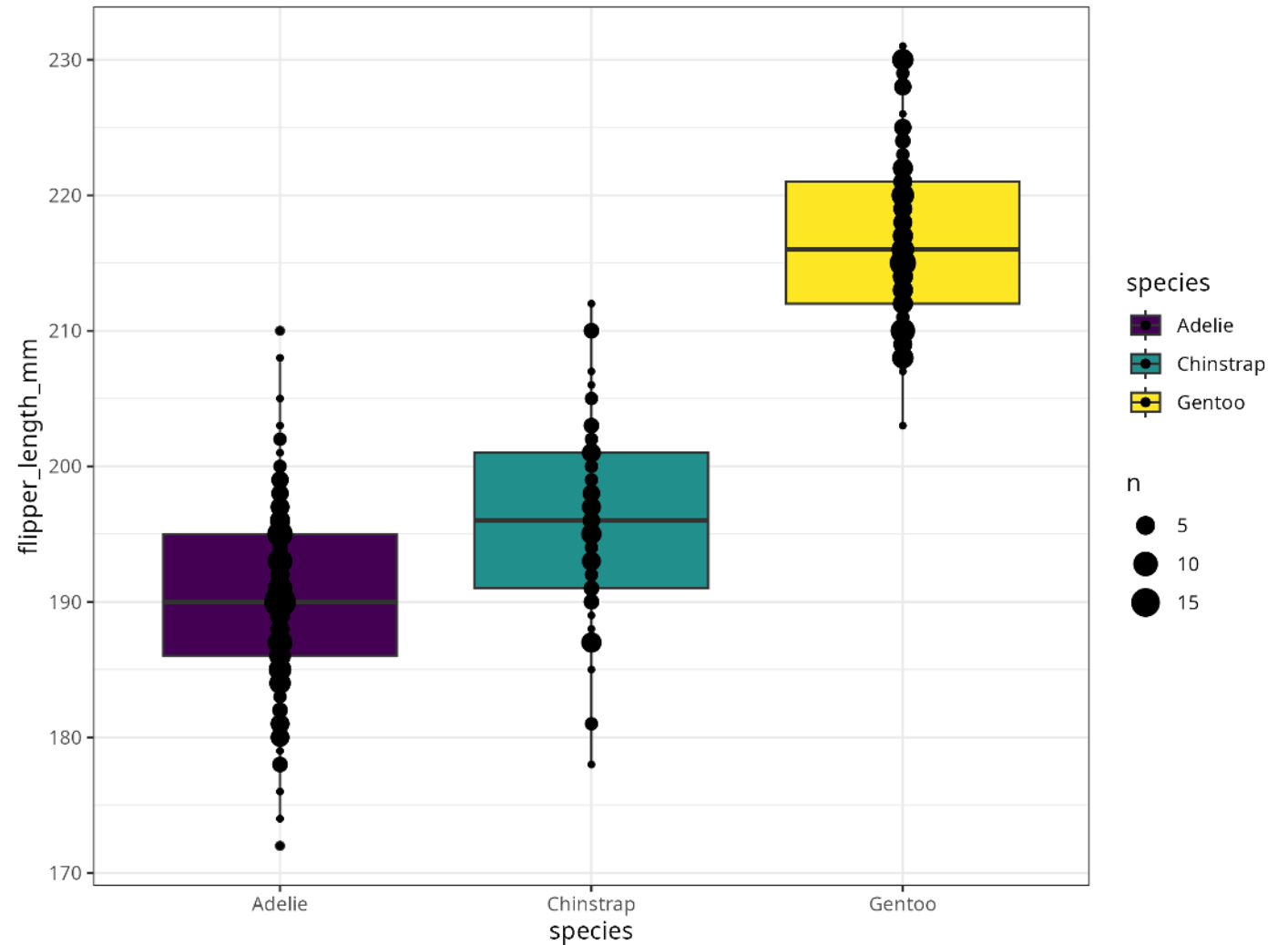


Visualizing Data in R

A primer on `ggplot2`

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Analysis and Data Tools for Science



First things first

 Save previous script

 Open New File

(make sure you're in the RStudio Project)

 Write `library(tidyverse)` at the top

 Save this new script

(consider names like `figs.R` or `2_figures.R`)

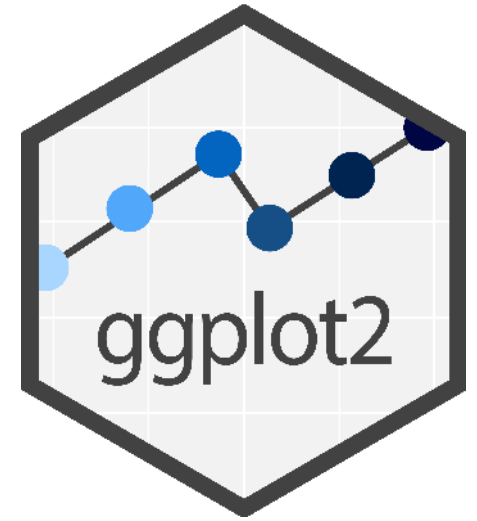
Outline

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

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

2. Combining figures with `patchwork`

3. Saving figures



ggplot2:

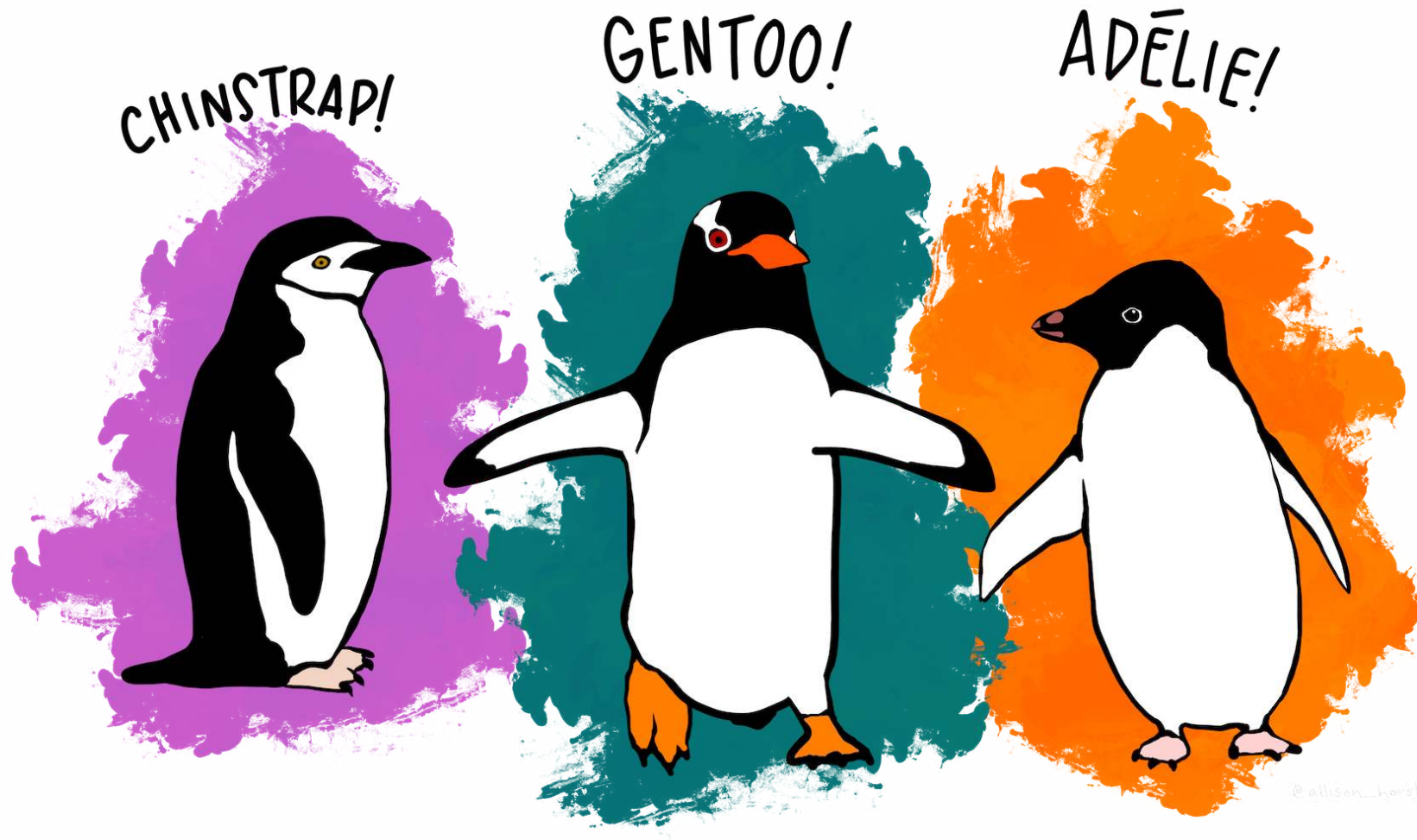
Build a data MASTERPIECE



HORST '18

Artwork by @allison_horst

Our data set: Palmer Penguins!



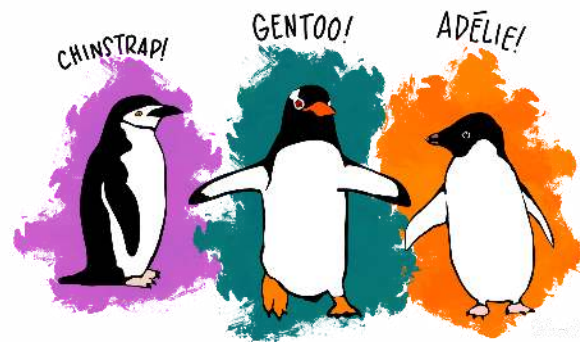
Artwork by [@allison_horst](#)

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
  <fct>    <fct>          <dbl>          <dbl>          <int>          <int>
1 Adelie  Torgersen         39.1           18.7           181           3750
2 Adelie  Torgersen         39.5           17.4           186           3800
3 Adelie  Torgersen         40.3            18           195           3250
4 Adelie  Torgersen         NA            NA            NA            NA
5 Adelie  Torgersen         36.7           19.3           193           3450
6 Adelie  Torgersen         39.3           20.6           190           3650
7 Adelie  Torgersen         38.9           17.8           181           3625
8 Adelie  Torgersen         39.2           19.6           195           4675
9 Adelie  Torgersen         34.1           18.1           193           3475
10 Adelie Torgersen         42            20.2           190           4250
# i 334 more rows
# i 2 more variables: sex <fct>, year <int>
```



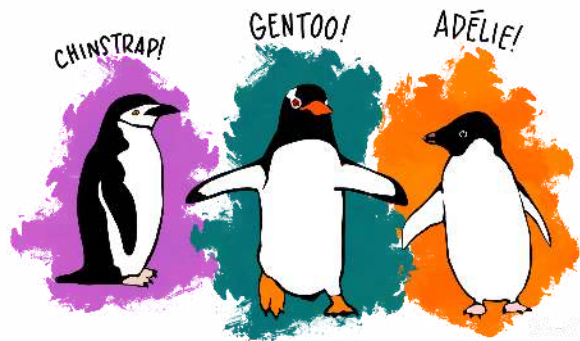
Artwork by [@allison_horst](#)

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
  <fct>   <fct>         <dbl>         <dbl>         <int>         <int>
1 Adelie Torgersen      39.1           18.7           181           3750
2 Adelie Torgersen      39.5           17.4           186           3800
3 Adelie Torgersen      40.3            18           195           3250
4 Adelie Torgersen      NA            NA            NA            NA
5 Adelie Torgersen      36.7           19.3           193           3450
6 Adelie Torgersen      39.3           20.6           190           3650
7 Adelie Torgersen      38.9           17.8           181           3625
8 Adelie Torgersen      39.2           19.6           195           4675
9 Adelie Torgersen      34.1           18.1           193           3475
10 Adelie Torgersen      42            20.2           190           4250
# i 334 more rows
# i 2 more variables: sex <fct>, year <int>
```



Your turn!

Run this code and look at the output in the console

Artwork by [@allison_horst](#)

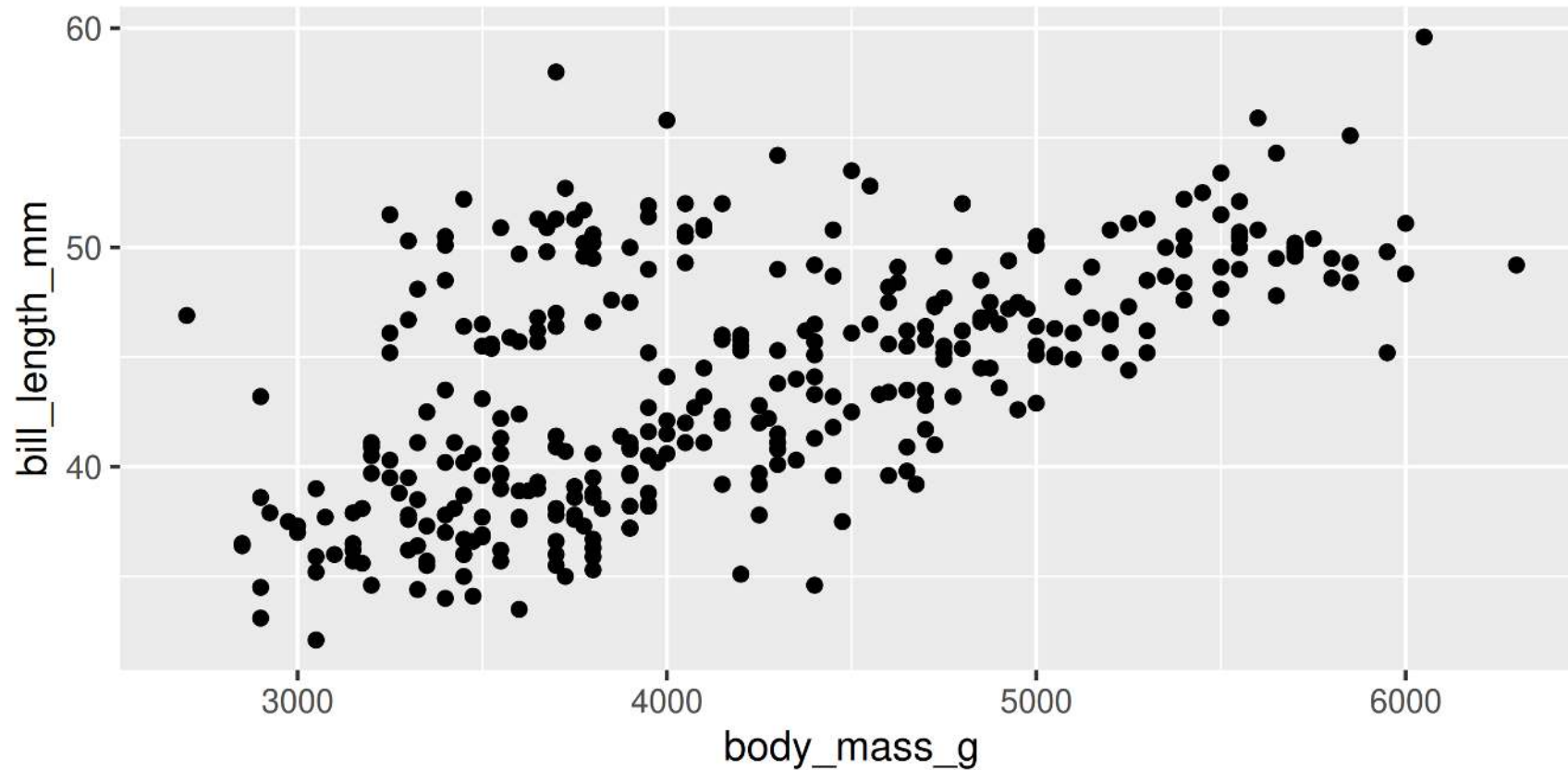
Side Note

Where did the `penguins` data set come from?

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

A basic plot

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

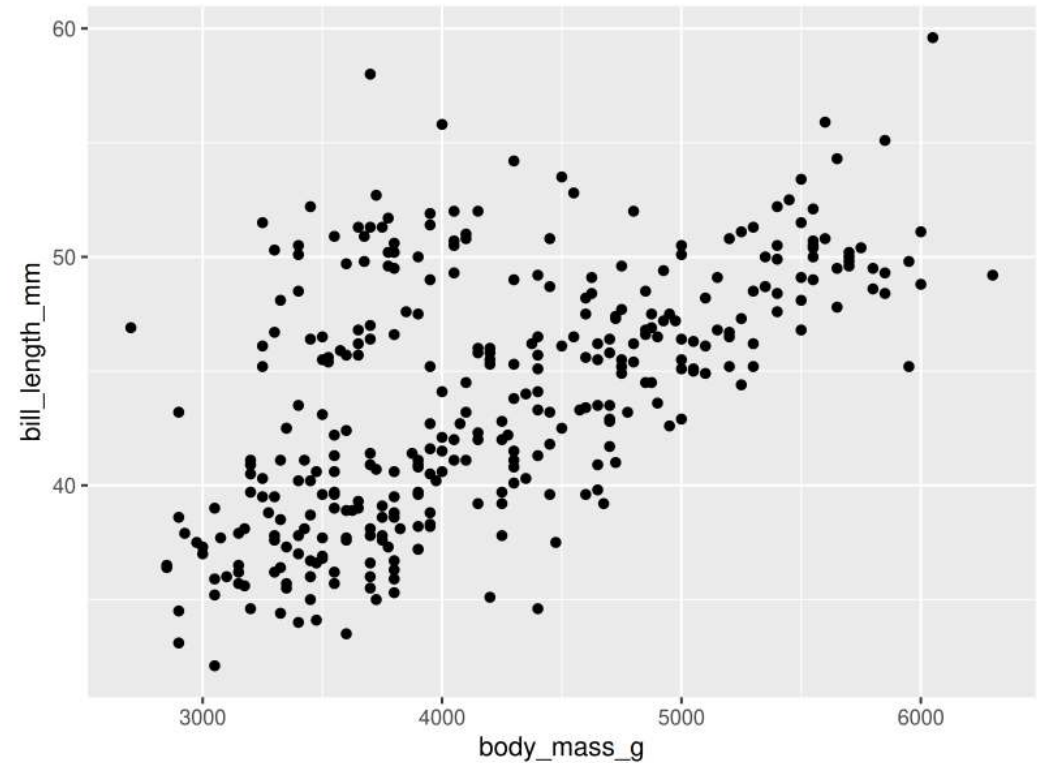


Break it down

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

library()

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

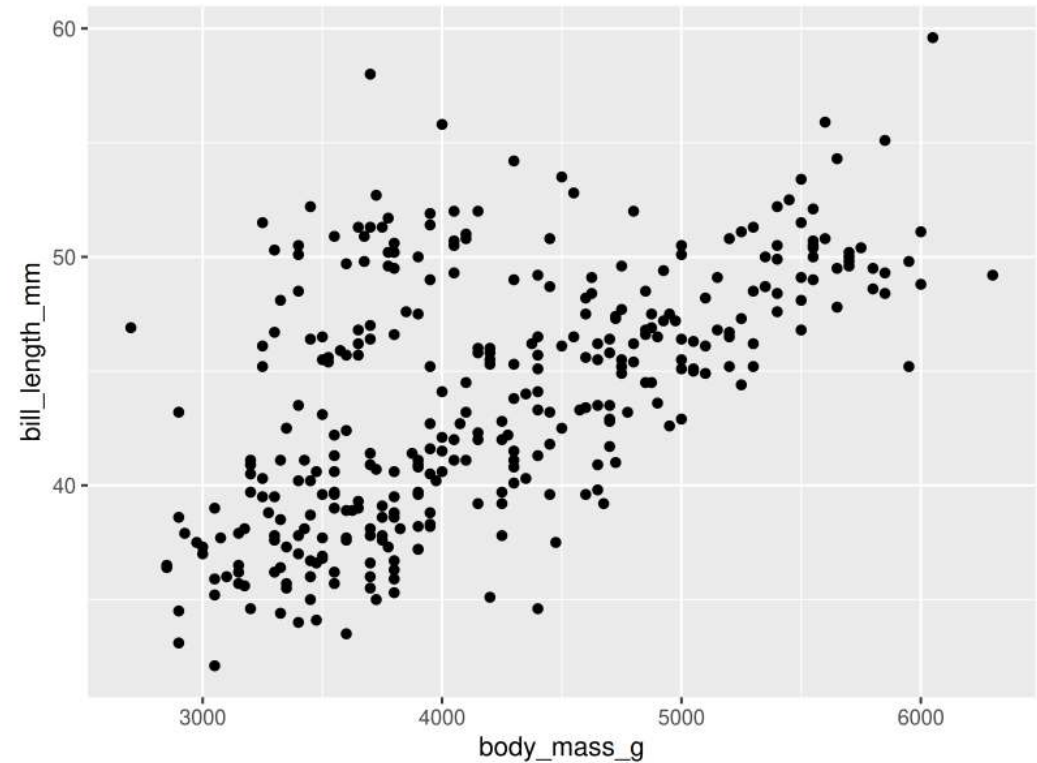


Break it down

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

library()

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

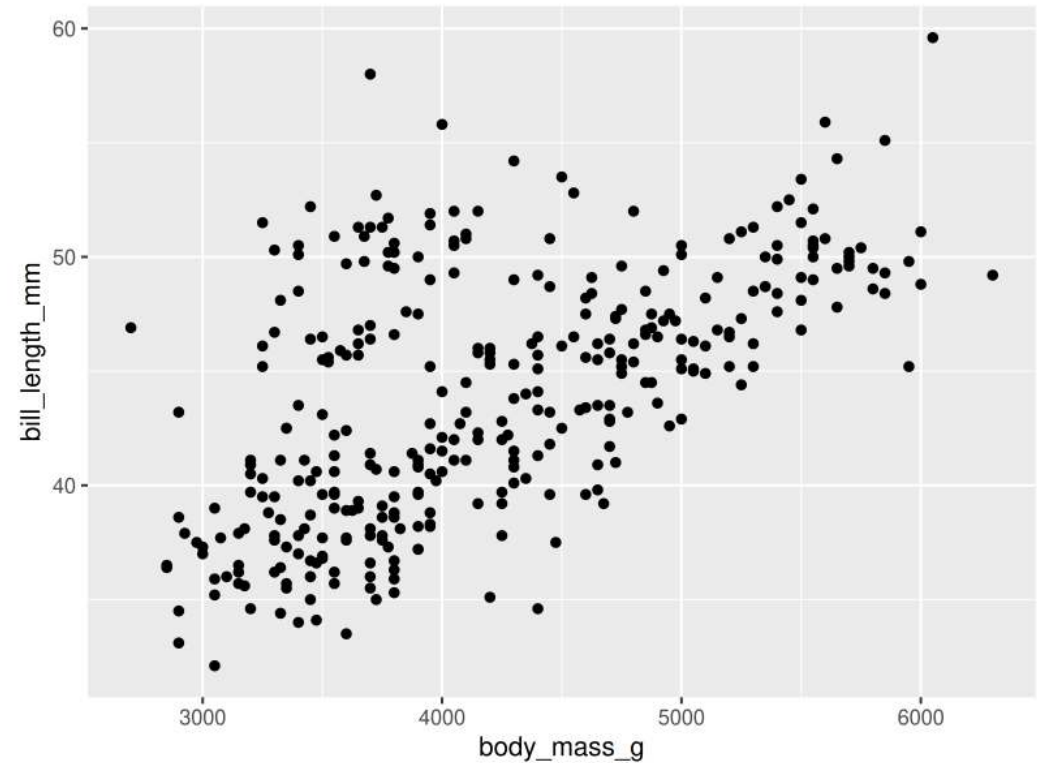


Break it down

```
1 library(palmerpenguins)
2 library(tidyverse)
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



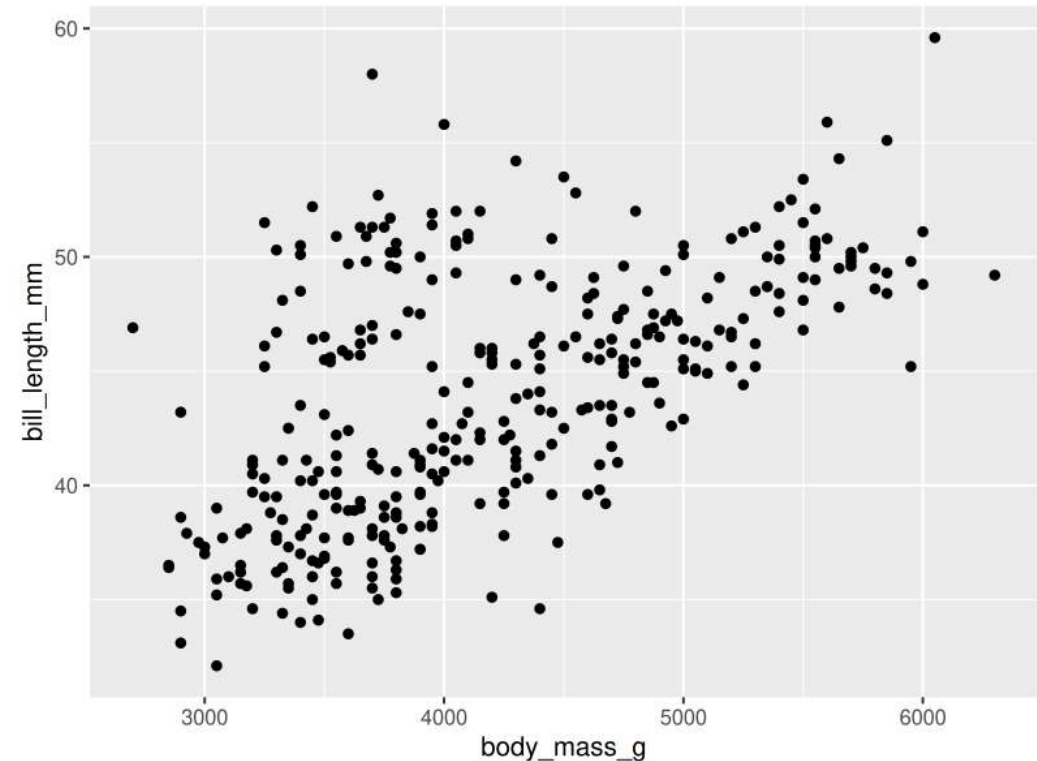
Break it down

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

geom_point()

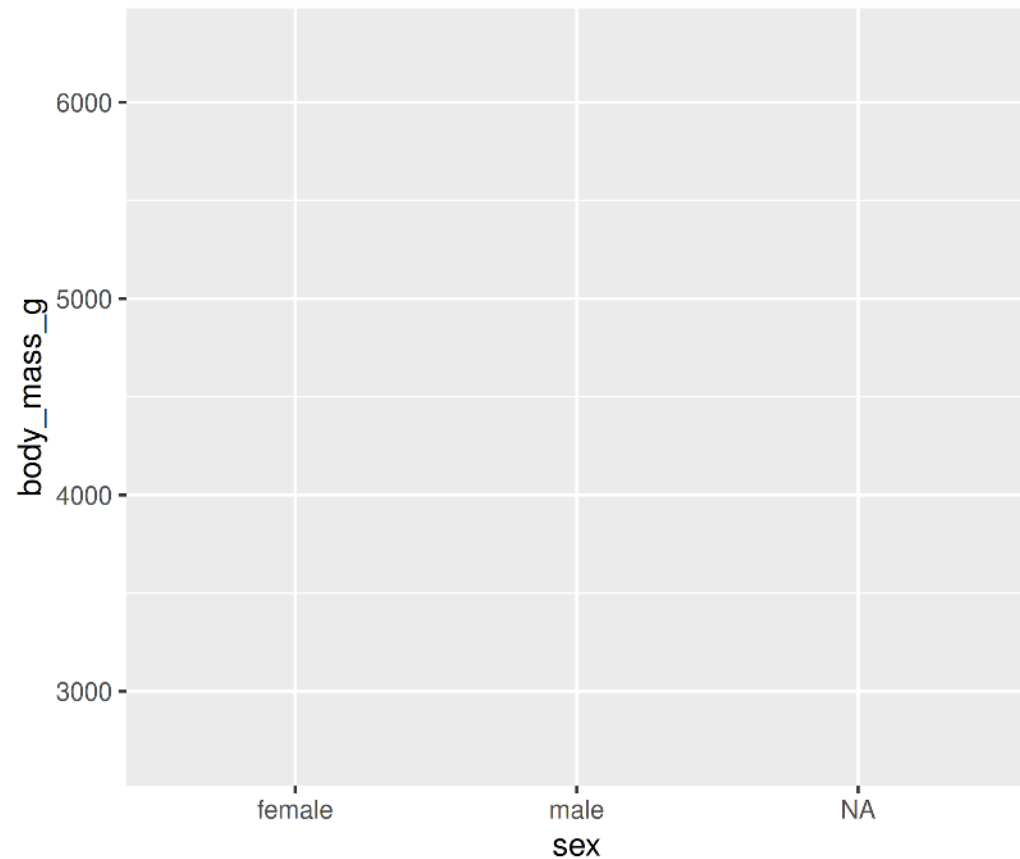
- Choose a `geom` function to display the data
- Always *added* to a `ggplot()` call with +

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

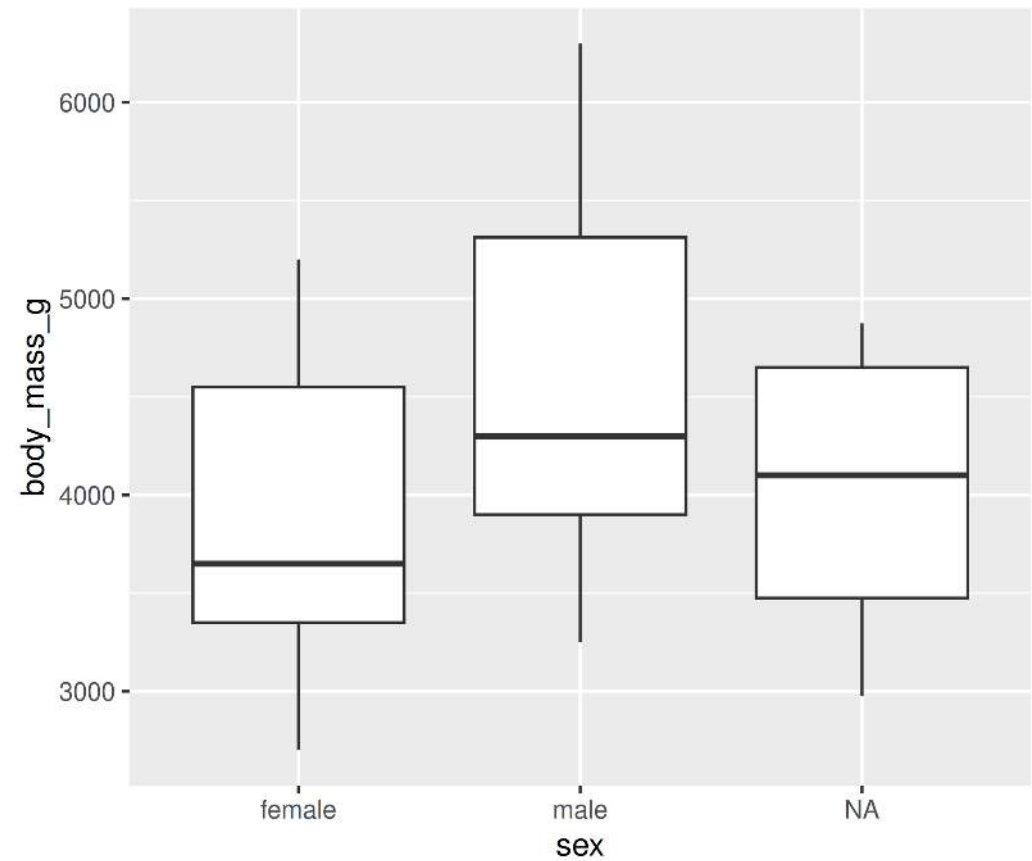


Plots are layered

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

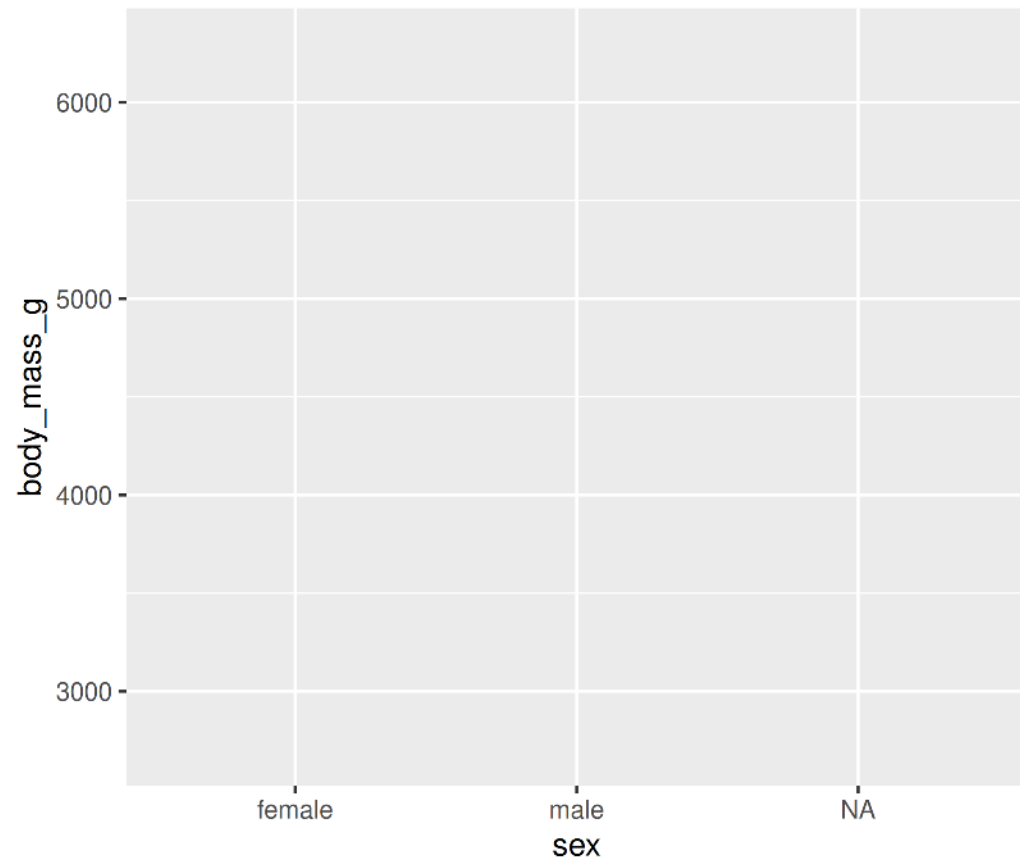


```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2   geom_boxplot()
```

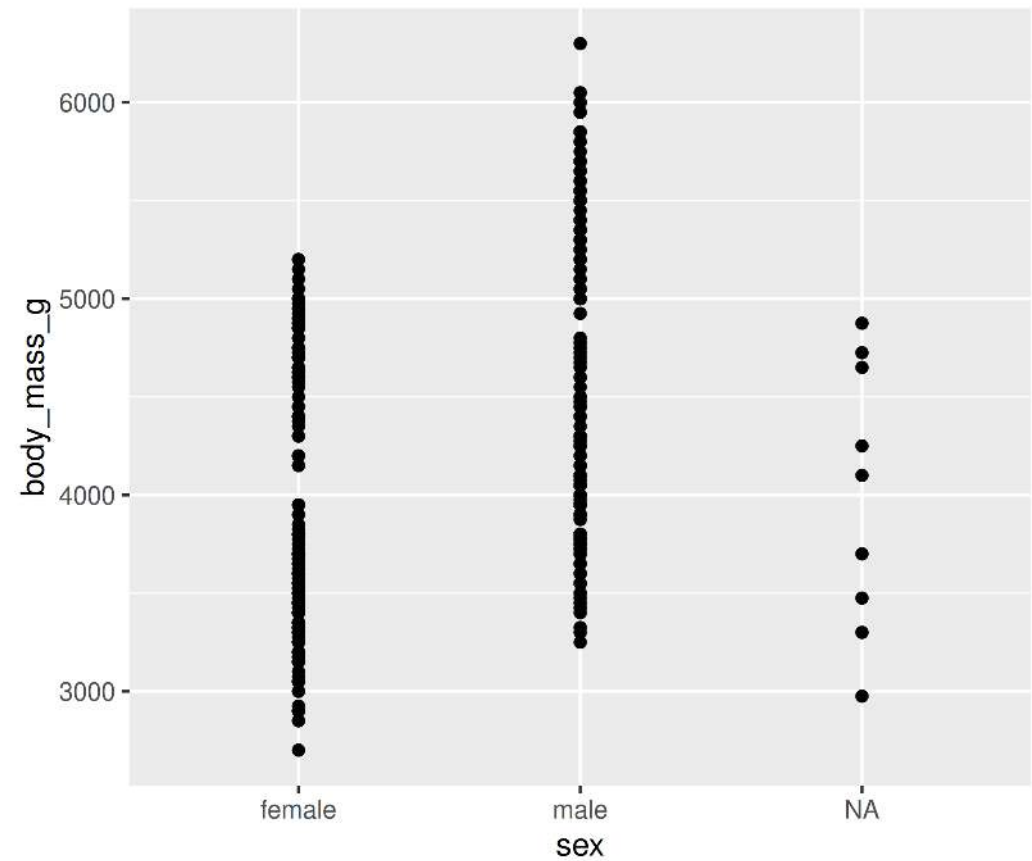


Plots are layered

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

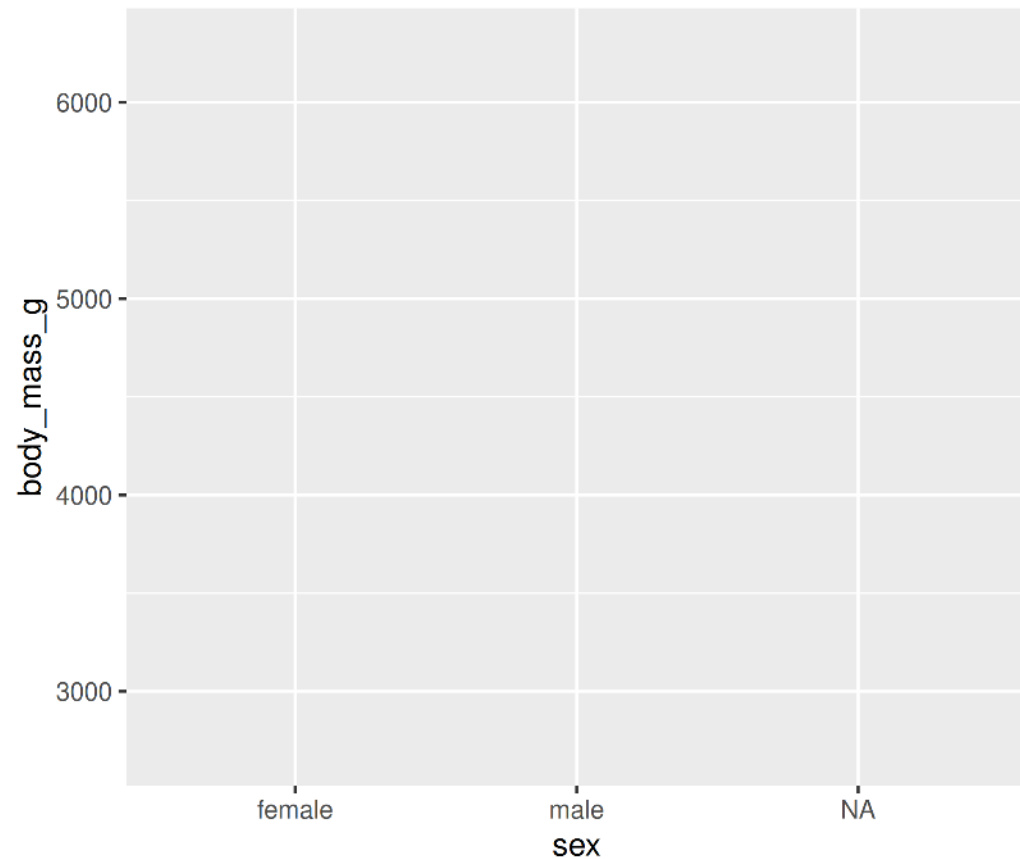


