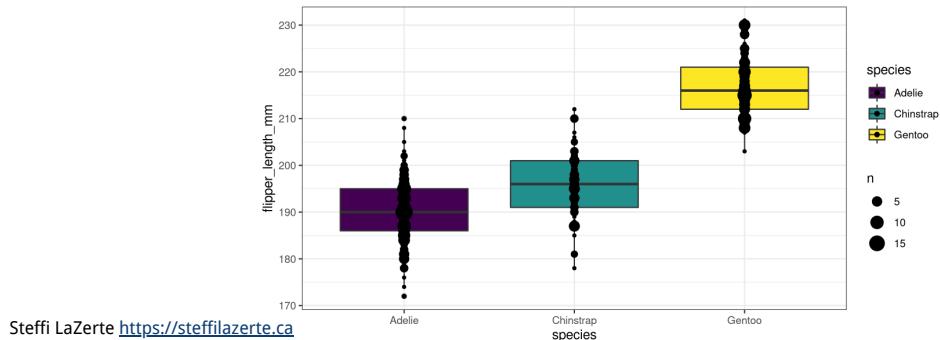


Visualizing Data in R

A primer on **ggplot2**



Steffi LaZerte <https://steffilazerte.ca>

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

3. Saving figures

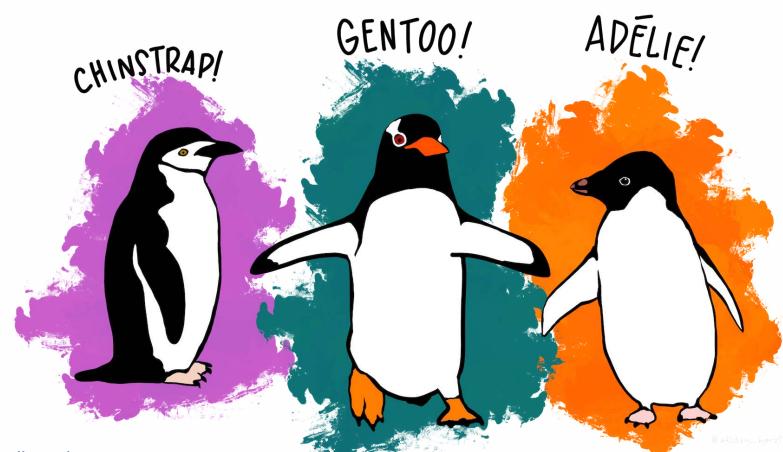
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Our data set: Palmer Penguins!



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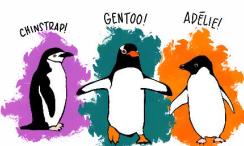
Our data set: Palmer Penguins!



```
library(palmerpenguins)
penguins
```



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



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Our data set: Palmer Penguins!



```
library(palmerpenguins)
penguins
```



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

Your turn!

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



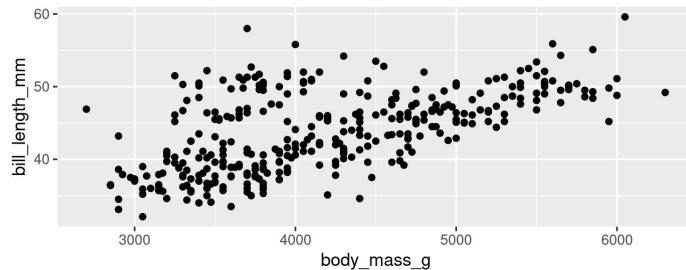
Artwork by [@allison_horst](#)

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A basic plot

```
library(palmerpenguins)
library(tidyverse)

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



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Break it down

```
library(palmerpenguins)
library(tidyverse)

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

library(palmerpenguins)

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

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Break it down

```
library(palmerpenguins)
library(tidyverse)

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

library(tidyverse)

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

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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

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Break it down

```
library(palmerpenguins)
library(tidyverse)

