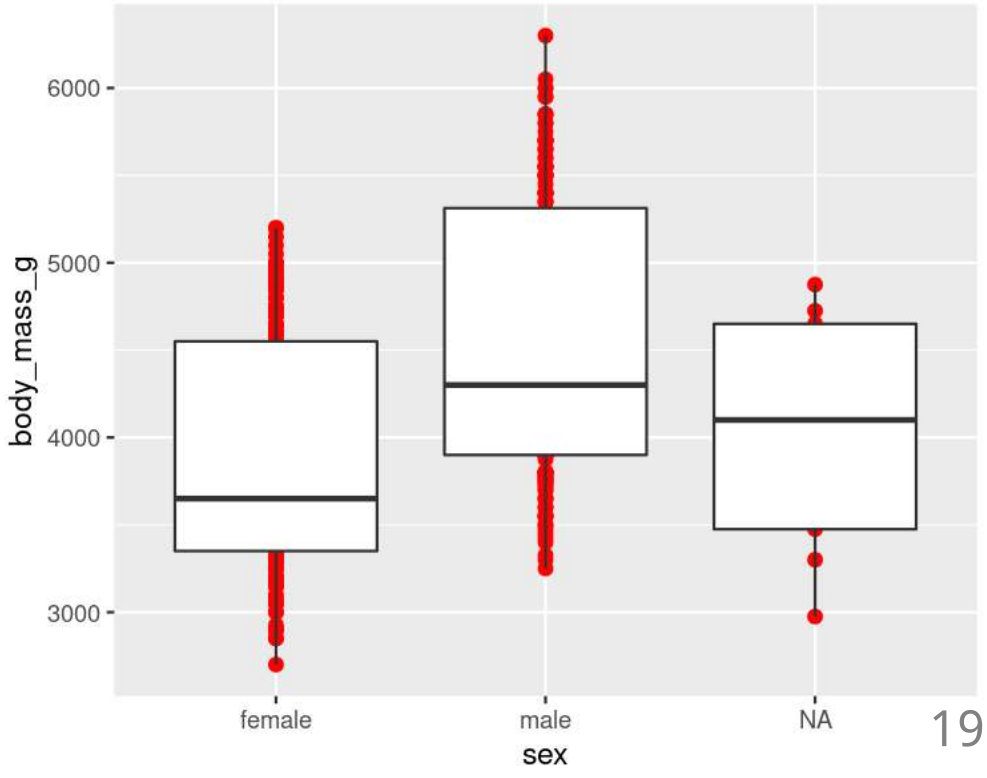


Order matters

```
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

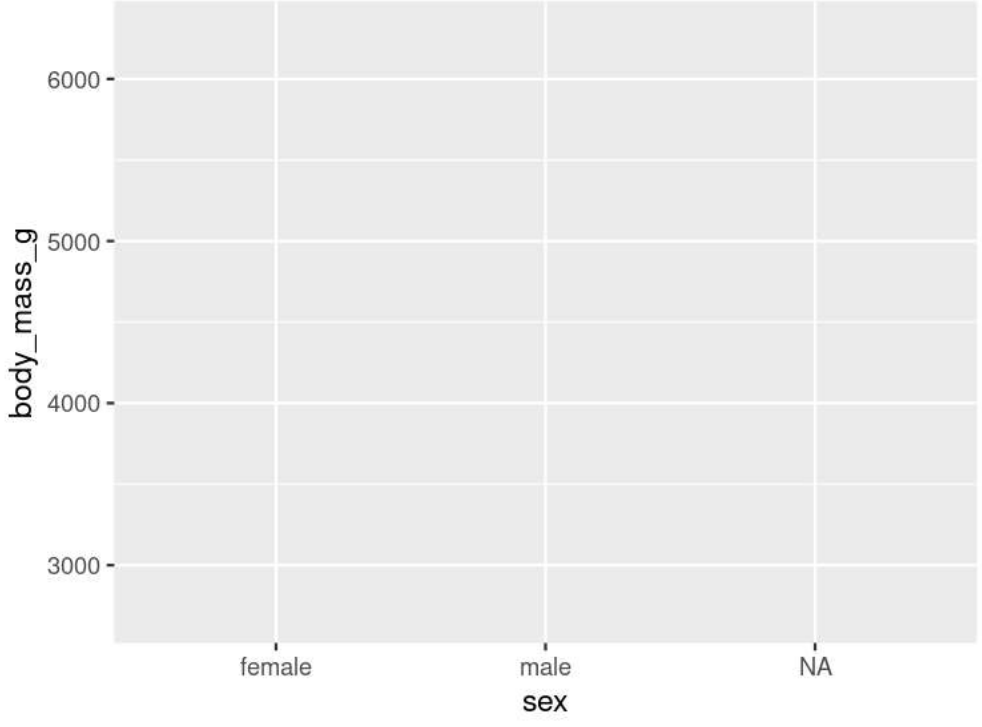
```
g <- ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

Plots are objects

Any ggplot can be saved as an object

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

```
g
```

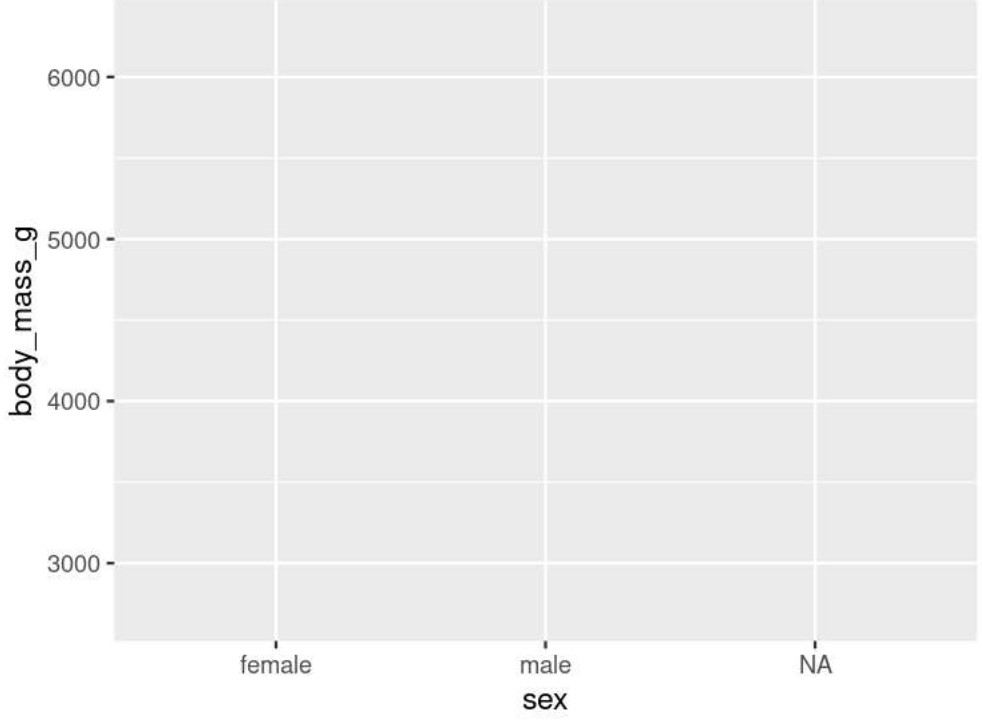


Plots are objects

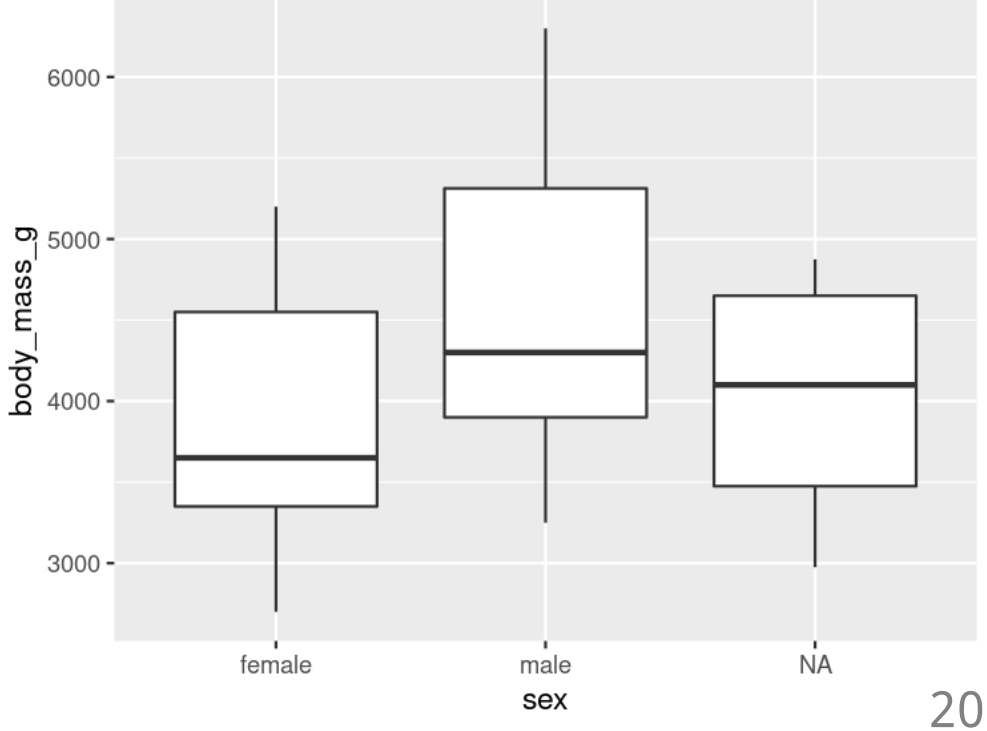
Any ggplot can be saved as an object

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

```
g
```




```
g + geom_boxplot()
```

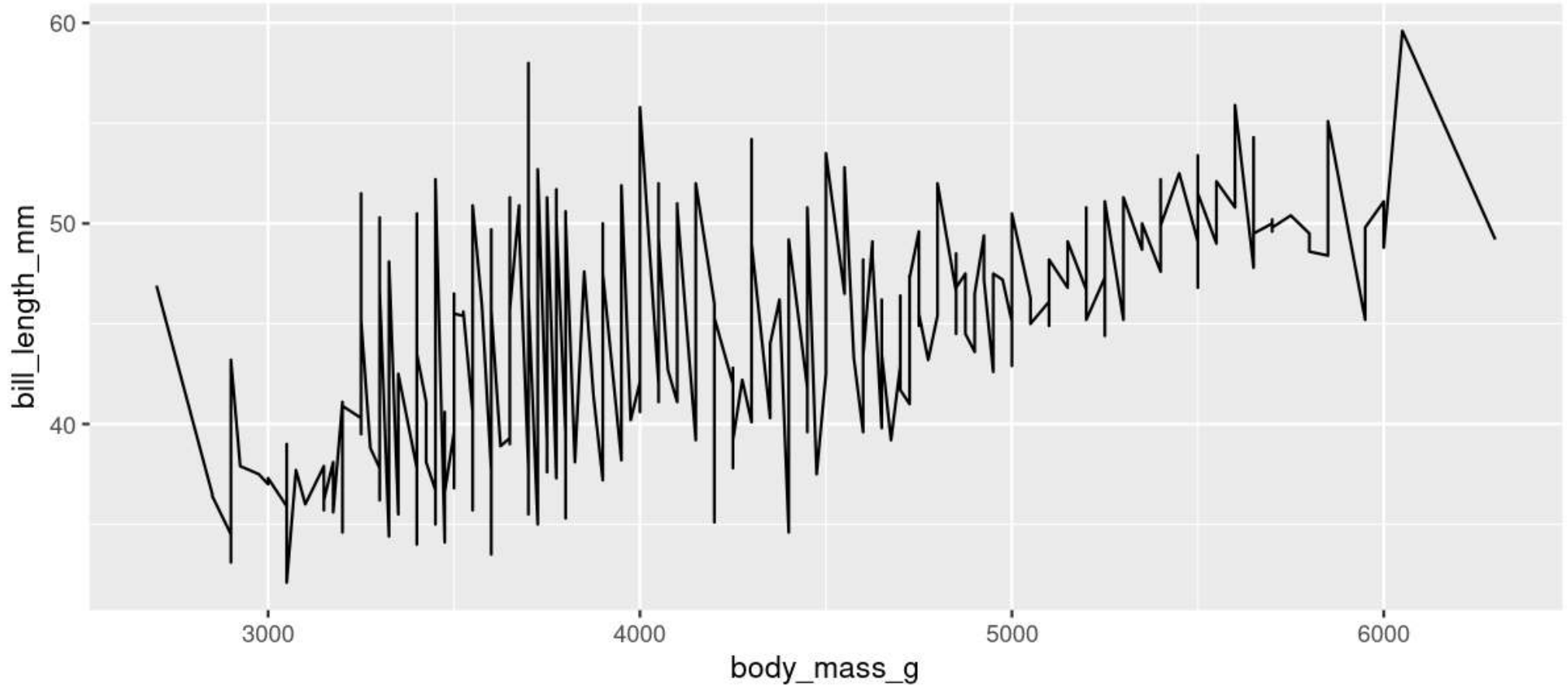


More Geoms

(Plot types)

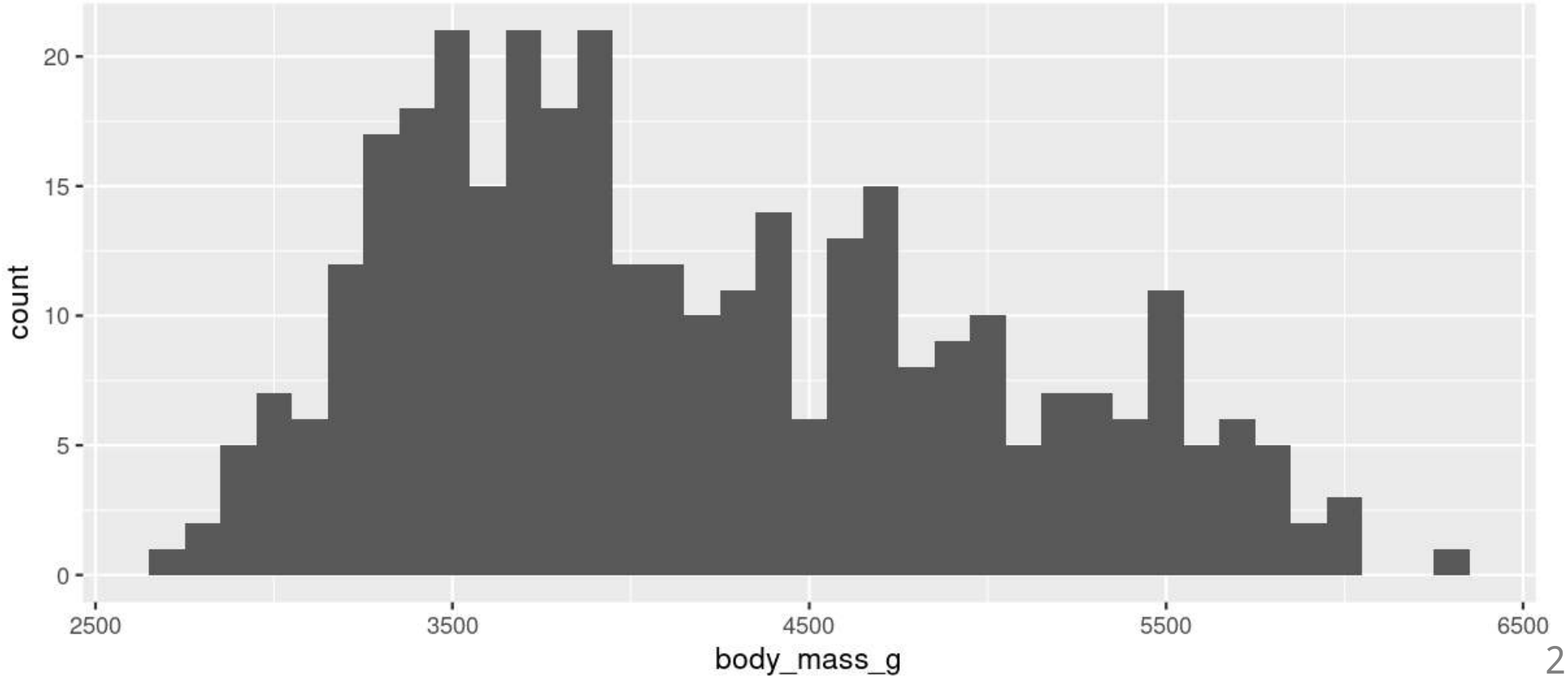
Geoms: Lines

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



Geoms: Histogram

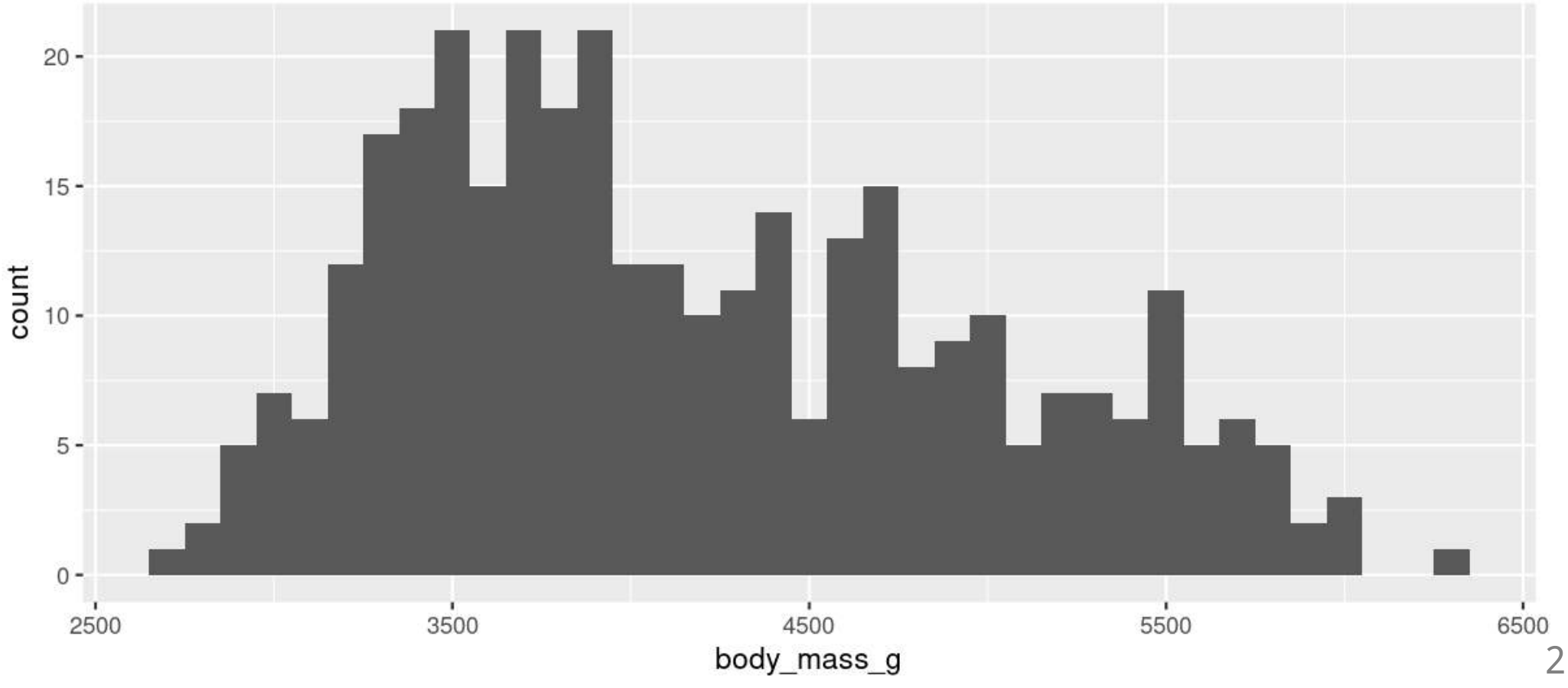
```
ggplot(data = penguins, aes(x = body_mass_g)) +
  geom_histogram(binwidth = 100)
```