```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2 geom_point()
```

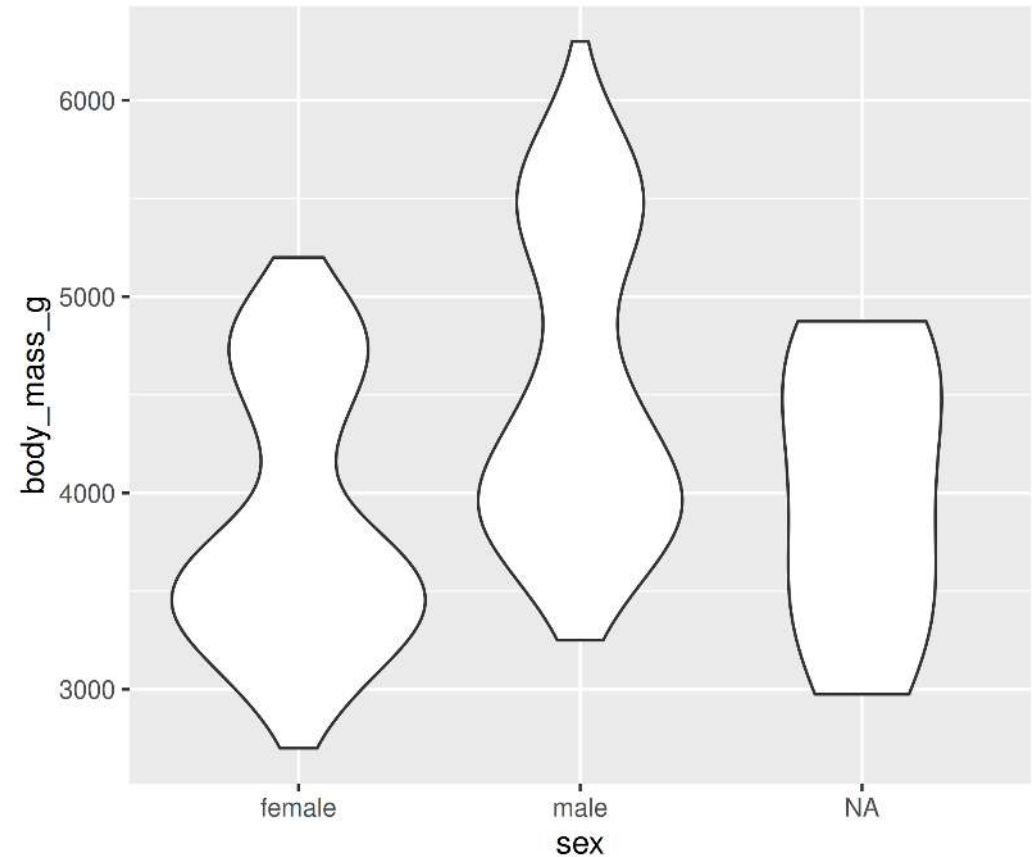


Plots are layered

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



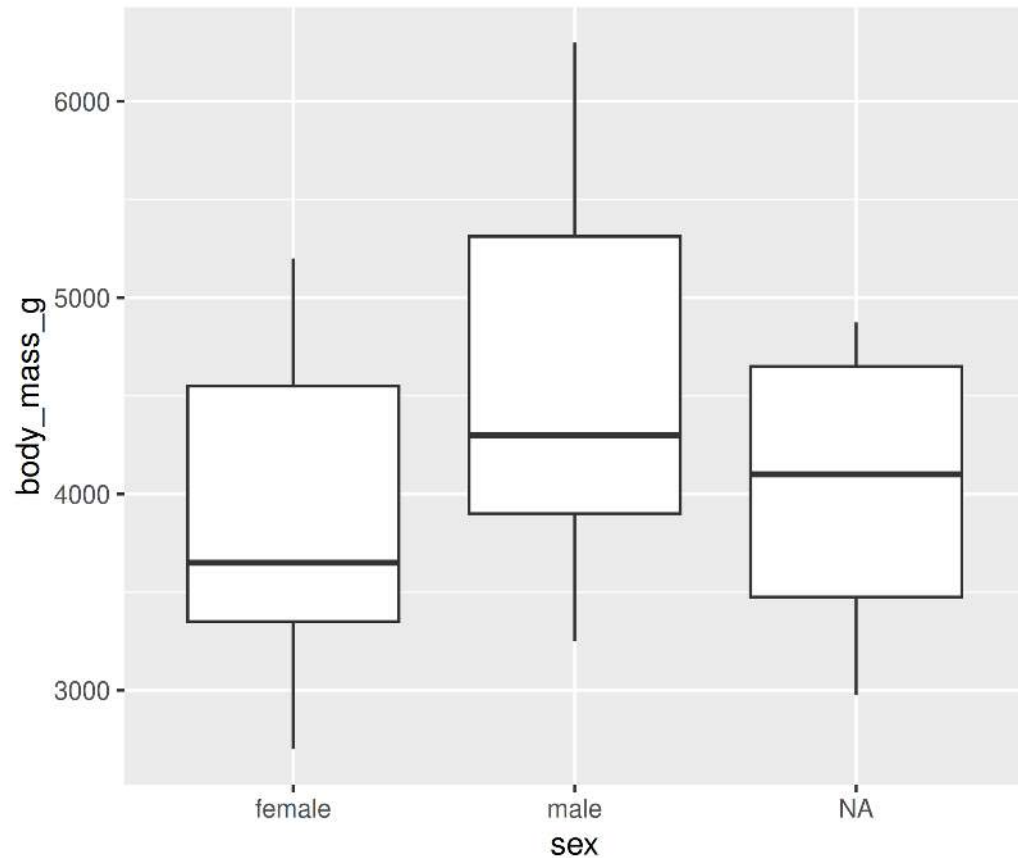
```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2   geom_violin()
```



Plots are layered

You can add multiple layers

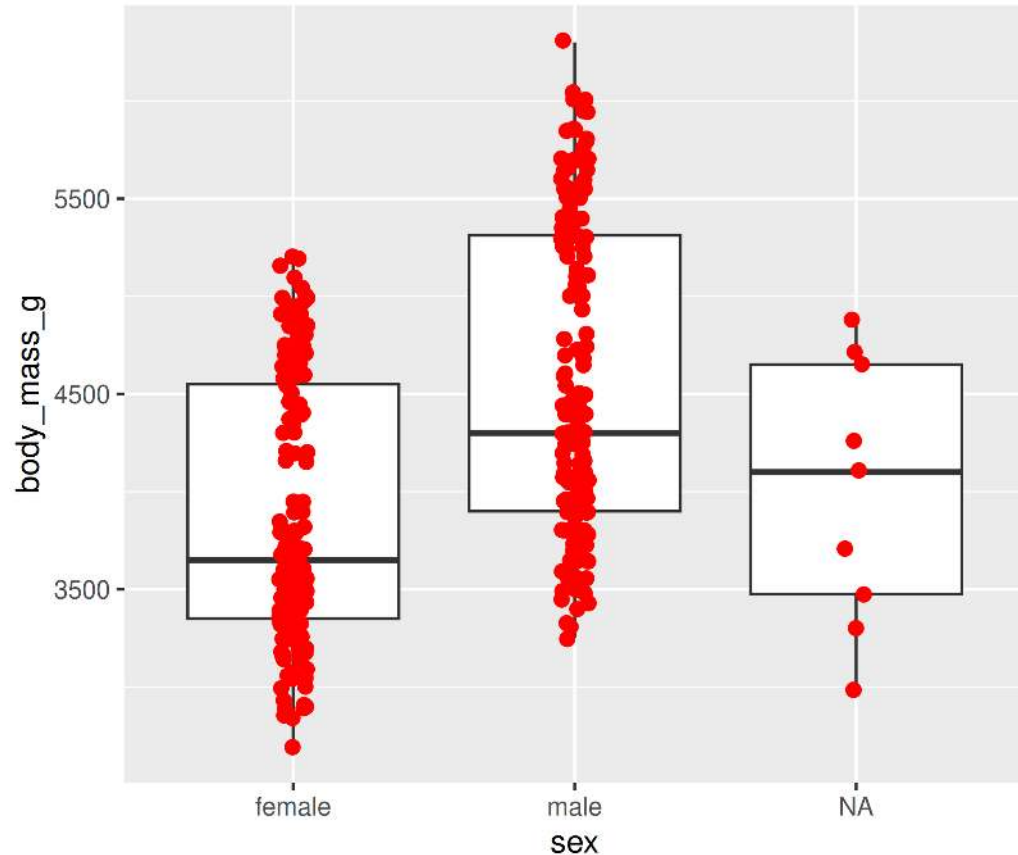
```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2   geom_boxplot()
```



Plots are layered

You can add multiple layers

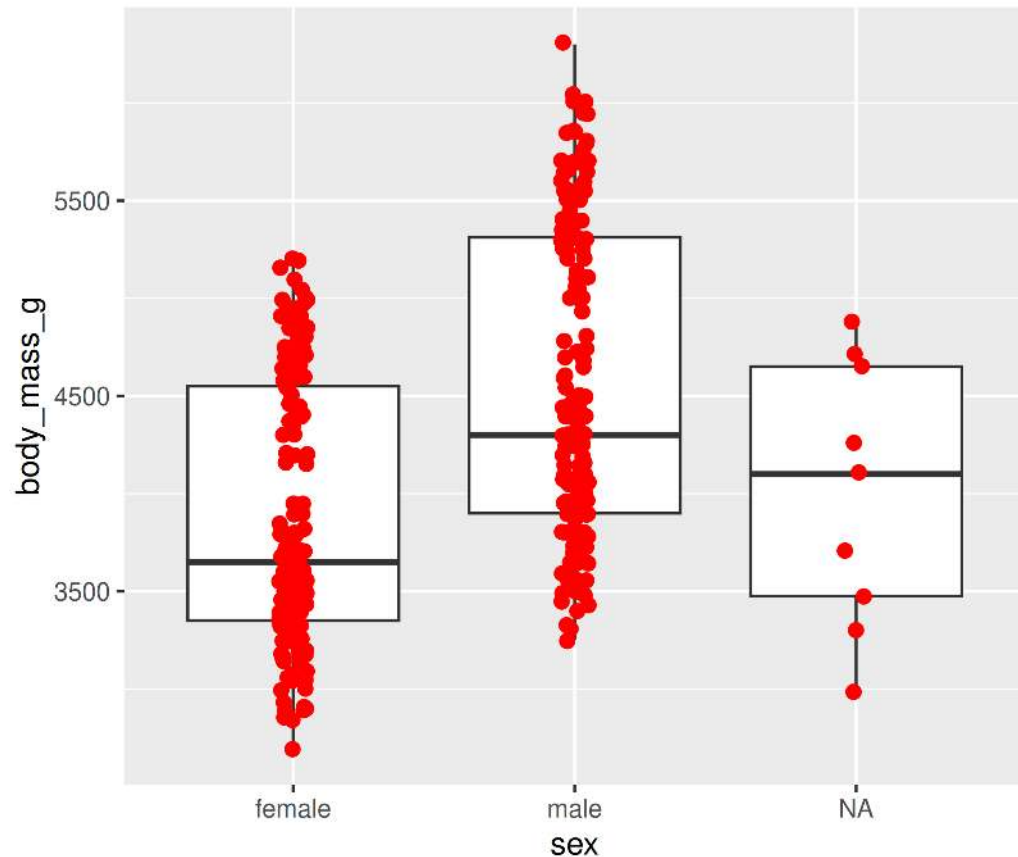
```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2   geom_boxplot() +  
3   geom_point(size = 2, colour = "red",  
4             position = position_jitter(width = 0.05))
```



Plots are layered

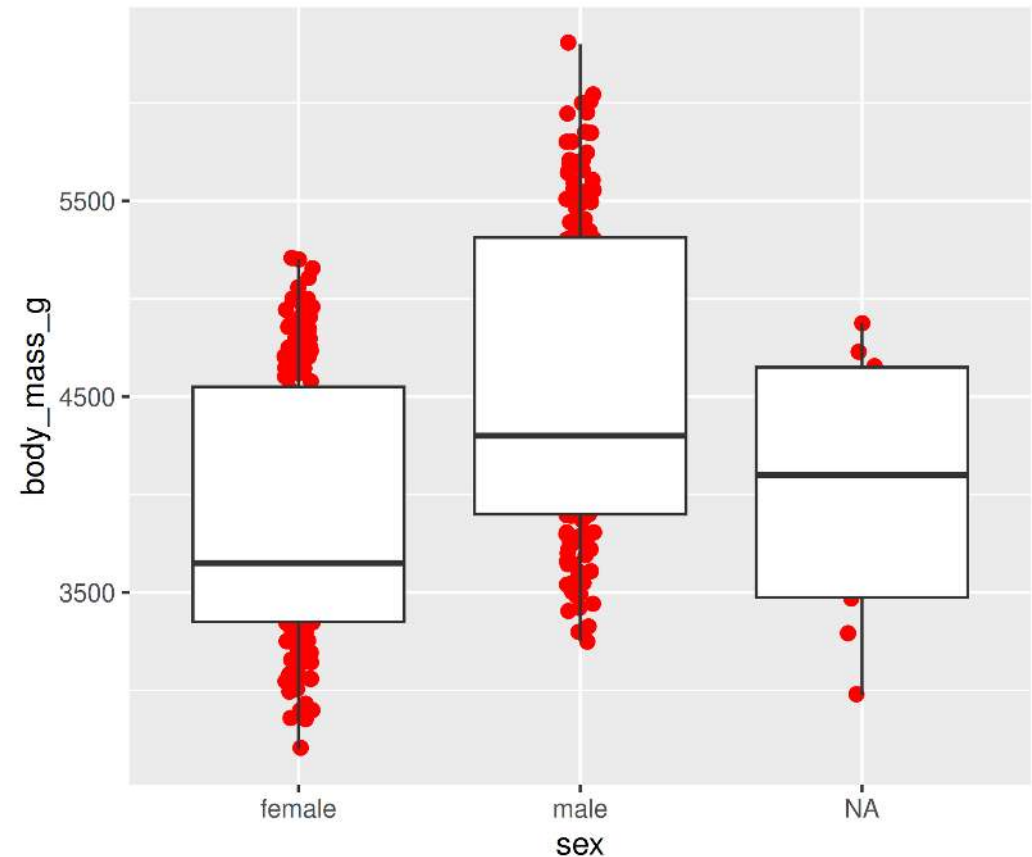
You can add multiple layers

```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2   geom_boxplot() +  
3   geom_point(size = 2, colour = "red",  
4             position = position_jitter(width = 0.05))
```



Order matters

```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2   geom_point(size = 2, colour = "red",  
3             position = position_jitter(width = 0.05)) +  
4   geom_boxplot()
```



Plots are objects

Any ggplot can be saved as an object

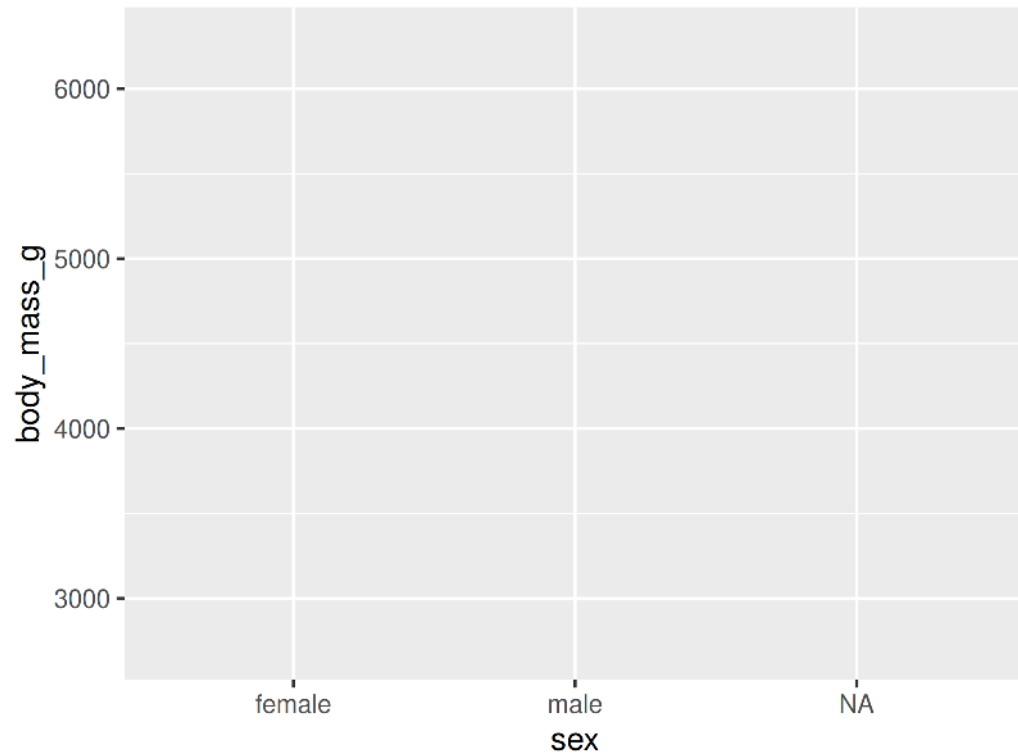
```
1 g <- ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

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
```

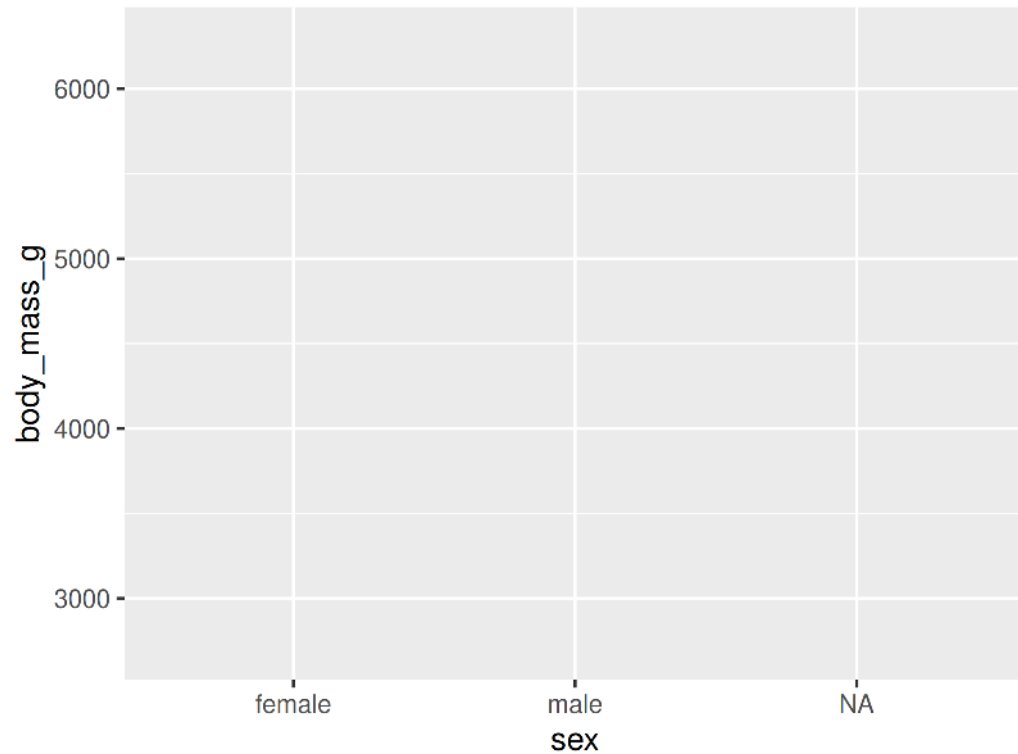


Plots are objects

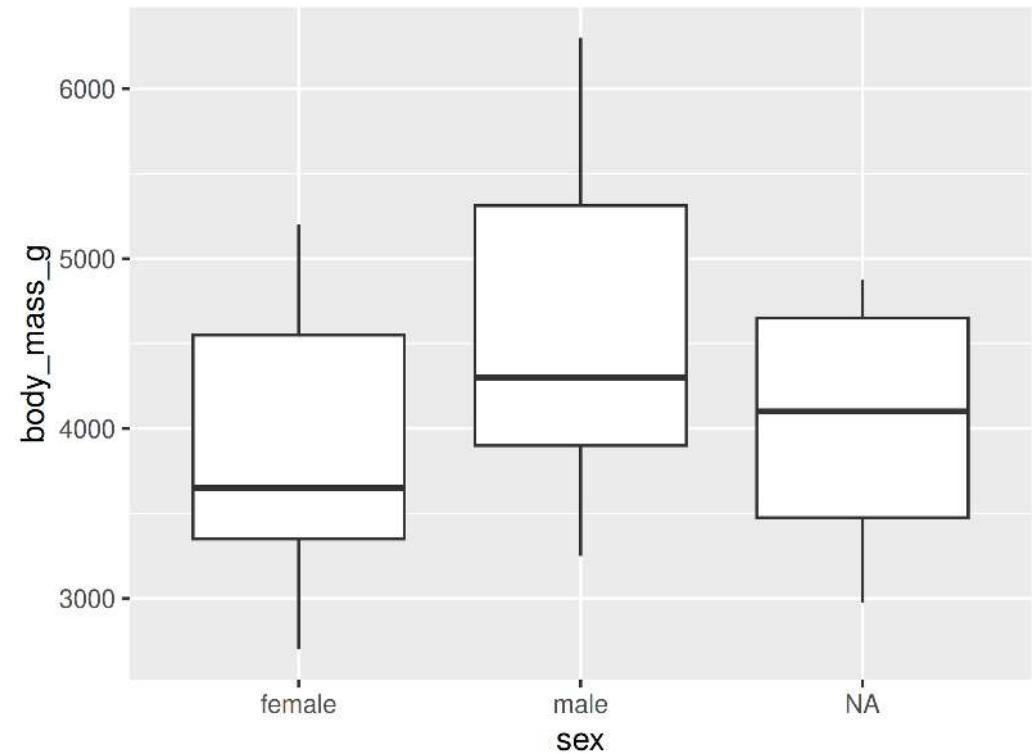
Any ggplot can be saved as an object

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