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

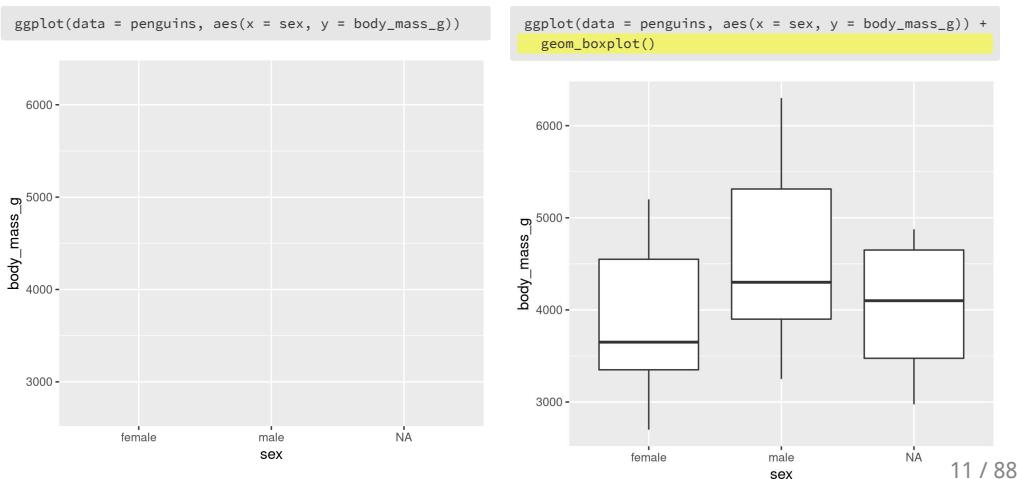
geom_point()

- 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()**

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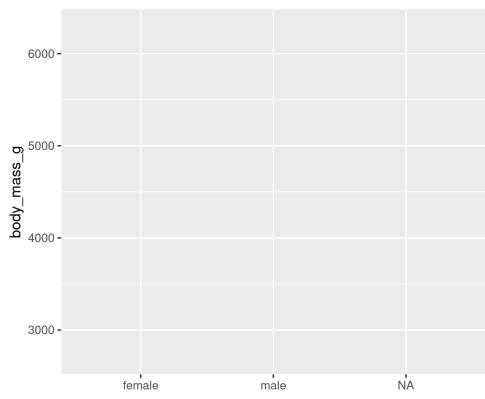
Plots are layered



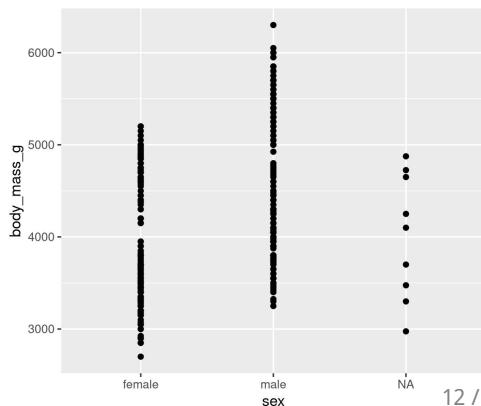
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Plots are layered

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



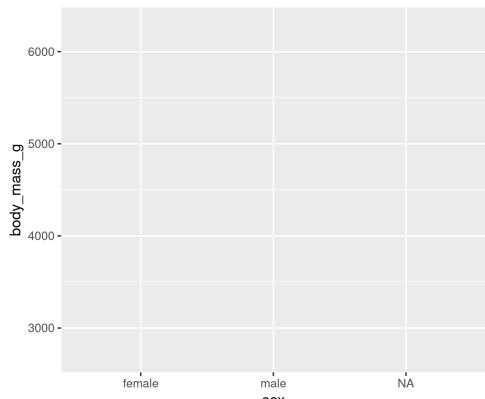
```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +  
  geom_point()
```



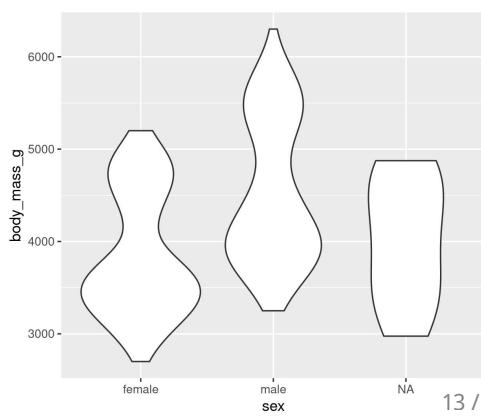
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Plots are layered