Geoms: Histogram

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

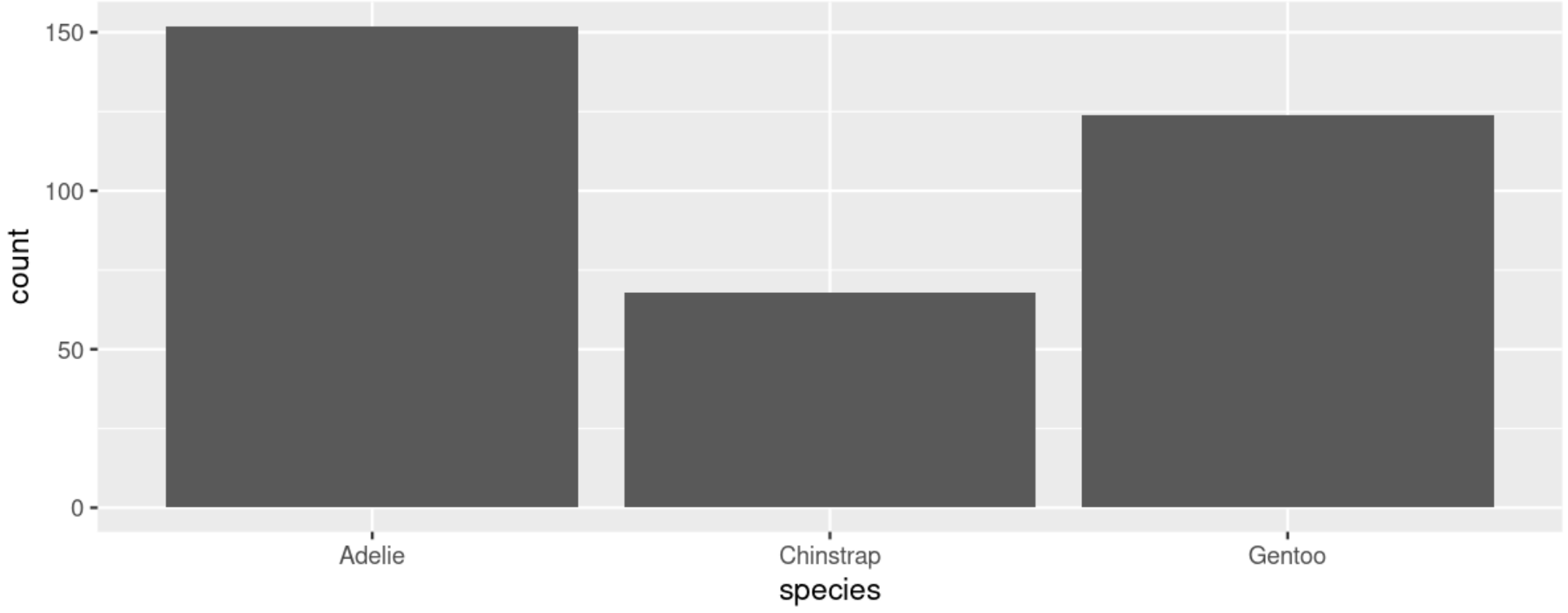
Note: We only need 1 aesthetic here (x)



Geoms: Barplots

Let `ggplot` count your data

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

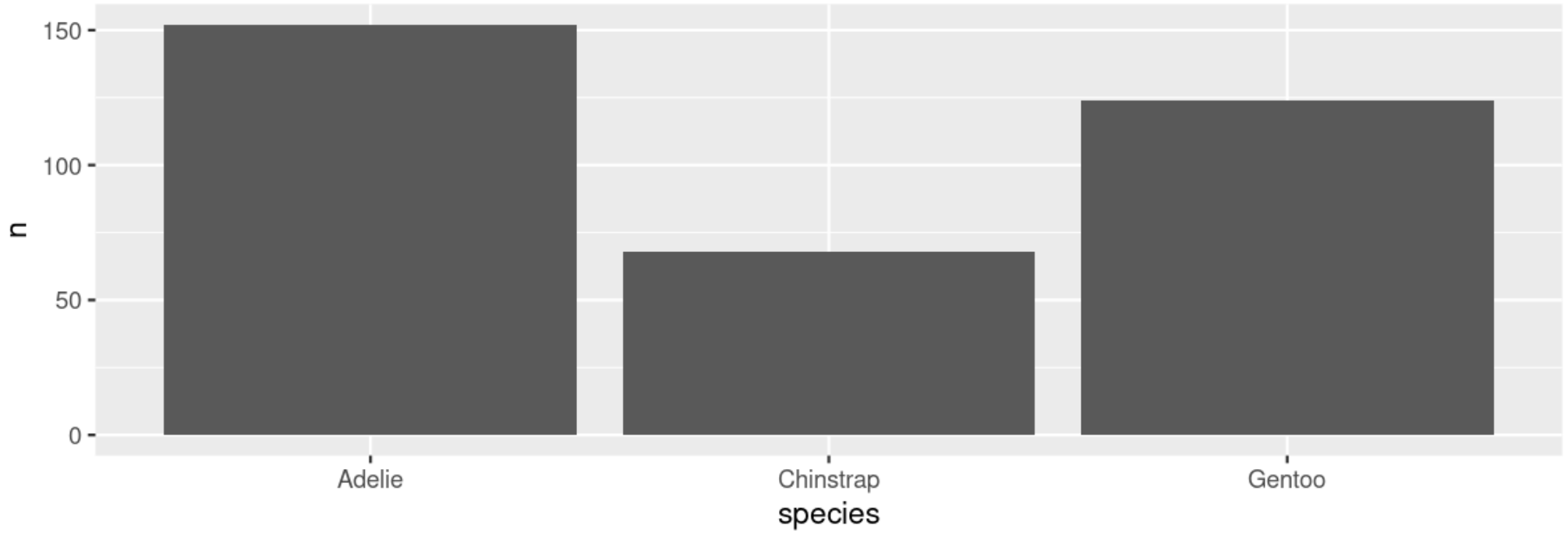


Geoms: Barplots

Or, you can provide the counts (makes more sense when you already/only have counts)

```
species_counts <- count(penguins, species)

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



Side Note: `tidyverse` functions

Or, you can provide the counts (makes more sense when you already/only have counts)

```
species_counts <- count(penguins, species)
```

`count()`

- **`tidyverse`** functions always start with the **data**, followed by other arguments
- you can reference any **column** from '**data**'
- **`count()`** the number of observations per unique **`column`** category

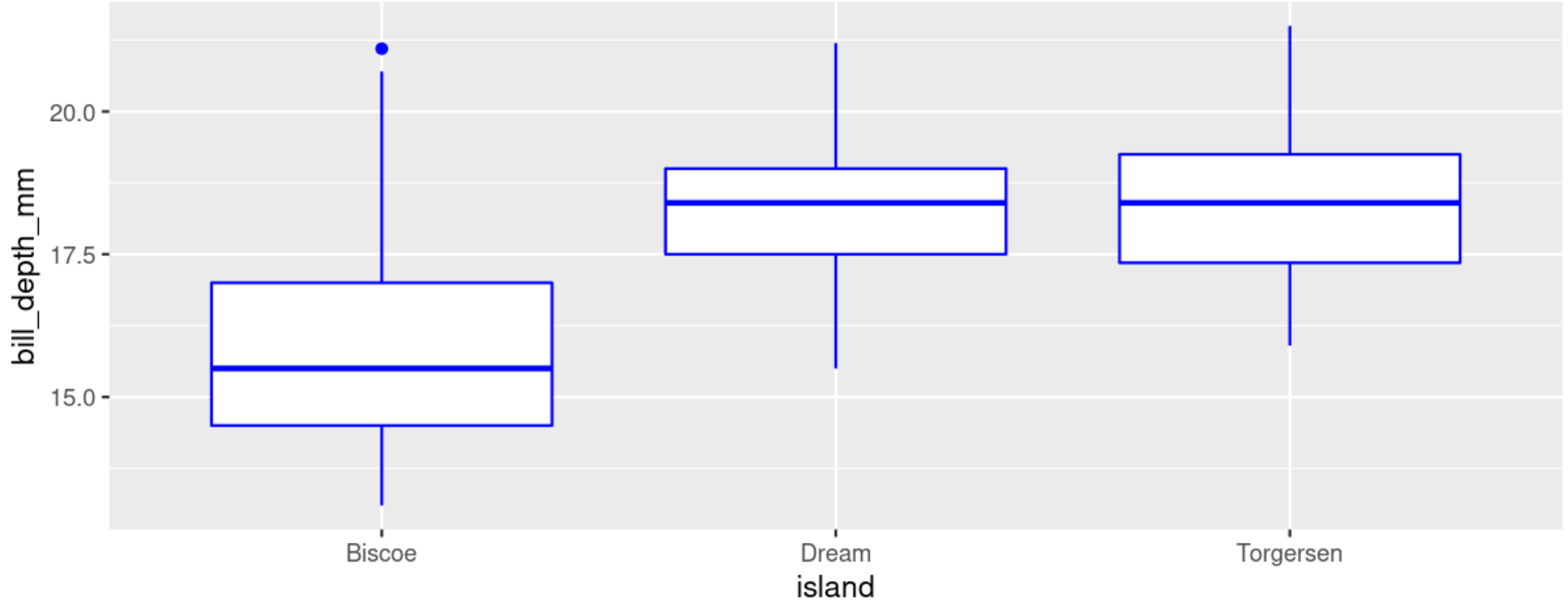
```
species_counts
```

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

Your Turn: Create this plot

```
library(ggplot2)

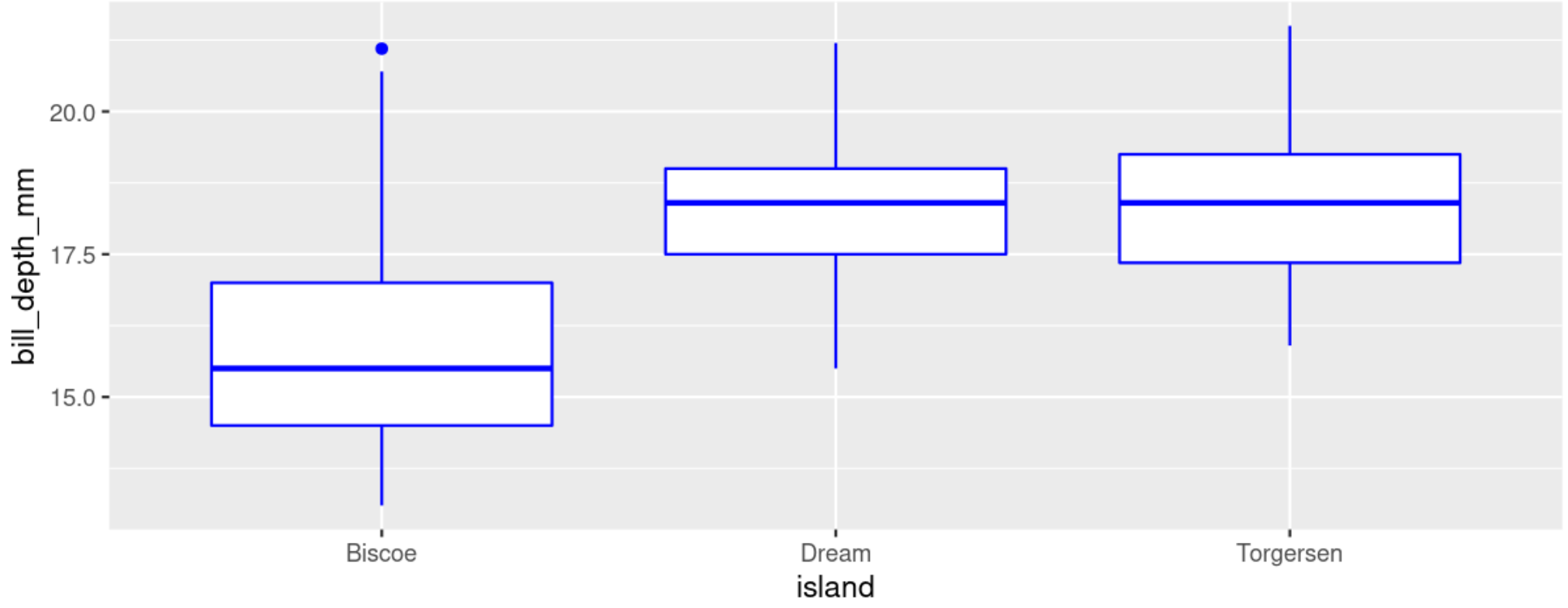
ggplot(data = _____, aes(x = _____, y = _____)) +
  geom_____(_____)
```



Your Turn: Create this plot

```
library(ggplot2)