```
1 g
```



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

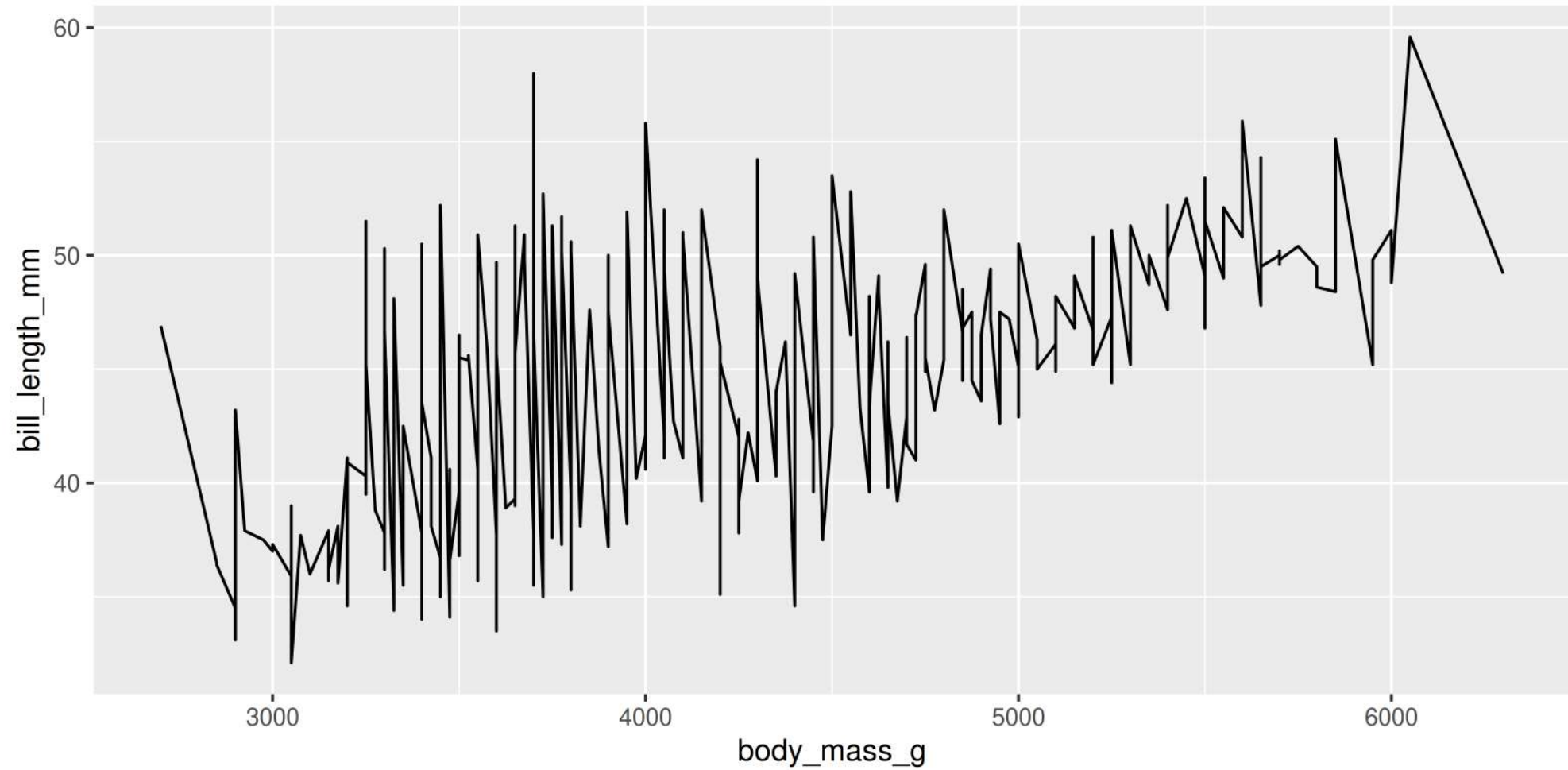


More Geoms

(Plot types)

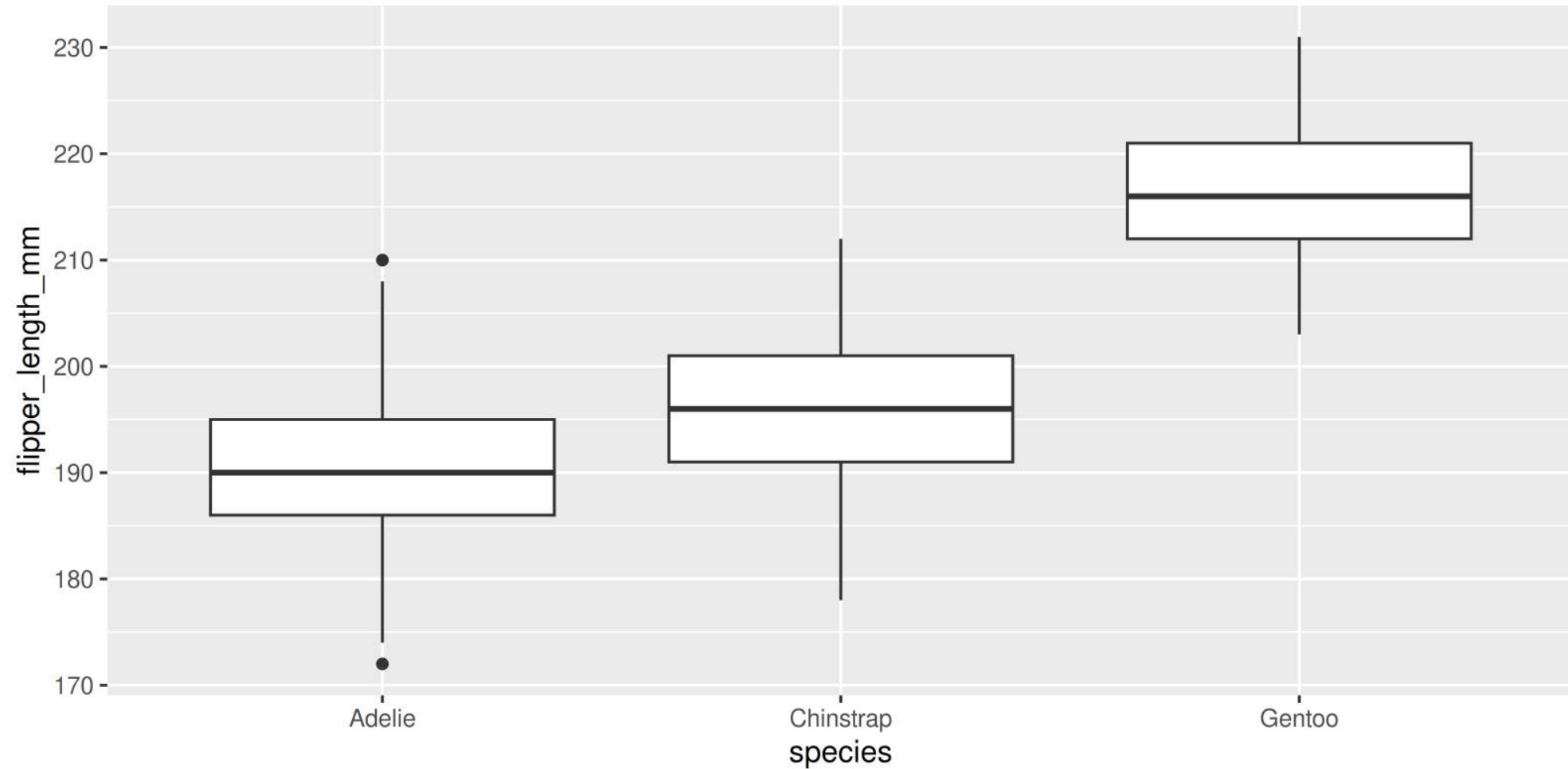
Geoms: Lines

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



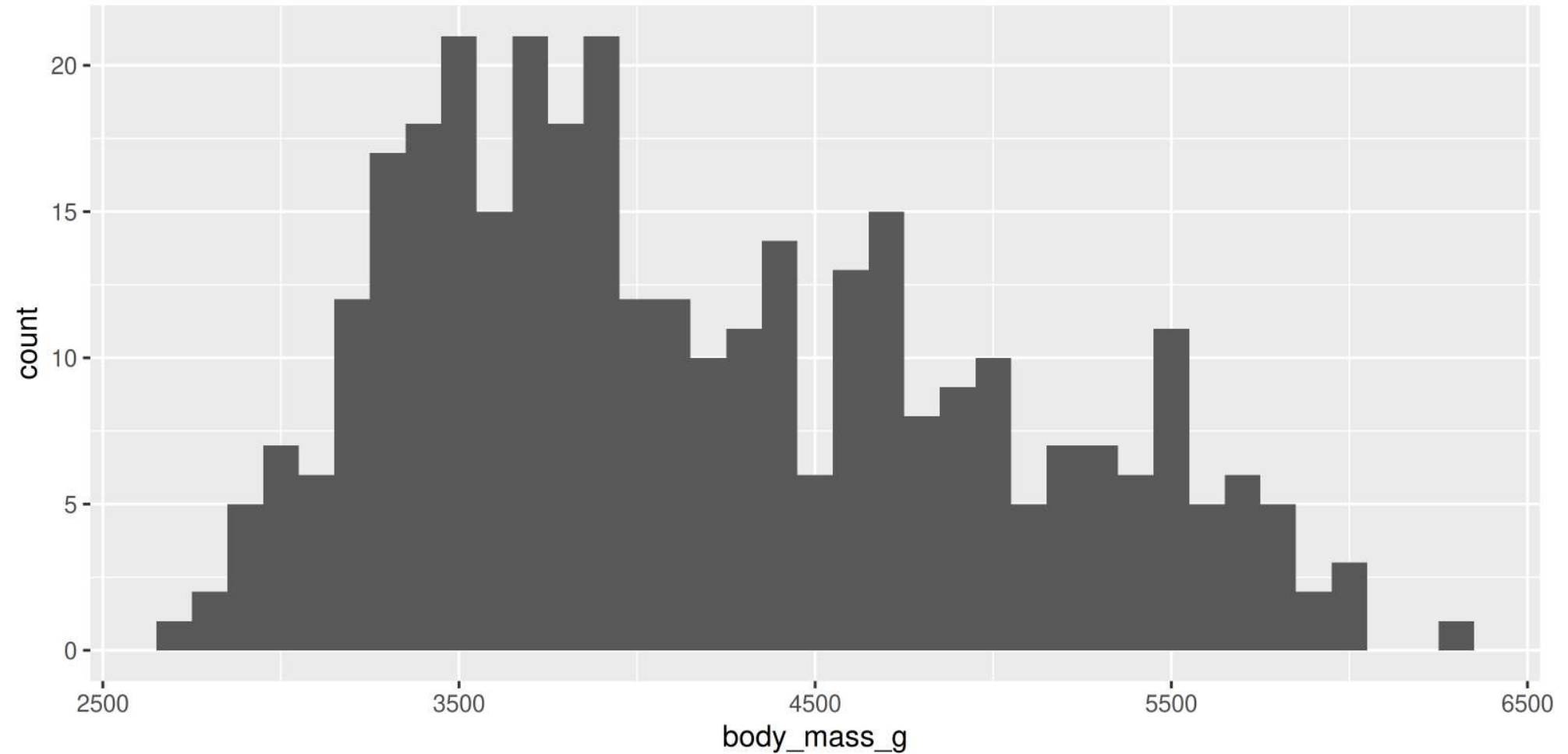
Geoms: Boxplots

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



Geoms: Histogram

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

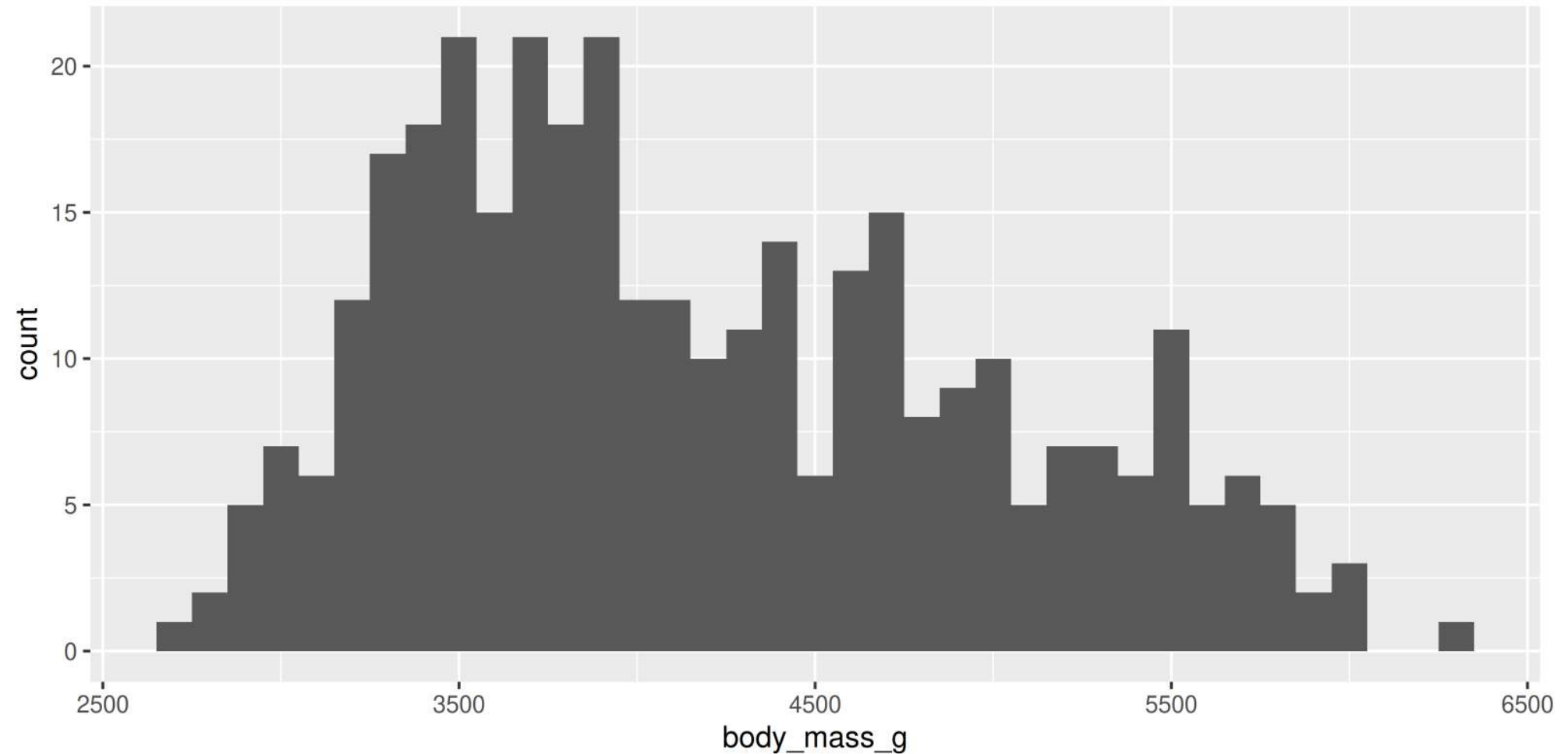


Geoms: Histogram

Note:

We only need 1 aesthetic here

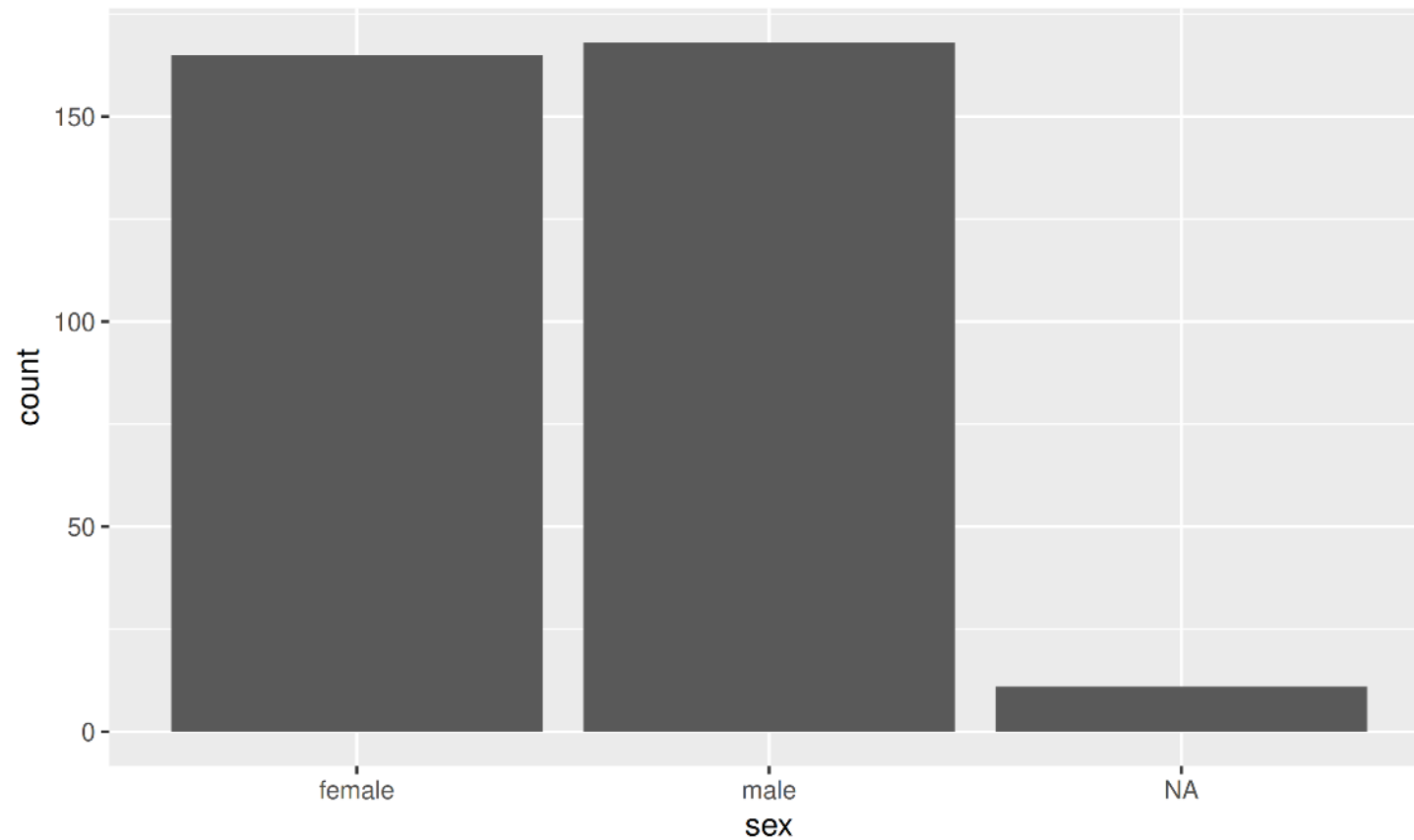
```
1 ggplot(data = penguins, aes(x = body_mass_g)) +  
2   geom_histogram(binwidth = 100)
```



Geoms: Barplots

Let `ggplot` count your data

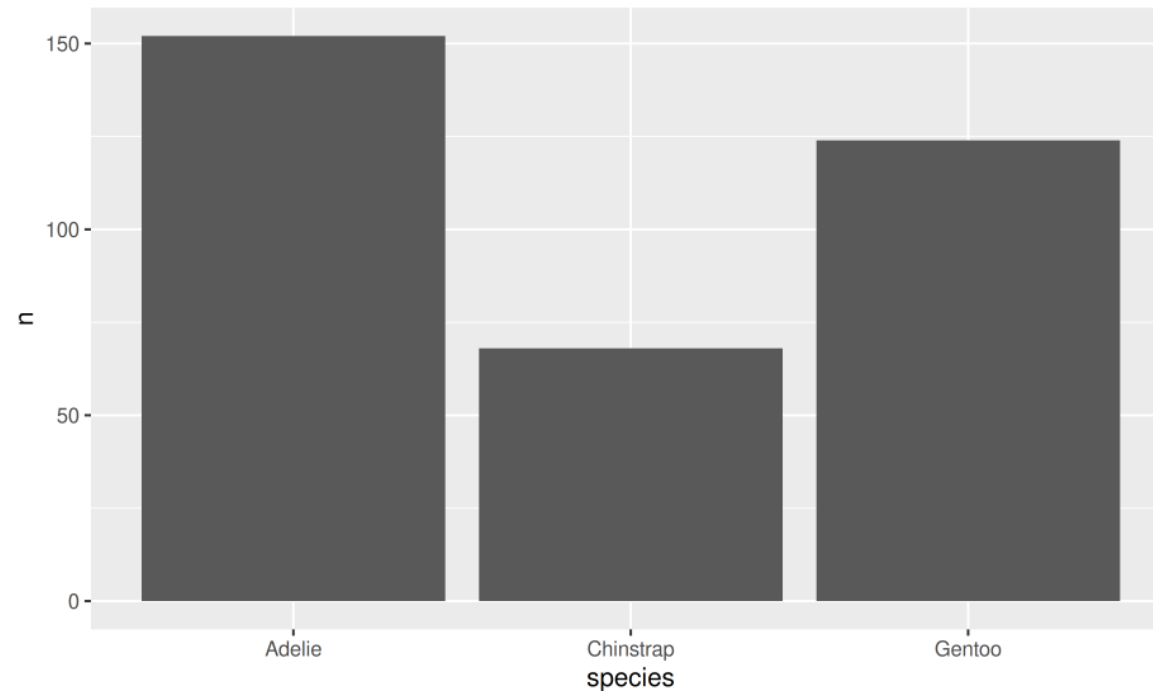
```
1 ggplot(data = penguins, aes(x = sex)) +  
2   geom_bar()
```



Geoms: Barplots

You can also provide the counts

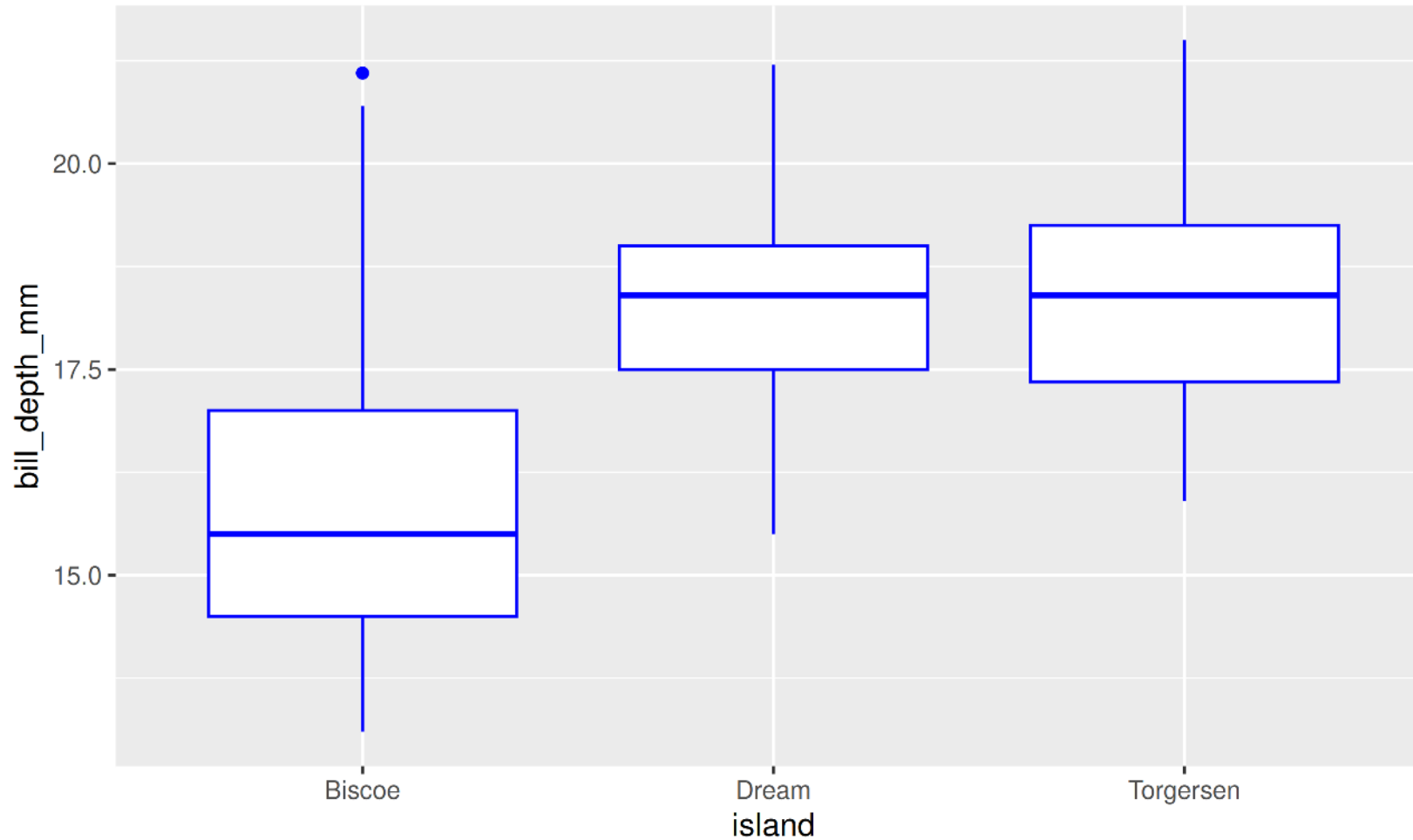
```
1 # Create our own data frame
2 species_counts <- data.frame(species = c("Adelie", "Chinstrap", "Gentoo"),
3                               n = c(152, 68, 124))
4
5 ggplot(data = species_counts, aes(x = species, y = n)) +
6   geom_bar(stat = "identity")
```



Your Turn: Create this plot

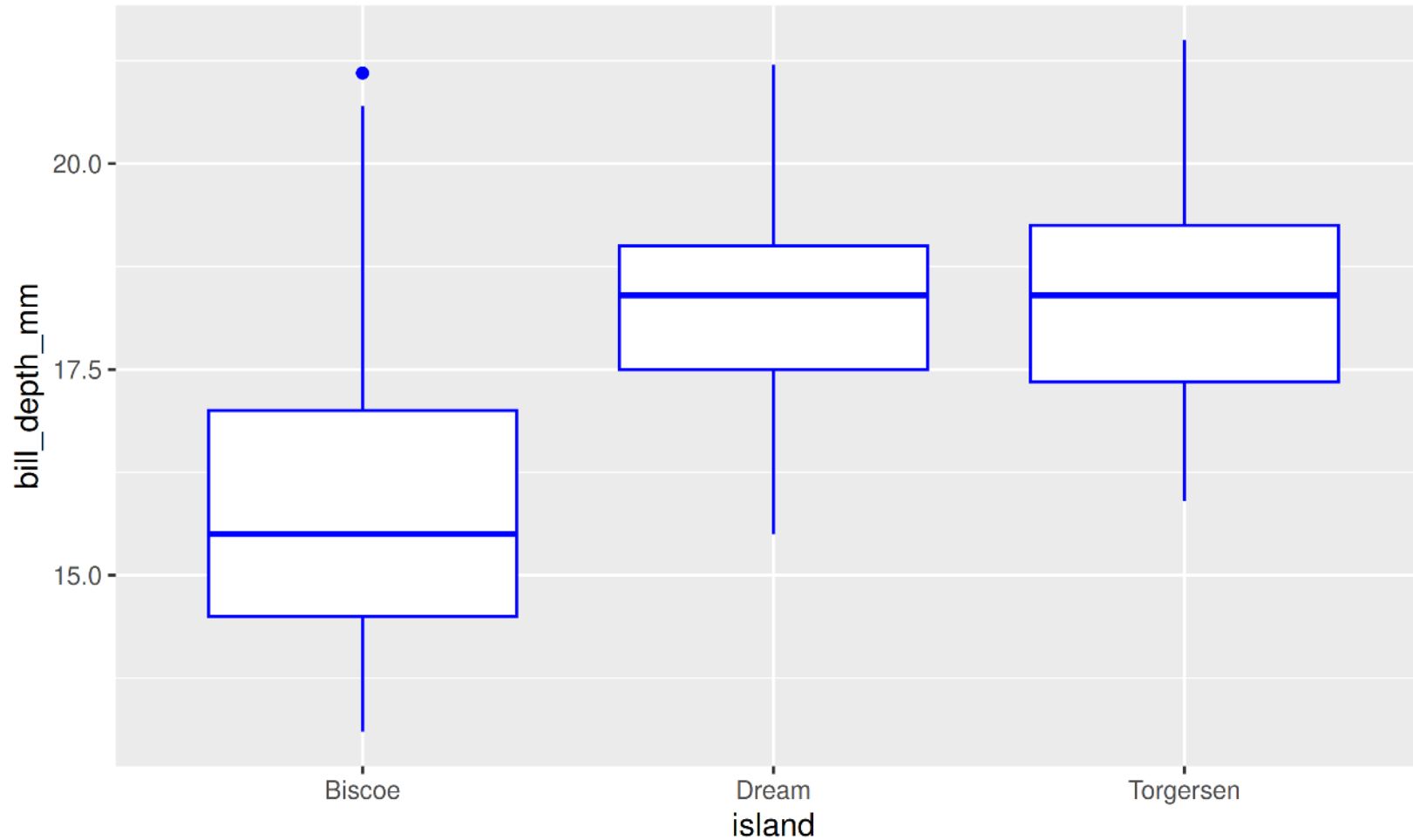
```
1 ggplot(data = ____, aes(x = ____, y = ____)) +  
2   geom____(____)
```

Too Easy?
Plot points on top
Why not consider jittering them?



Your Turn: Create this plot

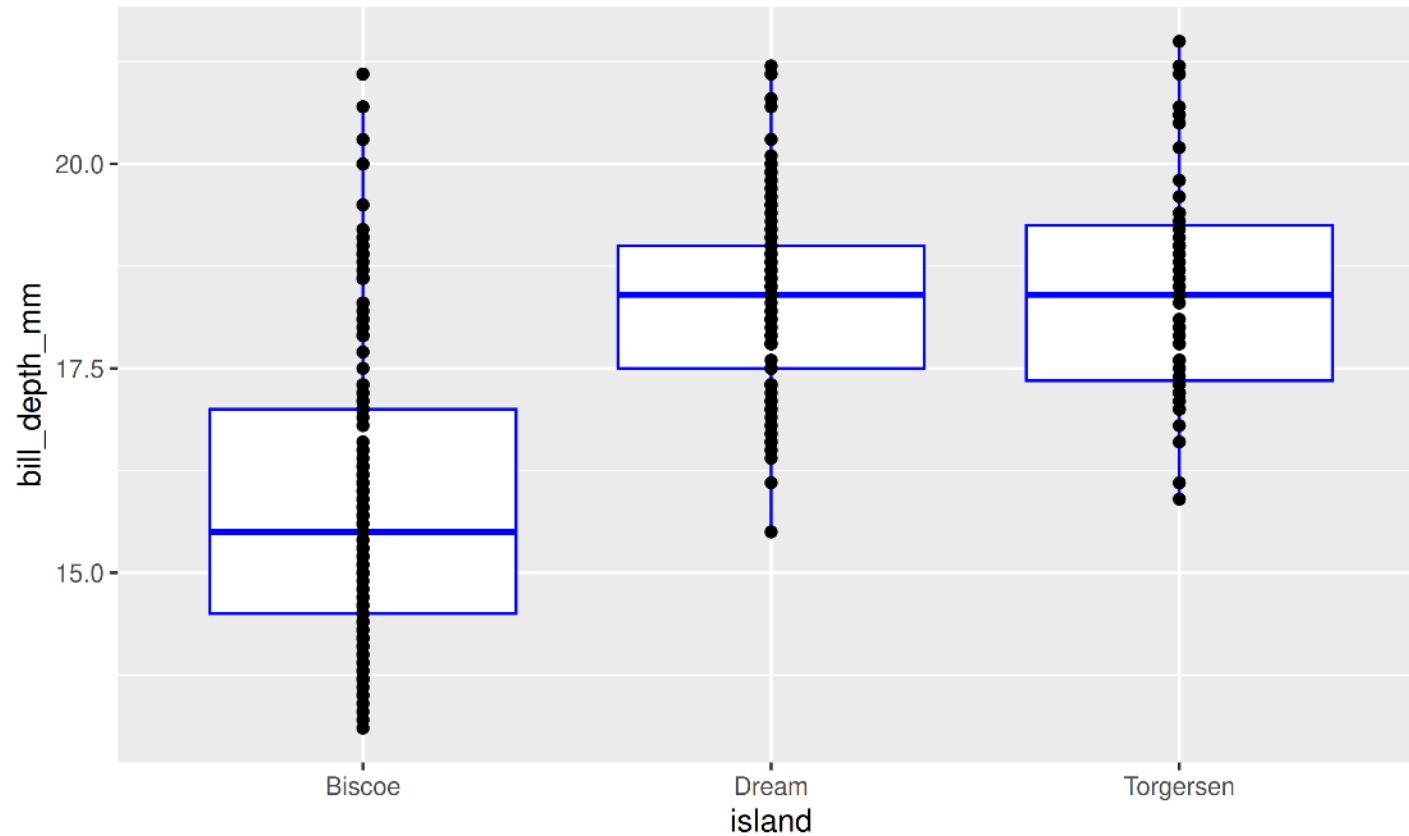
```
1 ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +  
2   geom_boxplot(colour = "blue")
```



Your Turn: Create this plot

Too Easy?

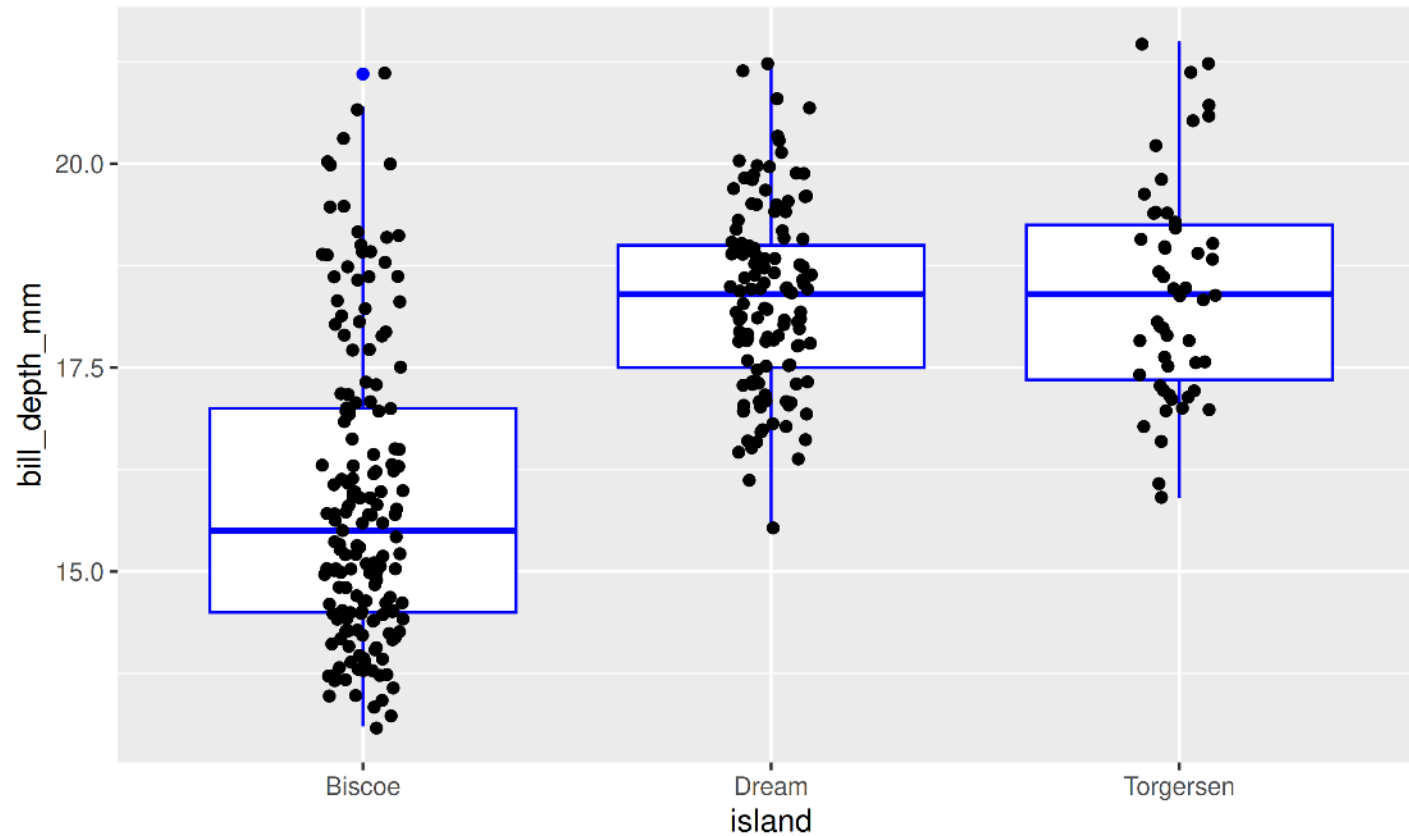
```
1 ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +  
2   geom_boxplot(colour = "blue") +  
3   geom_point()
```



Your Turn: Create this plot

Too Easy?

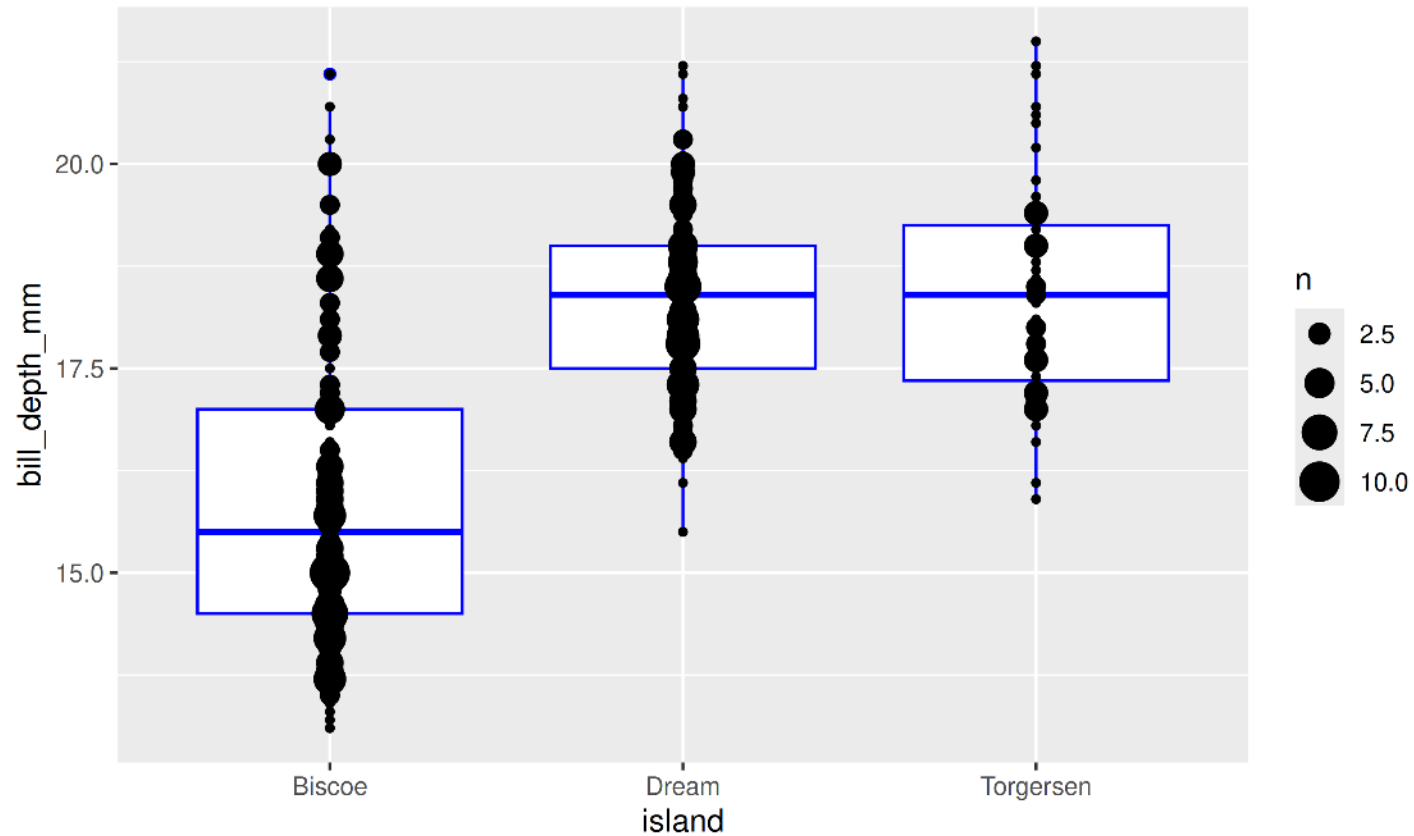
```
1 ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +  
2   geom_boxplot(colour = "blue") +  
3   geom_point(position = position_jitter(width = 0.1))
```



Your Turn: Create this plot

Too Easy?

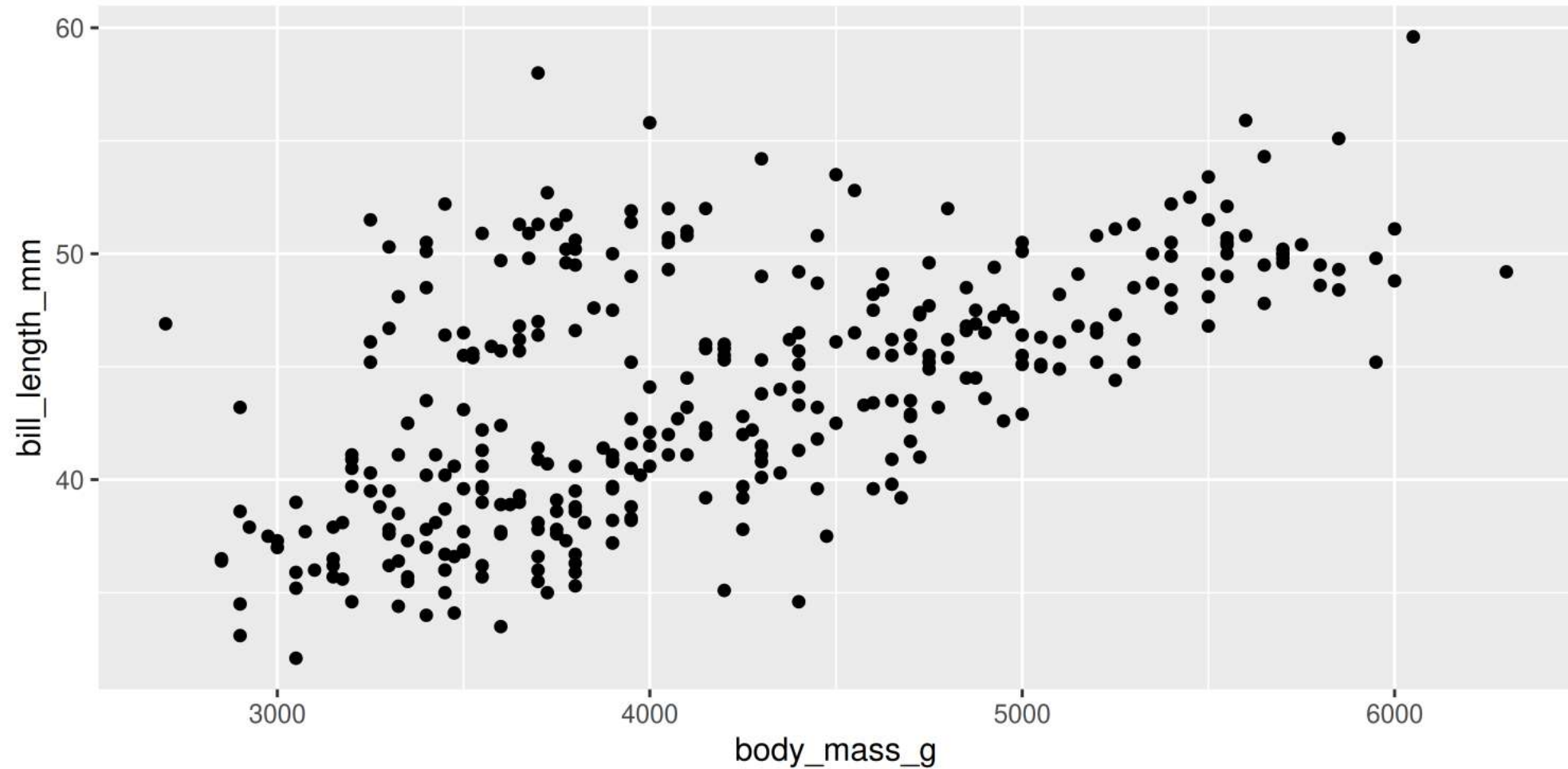
```
1 ggplot(data = penguins, aes(x = island, y = bill_depth_mm)) +  
2   geom_boxplot(colour = "blue") +  
3   geom_count()
```



Showing data by group

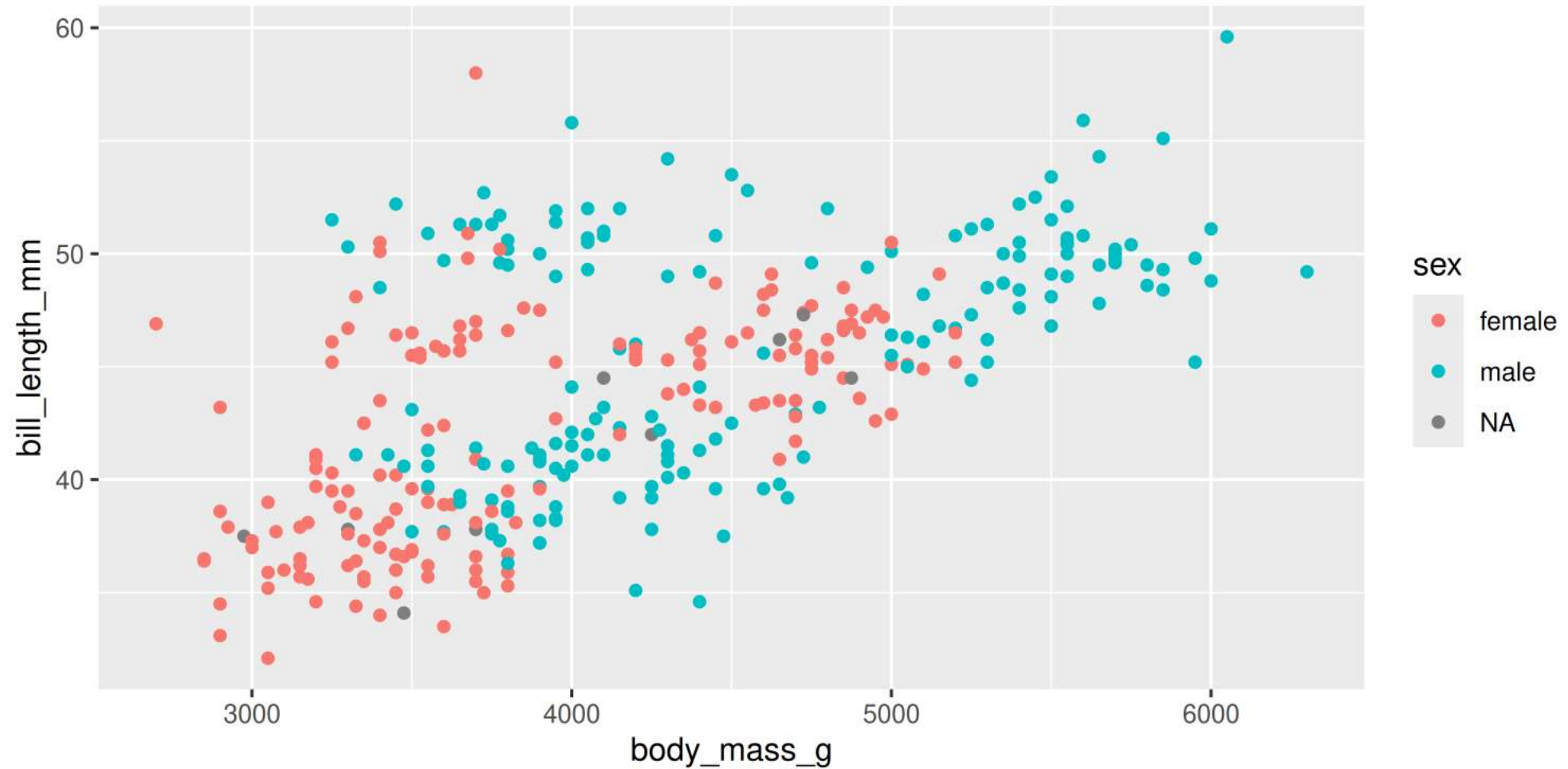
Mapping aesthetics

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



Mapping aesthetics

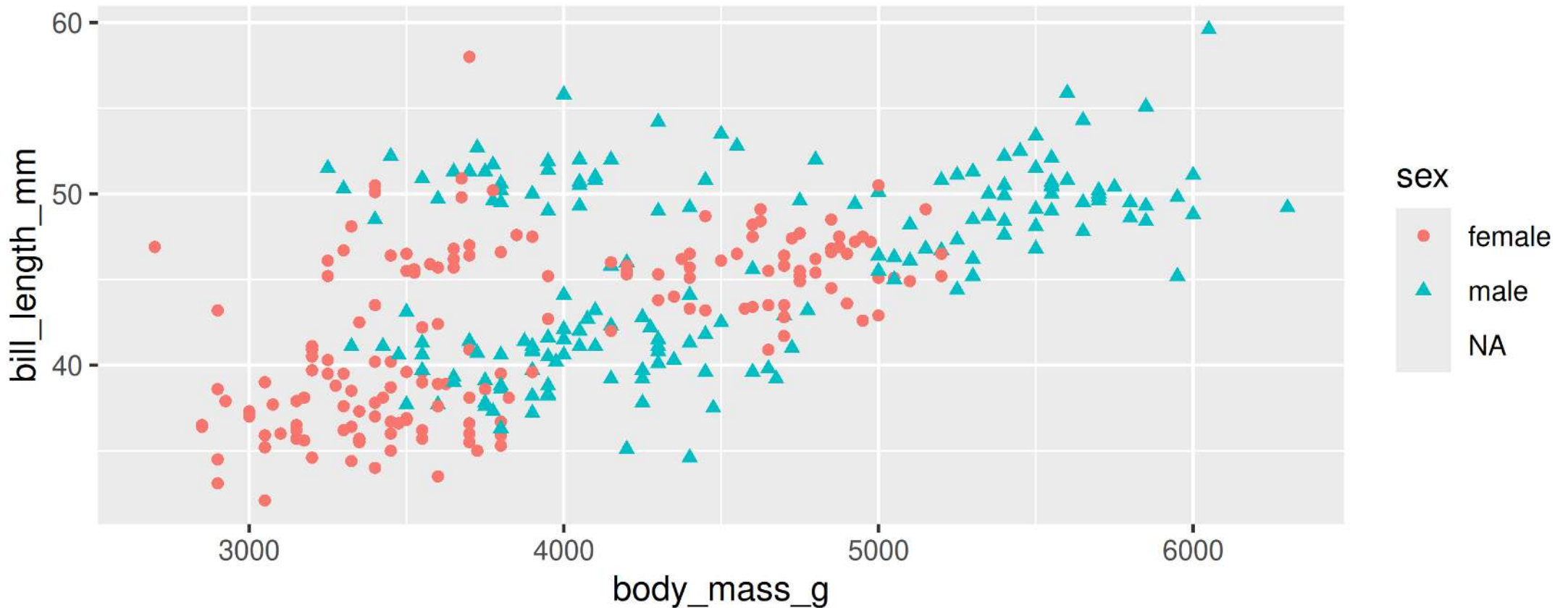
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
2   geom_point()
```