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



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

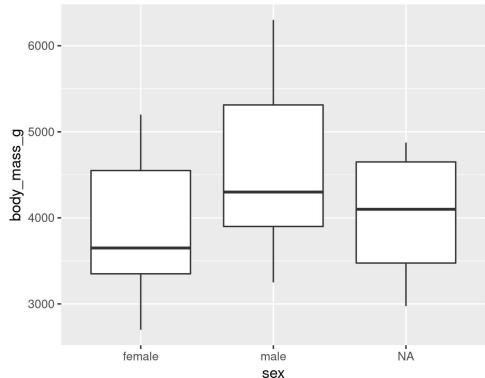


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Plots are layered

You can add multiple layers

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

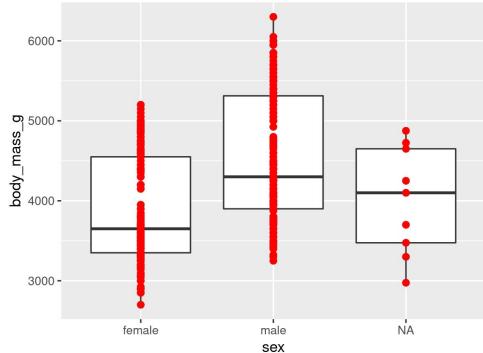


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Plots are layered

You can add multiple layers

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

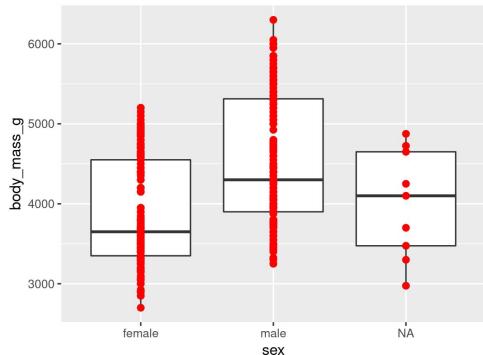


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Plots are layered

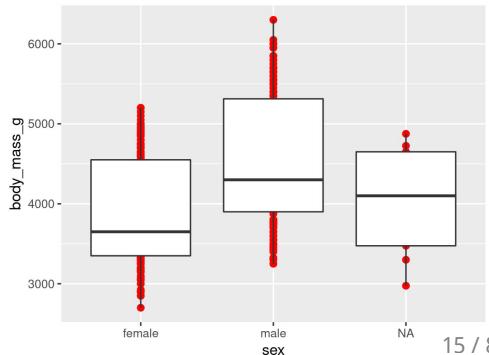
You can add multiple layers

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



Order matters

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



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Plots are objects

Any ggplot can be saved as an object

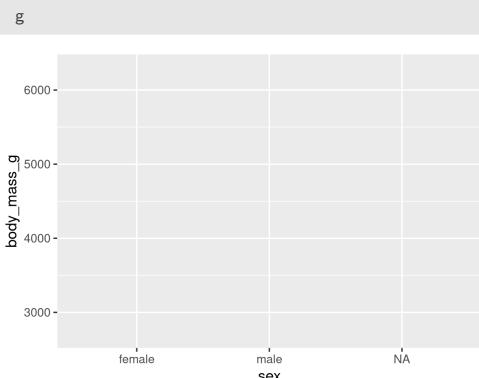
```
g <- ggplot(data = penguins, aes(x = sex, y = body_mass_g))
```

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Plots are objects

Any ggplot can be saved as an object

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

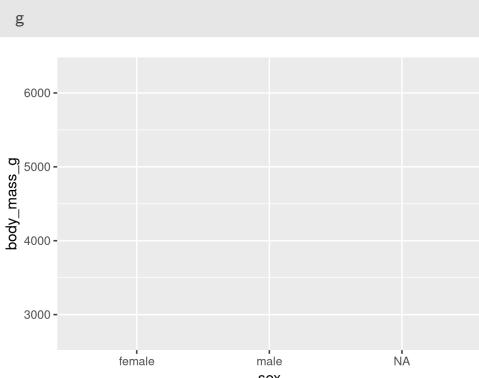


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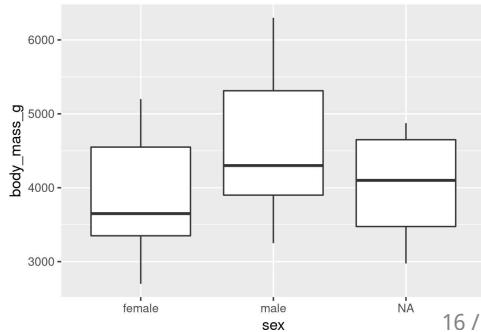
Plots are objects