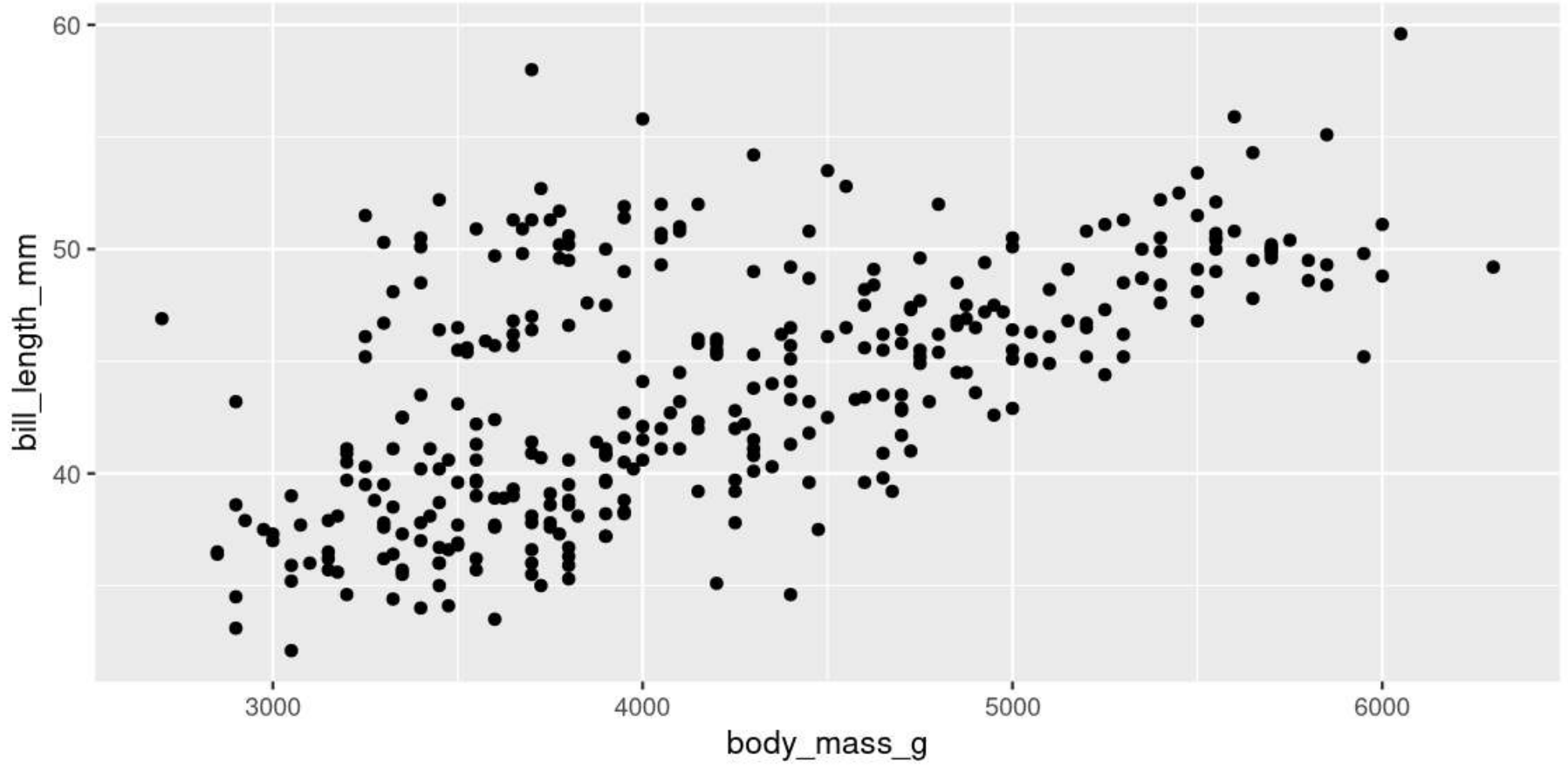
ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +
  geom_boxplot(colour = "blue")
```



Showing data by group

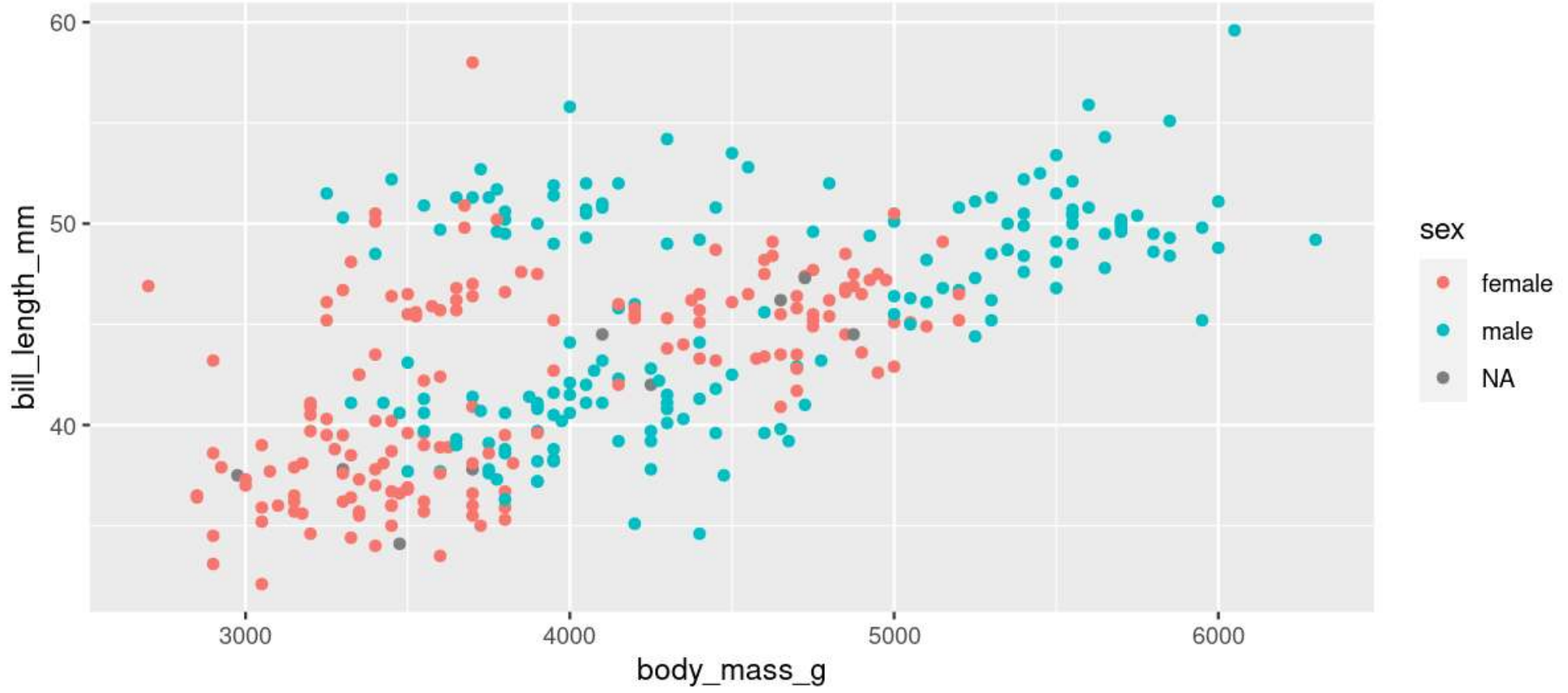
Mapping aesthetics

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



Mapping aesthetics

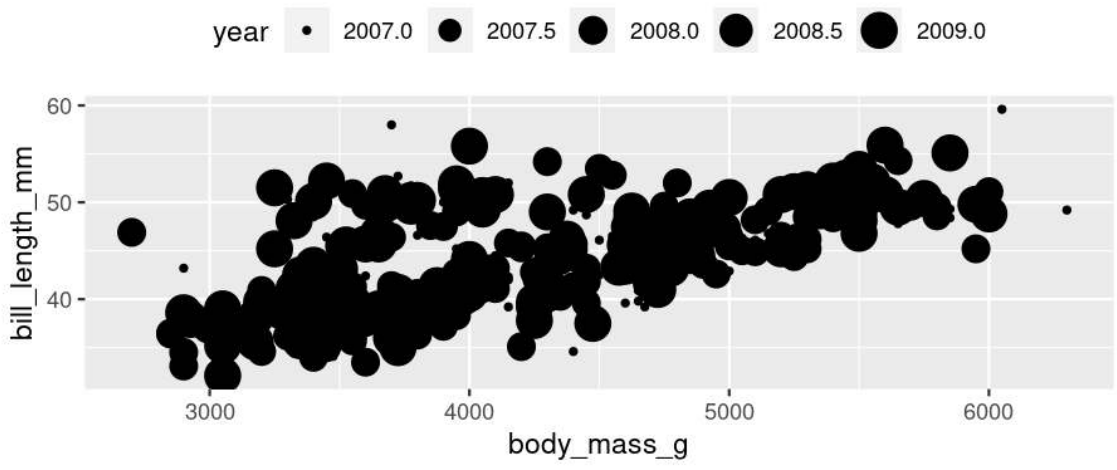
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +
  geom_point()
```



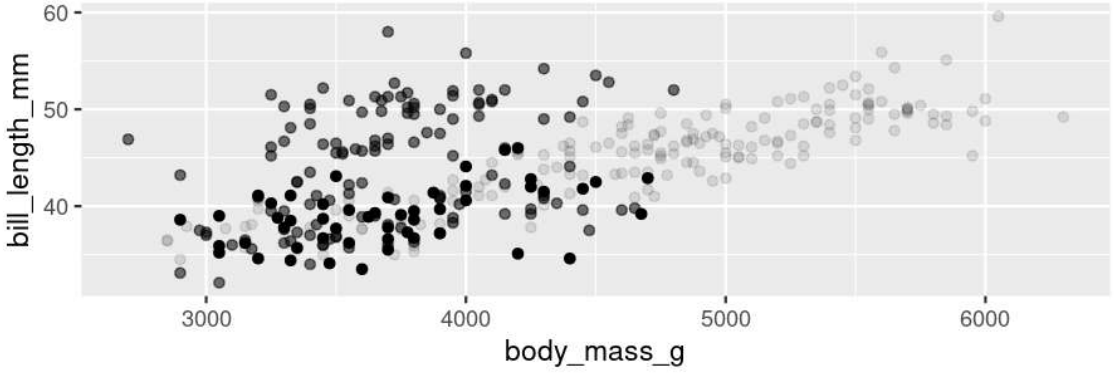
Mapping aesthetics

colour = sex

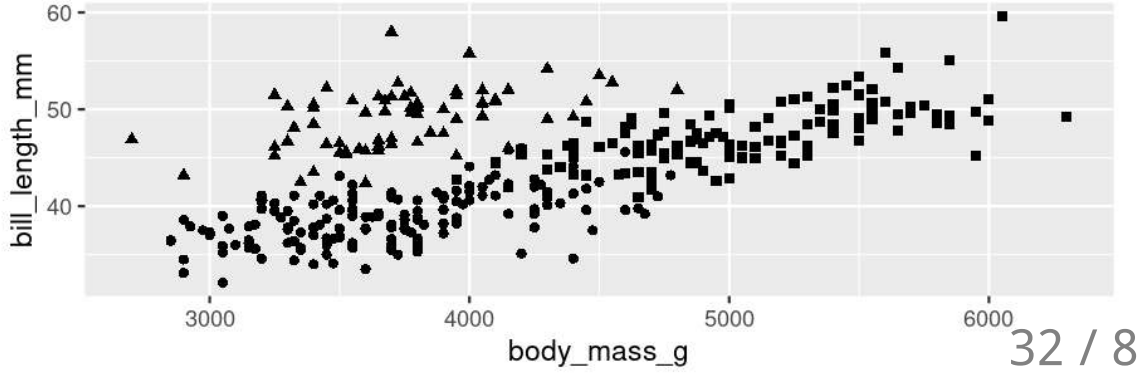
size = year



alpha = island



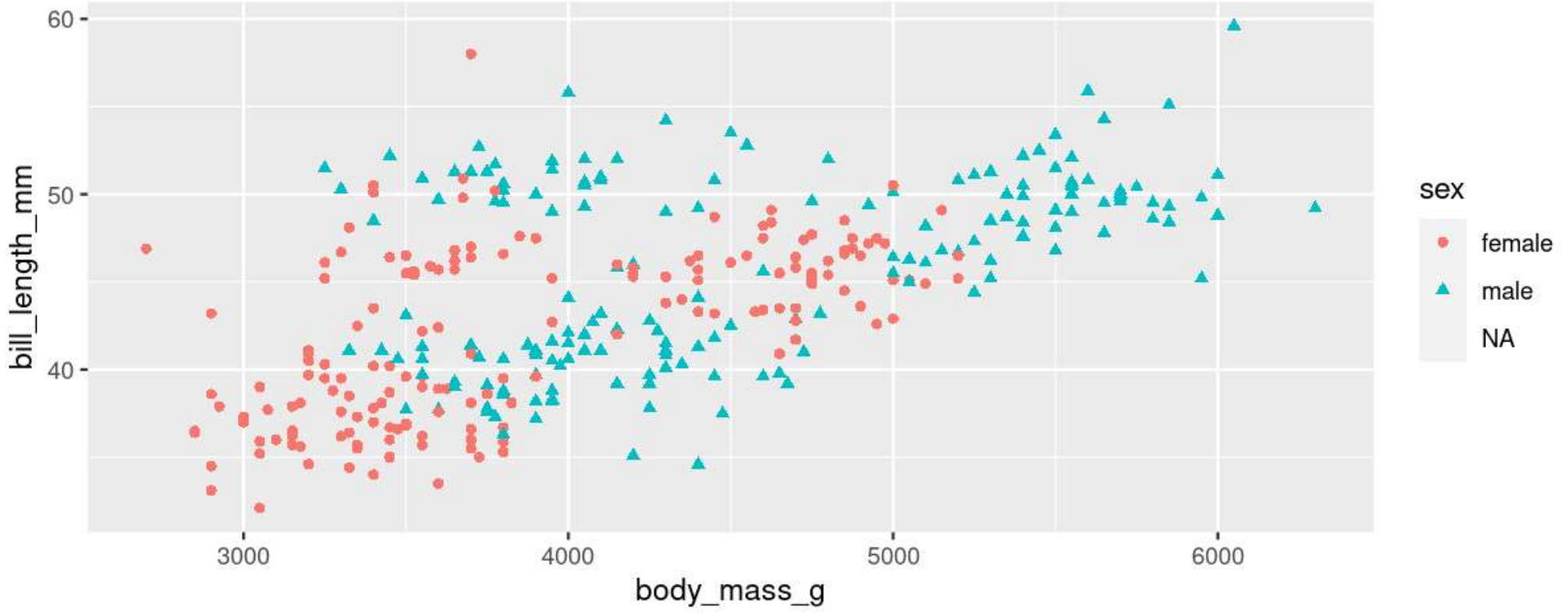
shape = species



Mapping aesthetics

`ggplot` automatically populates the legends (combining where it can)

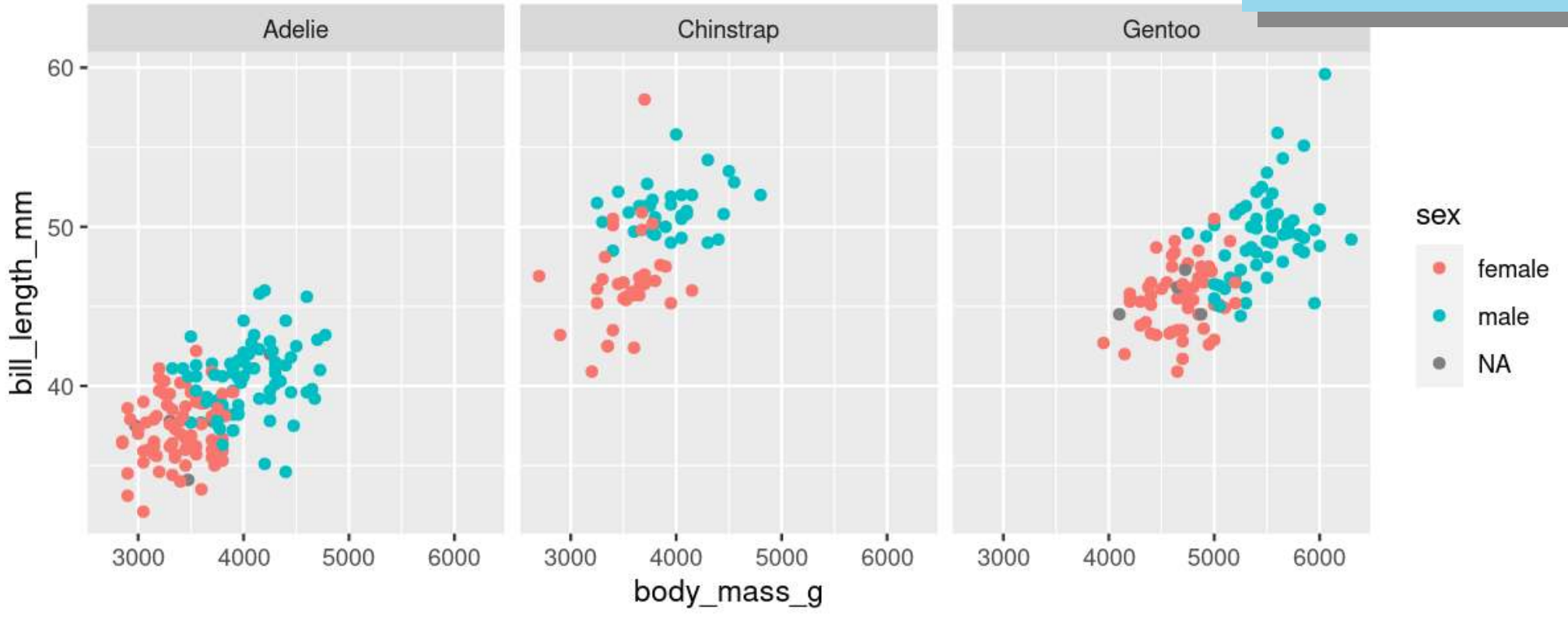
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex, shape = sex)) +
  geom_point()
```



Faceting: `facet_wrap()`

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

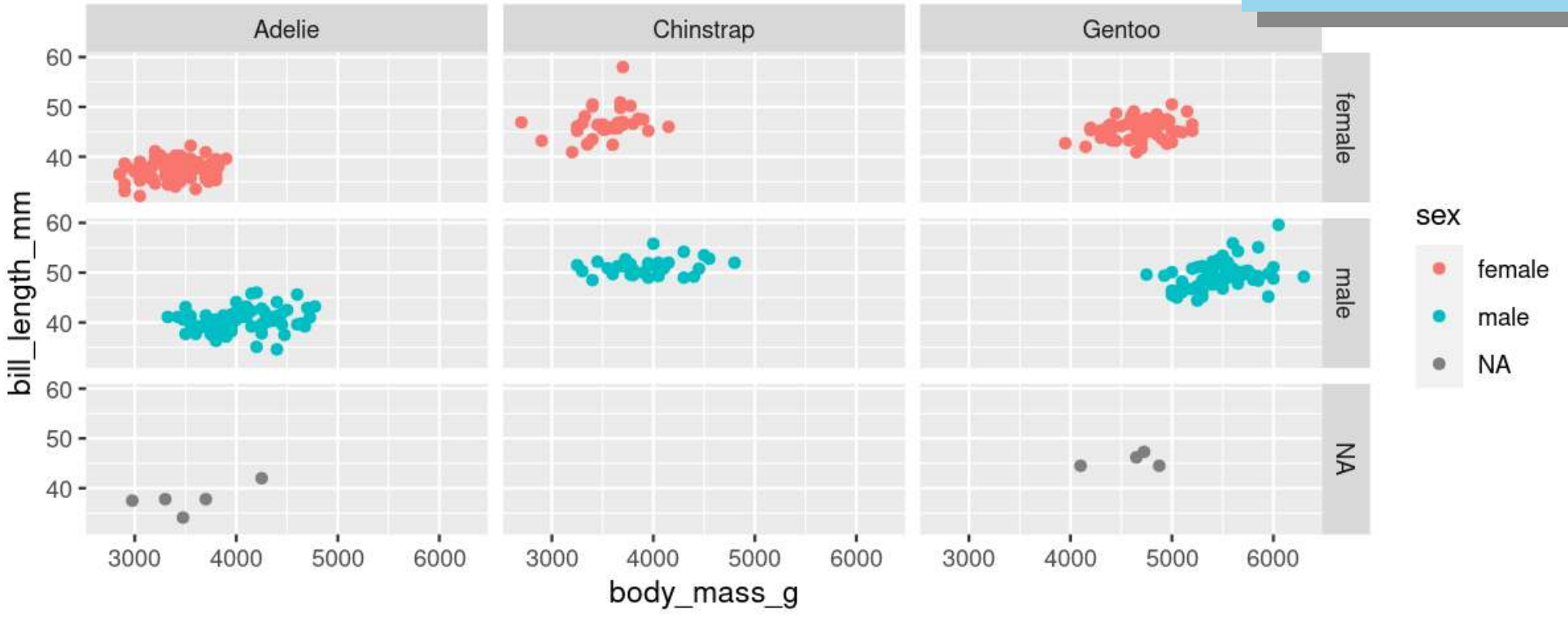
Split plots by **one** grouping variable



Faceting: `facet_grid()`

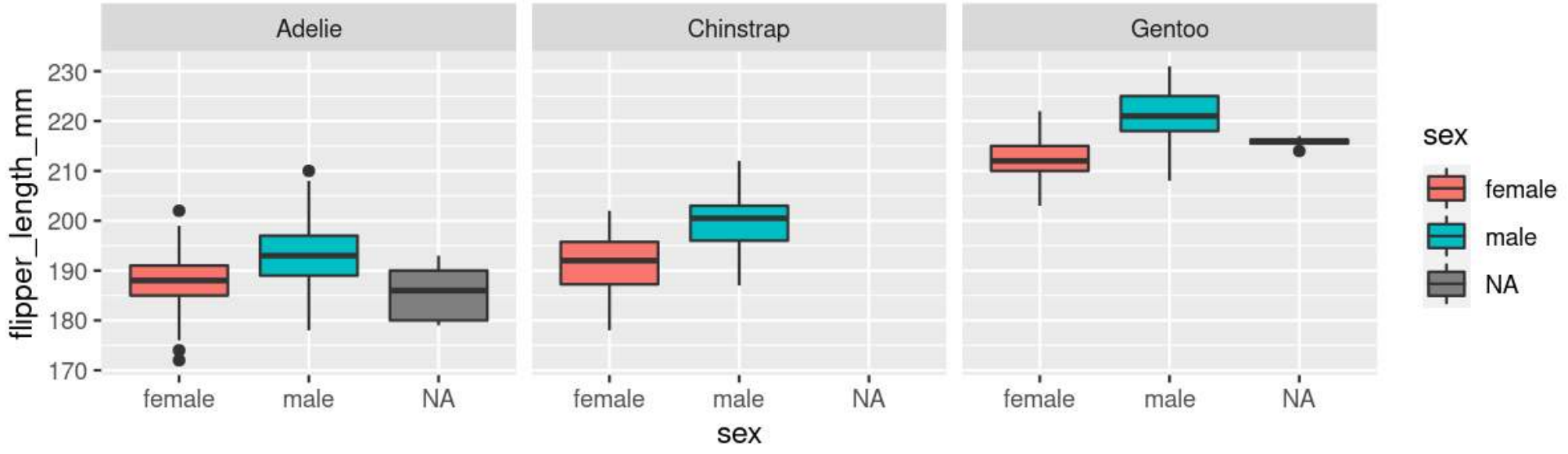
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +
  geom_point() +
  facet_grid(sex ~ species)
```