Mapping aesthetics

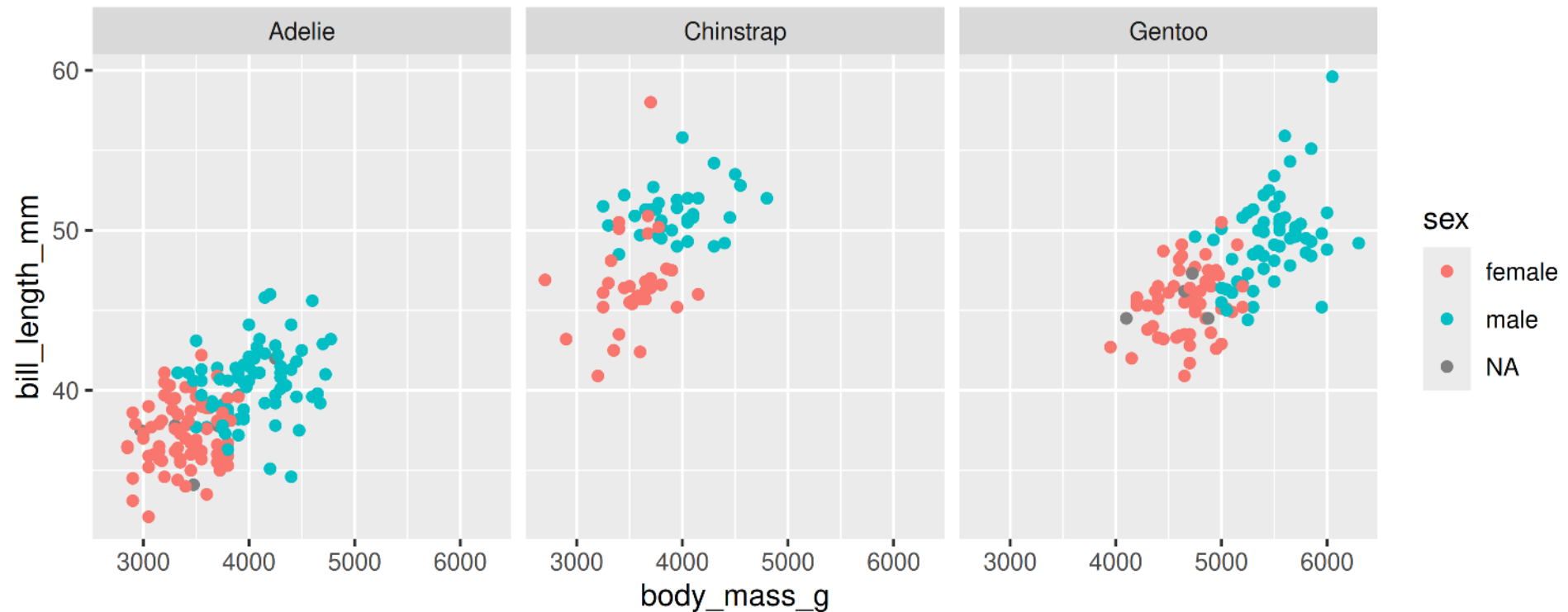
ggplot automatically populates the legends (combining where it can)

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



Faceting: `facet_wrap()`

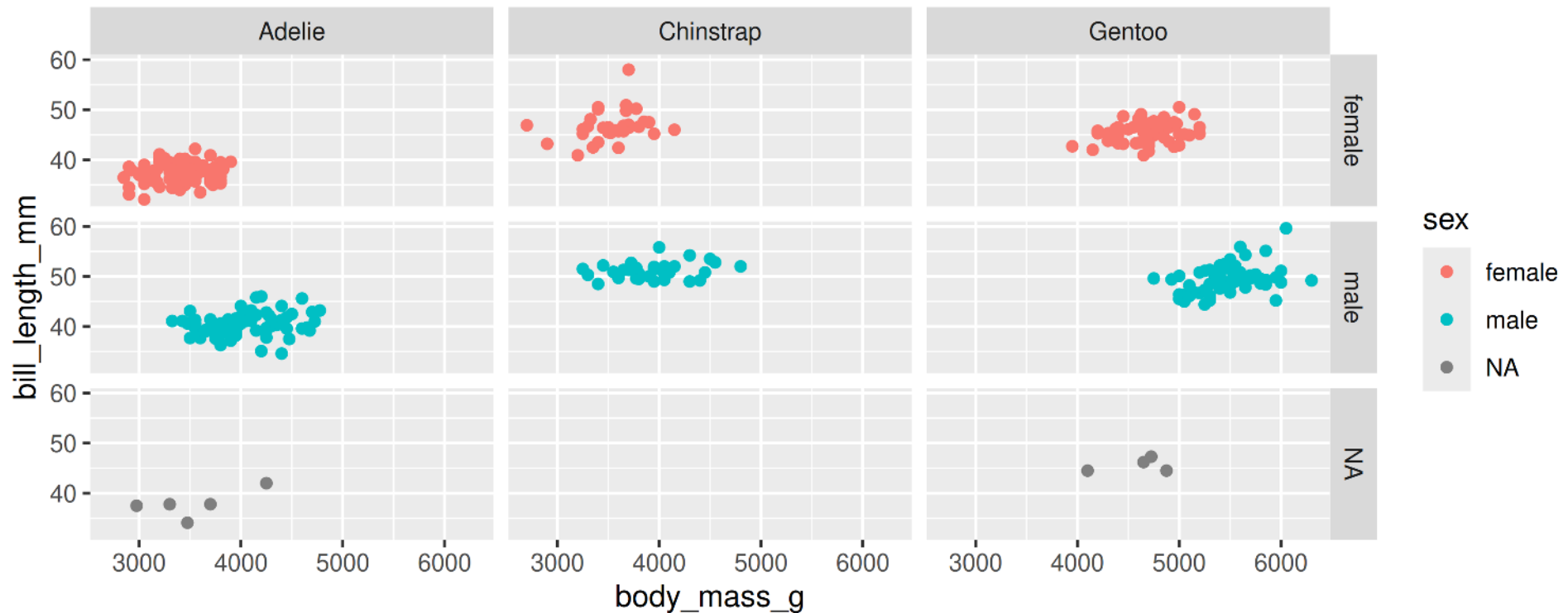
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
2   geom_point() +  
3   facet_wrap(~ species)
```



Split plots by **one** grouping variable

Faceting: facet_grid()

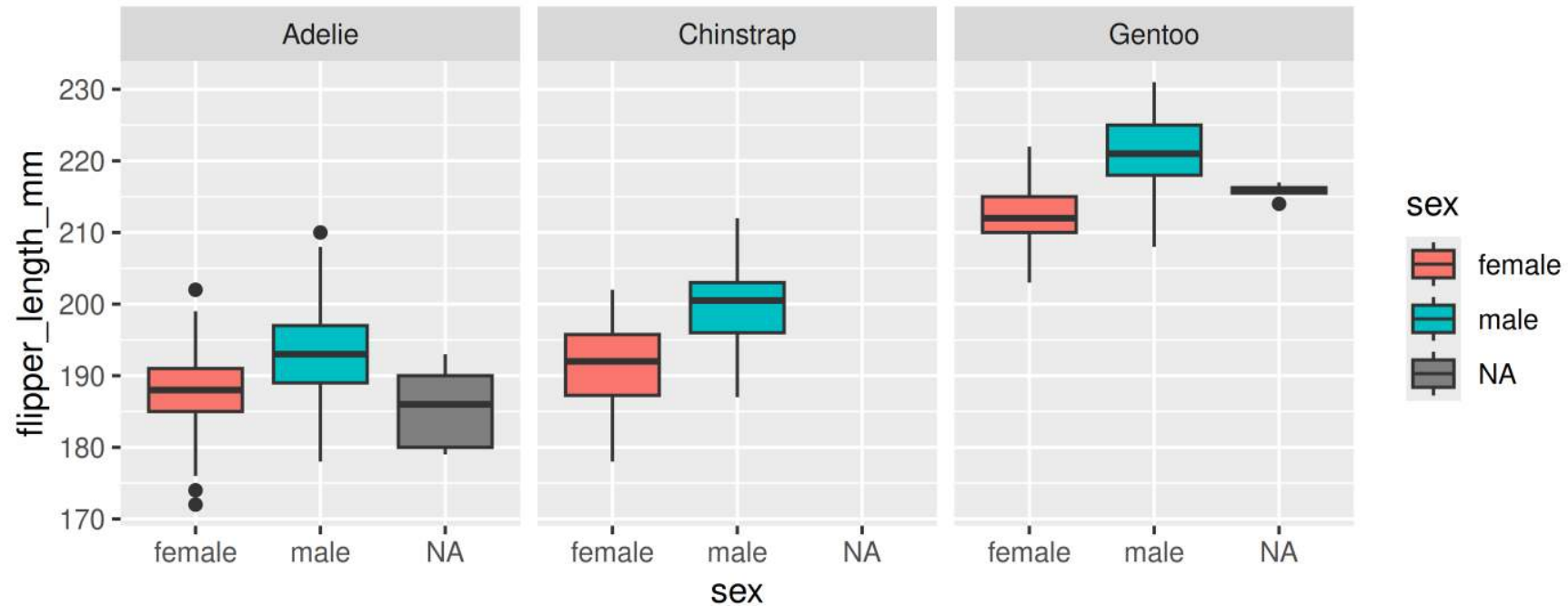
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
2   geom_point() +  
3   facet_grid(sex ~ species)
```



Split plots by **two** grouping variables

Your Turn: Create this plot

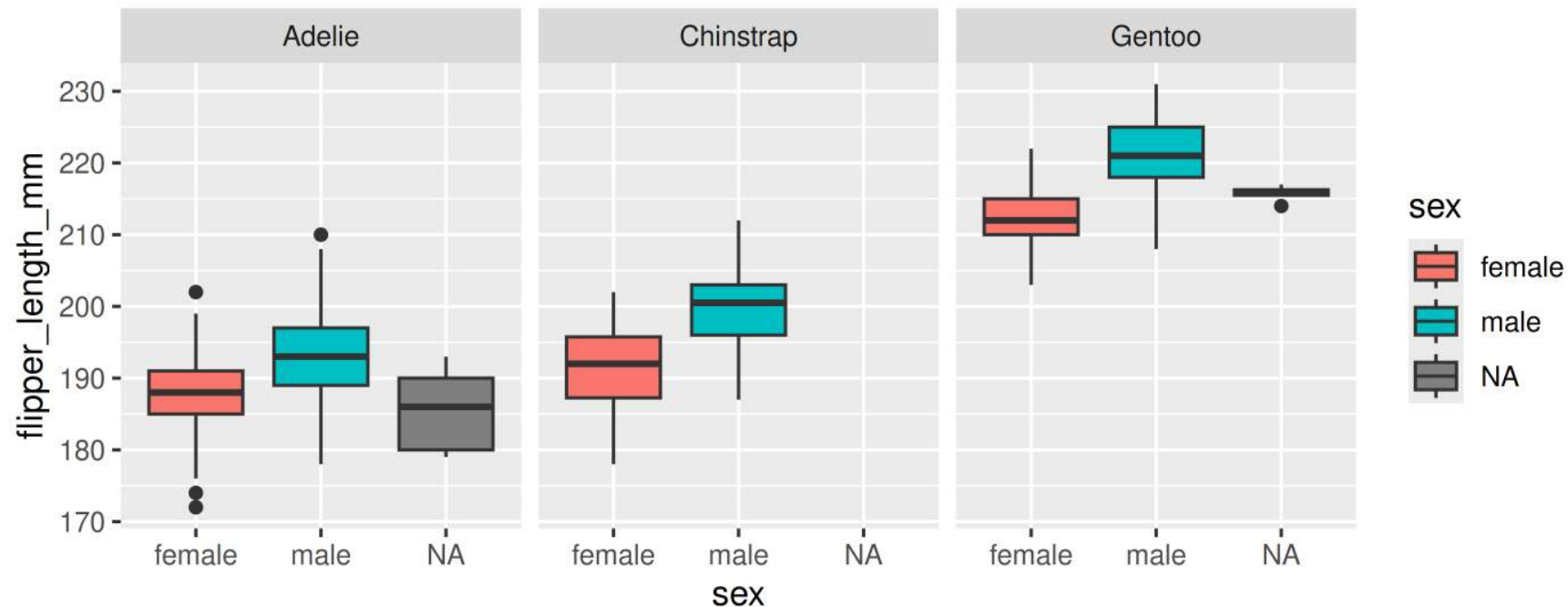
```
1 ggplot(data = _____, aes(_____)) +  
2 _____ +  
3 _____
```



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)
```

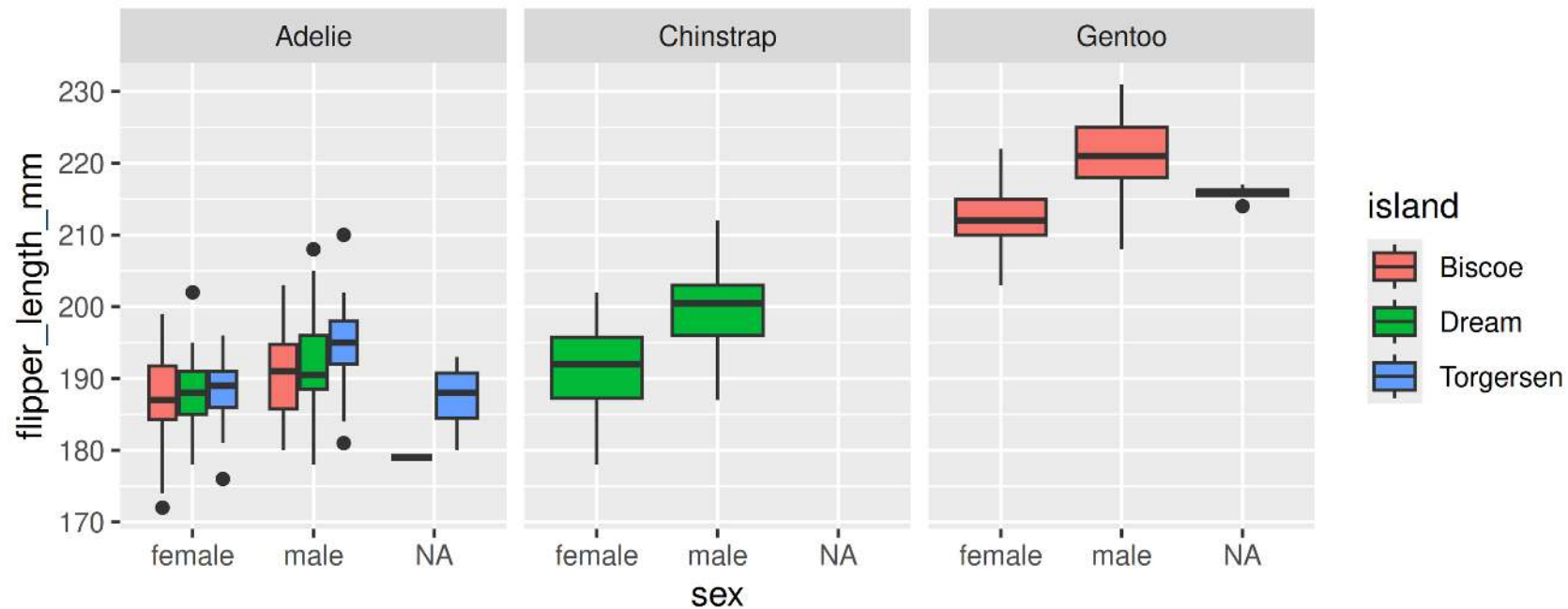


Hint: `colour` is for outlining with a colour, `fill` is for 'filling' with a colour
Too Easy? Split boxplots by sex **and** island

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)
```



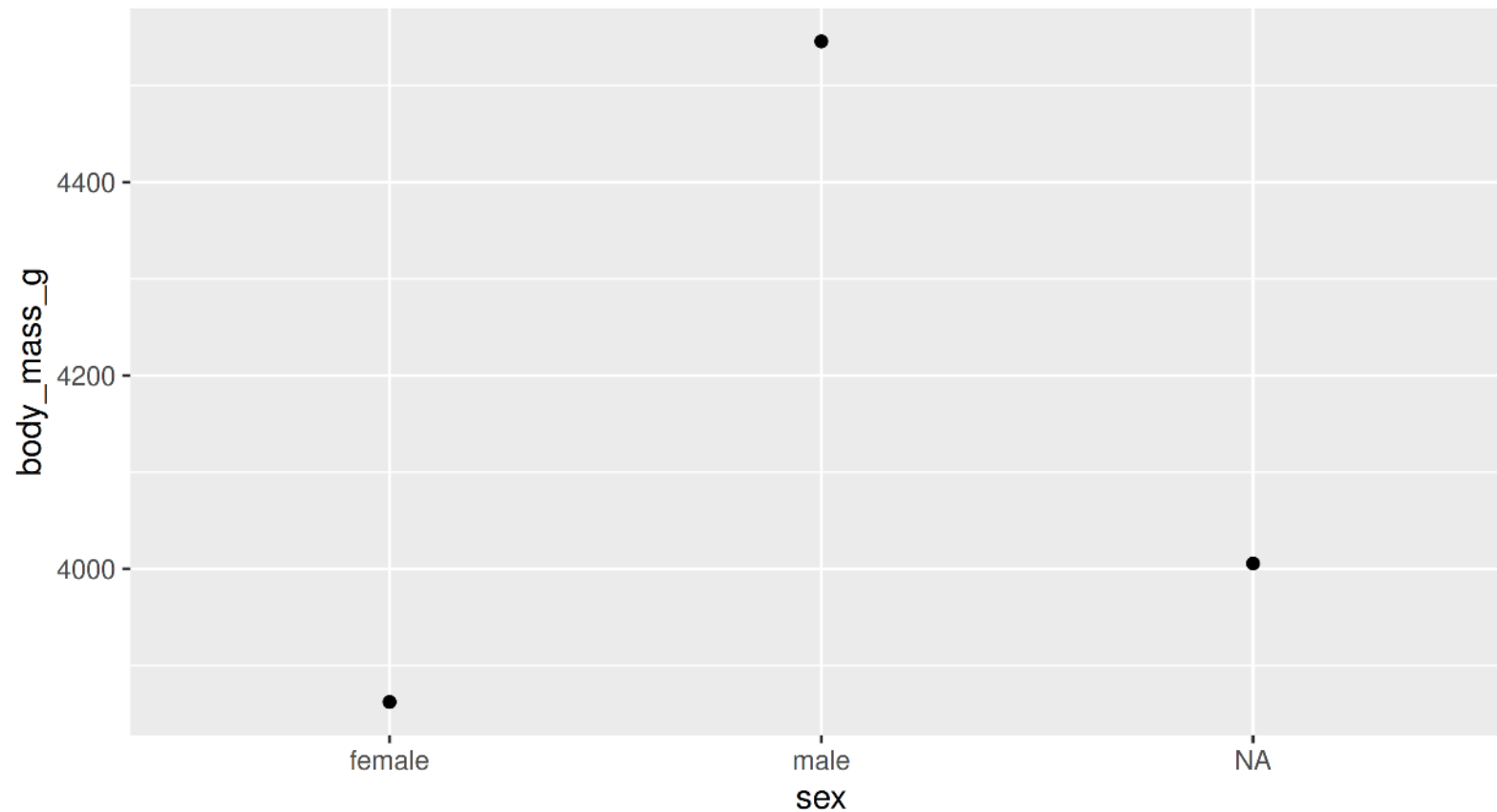
Small change (`fill = sex` to `fill = island`) results in completely different plot

Adding Statistics to Plots

Summarizing data

Add data means as points

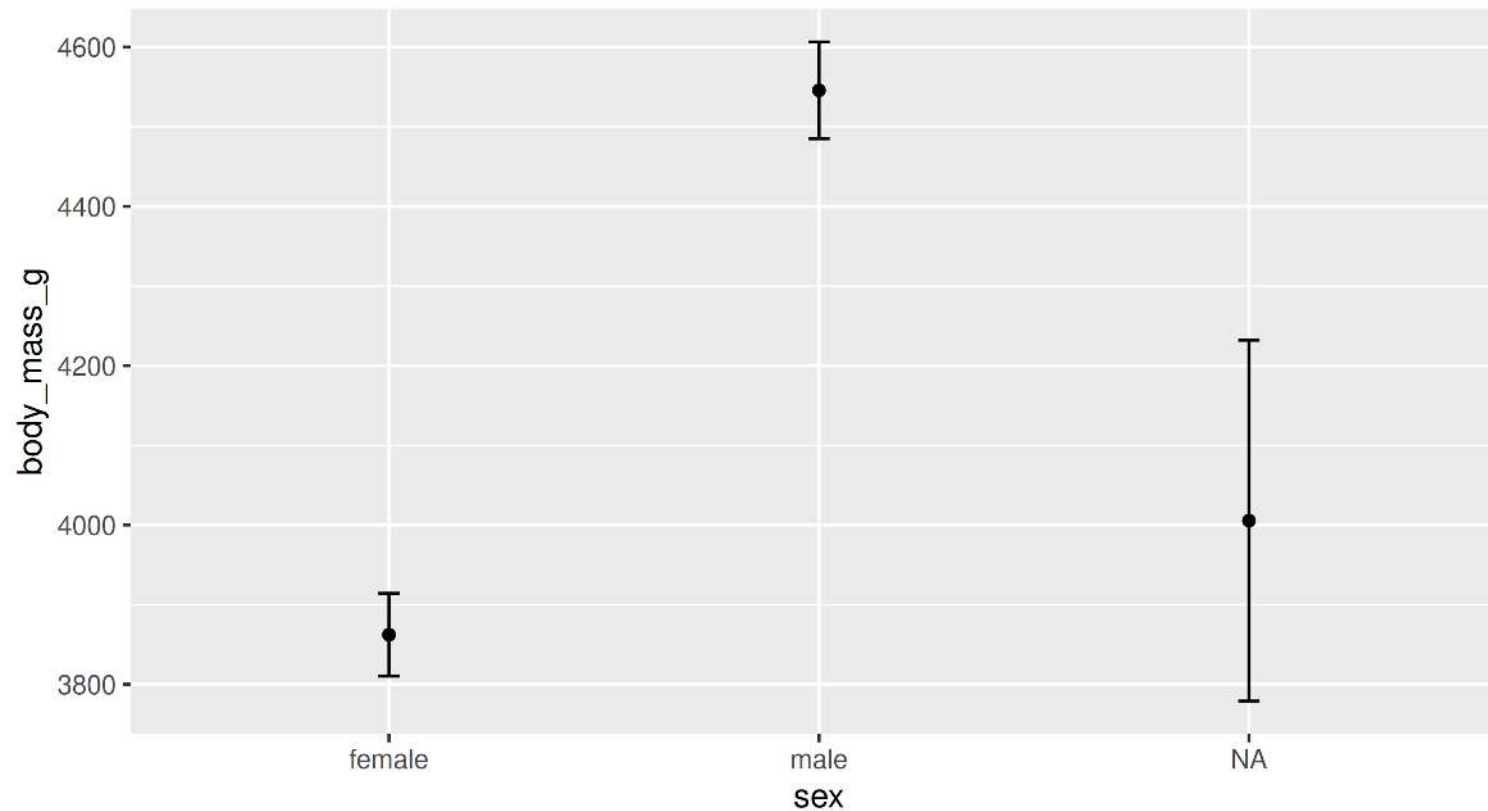
```
1 ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
2   stat_summary(geom = "point", fun = mean)
```



Summarizing data

Add error bars, calculated from the data

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

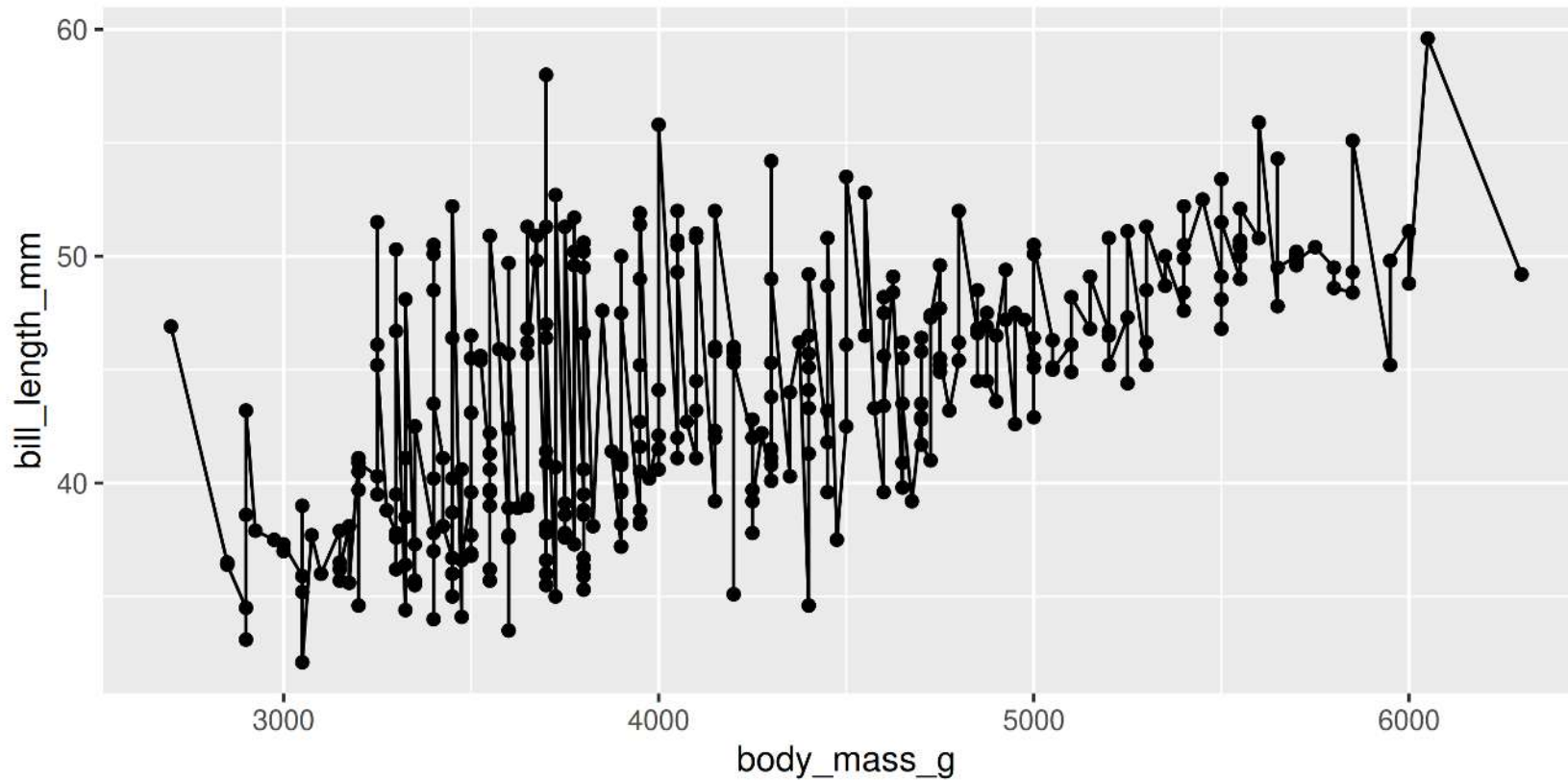


Trendlines / Regression Lines

Trendlines / Regression lines

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

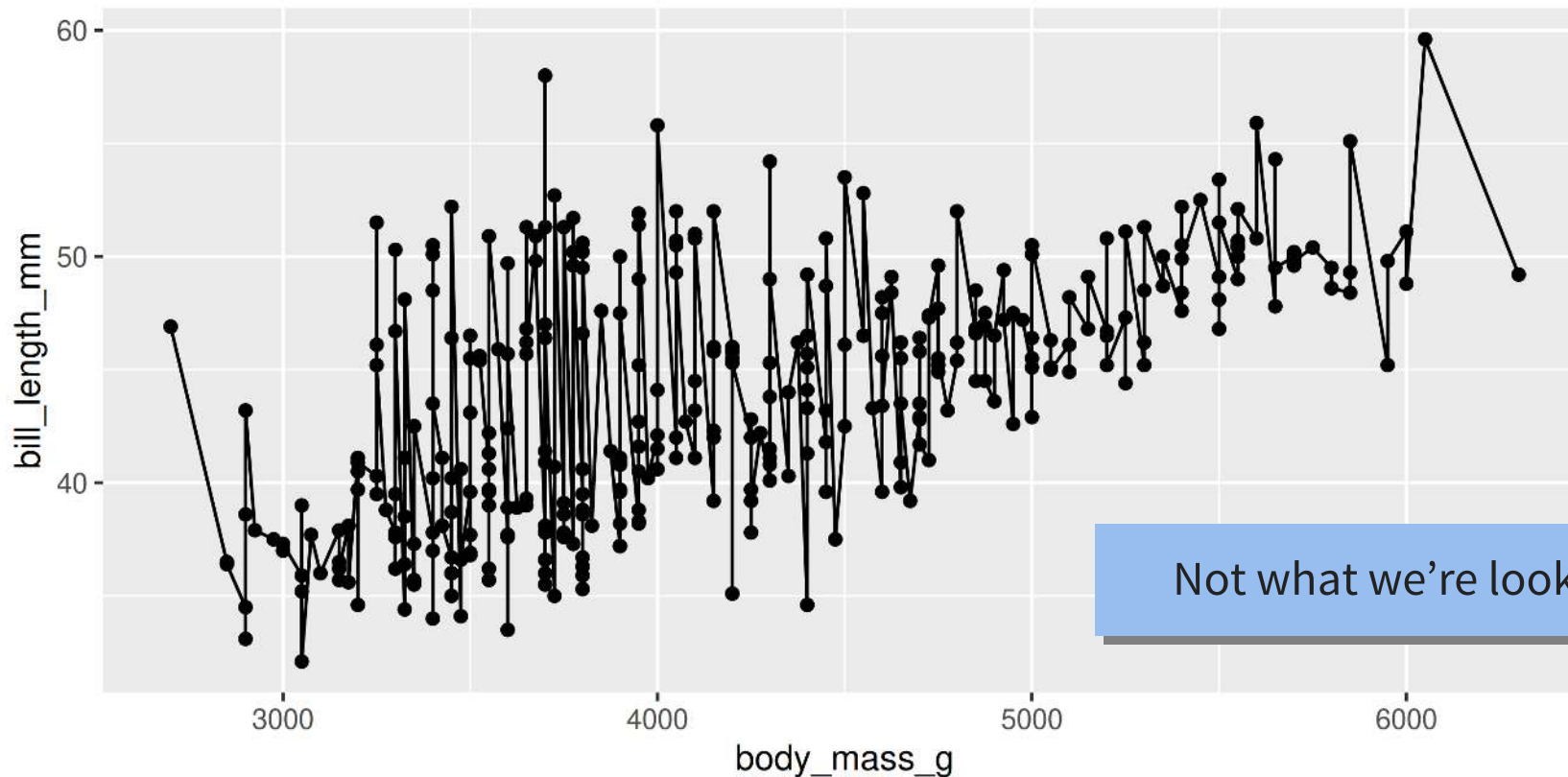
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +  
2   geom_point() +  
3   geom_line()
```



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()
```