Any ggplot can be saved as an object

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



```
g + geom_boxplot()
```



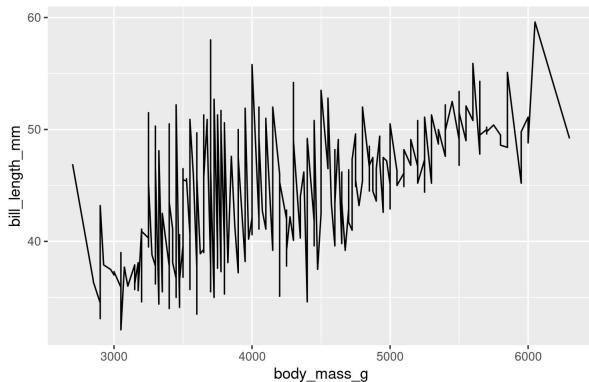
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More Geoms

(Plot types)

Geoms: Lines

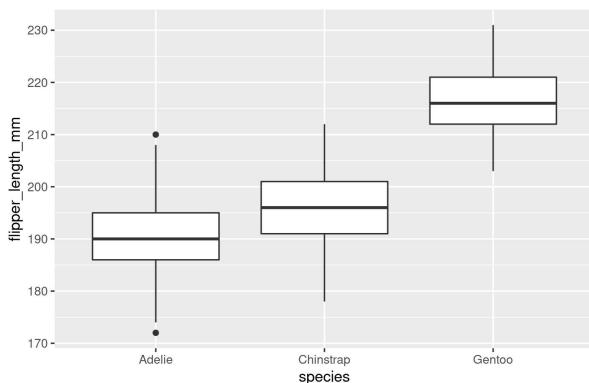
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +  
  geom_line()
```



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Geoms: Boxplots

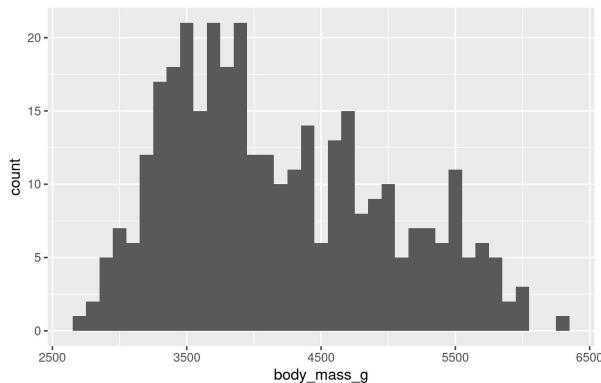
```
ggplot(data = penguins, aes(x = species, y = flipper_length_mm)) +  
  geom_boxplot()
```



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Geoms: Histogram

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

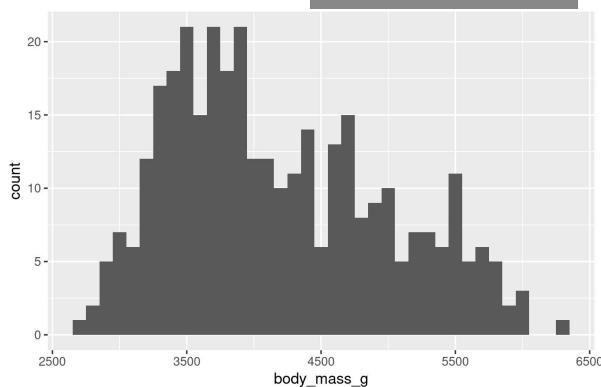


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Geoms: Histogram

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

Note: We only need 1 aesthetic here (x)

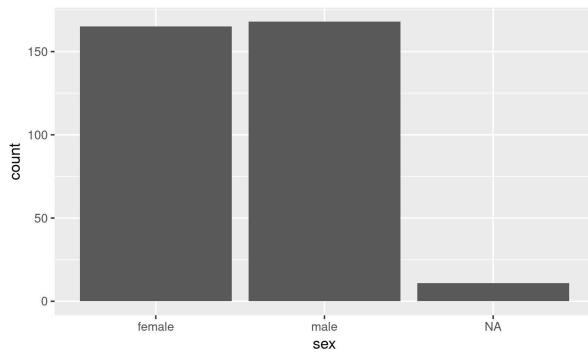


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Geoms: Barplots

Let **ggplot** count your data

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

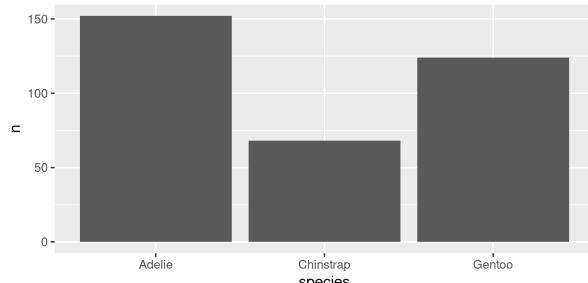


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Geoms: Barplots

You can also provide the counts