Split plots by **two** grouping variables



Your Turn: Create this plot

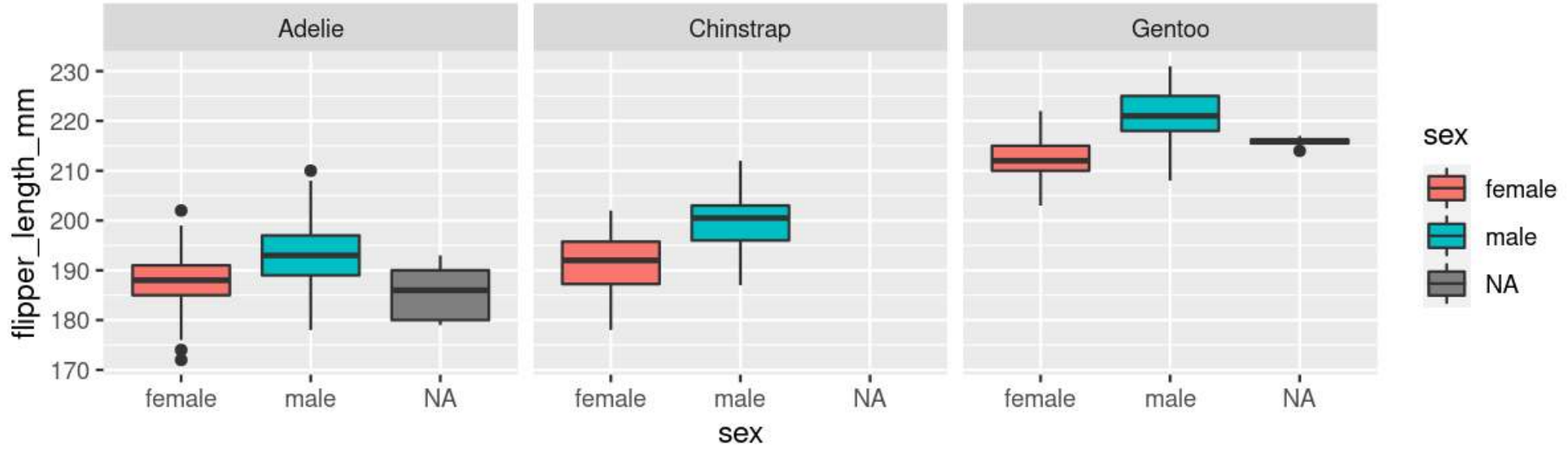
```
ggplot(data = ____, aes(____)) +
  ____ +
  ____
```



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

Your Turn: Create this plot

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



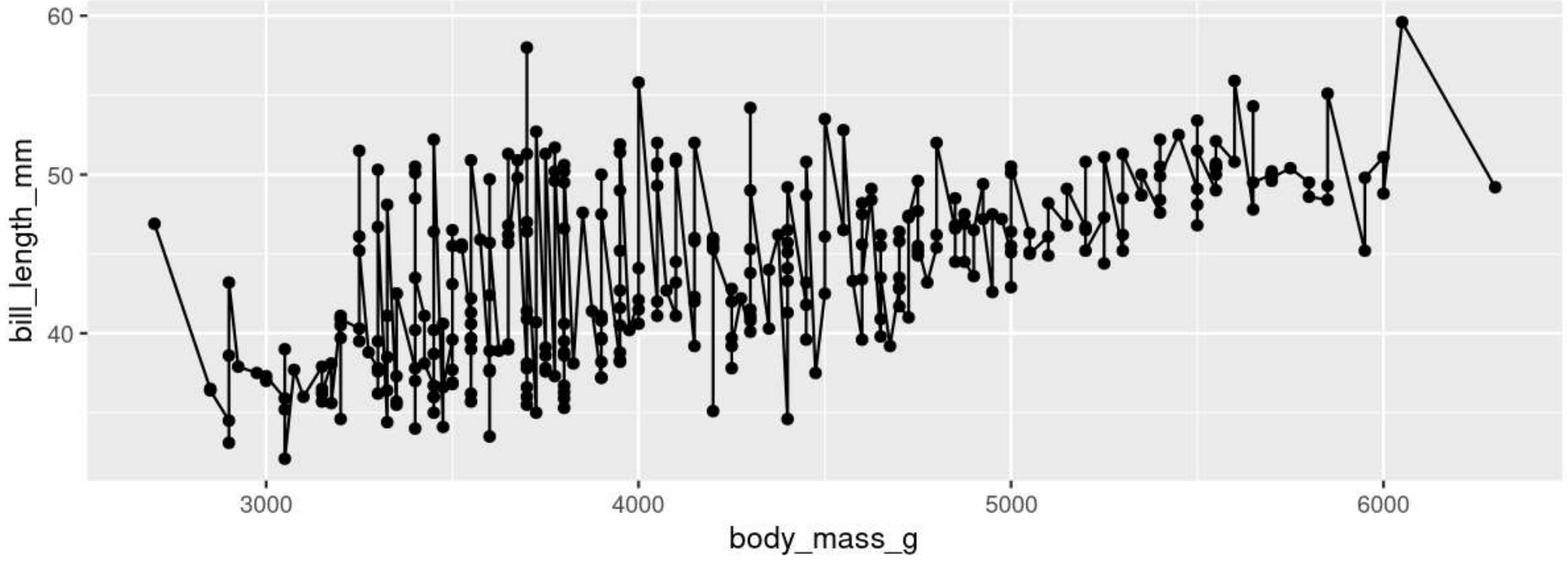
Hint: `colour` is for outlining with a colour, `fill` is for 'filling' with a colour

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()
```

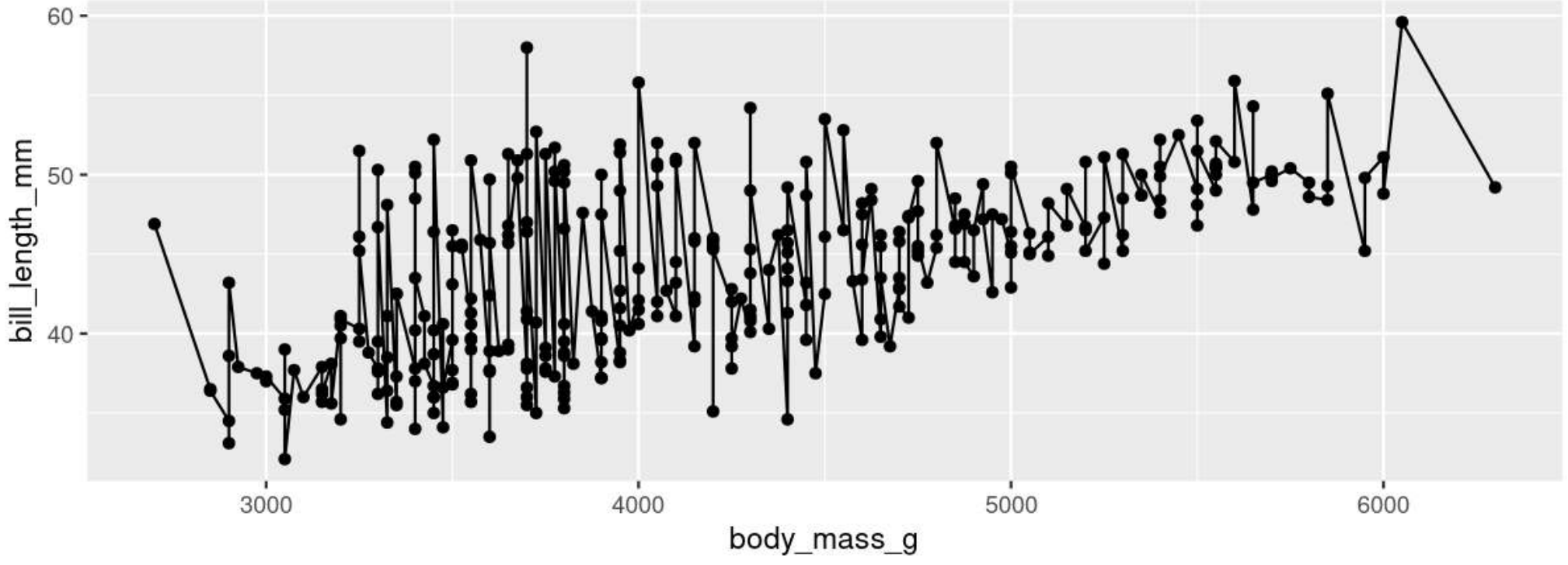


Trendlines / Regression lines

`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

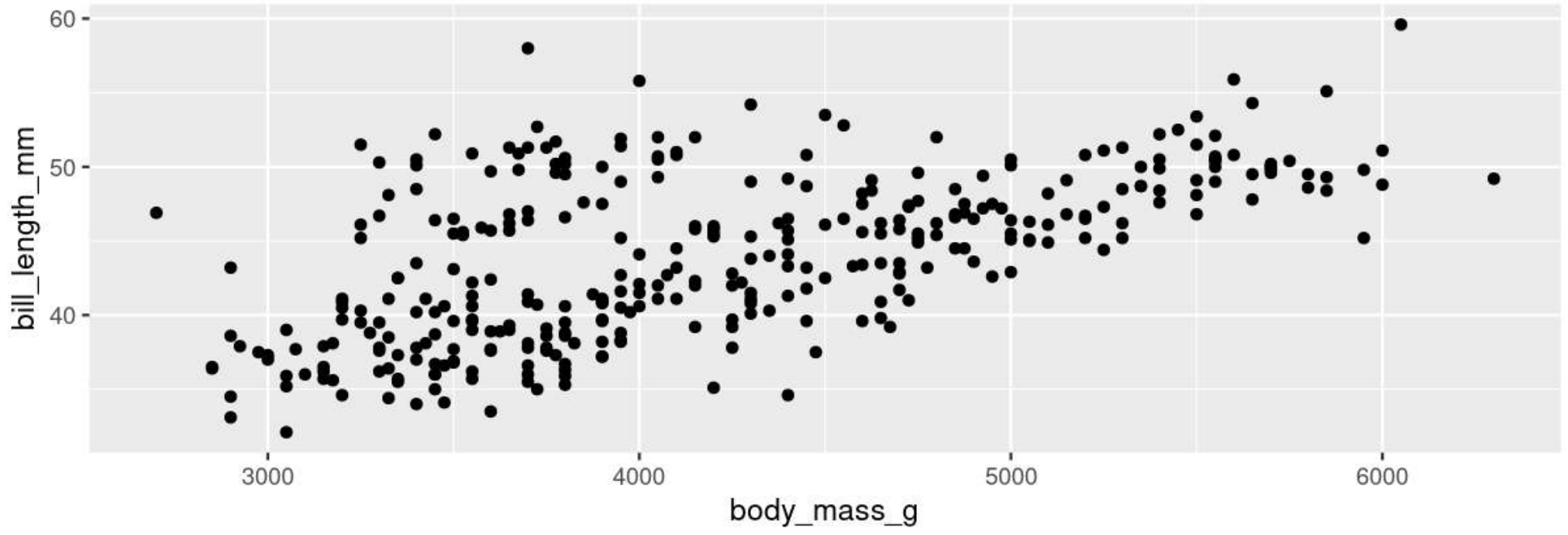


Trendlines / Regression lines

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
```