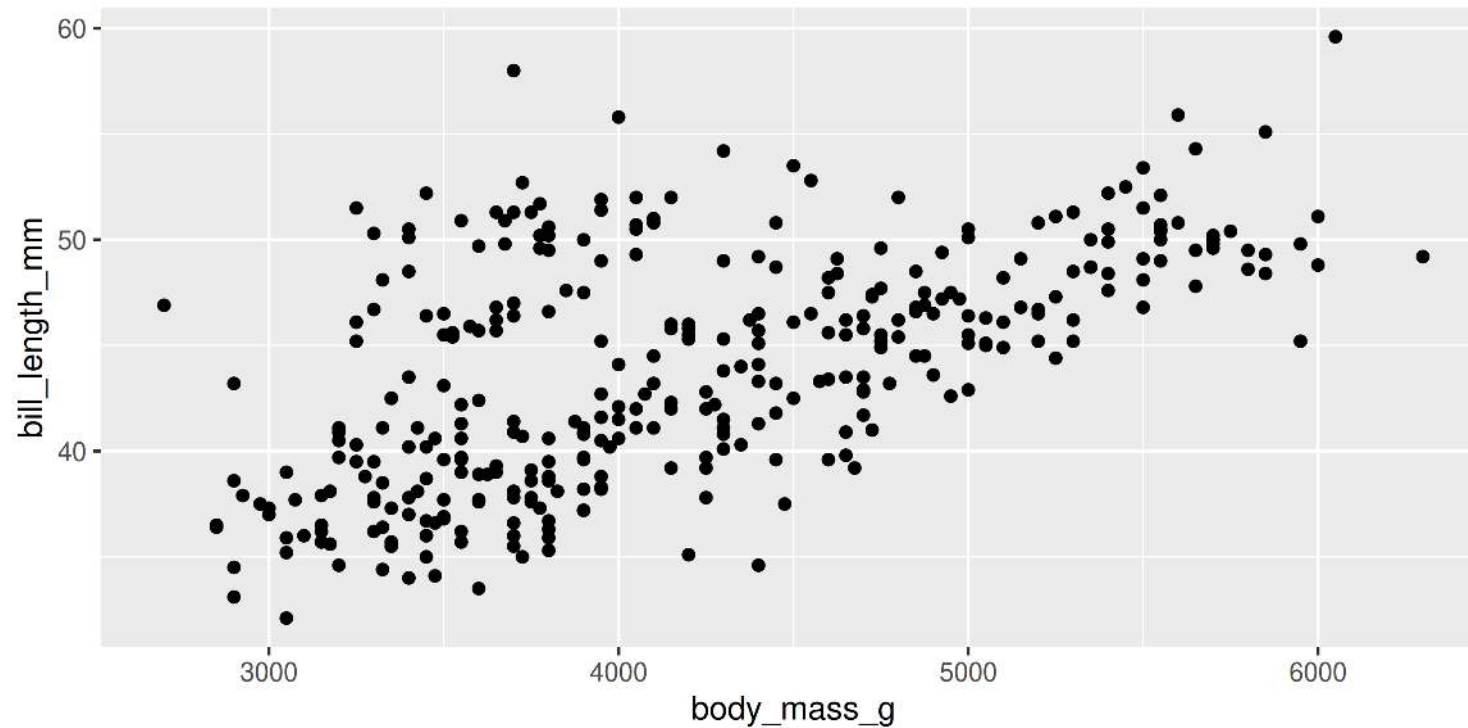
Not what we're looking for

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
```

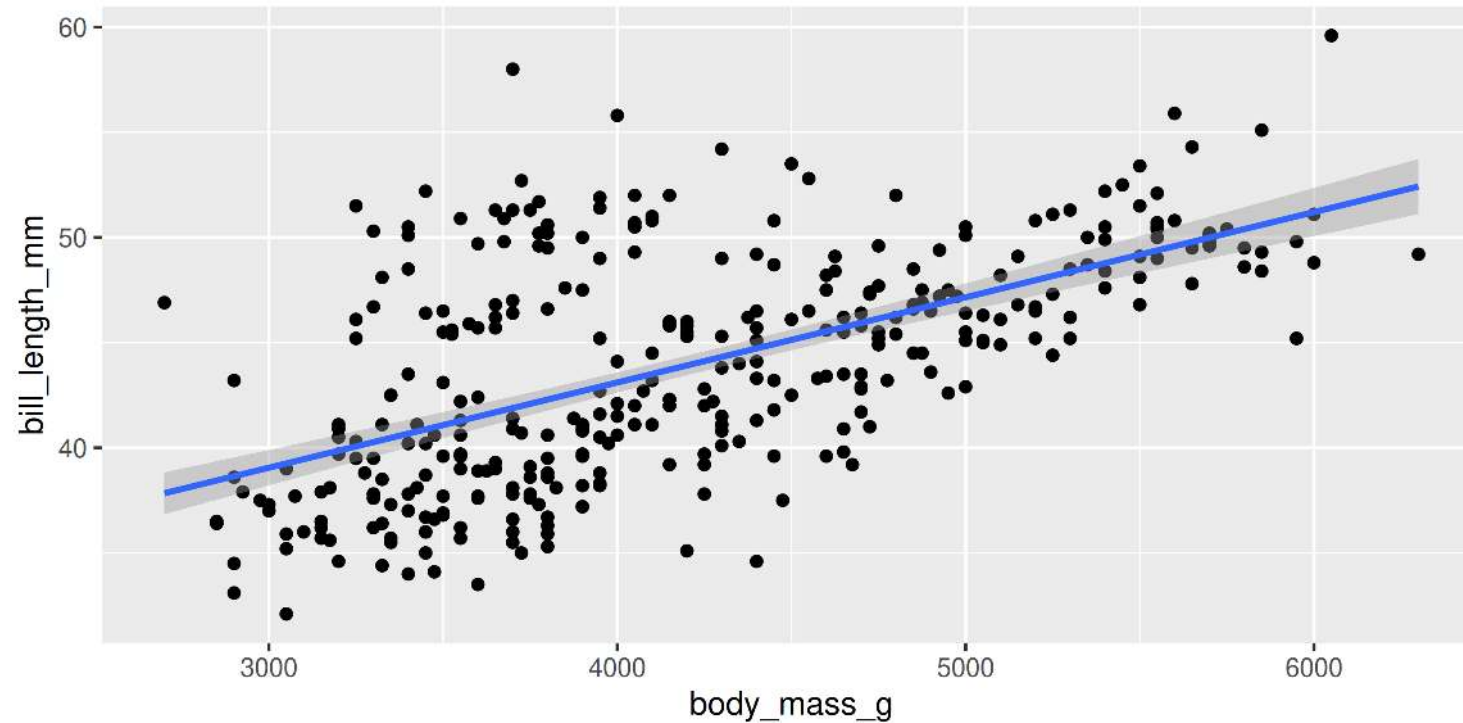


Trendlines / Regression lines

Add the `stat_smooth()`

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

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

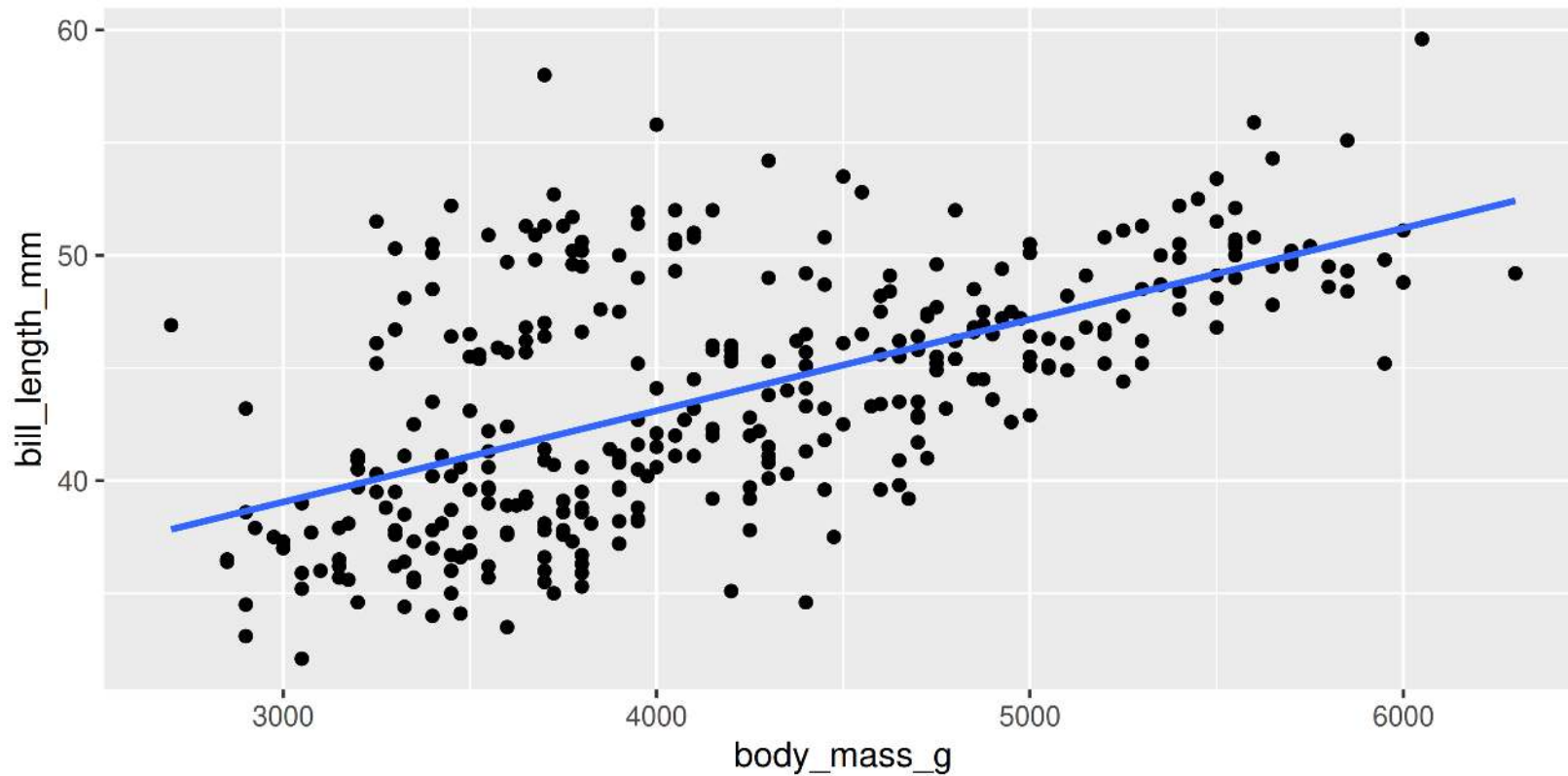


Trendlines / Regression lines

Add the `stat_smooth()`

- remove the grey ribbon `se = FALSE`

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

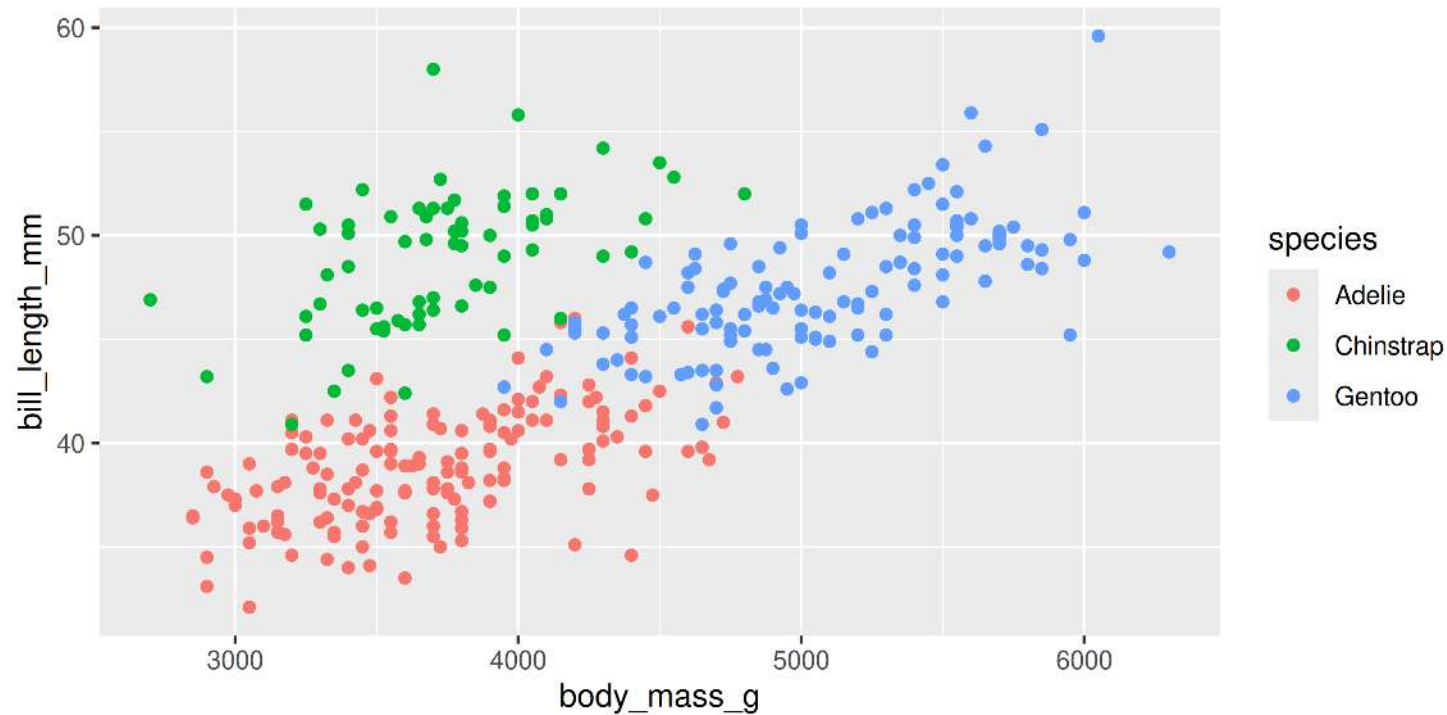


Trendlines / Regression lines

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
```

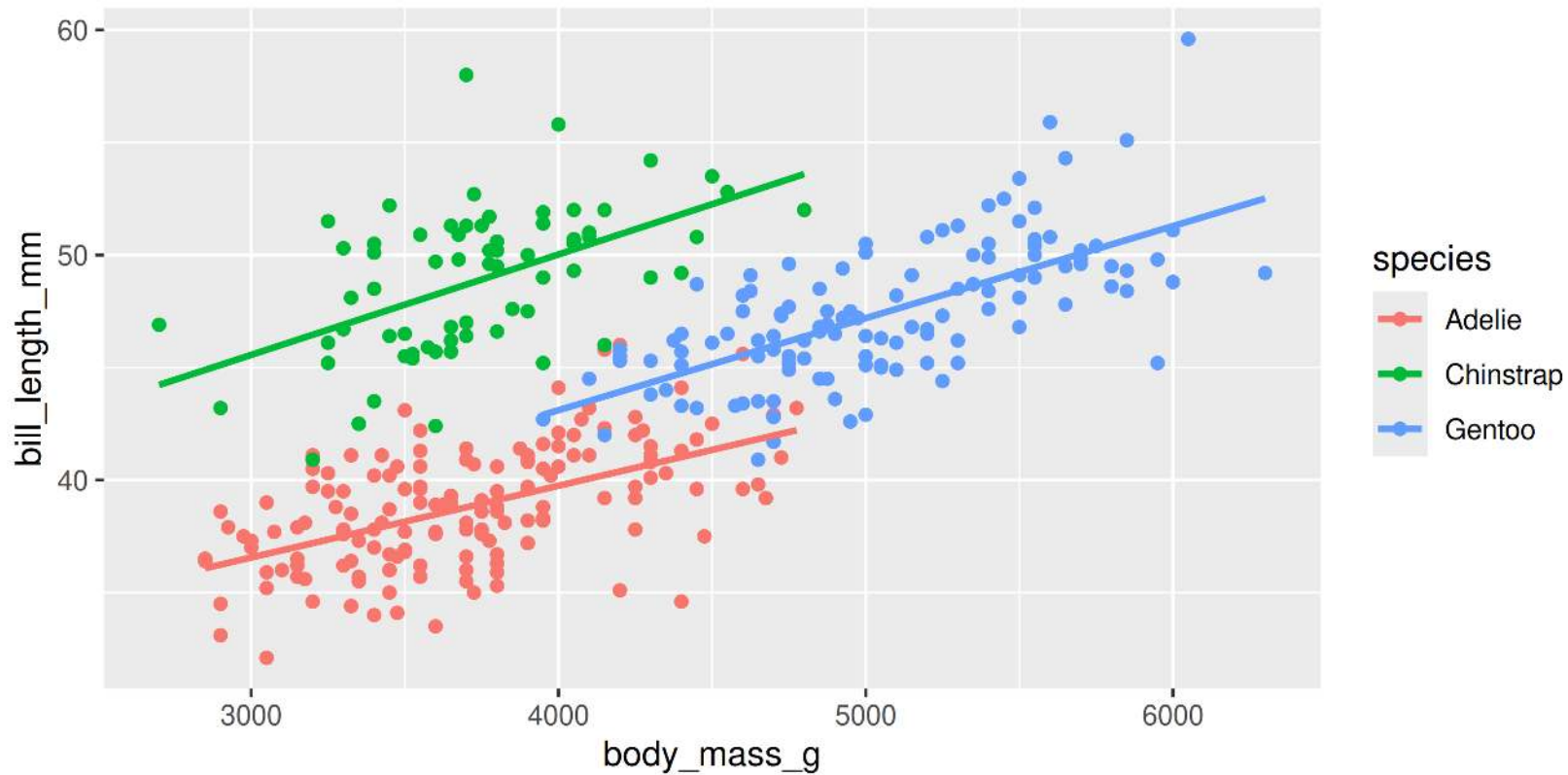


Trendlines / Regression lines

A line for each group

- `stat_smooth()` automatically uses the same grouping

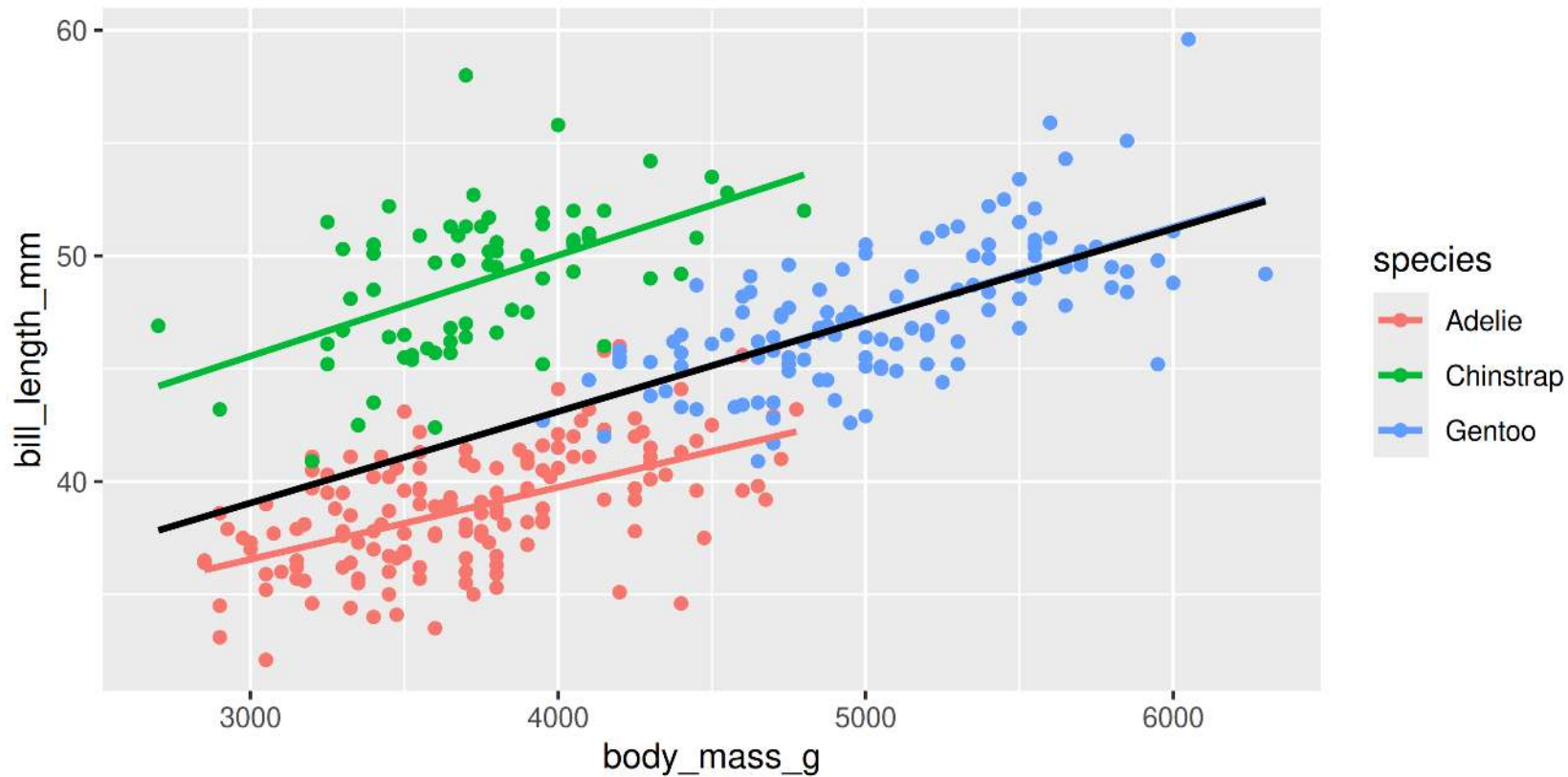
```
1 g + stat_smooth(method = "lm", se = FALSE)
```



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? Add regression lines for each species as well

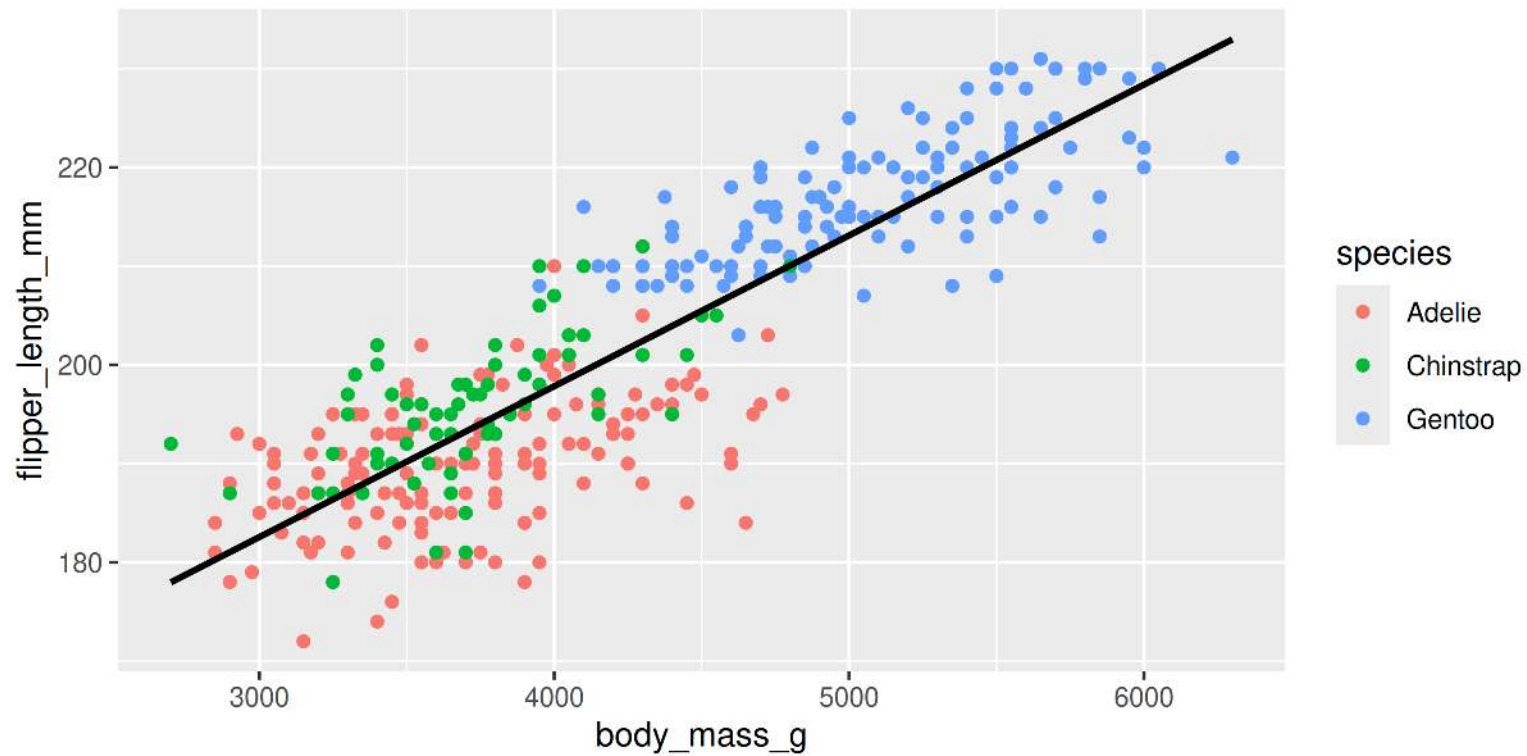
Can you make the species lines larger?

Can you indicate which points are female and which are male?

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*

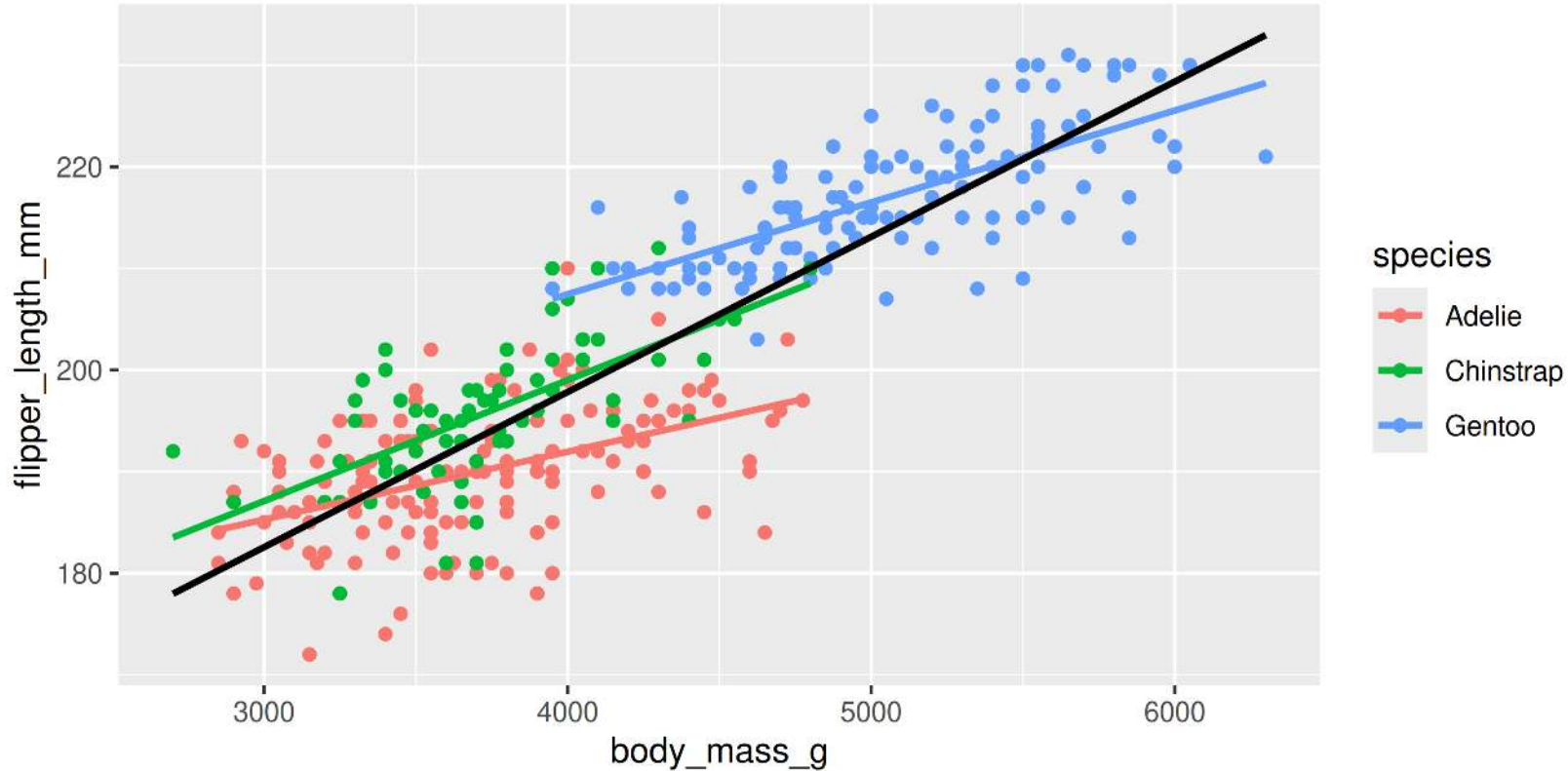
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
2   geom_point() +  
3   stat_smooth(method = "lm", se = FALSE, colour = "black")
```



Your Turn: Create this plot

Too Easy?

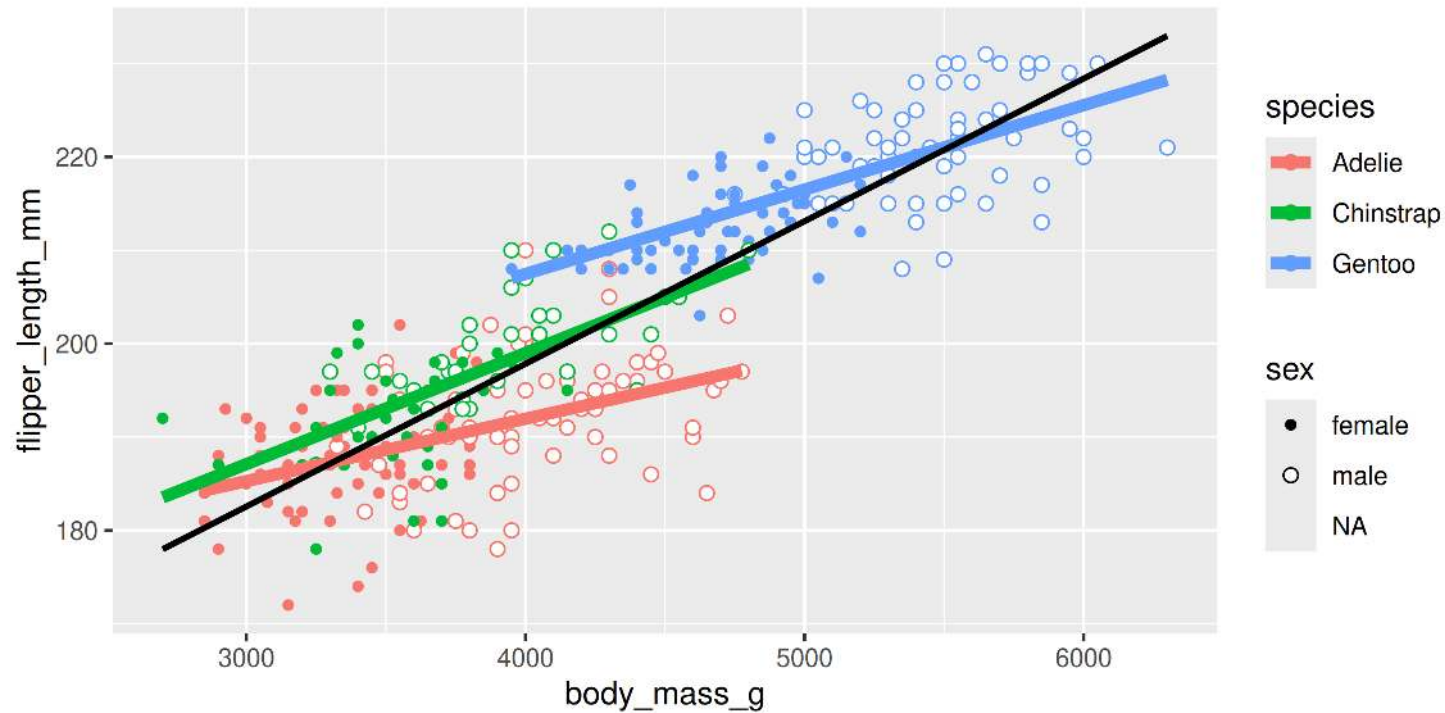
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
2   geom_point() +  
3   stat_smooth(method = "lm", se = FALSE) +  
4   stat_smooth(method = "lm", se = FALSE, colour = "black")
```



Your Turn: Create this plot

Too Easy?

```
1 ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm,  
2                             colour = species)) +  
3   geom_point(aes(shape = sex), size = 2, fill = "white") +  
4   stat_smooth(method = "lm", se = FALSE, linewidth = 2) +  
5   stat_smooth(method = "lm", se = FALSE, colour = "black") +  
6   scale_shape_manual(values = c(20, 21))
```

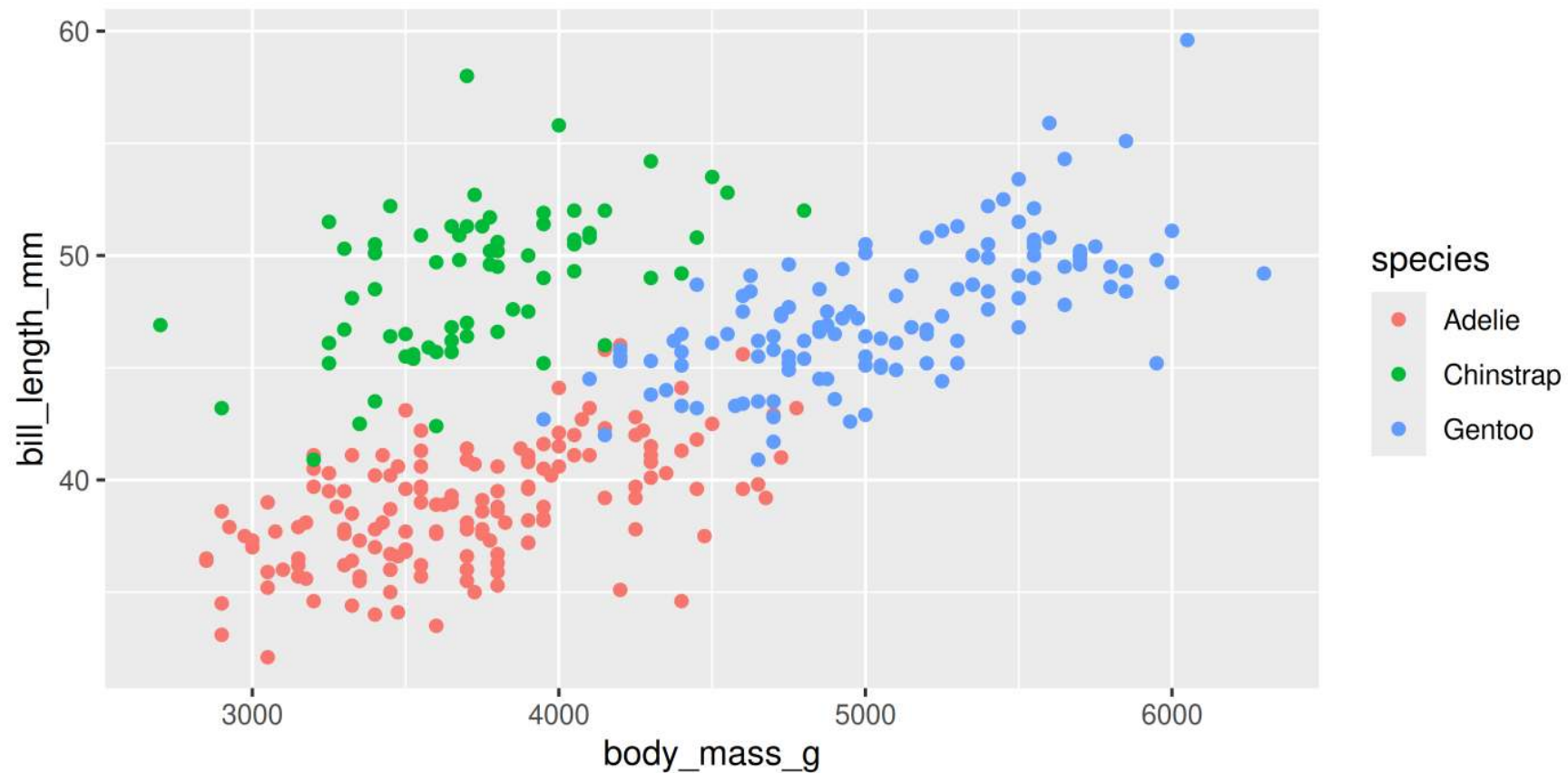


Customizing plots

Customizing: Starting plot

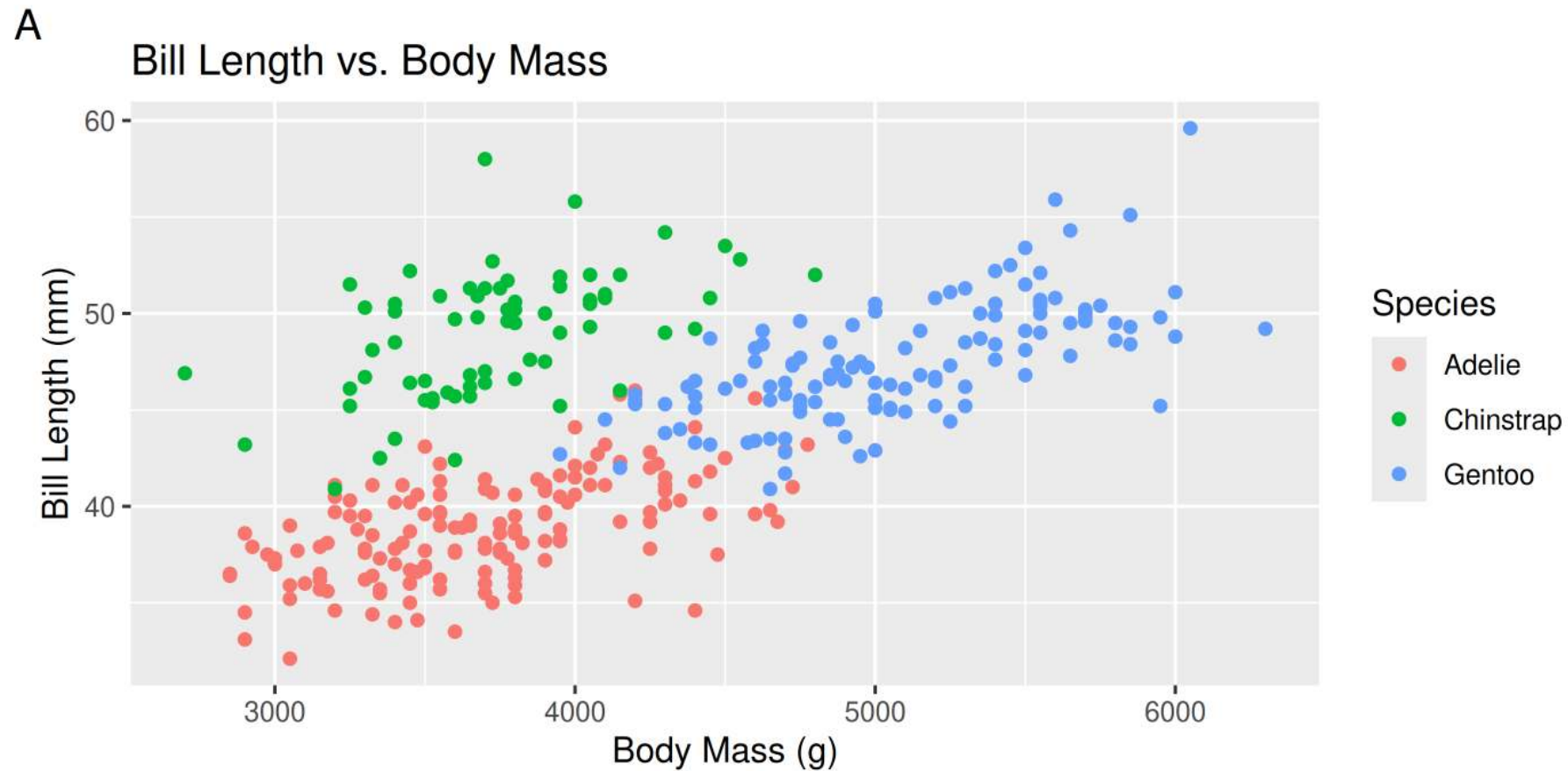
Let's work with this plot

```
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")
```

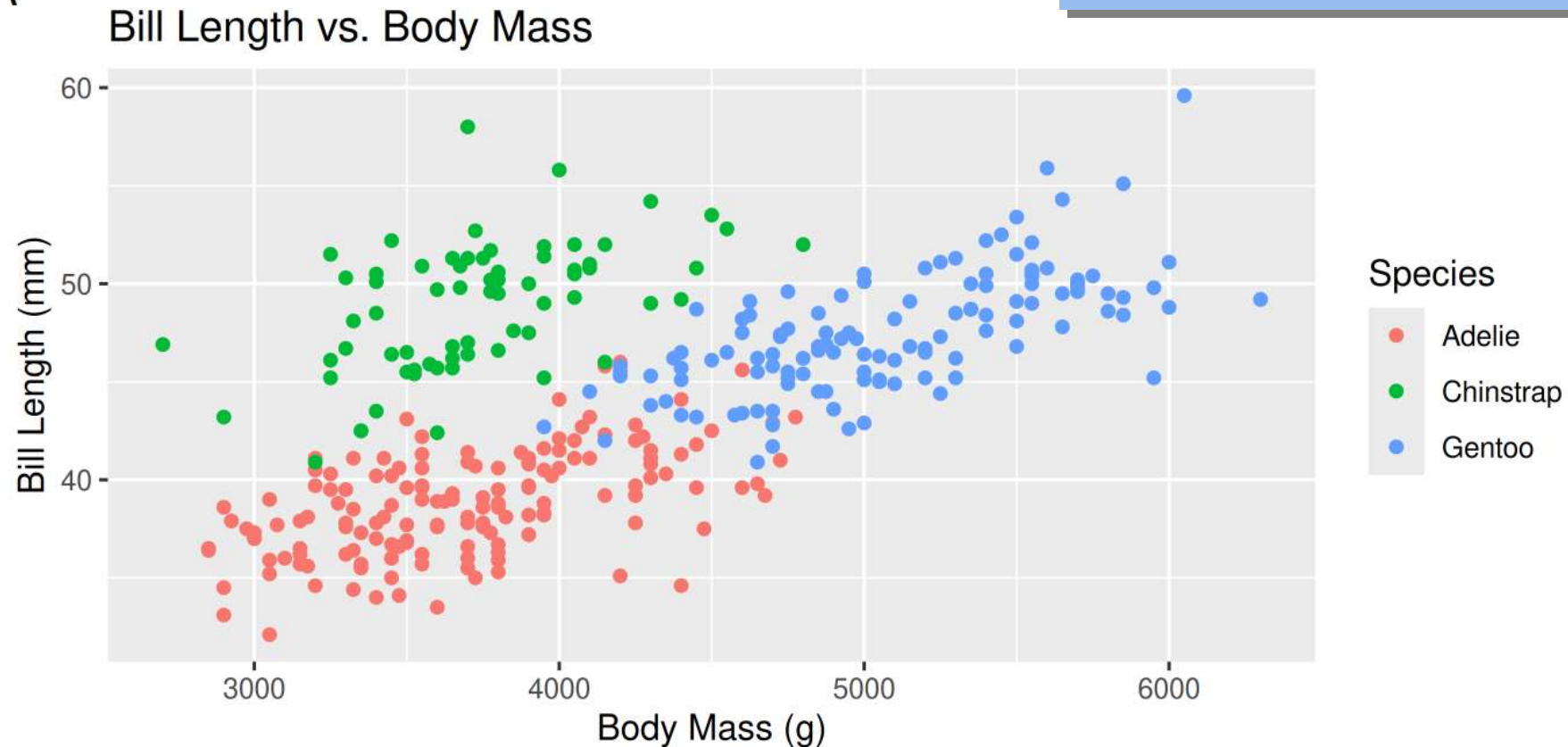


Customizing: Labels

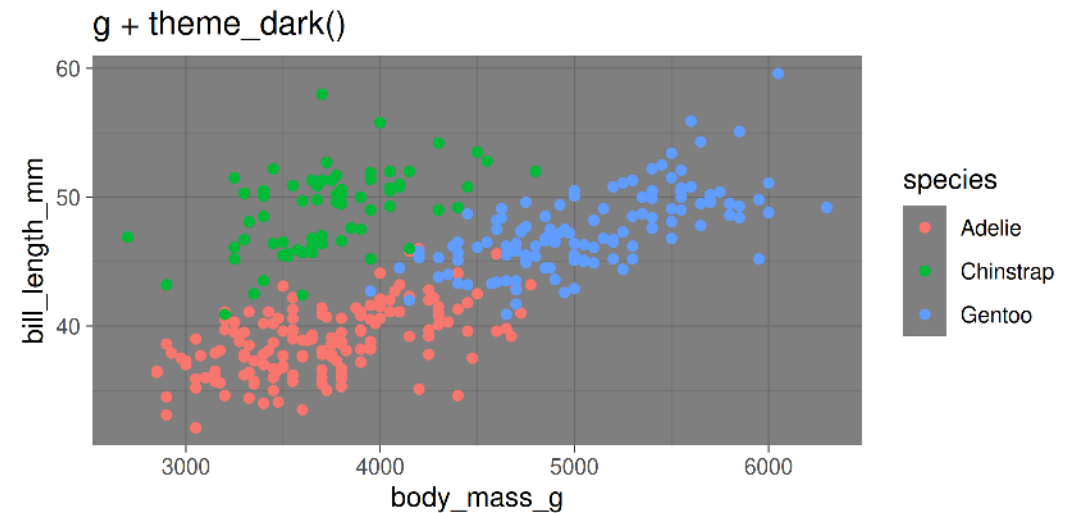
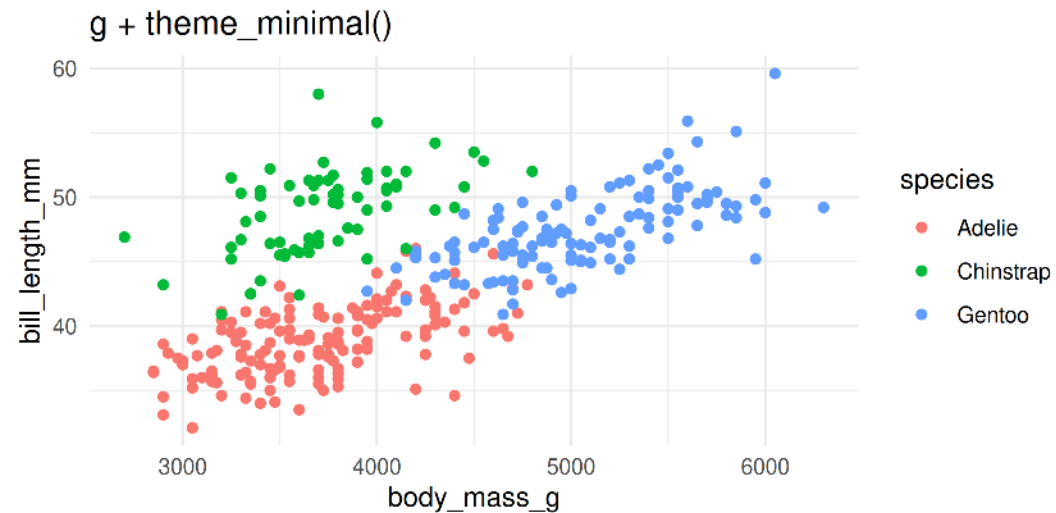
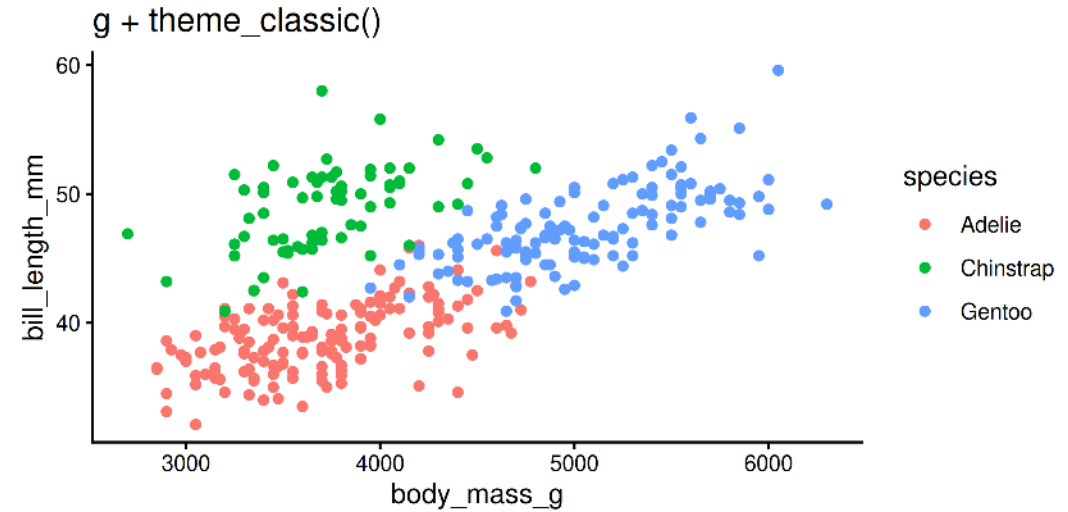
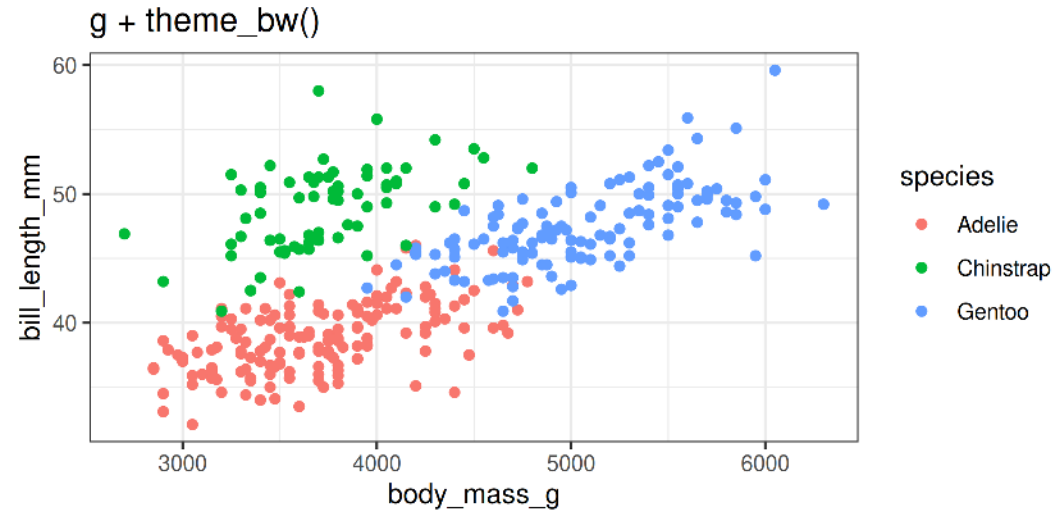
```
1 g + labs(title = "Bill Length vs. Body Mass",  
2           x = "Body Mass (g)",  
3           y = "Bill Length (mm)",  
4           colour = "Species", tag = "A")
```

Your Turn: Add proper labels to some of your previous plots

A



Customizing: Built-in themes



Customizing: Axes

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

- `scale_x_continuous()`
- `scale_y_discrete()`
- etc.

Common arguments

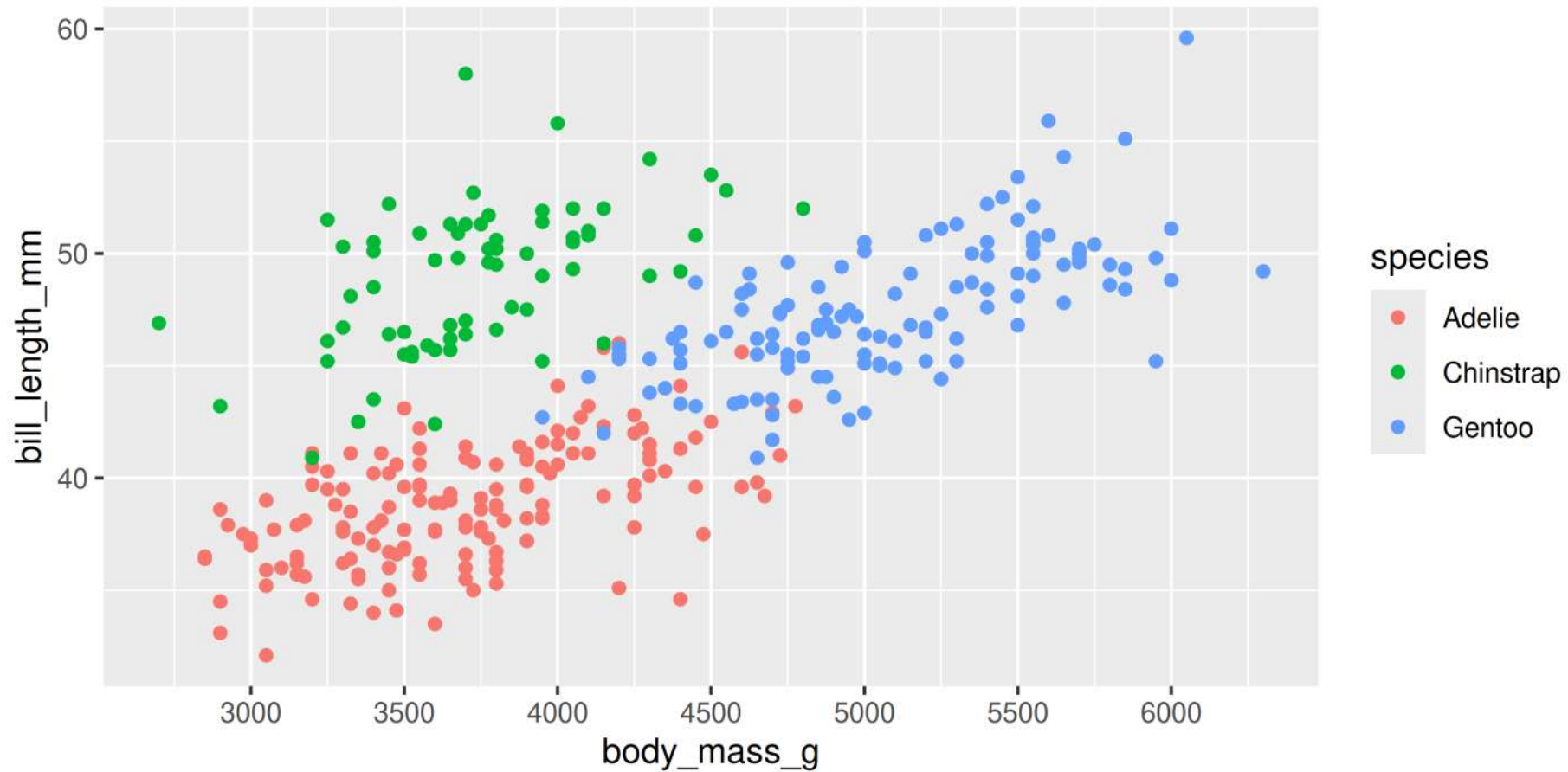
```
1 g + scale_x_continuous(breaks = seq(0, 20, 10)) # Tick breaks
2 g + scale_x_continuous(limits = c(0, 15))      # xlim() is a shortcut for this
3 g + scale_x_continuous(expand = c(0, 0))       # Space between axis and data
```

Let's take a look...

Customizing: Axes

Breaks

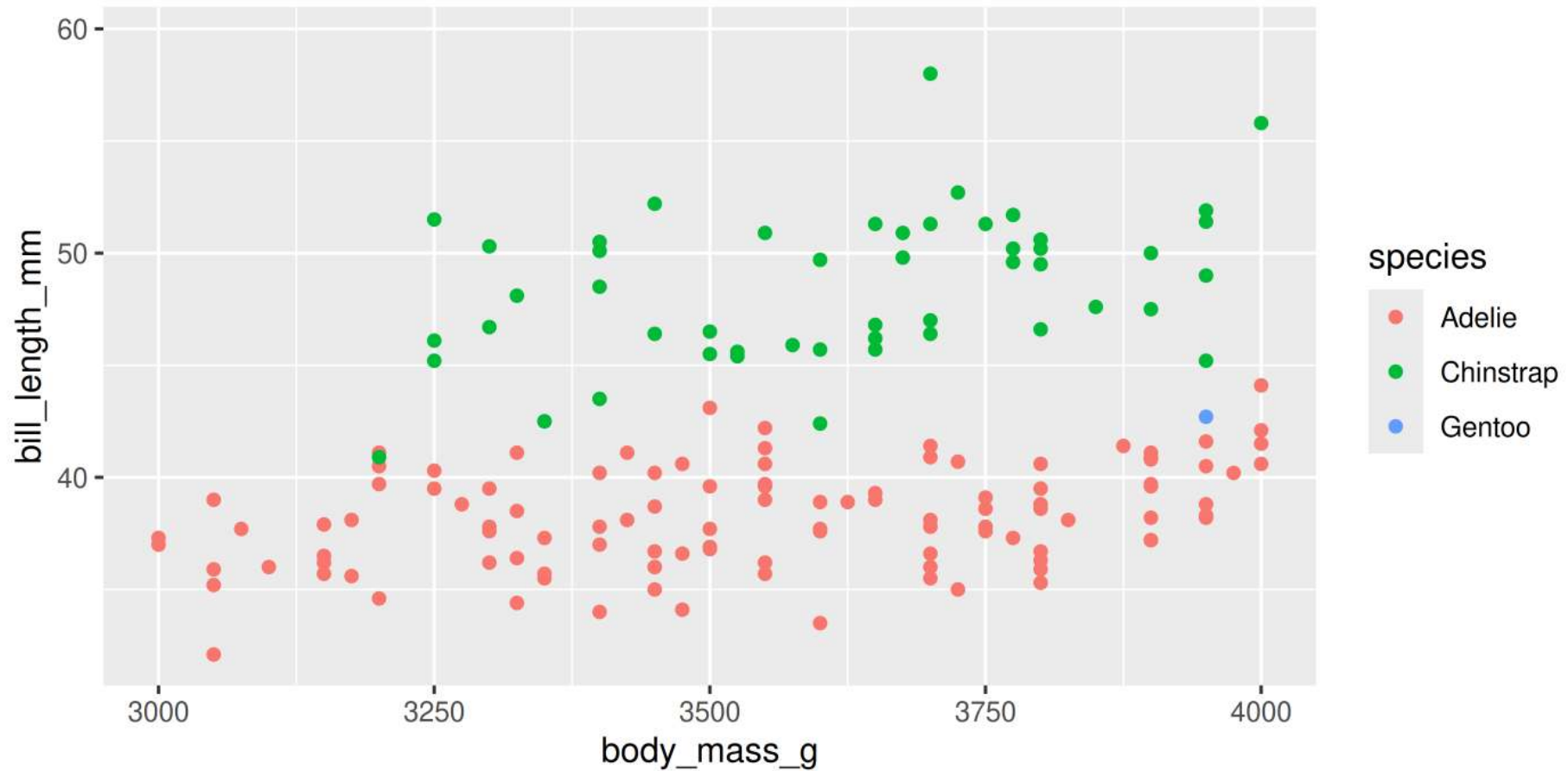
```
1 g + scale_x_continuous(breaks = seq(2500, 6500, 500))
```



Customizing: Axes

Limits

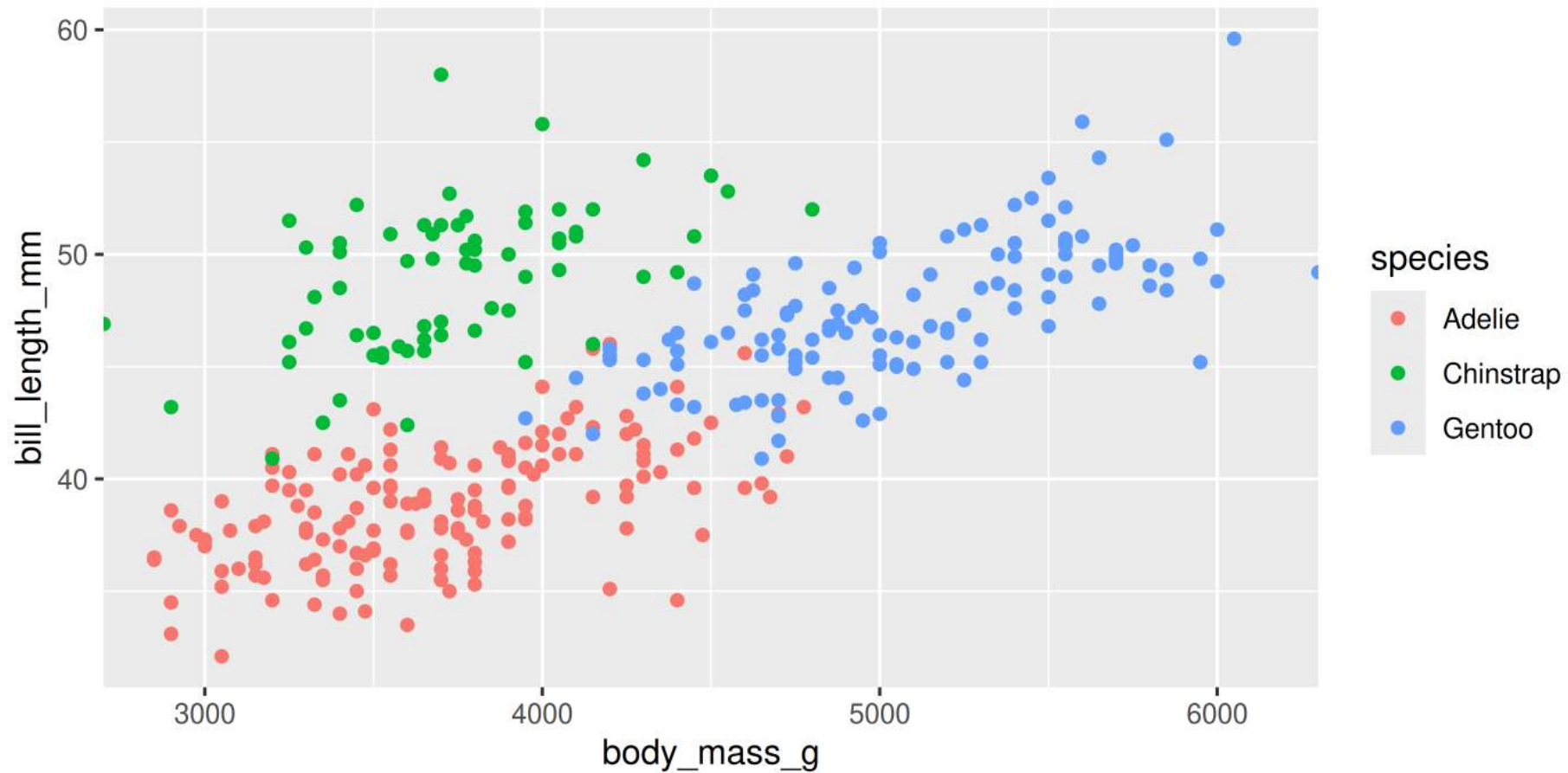
```
1 g + scale_x_continuous(limits = c(3000, 4000))
```



Customizing: Axes

Space between origin and axis start

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

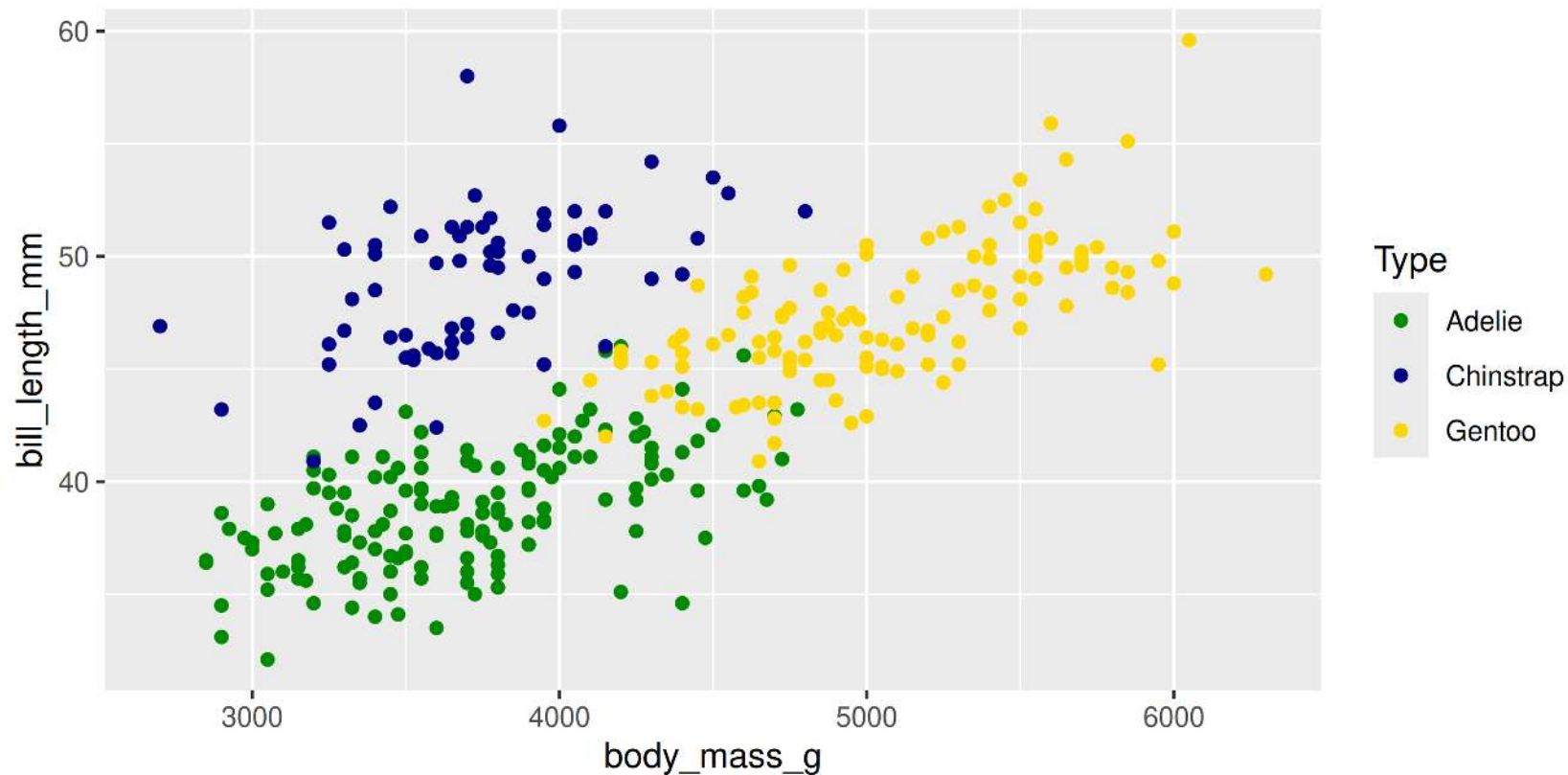


Customizing: Aesthetics

Using scales

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

```
1 g + scale_colour_manual(name = "Type", values = c("green4", "blue4", "gold"))
```

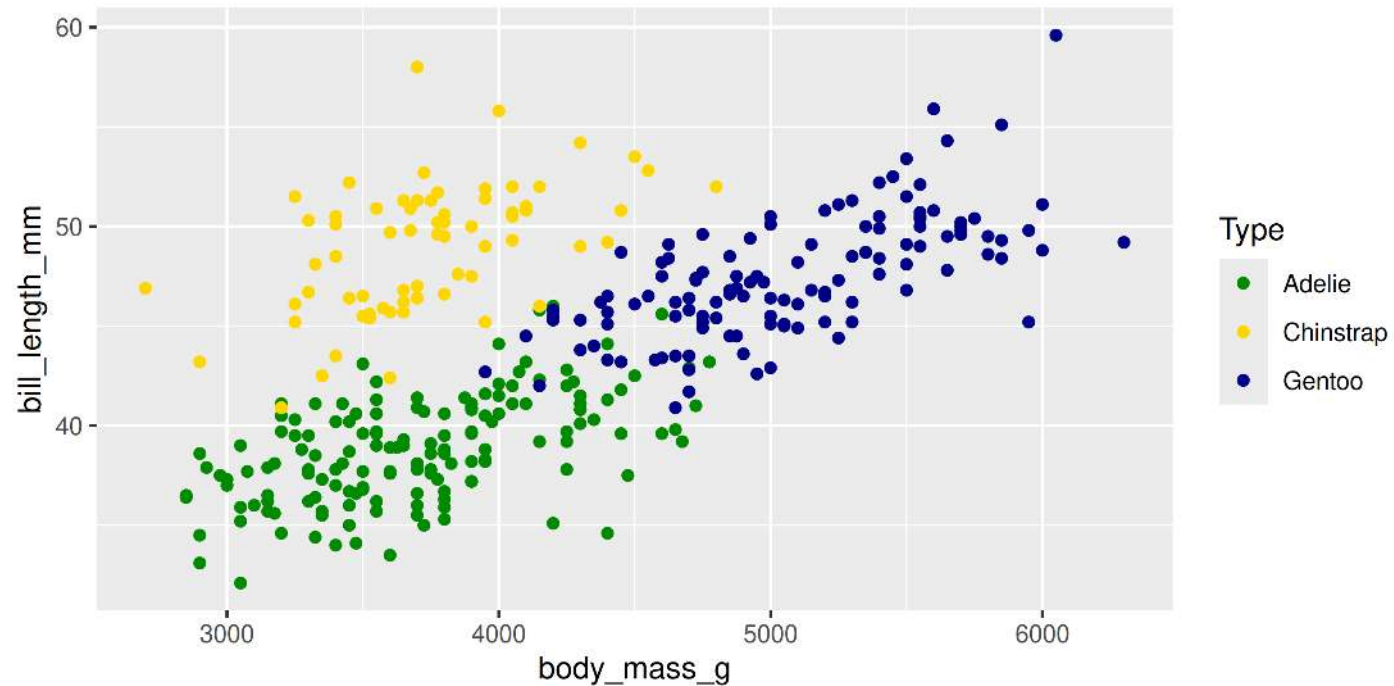


Customizing: Aesthetics

Using scales

Or be very explicit:

```
1 g + scale_colour_manual(  
2   name = "Type",  
3   values = c("Adelie" = "green4", "Gentoo" = "blue4", "Chinstrap" = "gold"),  
4   na.value = "black")
```

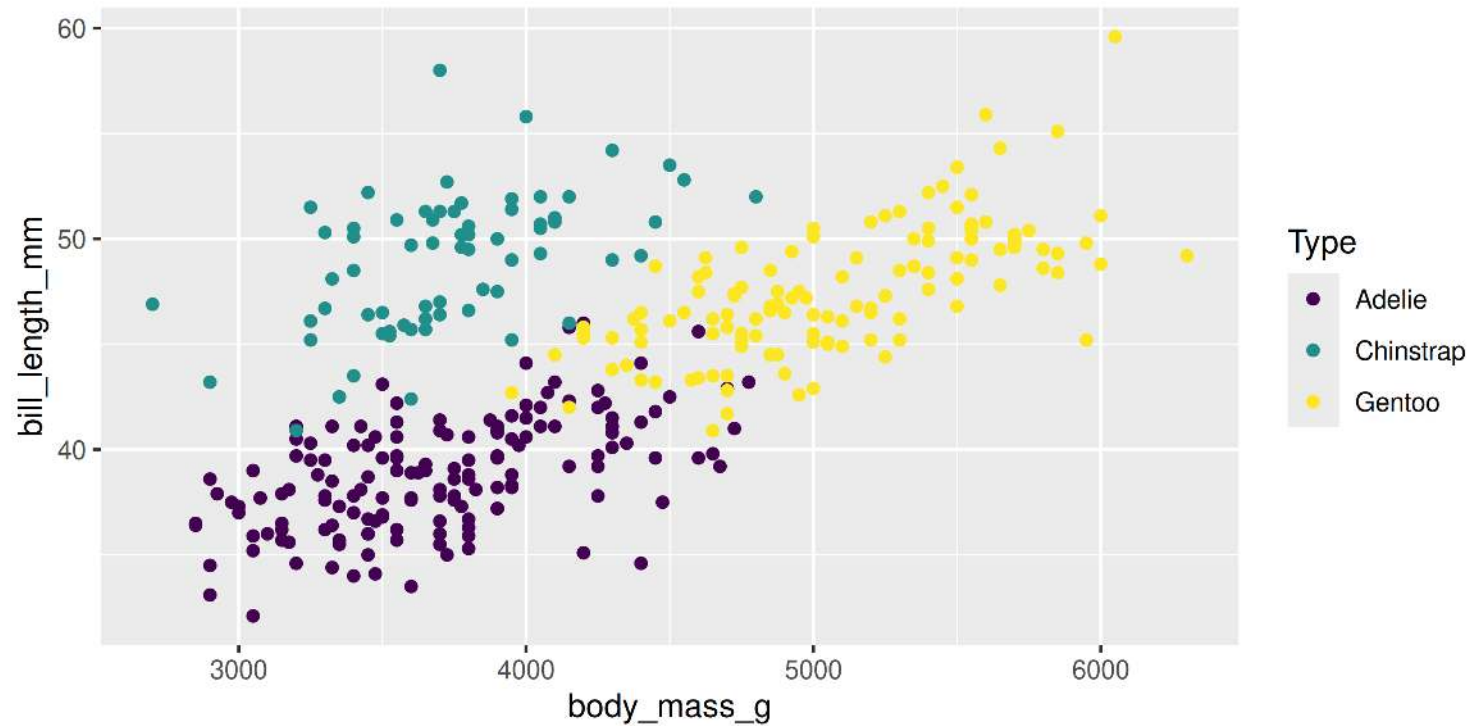


Customizing: Aesthetics

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")
```

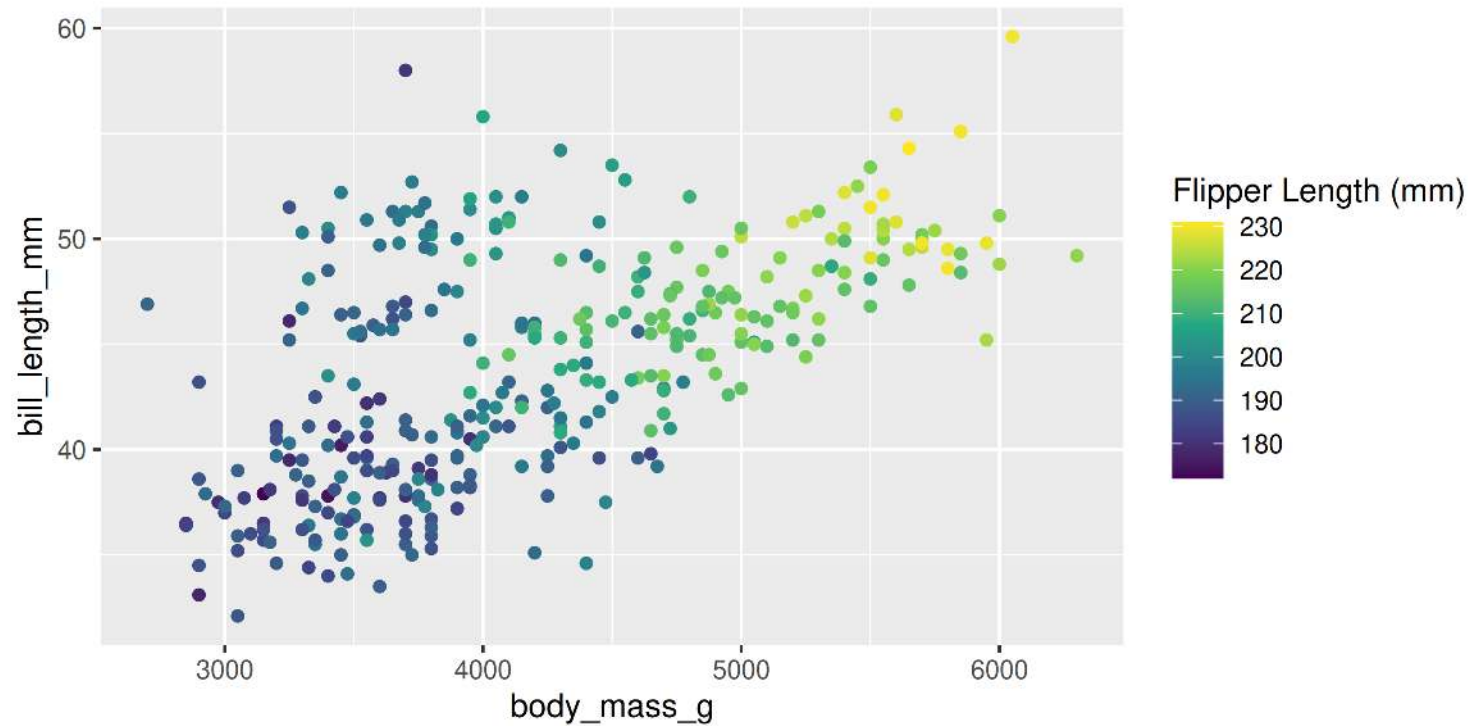


Customizing: Aesthetics

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)")
```