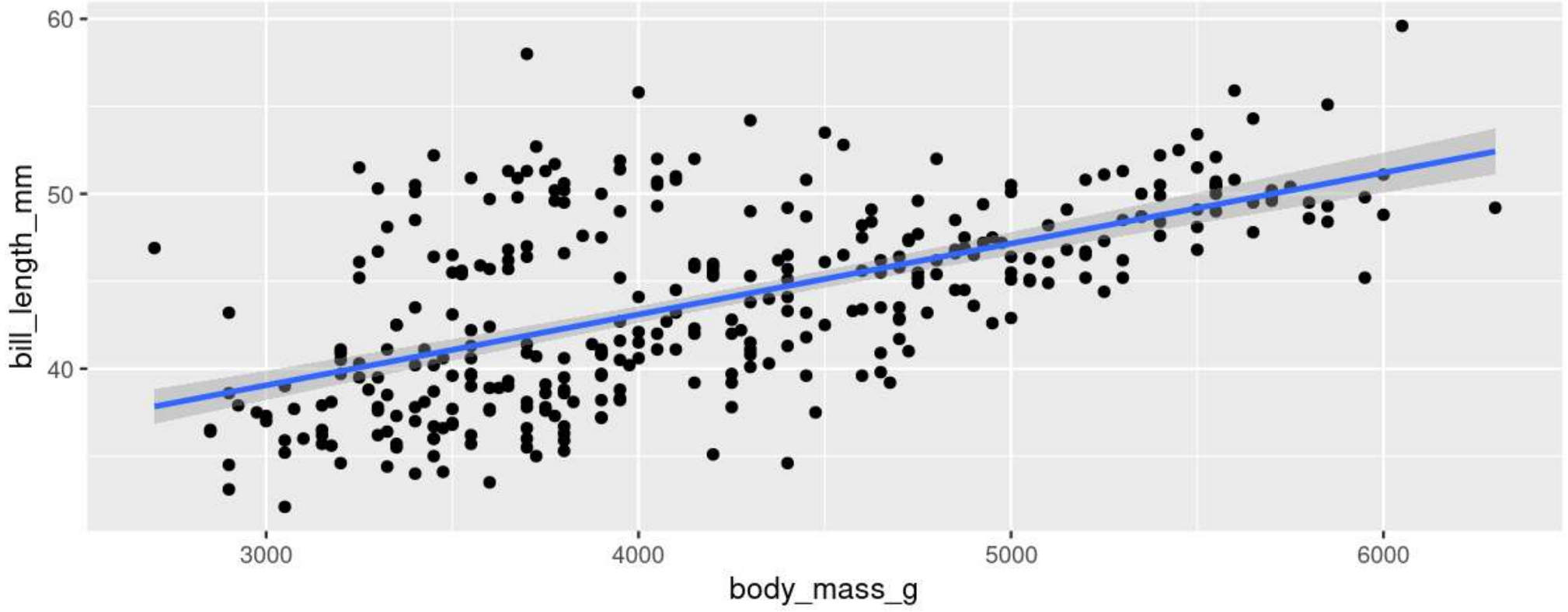


Trendlines / Regression lines

Add the `stat_smooth()`

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

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

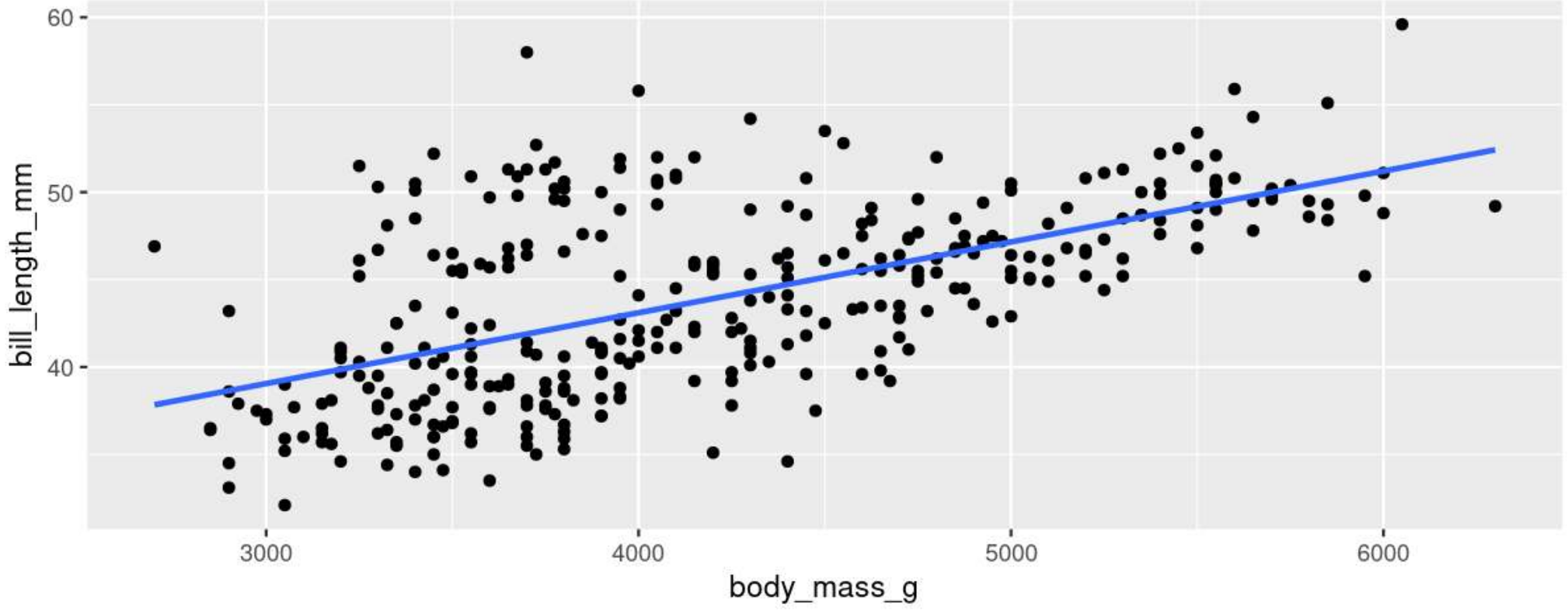


Trendlines / Regression lines

Add the `stat_smooth()`

- remove the grey ribbon **`se = FALSE`**

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

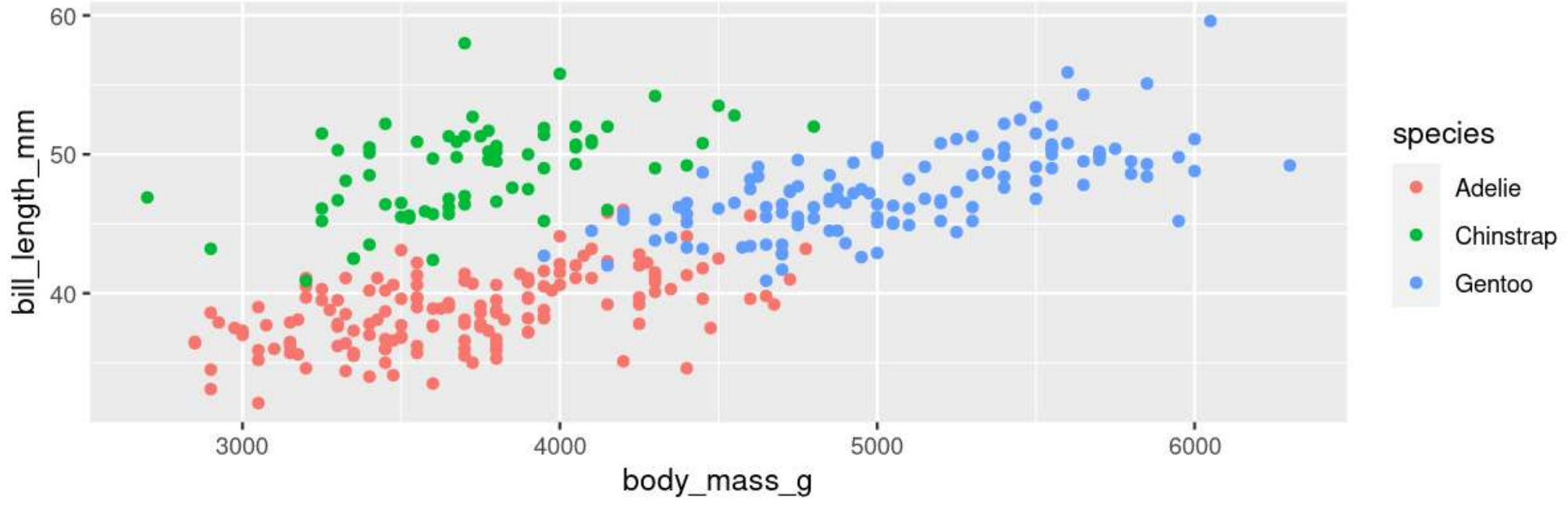


Trendlines / Regression lines

A line for each group

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

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

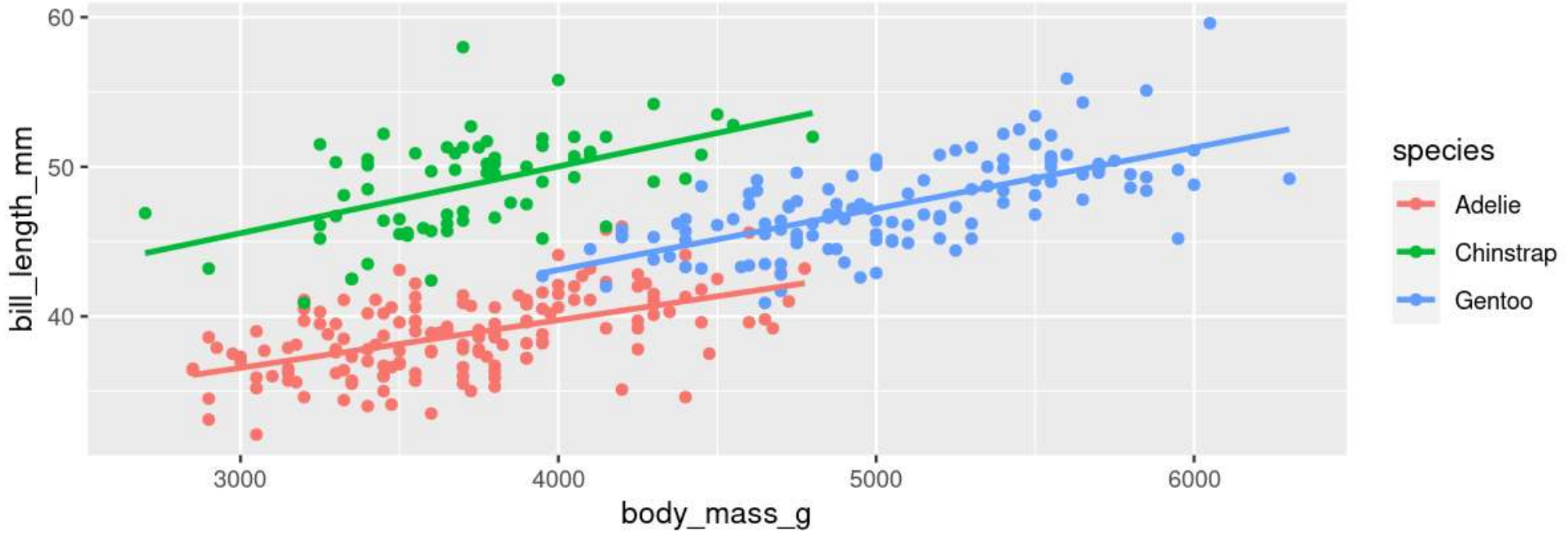


Using stats: Trendlines / Regression lines

A line for each group

- **`stat_smooth()`** automatically uses the same grouping

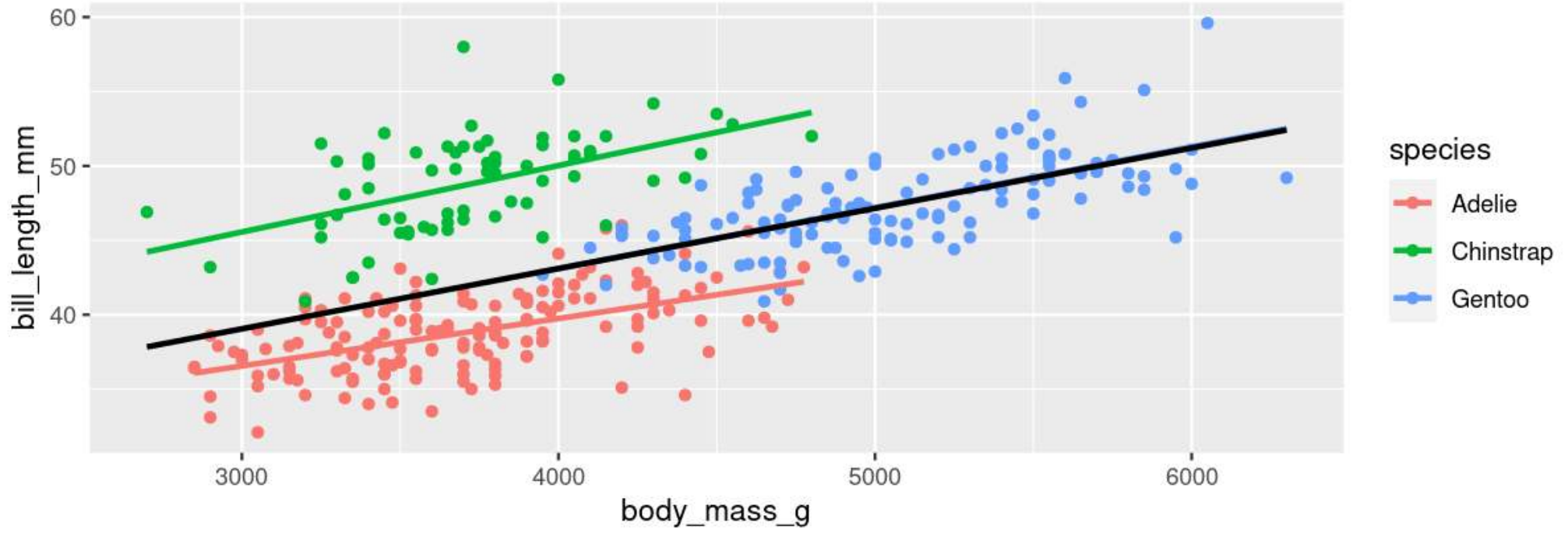
```
g + stat_smooth(method = "lm", se = FALSE)
```