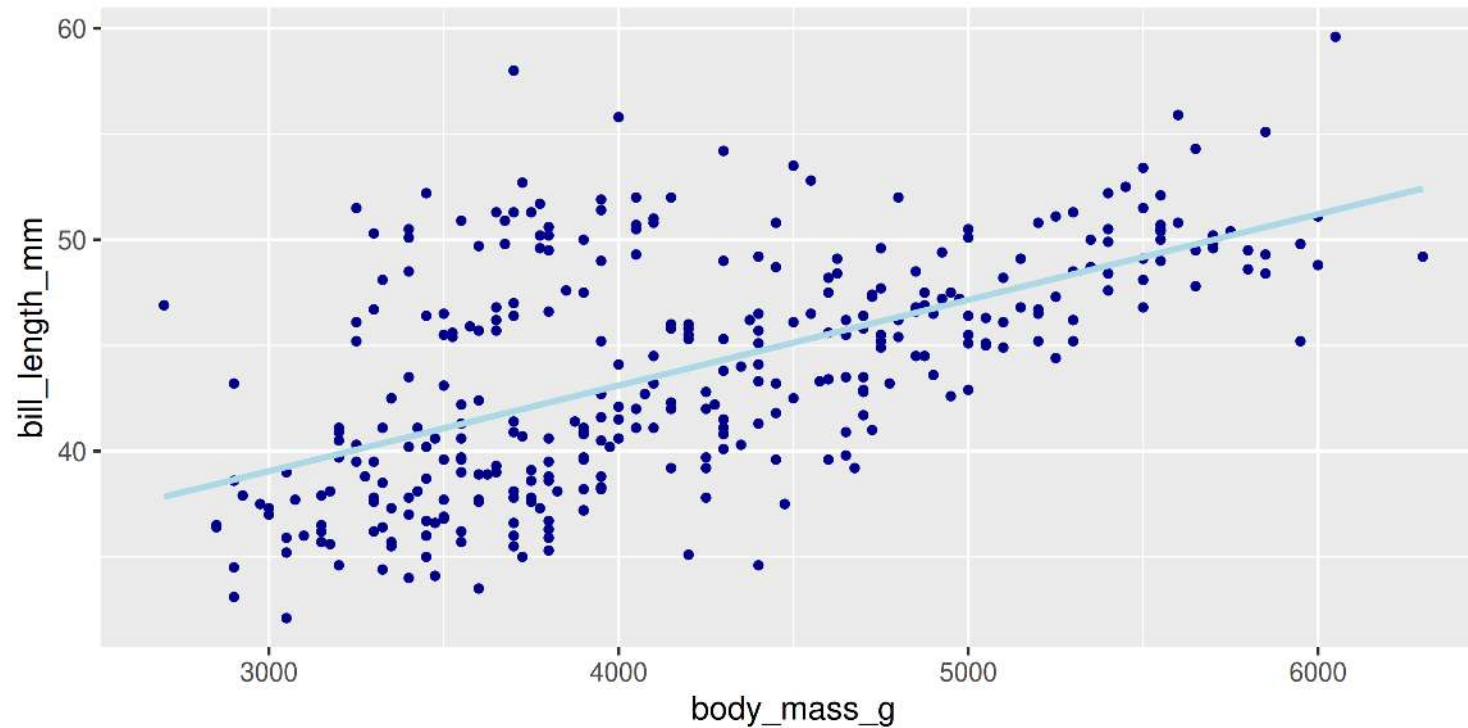


Customizing: Aesthetics

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")
```



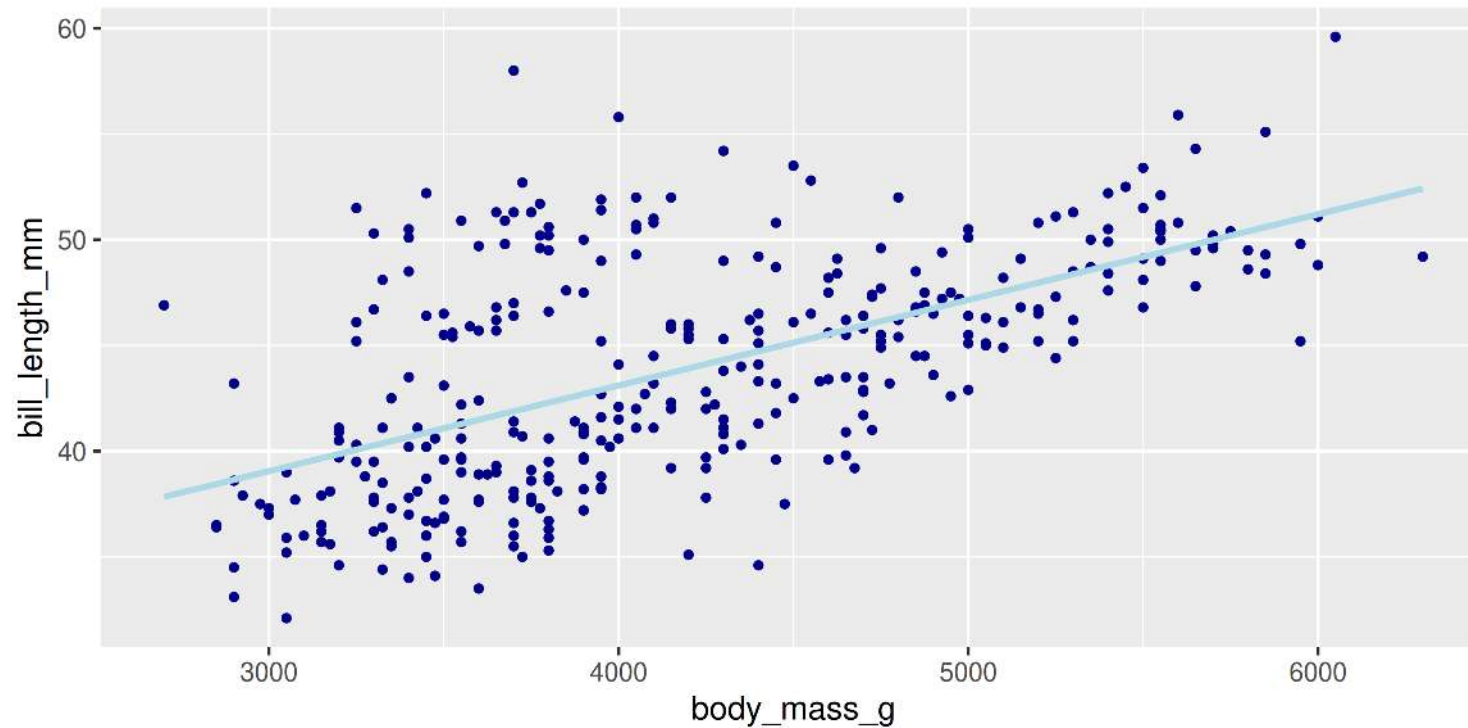
Customizing: Aesthetics

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

Forcing

Remove the association between a variable and an aesthetic

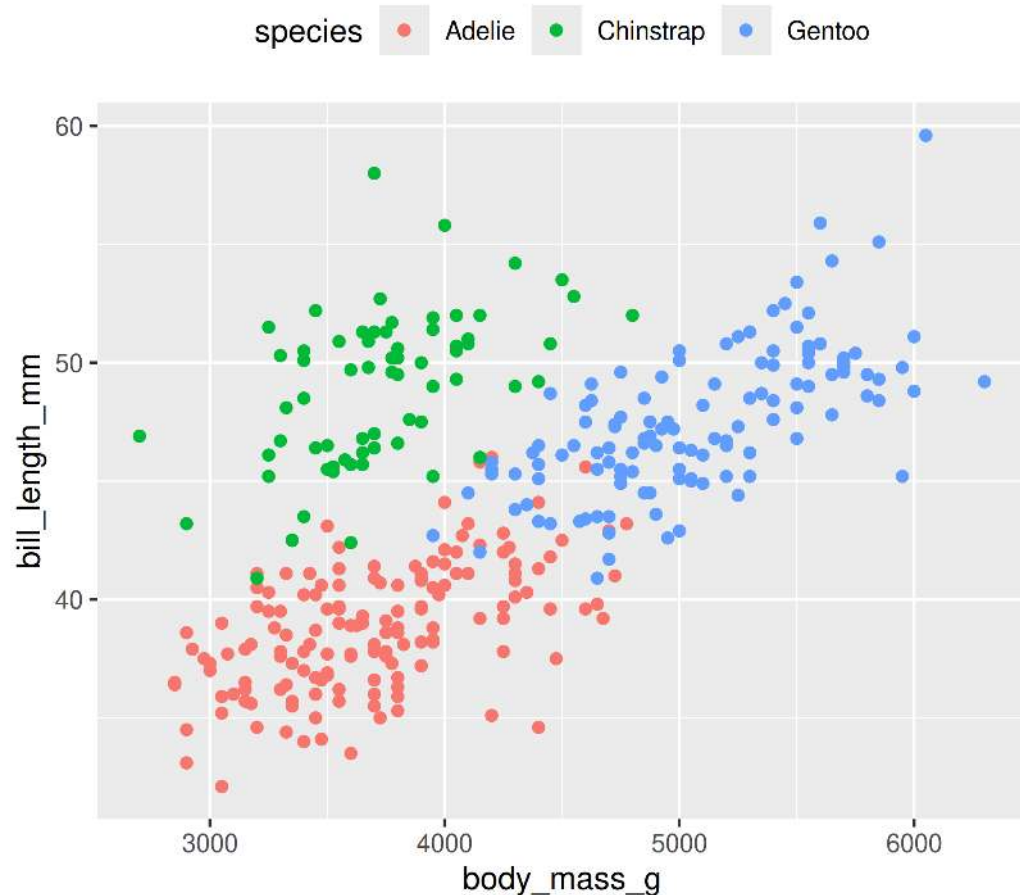
```
1 ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +  
2   geom_point(colour = "darkblue", size = 1) +  
3   stat_smooth(method = "lm", se = FALSE, colour = "lightblue")
```



Customizing: Legends placement

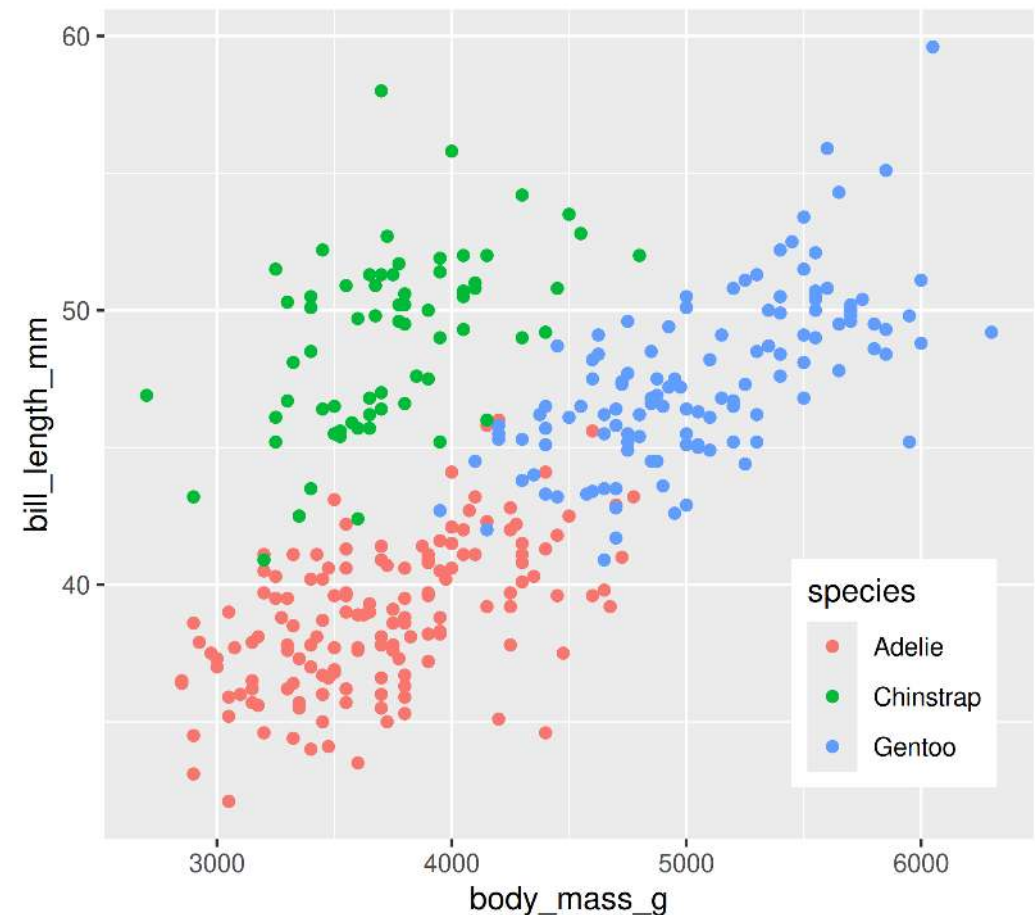
At the: top, bottom, left, right

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

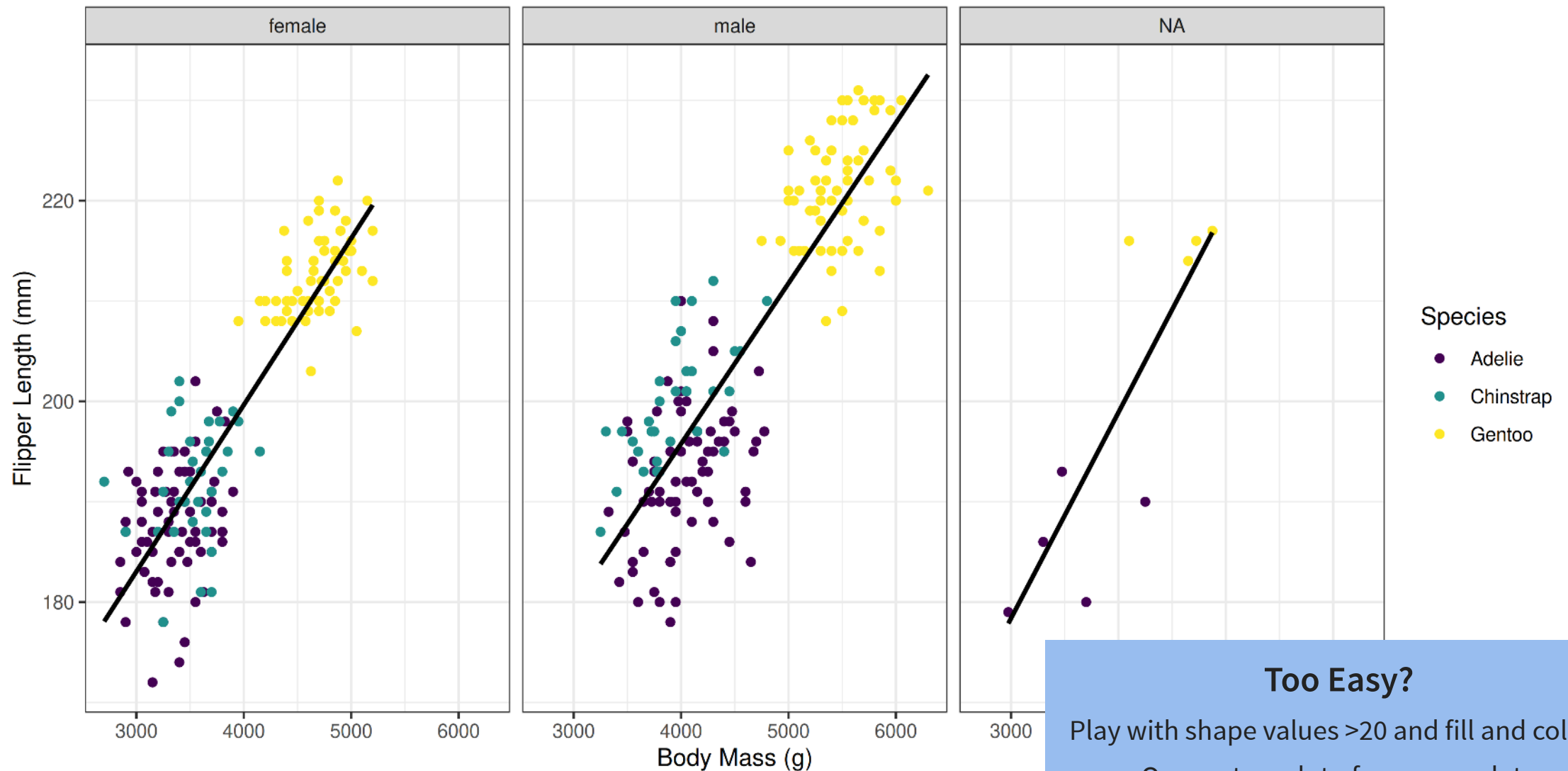


Exactly here

```
1 g + theme(legend.position = c(0.85, 0.2))
```

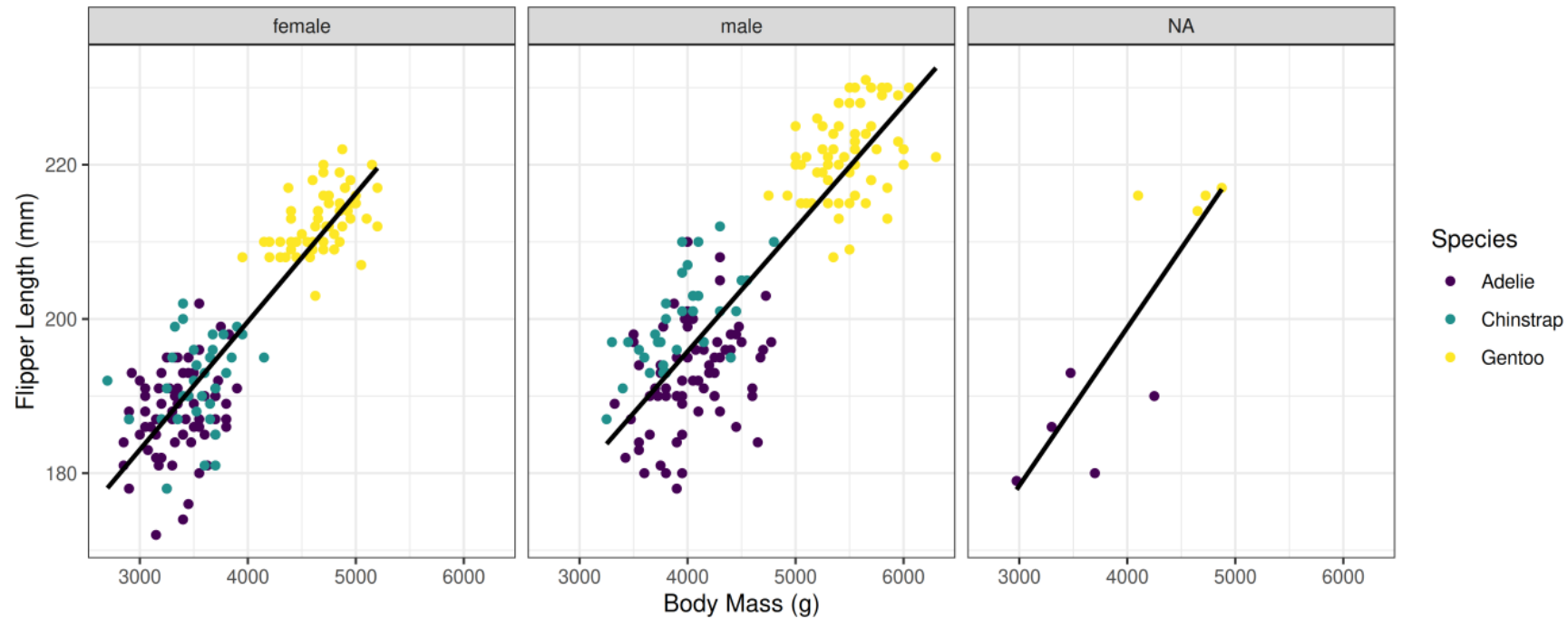


Your Turn: Create this plot



Your Turn: Create this plot

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

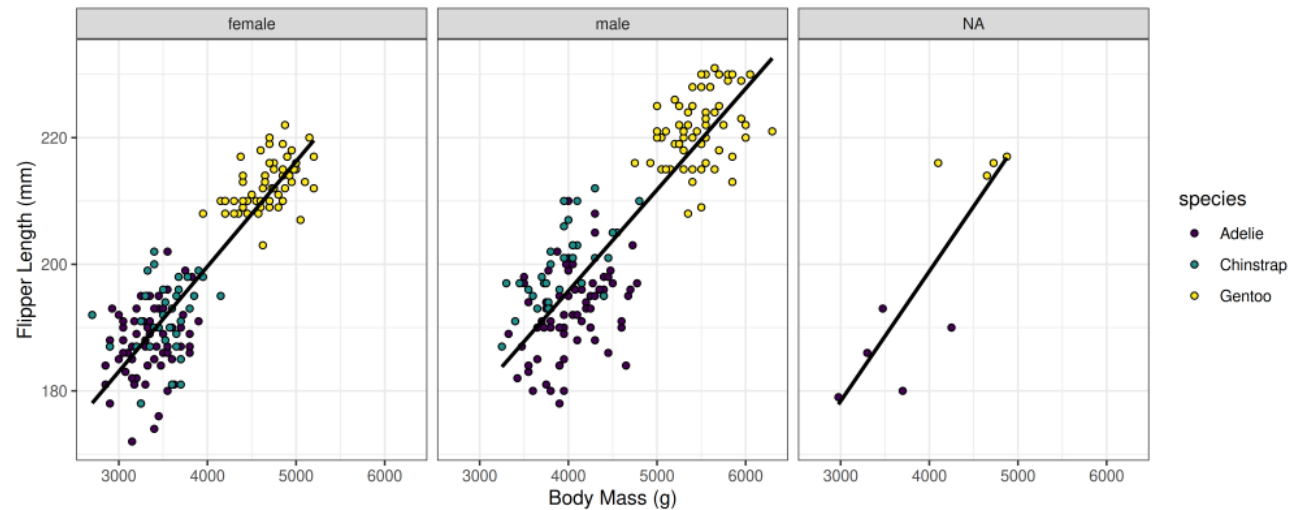


Your Turn: Create this plot

Too easy?

Shape values > 20 are fillable!

```
1 ggplot(penguins, aes(x = body_mass_g, y = flipper_length_mm, fill = species)) +  
2   theme_bw() +  
3   geom_point(shape = 21) +  
4   stat_smooth(method = "lm", se = FALSE, colour = "black", fill = NA) +  
5   scale_fill_viridis_d() +  
6   facet_wrap(~ sex) +  
7   labs(x = "Body Mass (g)",  
8        y = "Flipper Length (mm)",  
9        colour = "Species")
```

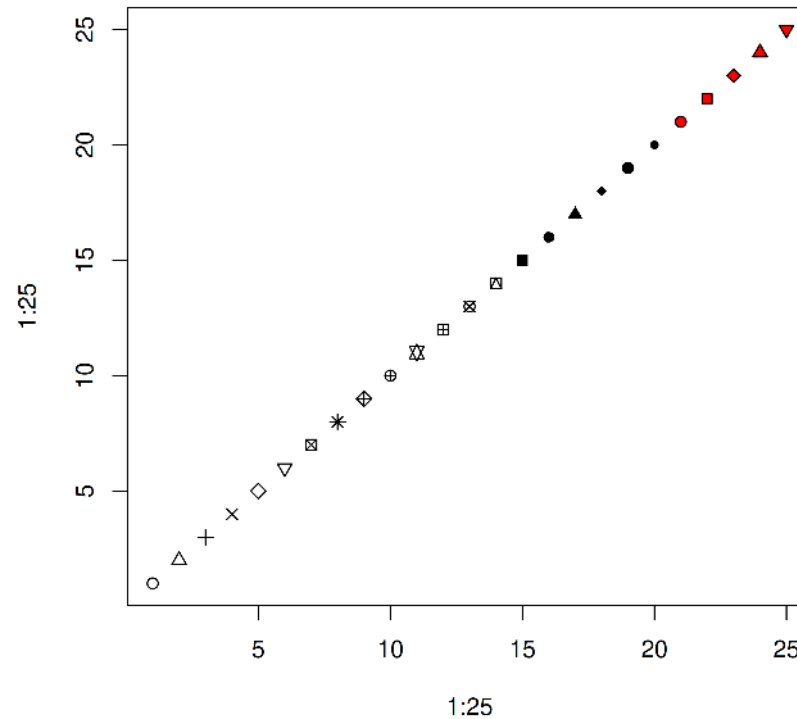


Your Turn: Create this plot

Too easy?

Shape values > 20 are fillable!

```
1 plot(1:25, 1:25, pch = 1:25, bg = "red")
```



Side note: Order of operations

Order of operations

Remember...

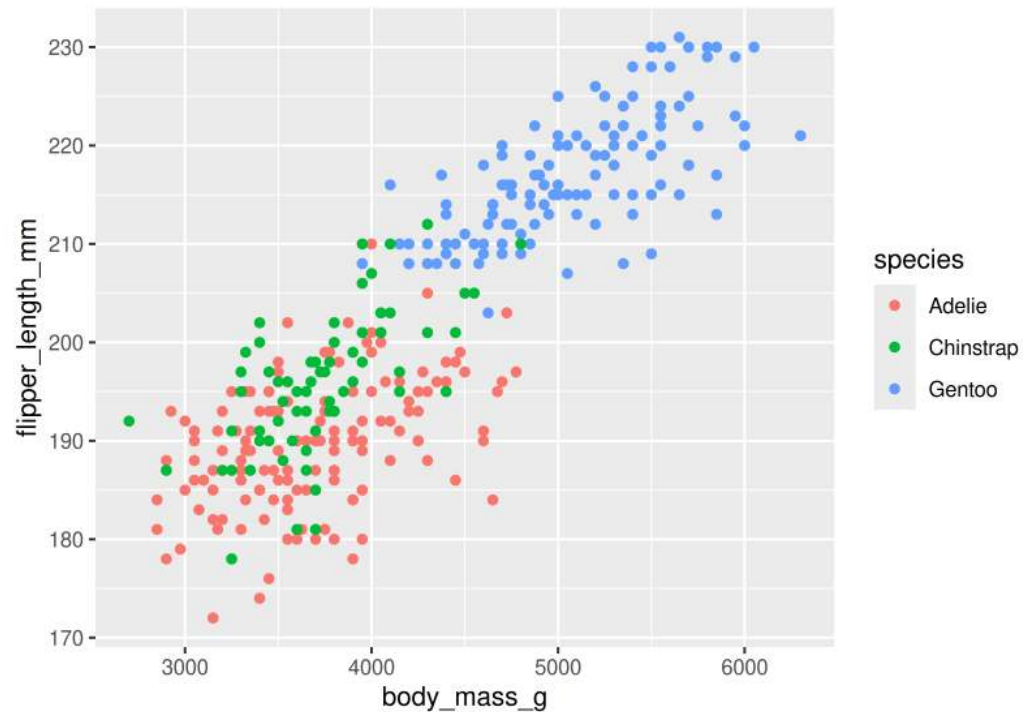
- `ggplot()` is the default line (all options passed down)
- The other lines are *added* with the `+` (options only apply to this line)

Order of operations

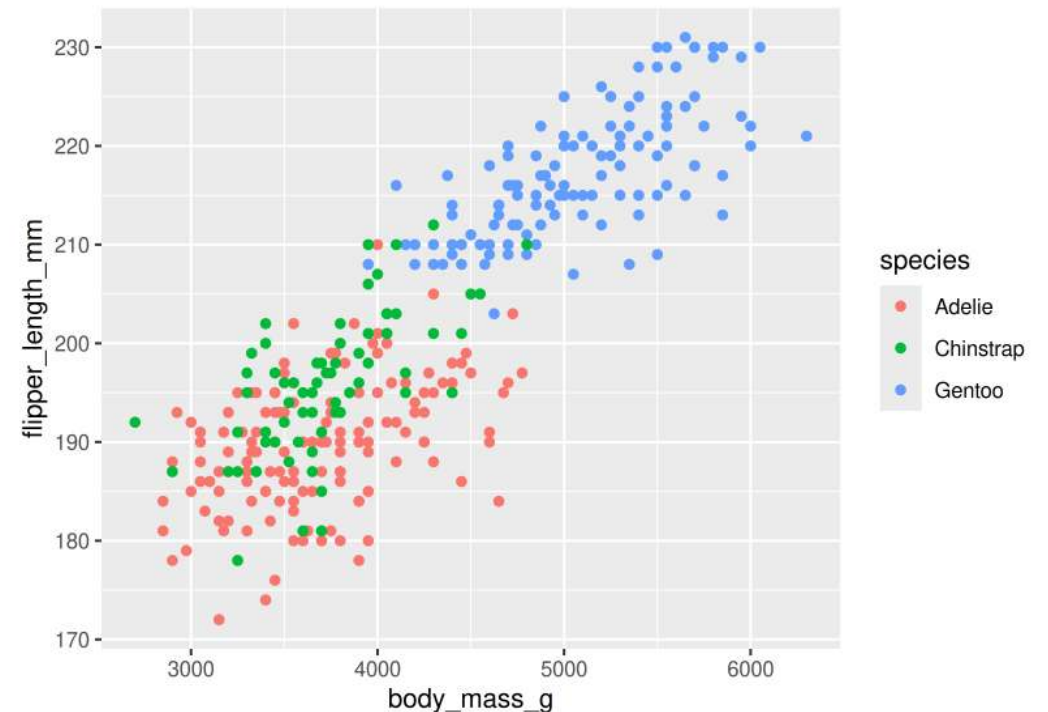
Where to put the `aes()`?

Sometimes it doesn't matter...

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



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

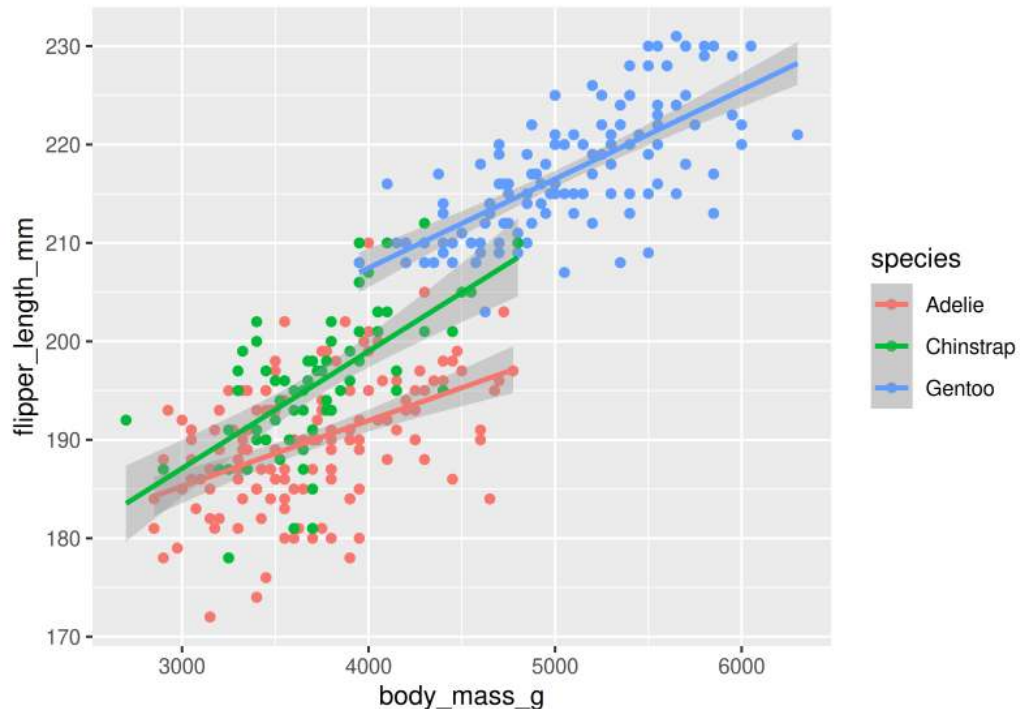


Order of operations

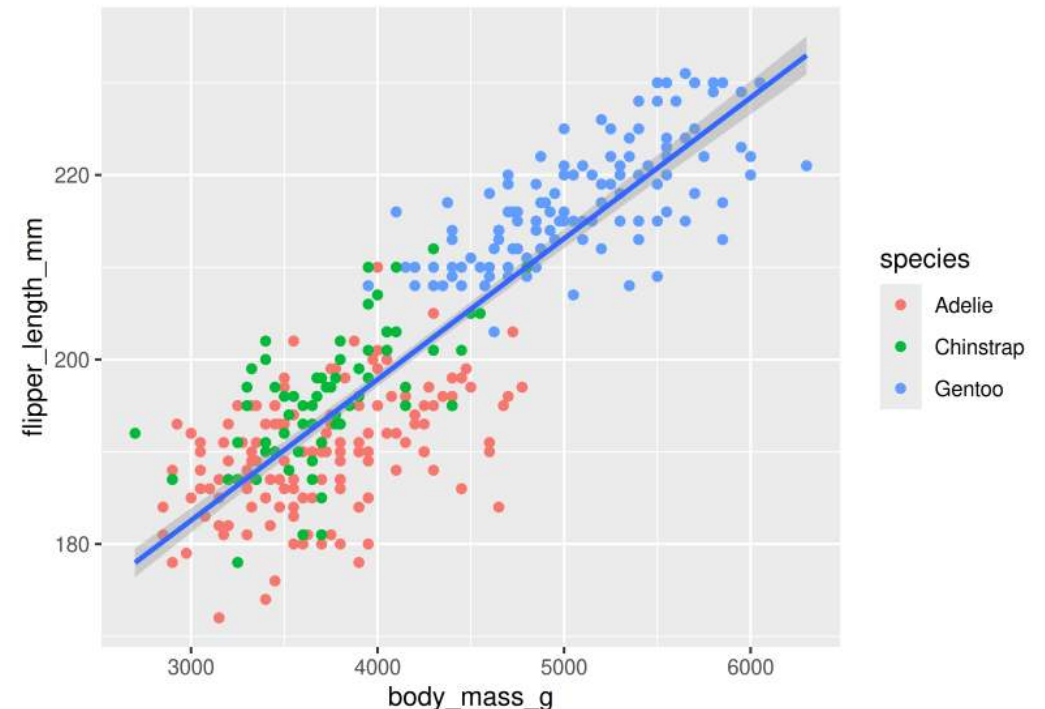
Where to put the `aes()`?

Sometimes it DOES matter...

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



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

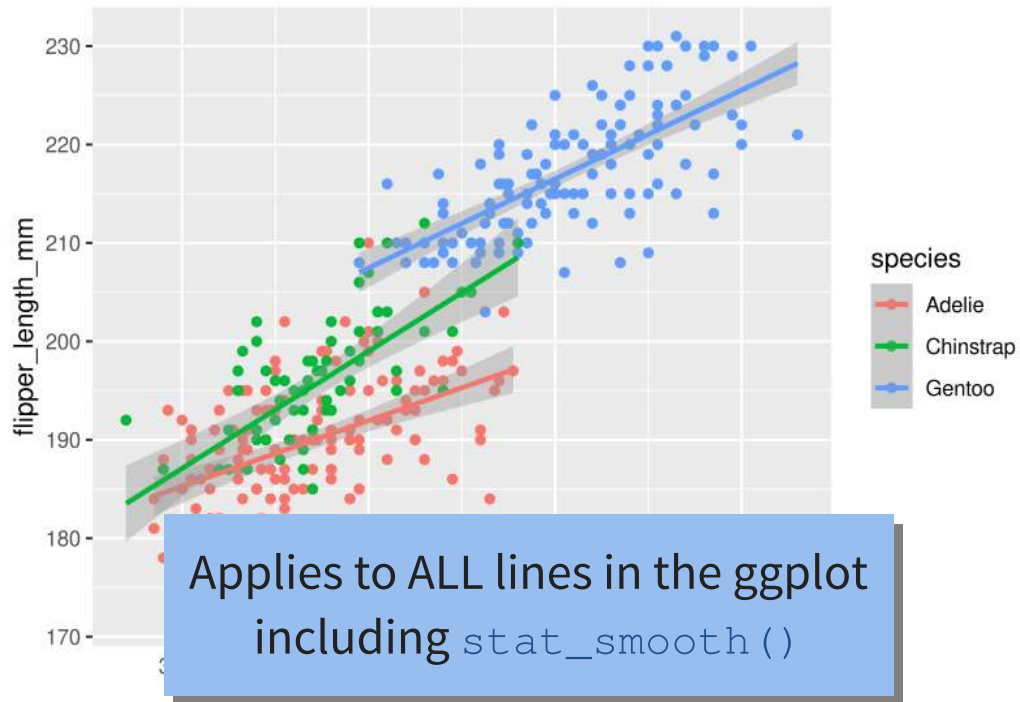


Order of operations

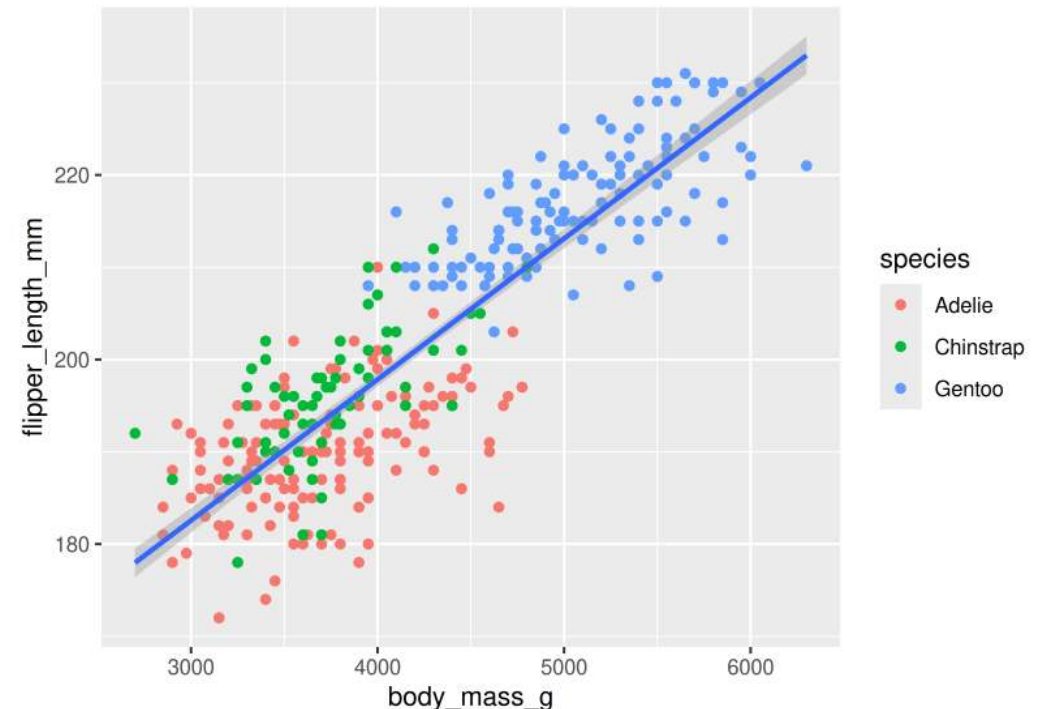
Where to put the `aes()`?

Sometimes it DOES matter...

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



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

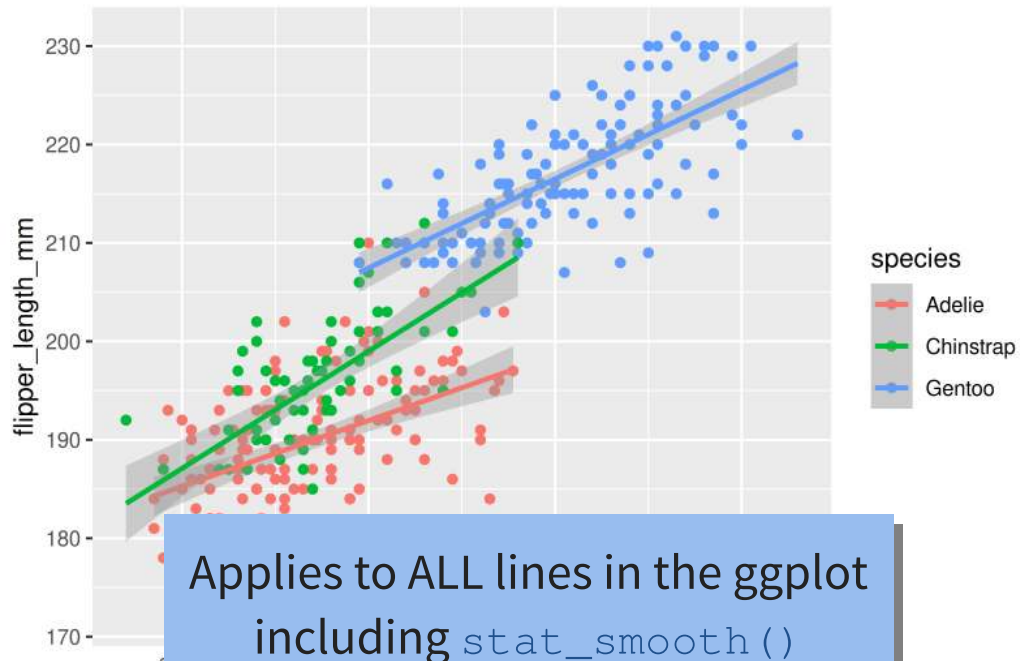


Order of operations

Where to put the `aes()` ?

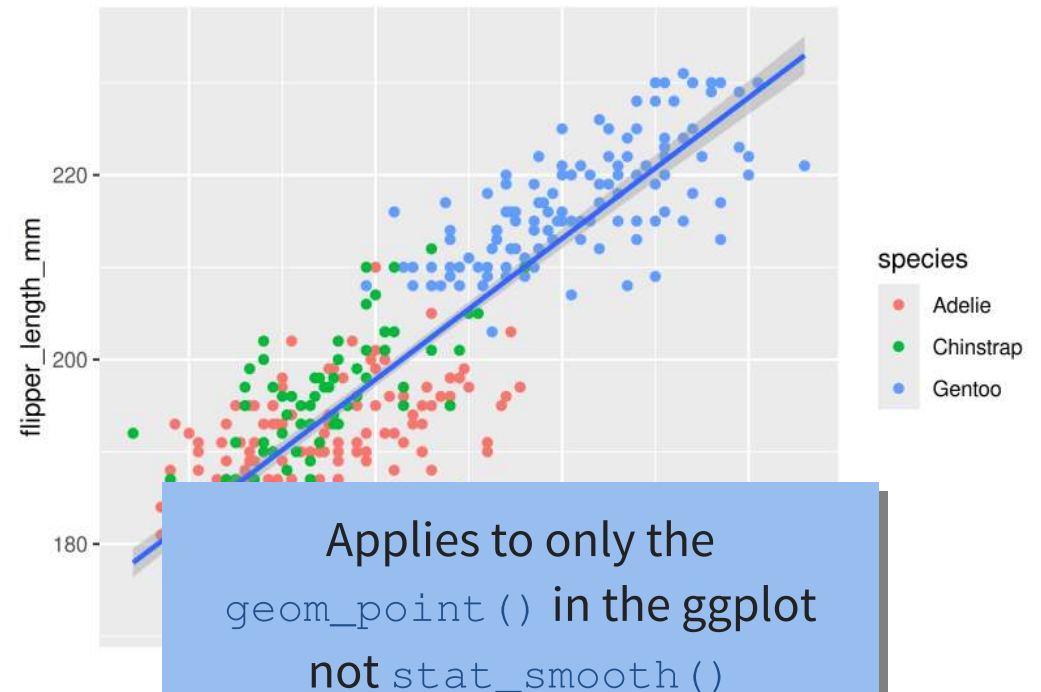
Sometimes it DOES matter...

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



Applies to ALL lines in the ggplot
including `stat_smooth()`

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



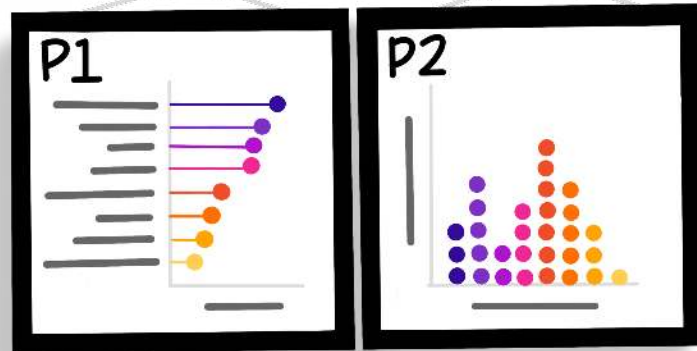
Applies to only the
`geom_point()` in the ggplot
not `stat_smooth()`

Combining plots with patchwork



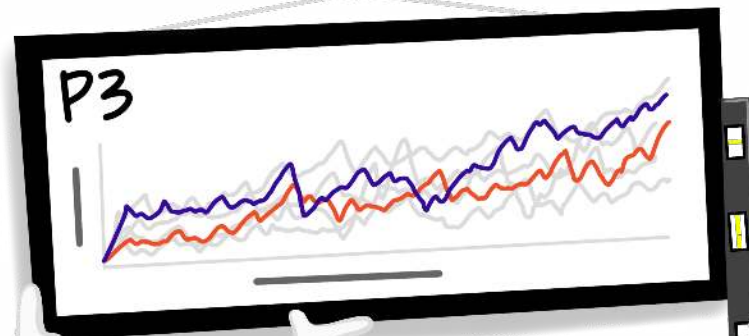
patchwork

Combine + arrange
your ggplots!



PLAN:
 $(P1 + P2) / P3$

P1	P2
P3	



Artwork by [@allison_horst](#)

Combining plots

Setup

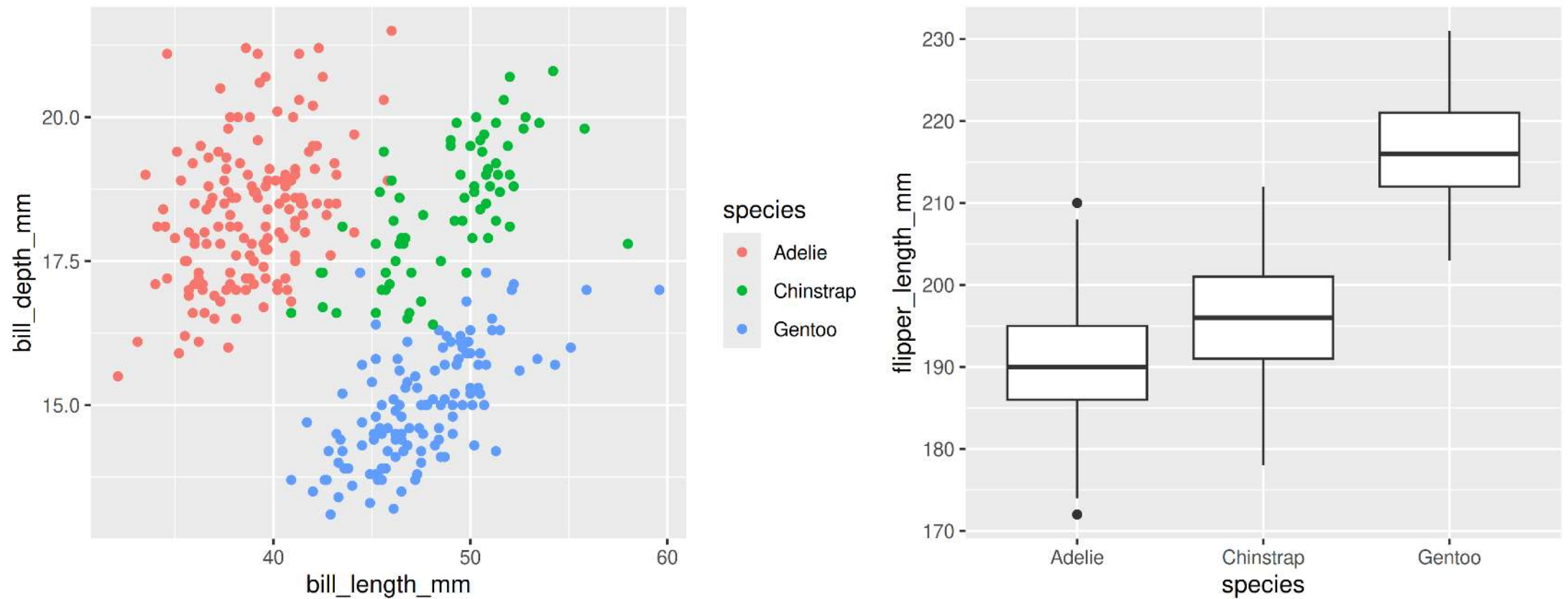
- Load `patchwork`
- Create a couple of different plots