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")
```



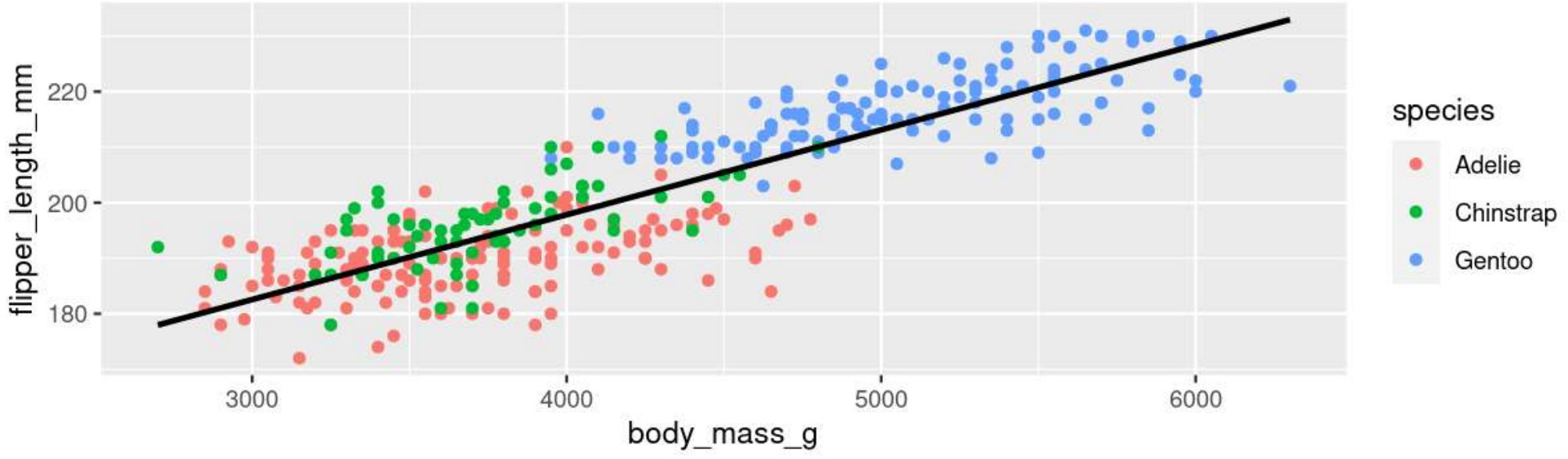
Your Turn: Create this plot

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

Your Turn: Create this plot

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

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

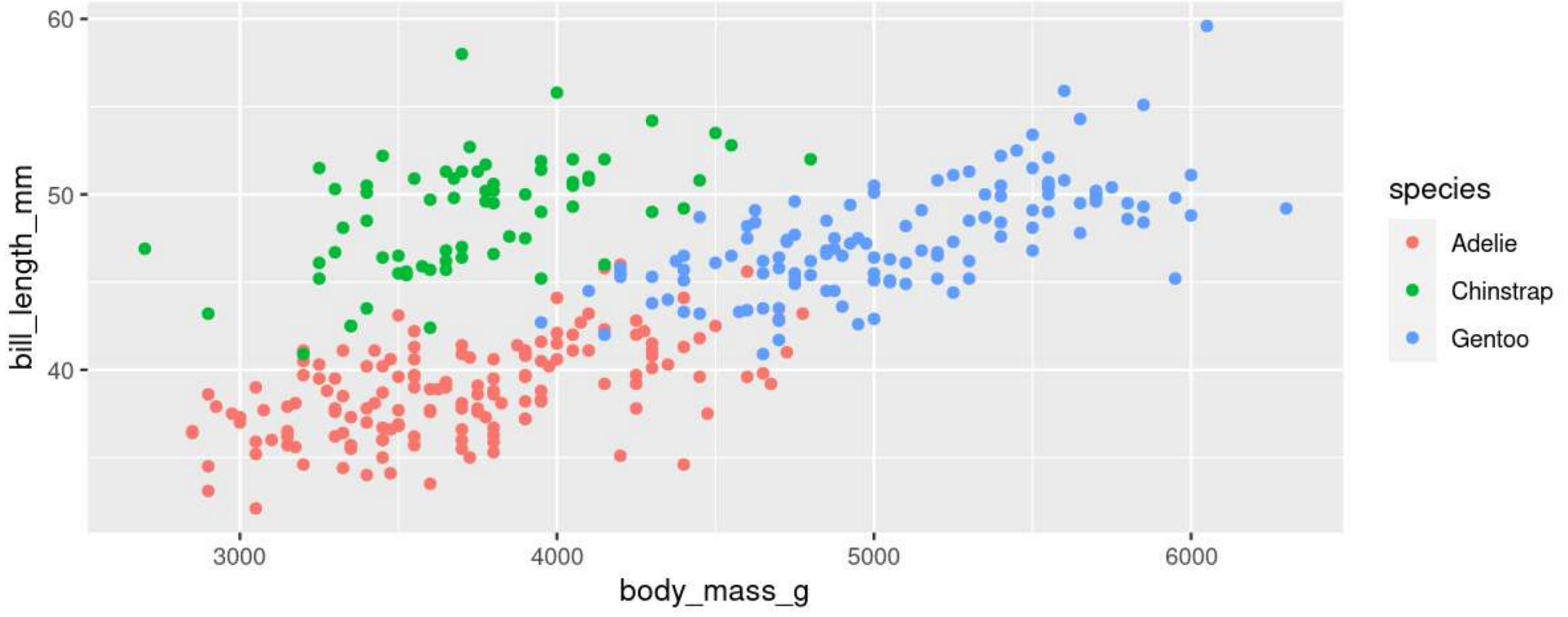


Customizing plots

Customizing: Starting plot

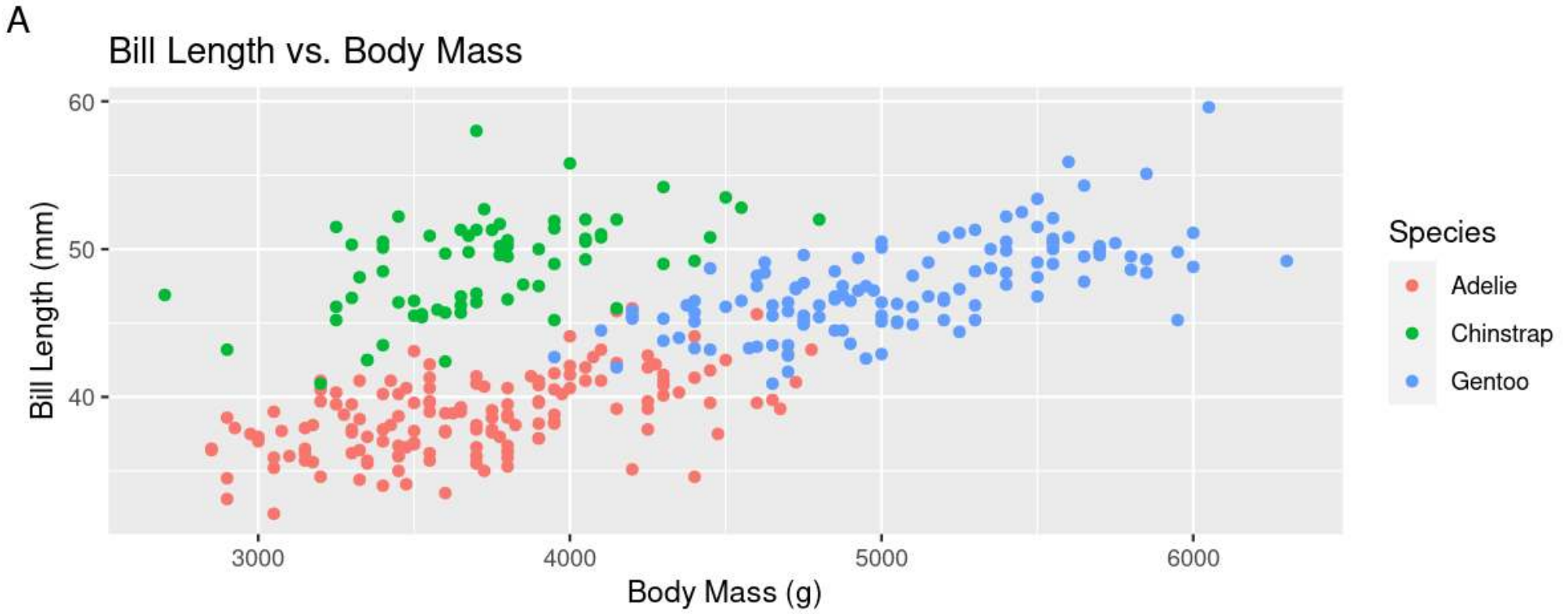
Let's work with this plot

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



Customizing: Labels

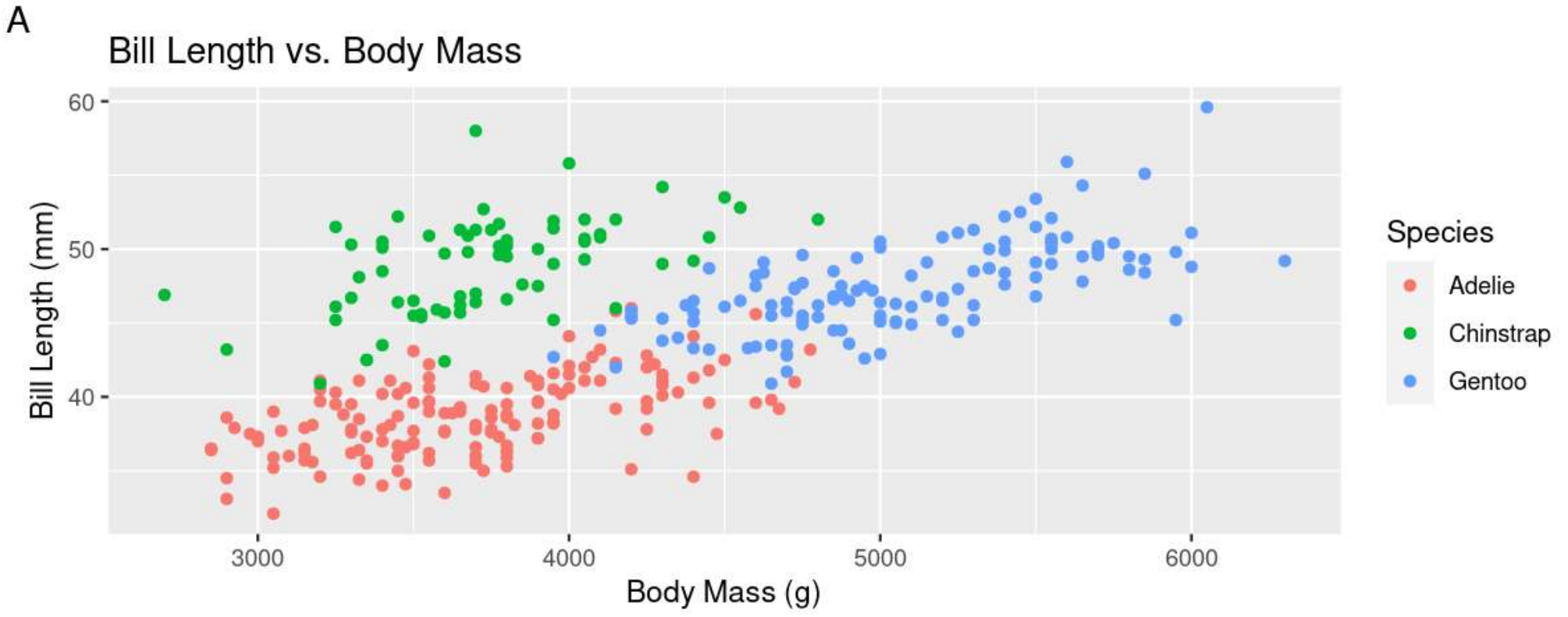
```
g + labs(title = "Bill Length vs. Body Mass",
         x = "Body Mass (g)",
         y = "Bill Length (mm)",
         colour = "Species", tag = "A")
```



Customizing: Labels

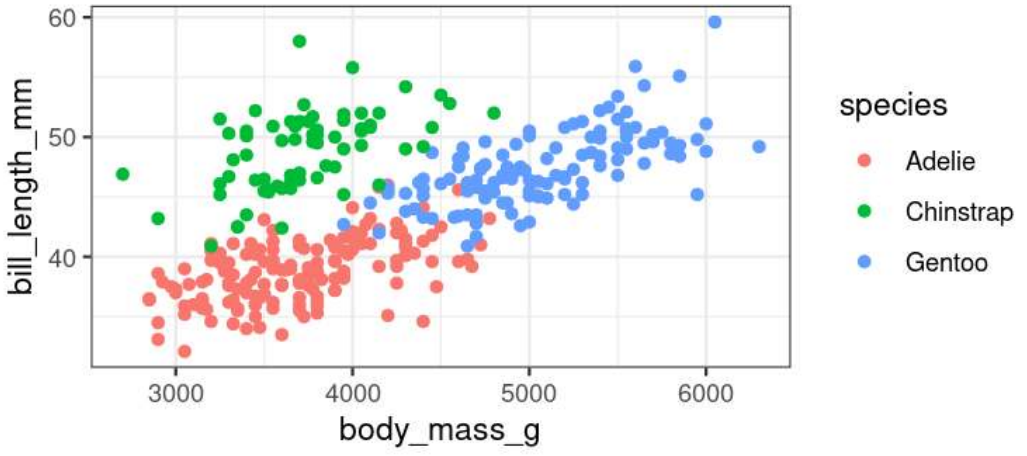
```
g + labs(title = "Bill Length vs. Body Mass",
         x = "Body Mass (g)",
         y = "Bill Length (mm)",
         colour = "Species", tag = "A")
```

Practice for later
Add proper labels to some of your previous plots

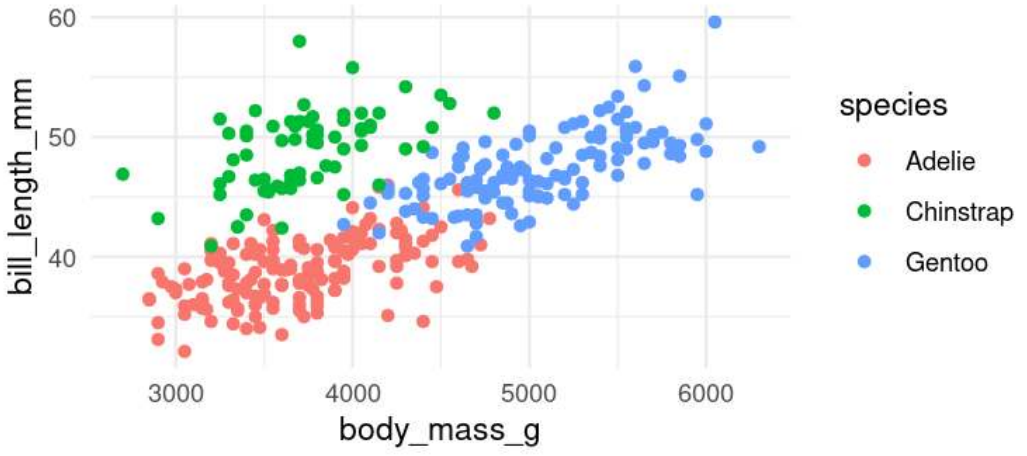


Customizing: Built-in themes

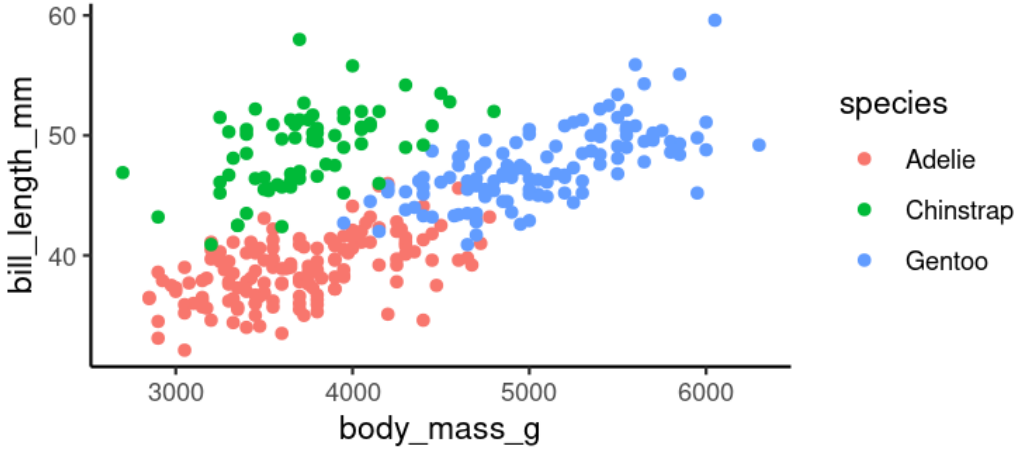
g + theme_bw()



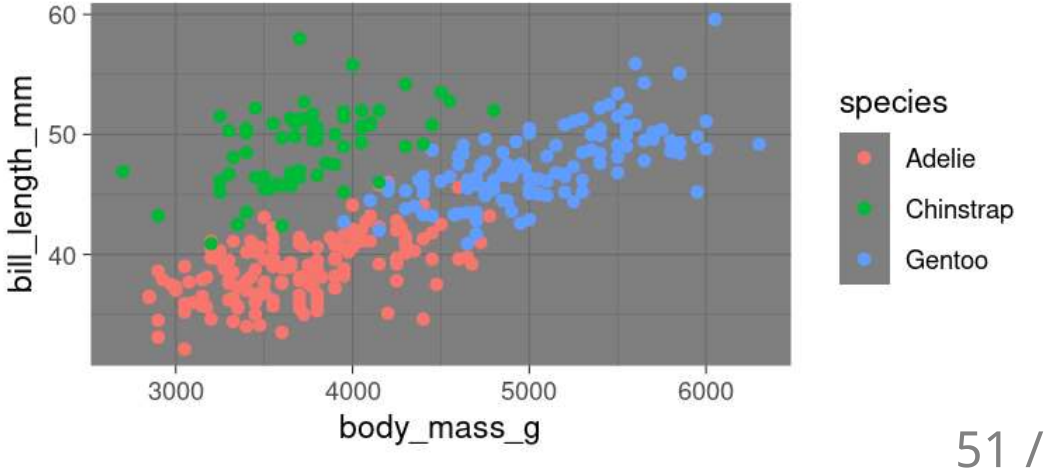
g + theme_minimal()



g + theme_classic()



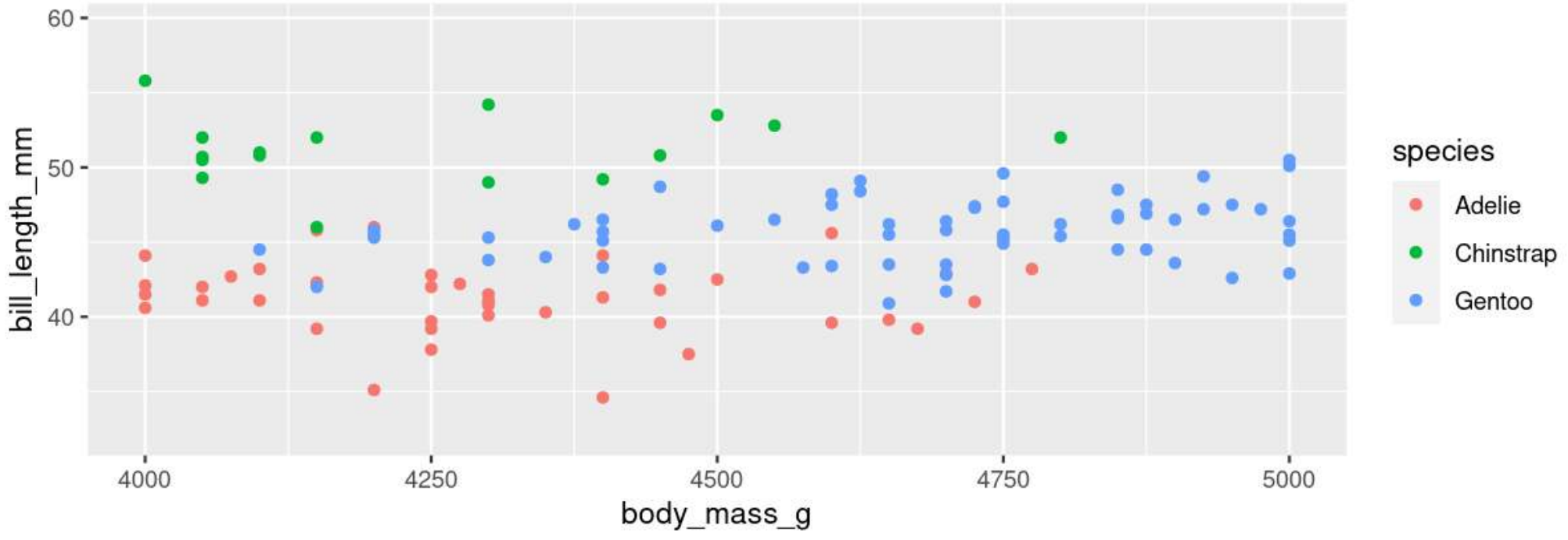
g + theme_dark()



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 (**contiuous**, **discrete**, **date**, **datetime**)

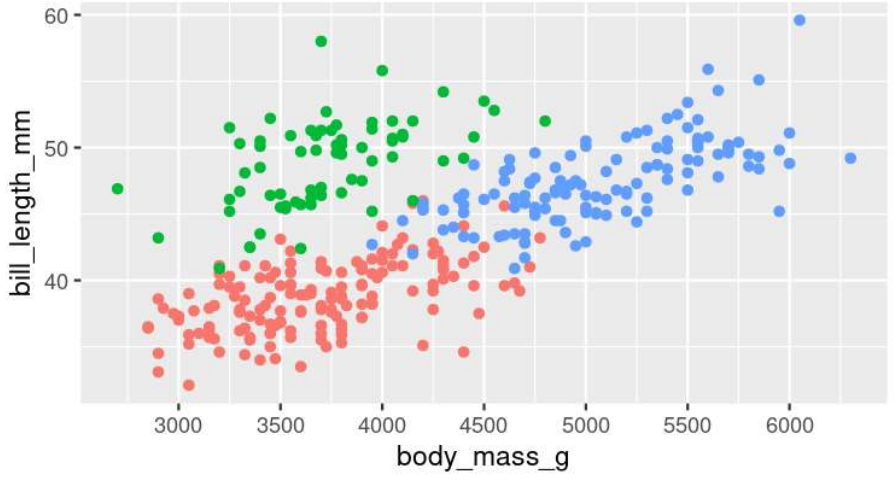
- **scale_x_continuous()**
- **scale_y_discrete()**
- etc.

Common arguments

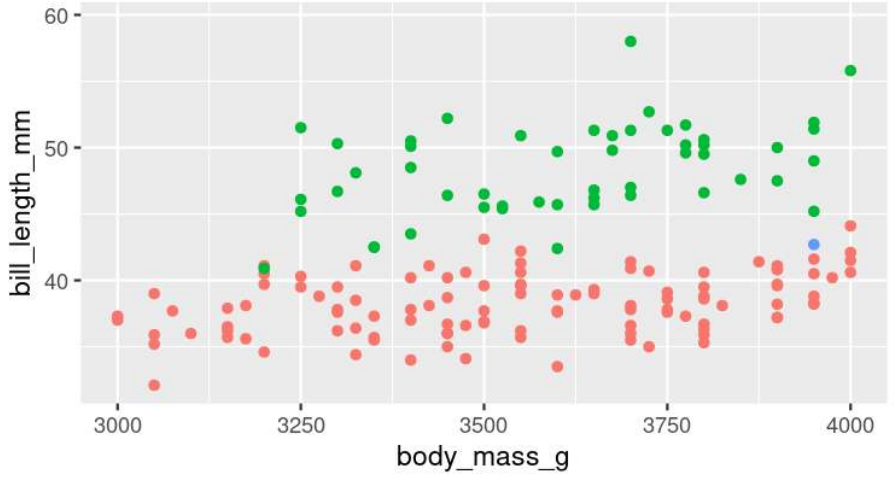
```
g + scale_x_continuous(breaks = seq(0, 20, 10)) # Tick breaks
g + scale_x_continuous(limits = c(0, 15))       # xlim() is a shortcut for this
g + scale_x_continuous(expand = c(0, 0))        # Space between axis and data
```

Customizing: Axes

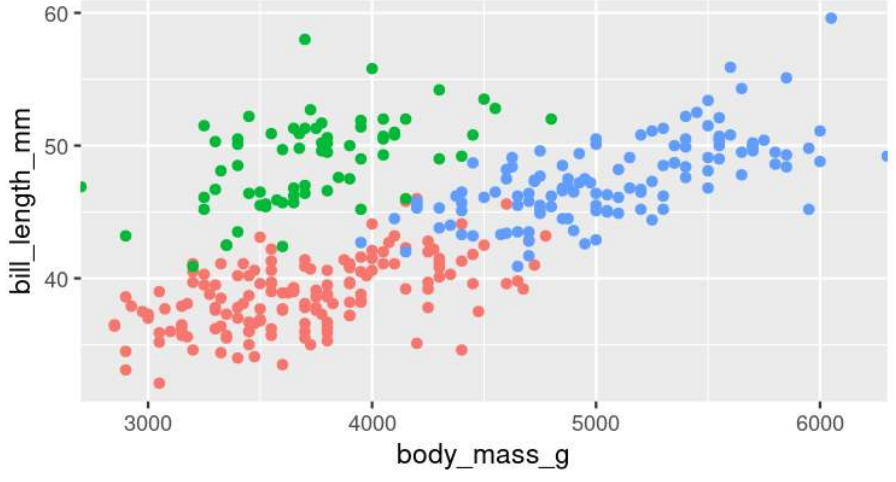
g + scale_x_continuous(breaks = seq(2500, 6500, 500))



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



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

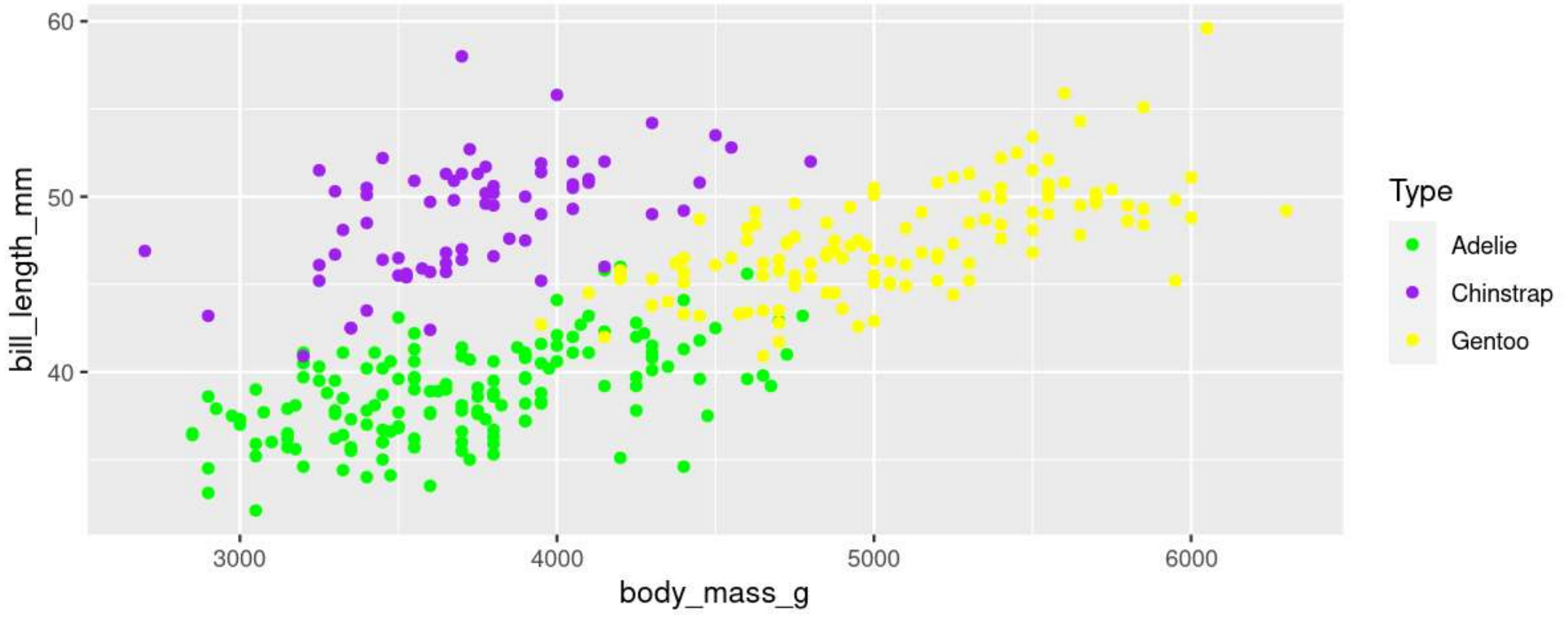


Customizing: Aesthetics

Using scales

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

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

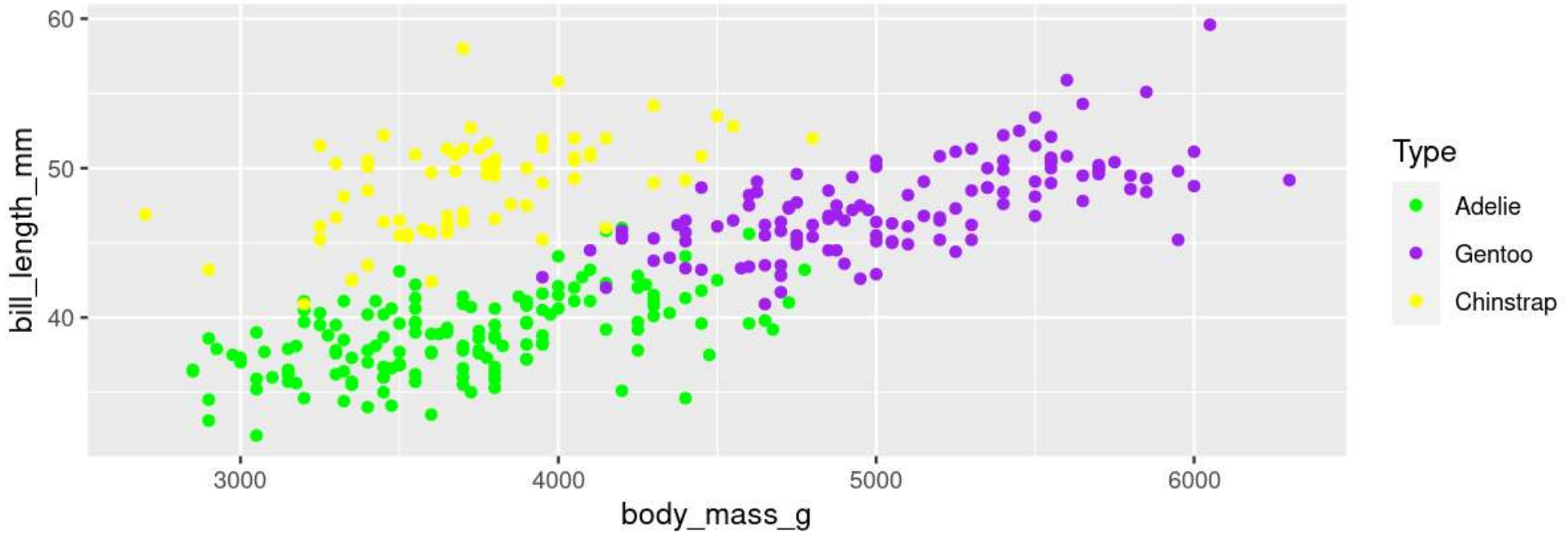


Customizing: Aesthetics

Using scales

Or be very explicit:

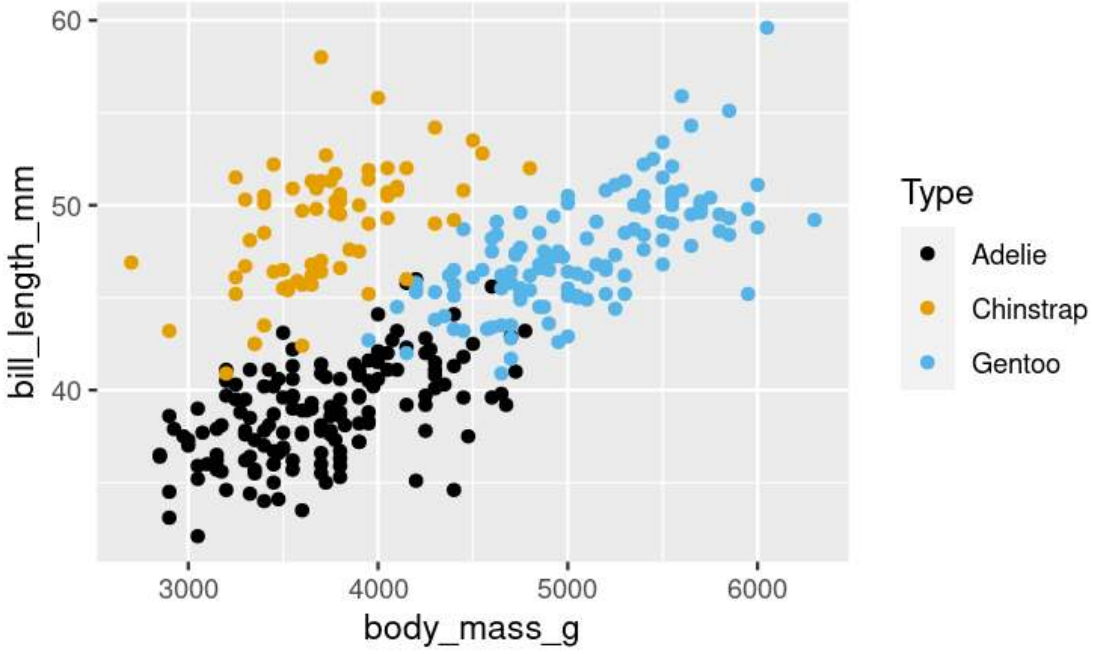
```
g + scale_colour_manual(name = "Type",
                        values = c("Adelie" = "green", "Gentoo" = "purple", "Chinstrap" = "yellow"),
                        na.value = "black")
```

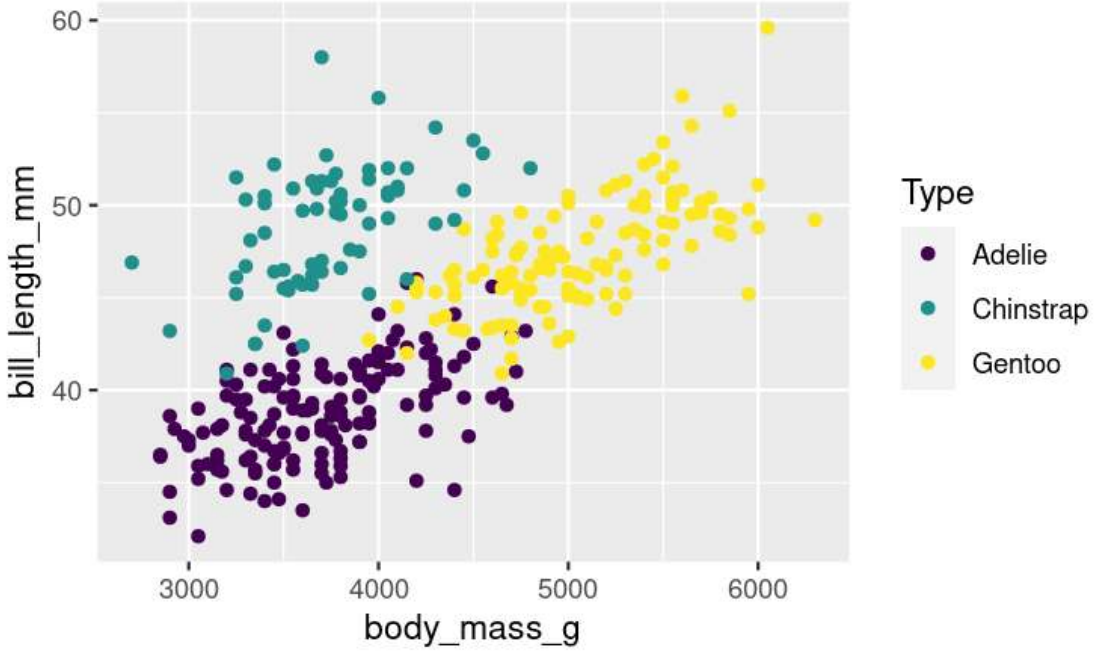


Customizing: Aesthetics

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

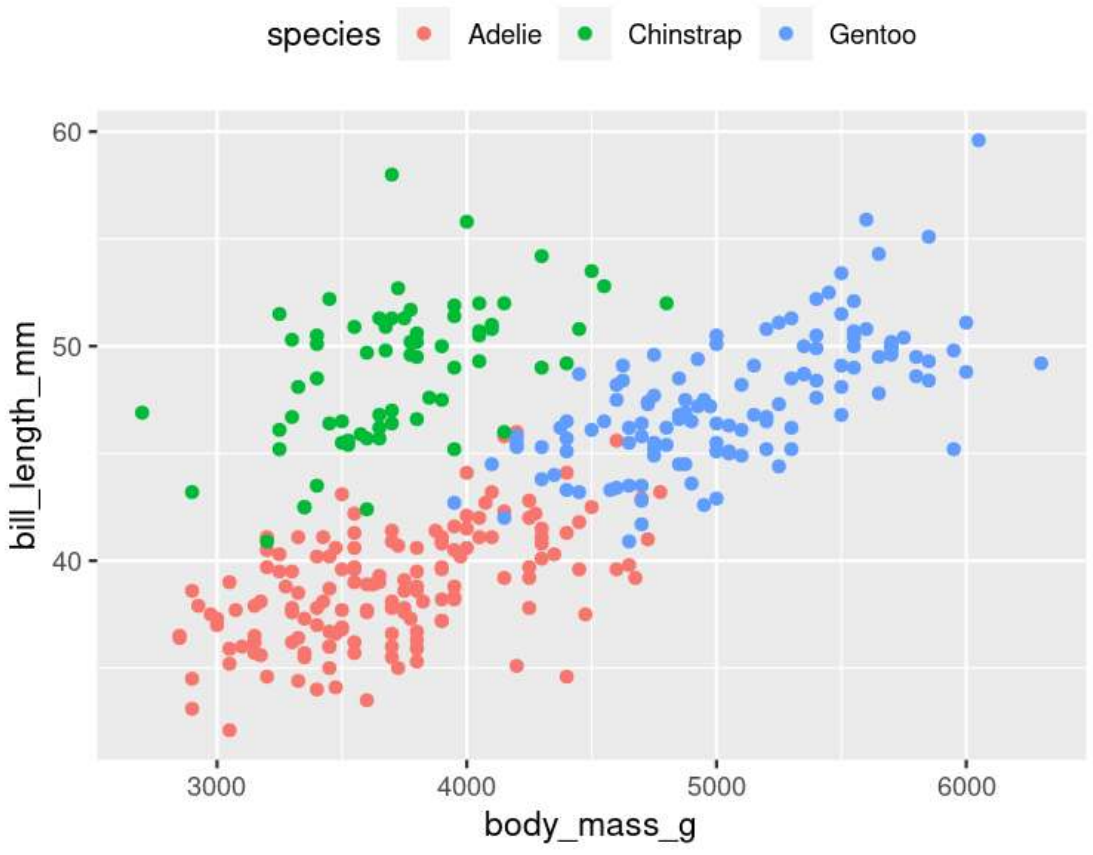
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +
  geom_point(colour = "green", size = 5) +
  stat_smooth(method = "lm", se = FALSE, colour = "red")
```

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

Customizing: Legends placement

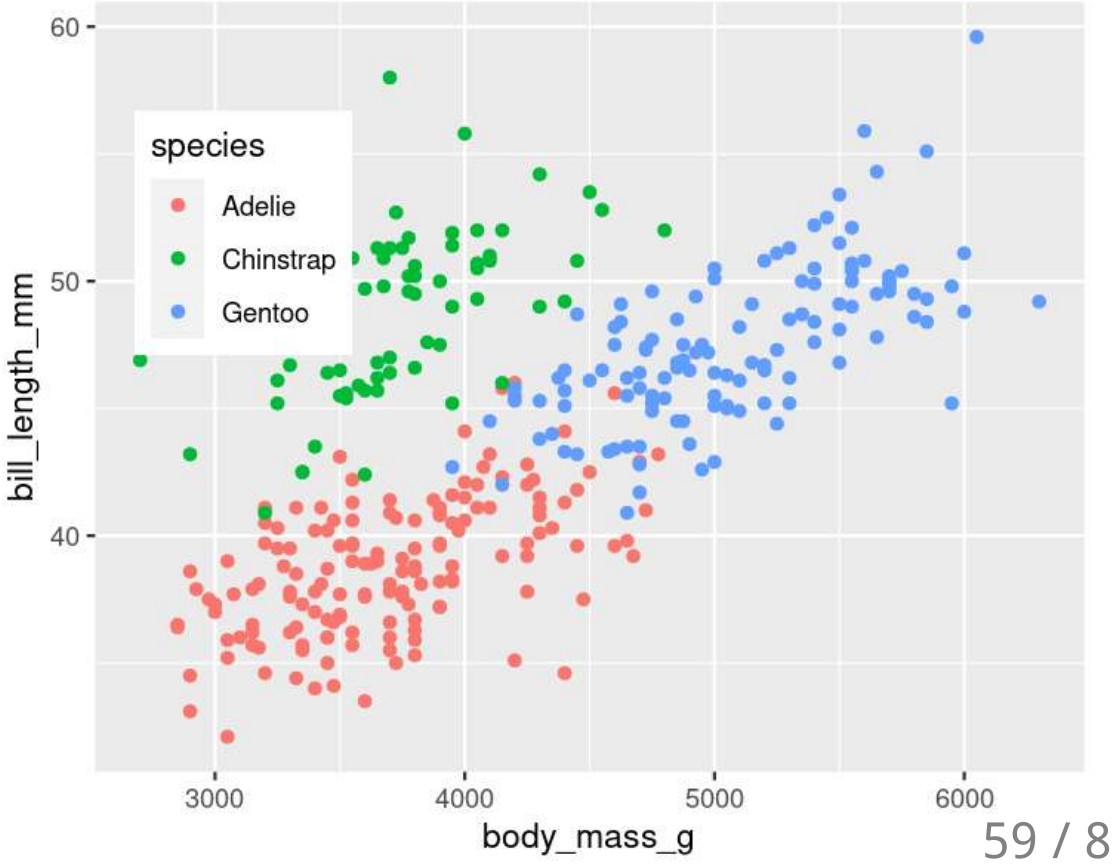
At the: top, bottom, left, right

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



Exactly here

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



Combining plots with `patchwork`

Further Reading: https://patchwork.data-imaginist.com/

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()

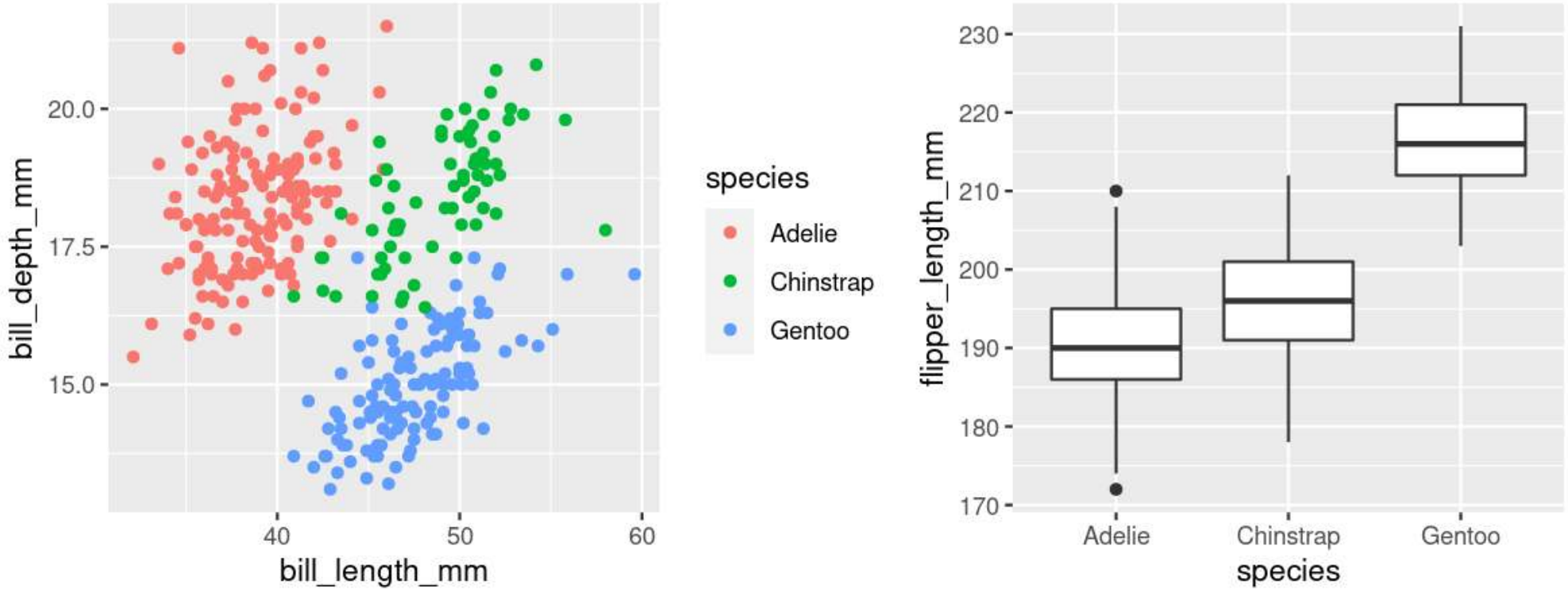
g2 <- ggplot(data = penguins, aes(x = species, y = flipper_length_mm)) +
  geom_boxplot()