```
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

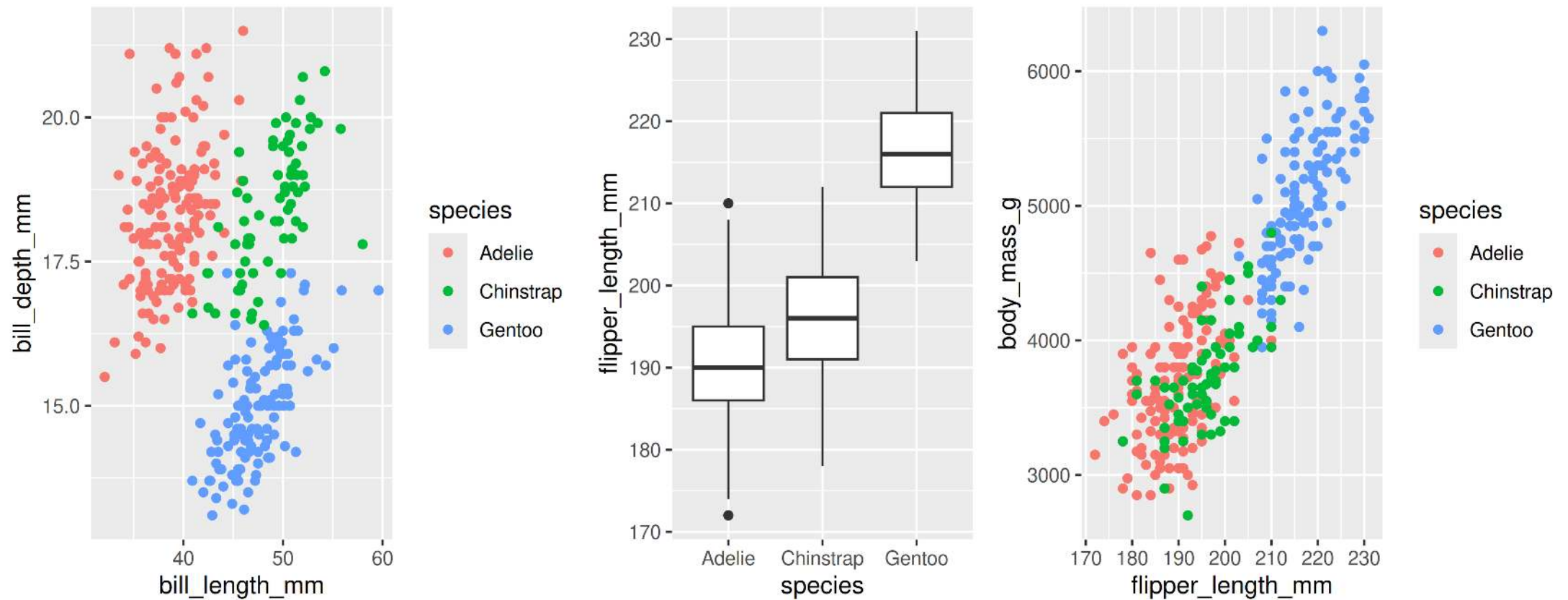
```
1 g1 + g2
```



Combining plots with patchwork

Side-by-Side 3 plots

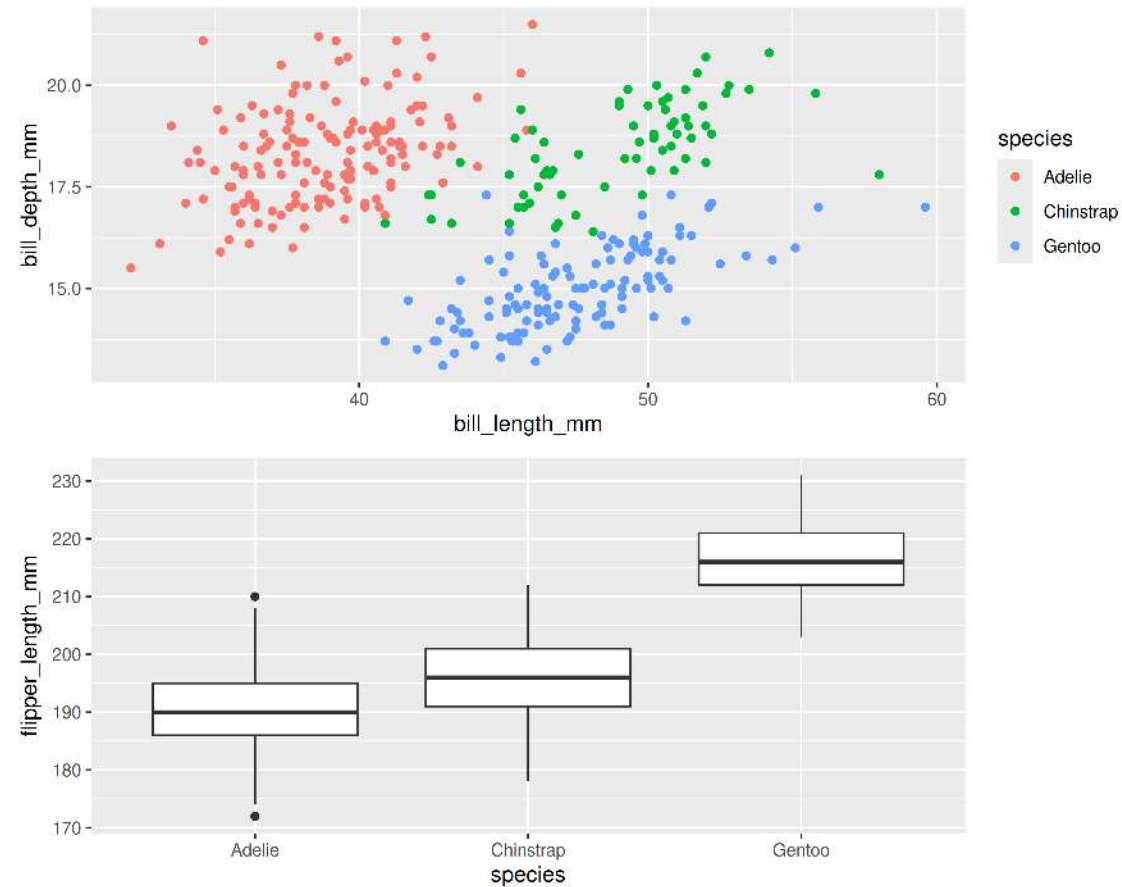
```
1 g1 + g2 + g3
```



Combining plots with patchwork

Stacked 2 plots

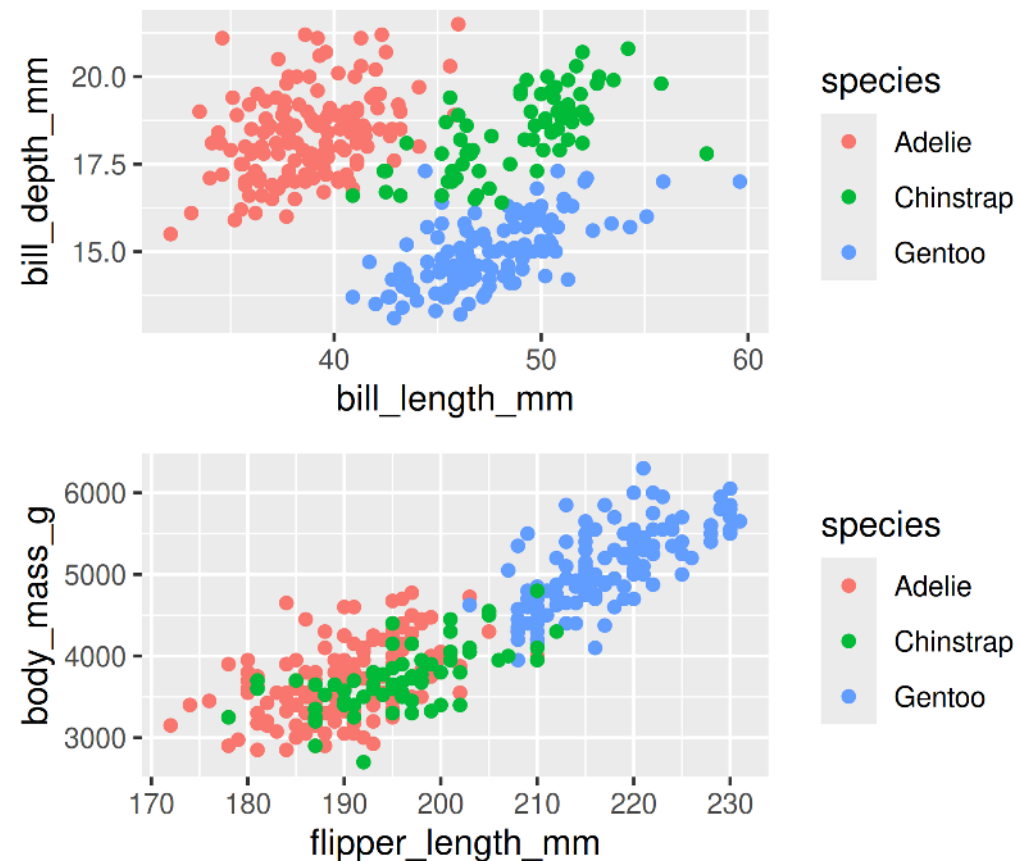
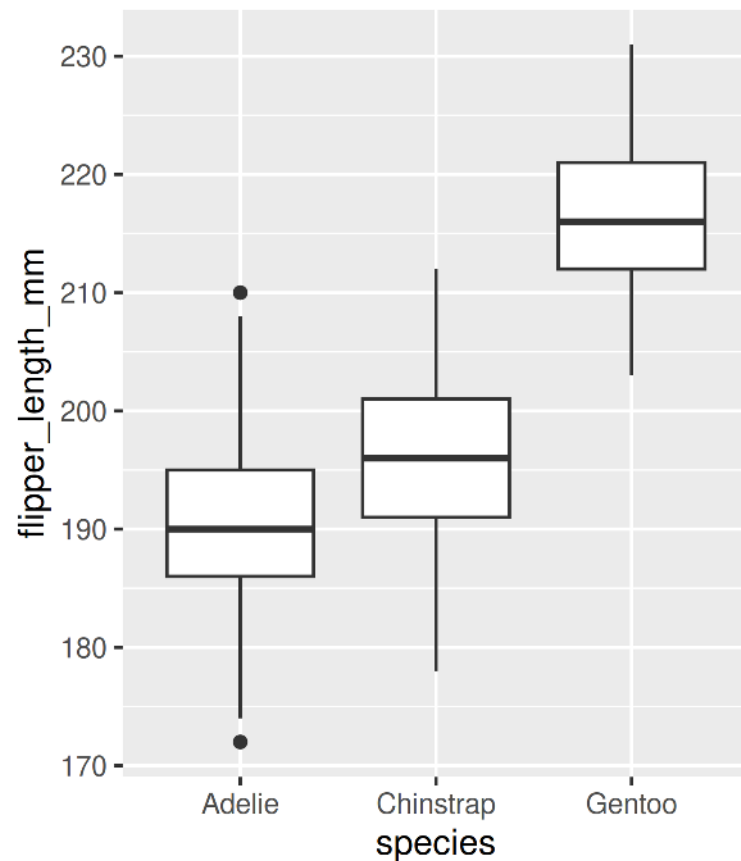
1 g1 / g2



Combining plots with patchwork

More complex arrangements

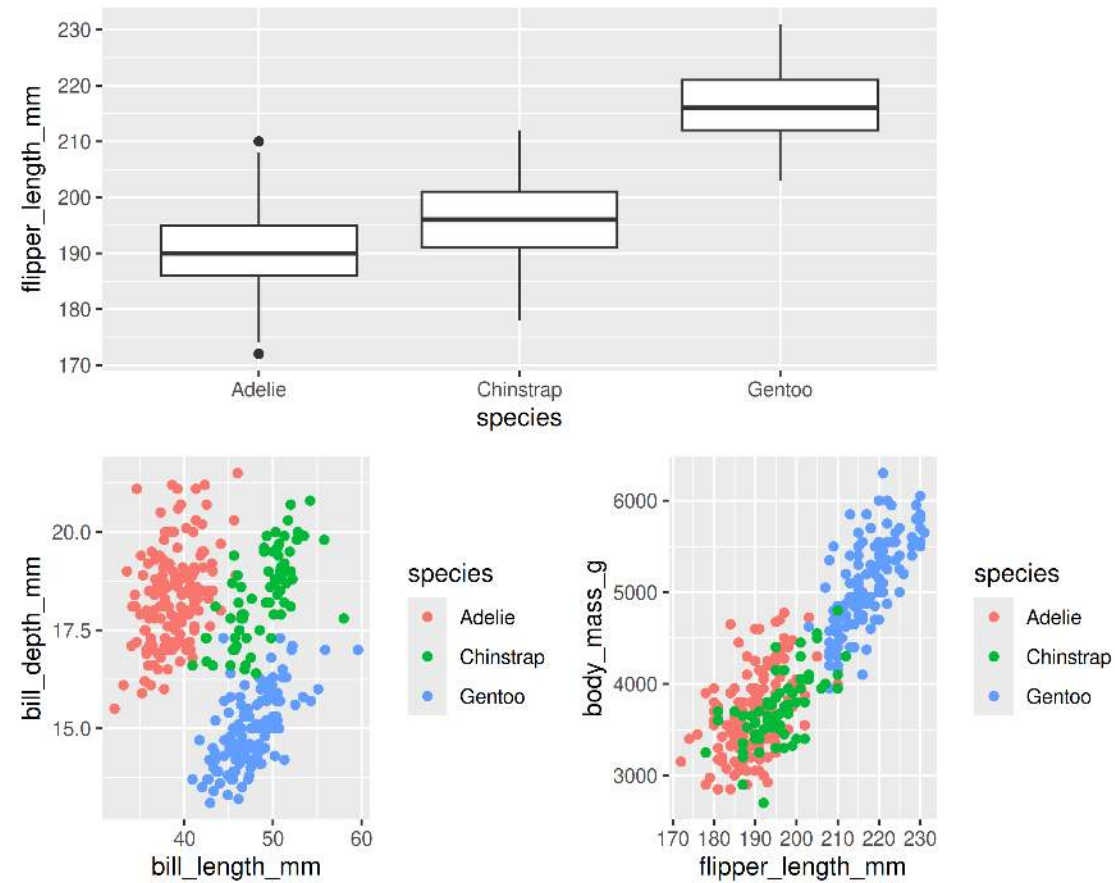
```
1 g2 + (g1 / g3)
```



Combining plots with patchwork

More complex arrangements

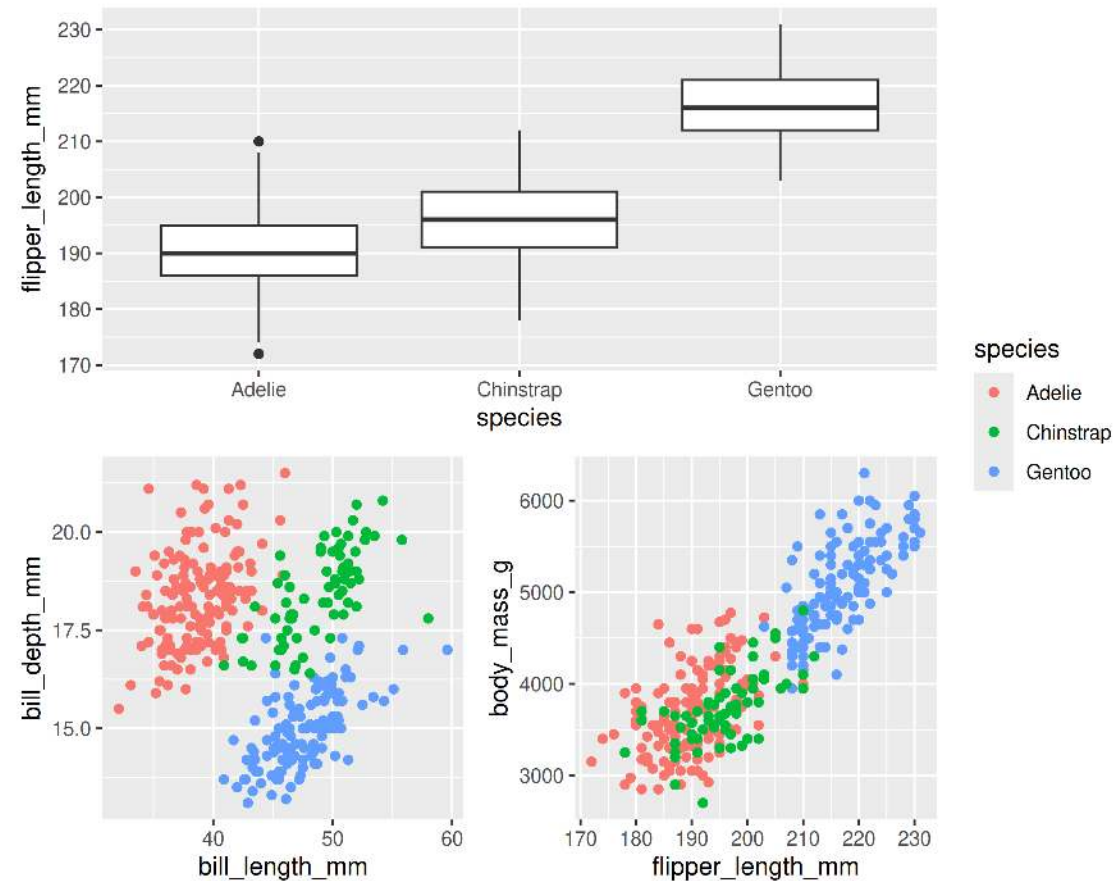
```
1 g2 / (g1 + g3)
```



Combining plots with patchwork

“collect” common legends

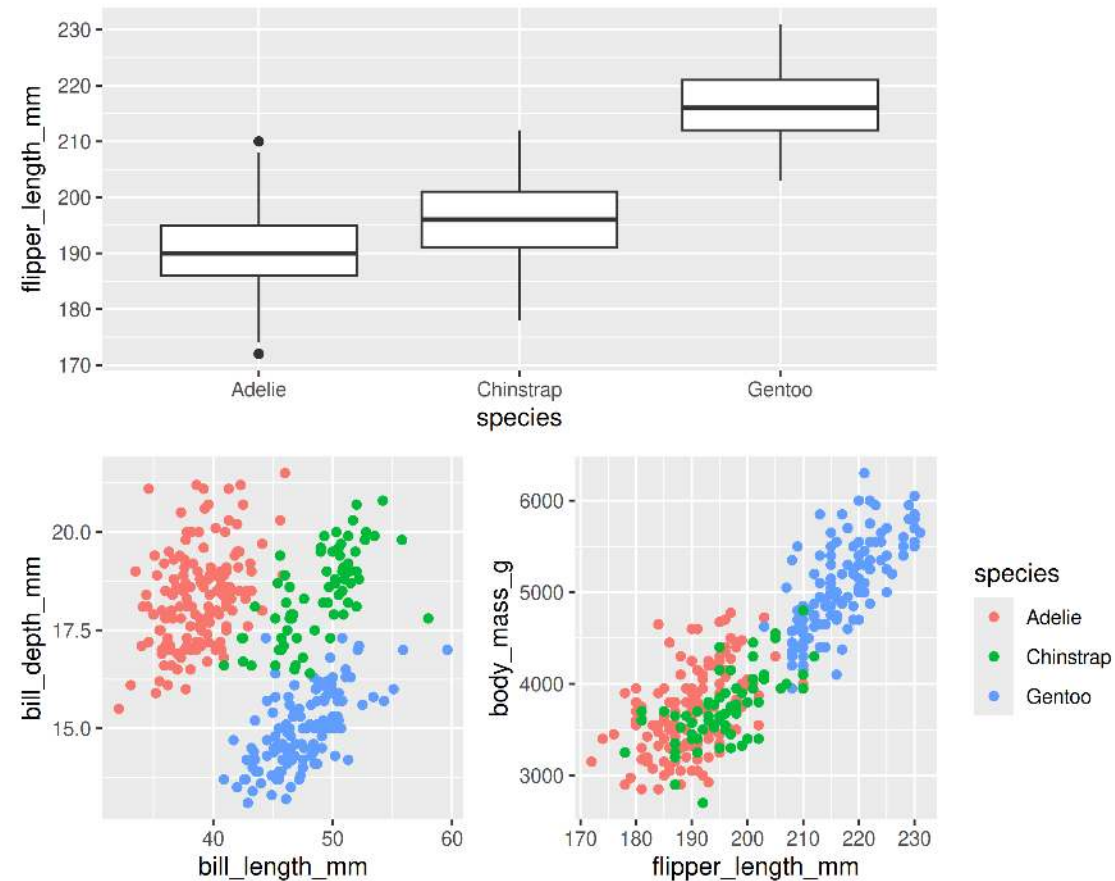
```
1 g2 / (g1 + g3) + plot_layout(guides = "collect")
```



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 = ")")
```

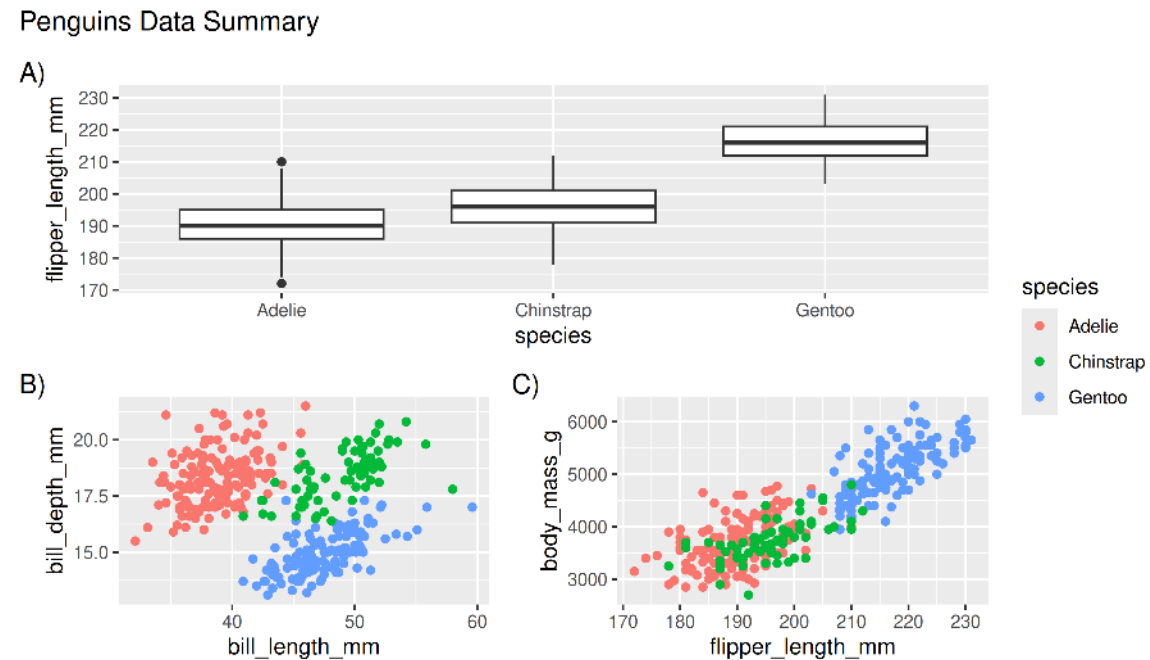


Fig 1. Penguins Data Summary

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 = ")")
```

Too Easy?

Can you figure out how to collect common axes as well?

Your Turn
Combine any 3 figures

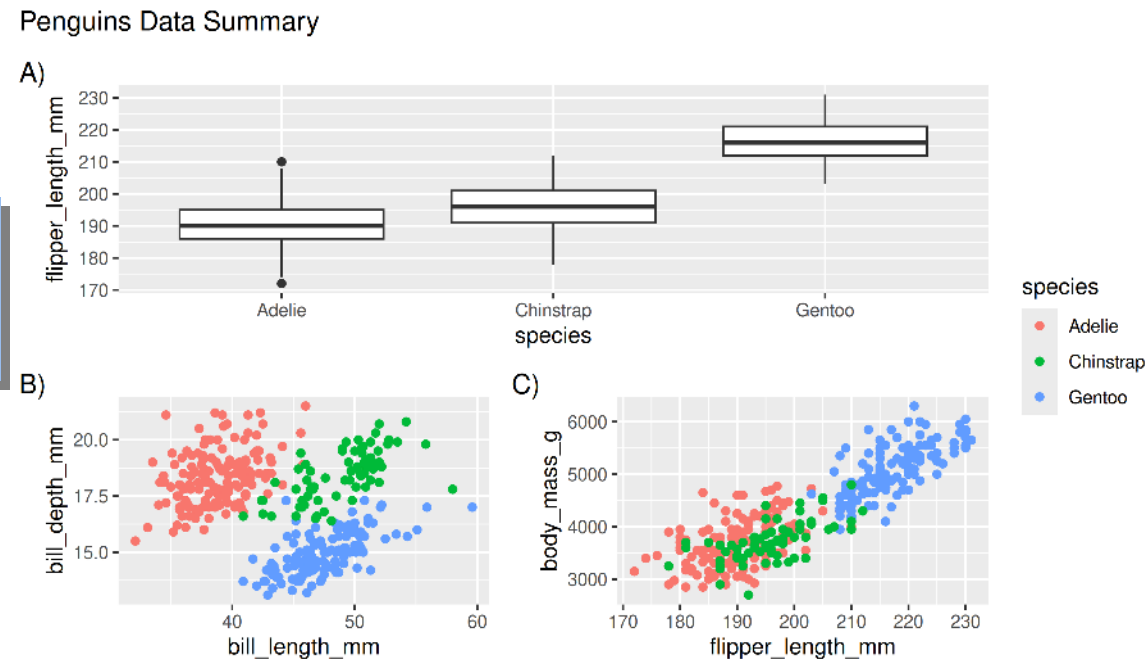
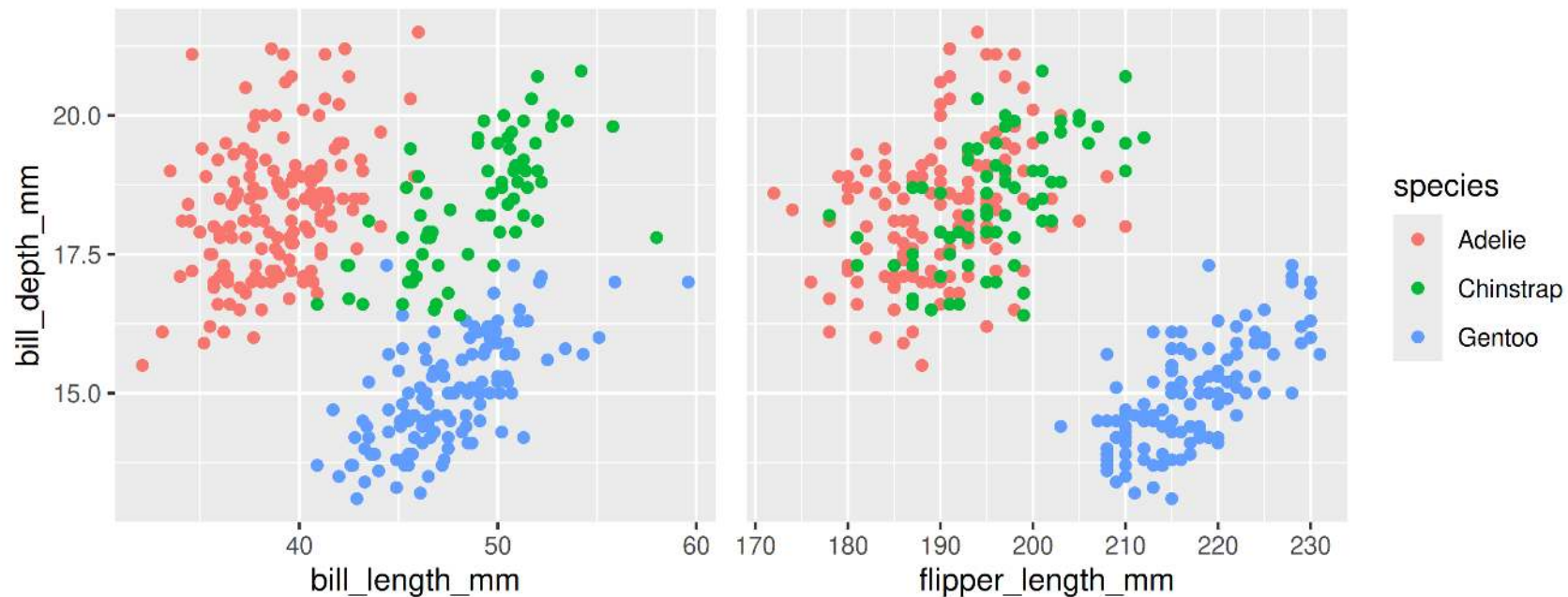


Fig 1. Penguins Data Summary

Your Turn: Combine plots

Too easy?

```
1 g1 <- ggplot(data = penguins, aes(x = bill_length_mm, y = bill_depth_mm, colour = species)) +  
2   geom_point()  
3  
4 g2 <- ggplot(data = penguins, aes(x = flipper_length_mm, y = bill_depth_mm, colour = species)) +  
5   geom_point()  
6  
7 g1 + g2 + plot_layout(guides = "collect", axes = "collect")
```



Saving plots

Saving plots

RStudio Export

Demo

Saving plots

RStudio Export

Demo

ggsave()

```
1 g <- ggplot(penguins, aes(x = sex, y = bill_length_mm)) +  
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: 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: Common mistakes

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

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

```
1 n <- count(penguins, island)
2
3 ggplot(data = penguins, aes(x = flipper_length_mm, y = bill_length_mm, colour = species)) +
4   geom_point() +
5   facet_wrap(~ island) +
6   geom_text(data = n, aes(label = n),
7             x = -Inf, y = +Inf, hjust = 0, vjust = 1)
```

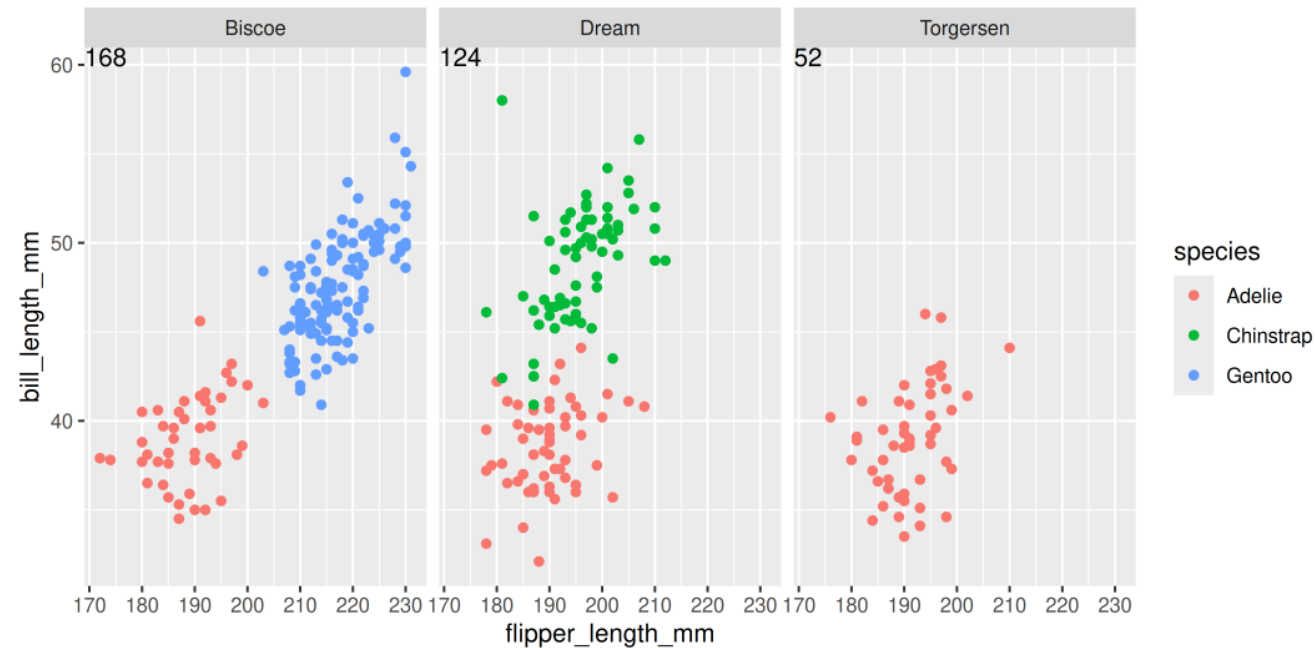
```
Error in `geom_text()` :
! Problem while computing aesthetics.
i Error occurred in the 2nd layer.
Caused by error:
! object 'species' not found
```

Wrapping up: Common mistakes

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

Either move the aesthetic...

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



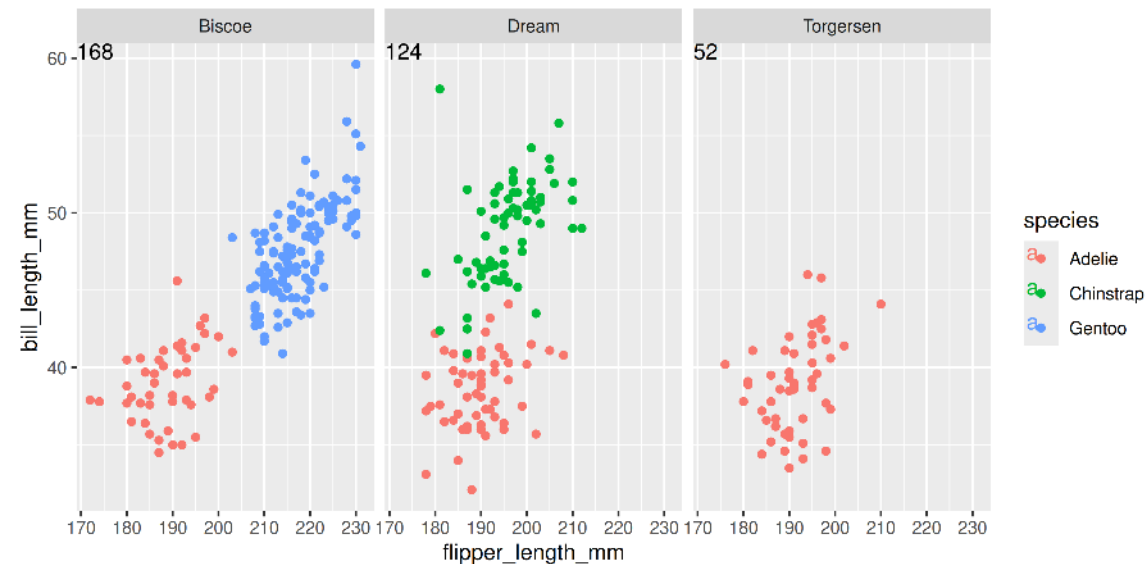
Wrapping up: Common mistakes

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

Either move the aesthetic...

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

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



Wrapping up: Further reading (all Free!)

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