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

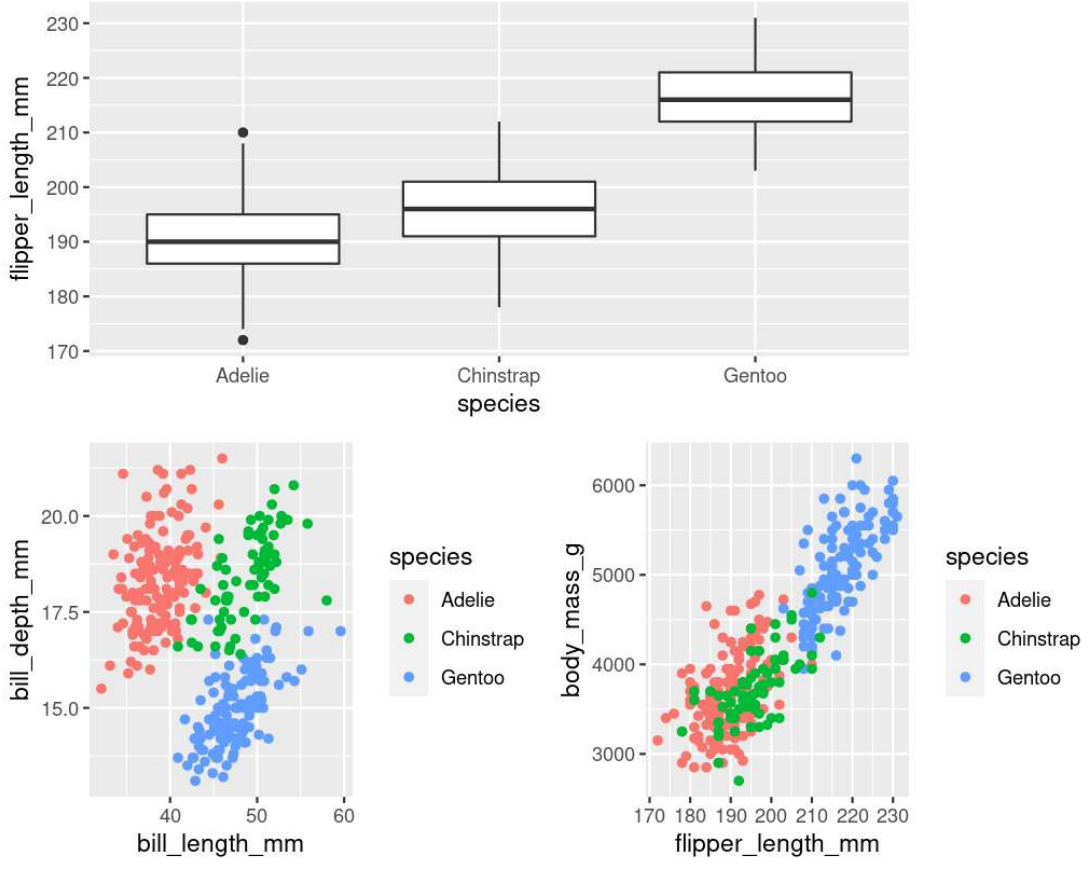
```
g1 + g2
```



Combining plots with **patchwork**

More complex arrangements

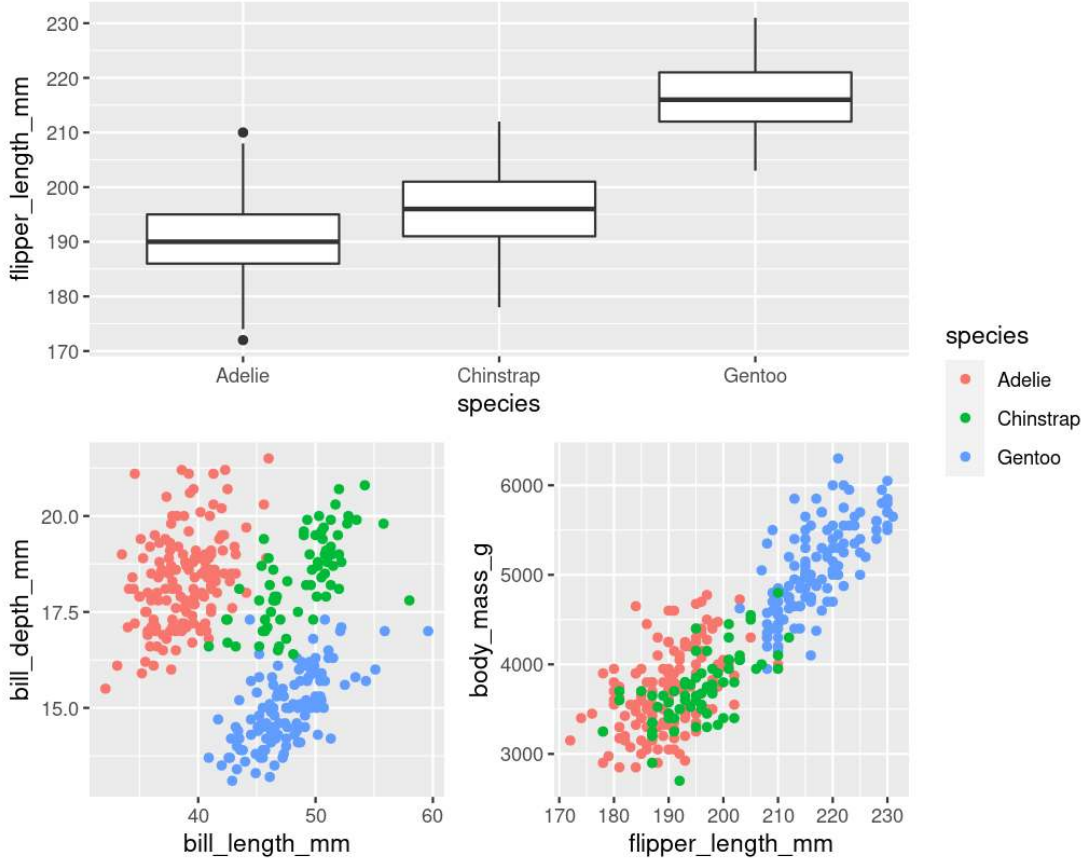
```
g2 / (g1 + g3)
```



Combining plots with **patchwork**

"collect" common legends

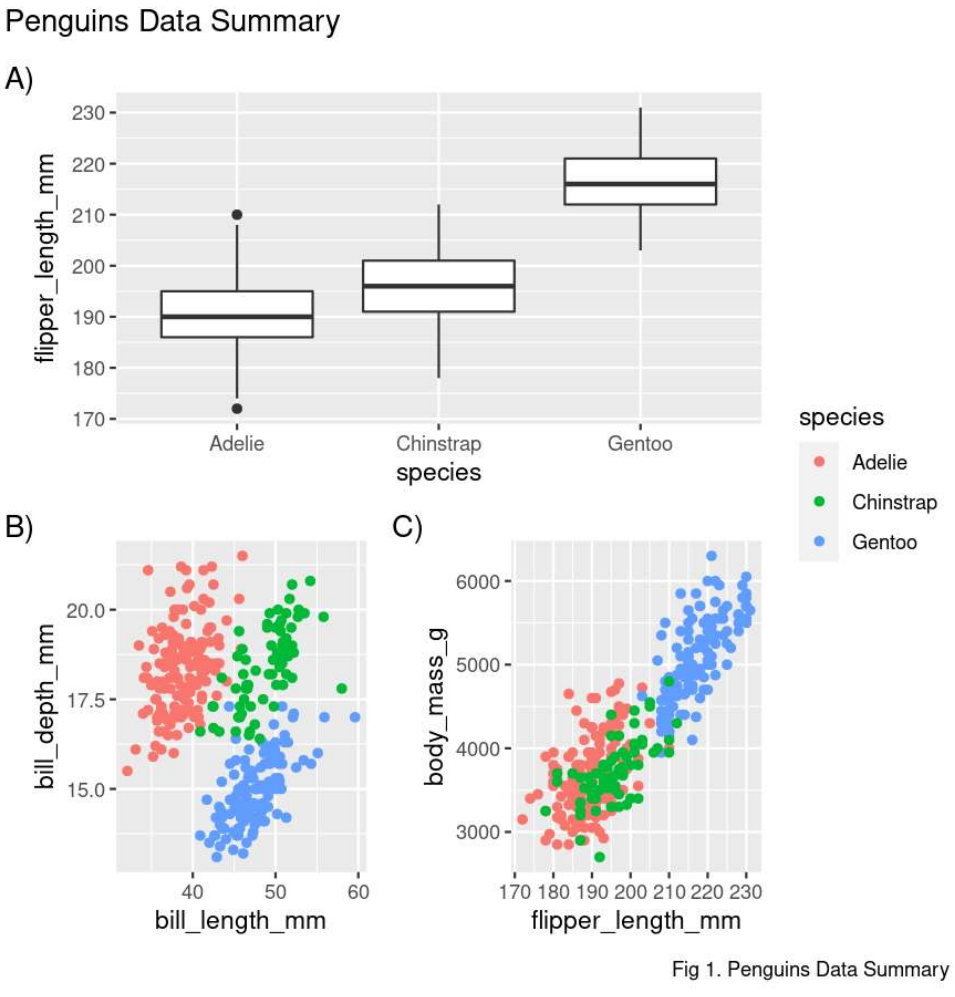
```
g2 / (g1 + g3) + plot_layout(guides = "collect")
```



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 = ")")
```



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 = "penguin_mass.pdf", plot = g, dpi = 300,
       height = 80, width = 129, units = "mm")
```

Loading Data

Data types: What kind of data do you have?

Specific program files

Type	R Package	Function (example usage)
Excel (.xls, .xlsx)	`readxl`	`read_excel("file.xlsx", sheet = 1)`
Comma separated (.csv)	`readr`	`read_csv("file.csv")`
Tab separated (e.g, .txt, .dat)	`readr`	`read_tsv("file.txt")`
Space separated (e.g, .txt, .dat)	`readr`	`read_delim("file.dat", delim = " ")`
Fixed-width (e.g, .txt, .dat)	`readr`	`read_fwf("file.dat")`

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Space separated (e.g, .txt, .dat)	`readr`	`read_delim("file.dat", delim = " ")`
Fixed-width (e.g, .txt, .dat)	`readr`	`read_fwf("file.dat")`

Notes

1. You may be familiar with base functions (i.e. `read.csv()`, `read.table()`)
   These are perfectly acceptable, but `readr` is a bit more powerful and quick
2. It can be quicker and safer to save Excel files as a *.csv (Comma-separated-variables file) and then use `readr` package and `read_csv()` function
3. `readr` is a tidyverse package

Where is my data?

```
library(tidyverse) # Load tidyverse which includes readr package

my_data <- read_csv("weather.csv")
```

```
## Error: 'weather.csv' does not exist in current working directory
('/home/steffi/Projects/Teaching/UofM - NRI/NRI_7350/_labs').
```

With no folder (just file name) R expects file to be in **Working directory**

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## Error: 'weather.csv' does not exist in current working directory
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Working directory is:

- Where your RStudio project is
- Your home directory (My Documents, etc.) [If not using RStudio Projects]
- Where you've set it (using **`setwd()`** or RStudio's Session > Set Working Directory)

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> Using Projects in RStudio is a great idea

Where is my data?

Absolute Paths

OS	Absolute Path
LINUX	/home/steffi/Documents/R Projects/mydata.csv
WINDOWS	C:/Users/steffi/My Documents/R Projects/mydata.csv
MAC	/users/steffi/Documents/R Projects/mydata.csv

Relative Paths

Path	Where to look
./mydata.csv	Here (current directory) (./)
../mydata.csv	Go up one directory (../)
./data/mydata.csv	Stay here (./), go into "data" folder (data/)
../data/mydata.csv	Go up one directory (../), then into "data" folder (data/)

Where is my data?

Absolute Paths

OS	Absolute Path
LINUX	/home/steffi/Documents/R Projects/mydata.csv
WINDOWS	C:/Users/steffi/My Documents/R Projects/mydata.csv
MAC	/users/steffi/Documents/R Projects/mydata.csv

With RStudio 'Projects' only need to use **relative** paths

Relative Paths

Path	Where to look
./mydata.csv	Here (current directory) (./)
../mydata.csv	Go up one directory (../)
./data/mydata.csv	Stay here (./), go into "data" folder (data/)
../data/mydata.csv	Go up one directory (../), then into "data" folder (data/)

Keep yourself organized

- Create an RStudio Project for each Project (e.g. **`My Project`**)
- Create a specific **`Data`** folder within each project (one per project)

Folders look like:

```
- My Project
    - Data
        - mydata1.csv
        - mydata2.csv
    - myscript.R
    - My Project.Rproj
```

Now when you load data, you can use something like this: **`"Data/mydata1.csv"`**

Checking / Cleaning your data

```
library(readxl)
my_data <- read_excel("my_data.xlsx")
```

```
head(my_data)
```

```
## # A tibble: 6 × 6
##   `Sample Number` Stage              `Date Egg`          `Body Mass (g)` ...5  ...6
##             <dbl> <chr>              <dttm>                        <dbl> <lgl> <lgl>
## 1               1 Adult, 1 Egg Stage 2007-11-11 00:00:00            3750 NA    NA
## 2               2 Adult, 1 Egg Stage 2007-11-11 00:00:00            3800 NA    NA
## 3               3 Adult, 1 Egg Stage 2007-11-16 00:00:00            3250 NA    NA
## 4               4 Adult, 1 Egg Stage 2007-11-16 00:00:00              NA NA    NA
## 5               5 Adult, 1 Egg Stage 2007-11-16 00:00:00            3450 NA    NA
## 6               6 Adult, 1 Egg Stage 2007-11-16 00:00:00            3650 NA    NA
```

Checking / Cleaning your data

```
tail(my_data)
```

```
## # A tibble: 6 × 6
##   `Sample Number` Stage              `Date Egg`          `Body Mass (g)` ...5  ...6
##             <dbl> <chr>              <dttm>                        <dbl> <lgl> <lgl>
## 1              63 Adult, 1 Egg Stage 2009-11-19 00:00:00            3650 NA    NA
## 2              64 Adult, 1 Egg Stage 2009-11-19 00:00:00            4000 NA    NA
## 3              65 Adult, 1 Egg Stage 2009-11-21 00:00:00            3400 NA    NA
## 4              66 Adult, 1 Egg Stage 2009-11-21 00:00:00            3775 NA    NA
## 5              67 Adult, 1 Egg Stage 2009-11-21 00:00:00            4100 NA    NA
## 6              68 Adult, 1 Egg Stage 2009-11-21 00:00:00            3775 NA    NA
```

Checking / Cleaning your data

```
tail(my_data)
```

```
## # A tibble: 6 × 6
##   `Sample Number` Stage              `Date Egg`          `Body Mass (g)` ...5  ...6
##             <dbl> <chr>              <dttm>                        <dbl> <lgl> <lgl>
## 1              63 Adult, 1 Egg Stage 2009-11-19 00:00:00            3650 NA    NA
## 2              64 Adult, 1 Egg Stage 2009-11-19 00:00:00            4000 NA    NA
## 3              65 Adult, 1 Egg Stage 2009-11-21 00:00:00            3400 NA    NA
## 4              66 Adult, 1 Egg Stage 2009-11-21 00:00:00            3775 NA    NA
## 5              67 Adult, 1 Egg Stage 2009-11-21 00:00:00            4100 NA    NA
## 6              68 Adult, 1 Egg Stage 2009-11-21 00:00:00            3775 NA    NA
```

- Looks like we have some extra, empty, columns... (`..5`, `..6`)
- Also looks like some column names might not work well in R
  - (Anything with a space or special character, i.e. `Date Egg` and `Body Mass (g)`

Checking / Cleaning your data

- When loading data that was in Excel (etc.) it can often have some funky things going on
- Use the **`janitor`** package to quickly fix some of those problems

Column names

```
library(janitor)

my_data <- clean_names(my_data)
head(my_data)
```

```
## # A tibble: 6 × 6
##   sample_number stage              date_egg            body_mass_g x5    x6
##           <dbl> <chr>              <dttm>                    <dbl> <lgl> <lgl>
## 1             1 Adult, 1 Egg Stage 2007-11-11 00:00:00        3750 NA    NA
## 2             2 Adult, 1 Egg Stage 2007-11-11 00:00:00        3800 NA    NA
## 3             3 Adult, 1 Egg Stage 2007-11-16 00:00:00        3250 NA    NA
## 4             4 Adult, 1 Egg Stage 2007-11-16 00:00:00          NA NA    NA
## 5             5 Adult, 1 Egg Stage 2007-11-16 00:00:00        3450 NA    NA
## 6             6 Adult, 1 Egg Stage 2007-11-16 00:00:00        3650 NA    NA
```

Checking / Cleaning your data

- When loading data that was in Excel (etc.) it can often have some funky things going on
- Use the **`janitor`** package to quickly fix some of those problems

Empty rows/columns

```
my_data <- remove_empty(my_data, which = c("rows", "cols"))
```

```
head(my_data)
```

```
## # A tibble: 6 × 4
##   sample_number stage              date_egg            body_mass_g
##           <dbl> <chr>              <dttm>                    <dbl>
## 1             1 Adult, 1 Egg Stage 2007-11-11 00:00:00        3750
## 2             2 Adult, 1 Egg Stage 2007-11-11 00:00:00        3800
## 3             3 Adult, 1 Egg Stage 2007-11-16 00:00:00        3250
## 4             4 Adult, 1 Egg Stage 2007-11-16 00:00:00          NA
## 5             5 Adult, 1 Egg Stage 2007-11-16 00:00:00        3450
## 6             6 Adult, 1 Egg Stage 2007-11-16 00:00:00        3650
```

Loading your data

This blazing fast intro to loading/cleaning will not cover the
many, *many*, **many**, **MANY** ways that data can be weird.

Let me know if (when) you run into problems and we can trouble shoot together!

Your Turn!

Prep for next class (be ready for class, but you don't have to share with me unless you want to!)

- Create a **new RStudio Project** for your class project
- Create a **"Data" folder** inside this project folder
  - Files pane > New Folder
- **Add data** to it (if you have data)
  - Use your computers folder navigator for this
- **Create a new script** in the main folder
  - [Menu] File > New > R Script
- Add code to this script to **load your data into R**
  - Load the appropriate packages (`tidyverse`, `readxl`, `janitor`)
  - Use the appropriate function given your data type (e.g., `read_csv()` for .csv, `read_excel` for .xlsx)
  - Use the appropriate file location (e.g, `"Data/my_data.csv"`)
    Remember quotes (" ") around the *entire* file location
- **Explore your data -** Click on your data in the Environment pane and take a look!

Wrapping Up!

Wrapping up: Common mistakes

Figures

- 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))`**

Loading data

- Not using RProjects which makes it hard to find your data
- Expecting your data to be something it's not
  - (open your data in a text editor or spreadsheet program to take a look)
- Using the wrong function (i.e you used **`read_csv()`** when you should have used **`read_tsv()`**)

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
- **`patchwork`** site
- R for Data Science
  - Data Visualization
  - Workflow and Projects
  - Data Import