```
# Create our own data frame of counts  
species <- count(penguins, species)  
  
ggplot(data = species, aes(x = species, y = n)) +  
  geom_bar(stat = "identity")
```

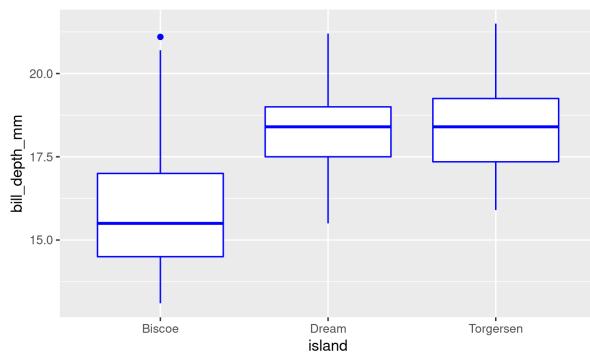


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Your Turn: Create this plot

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

Extra Challenge:
Plot points on top

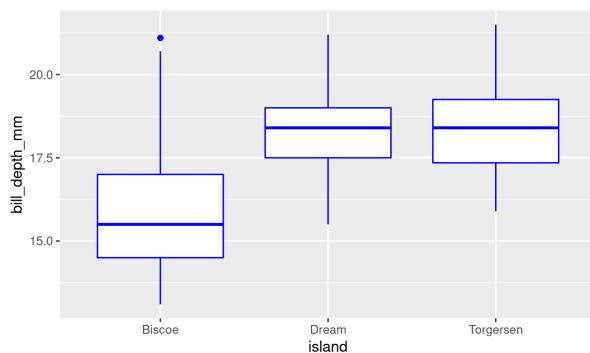


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Your Turn: Create this plot

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

Extra Challenge:
Plot points on top

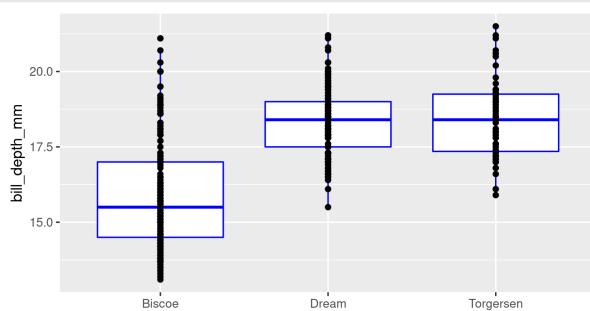


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Your Turn: Create this plot (Extra Challenge)

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

Extra Challenge
Plot points on top

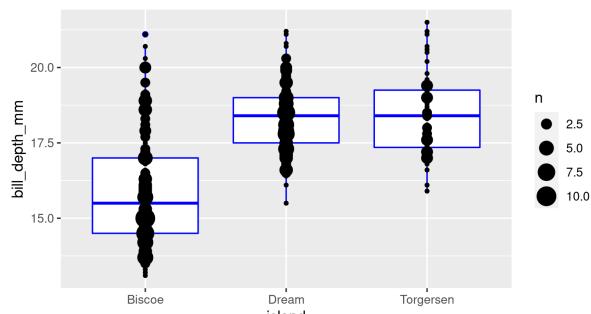


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Your Turn: Create this plot (Extra Challenge)

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

Extra Challenge
Plot points on top

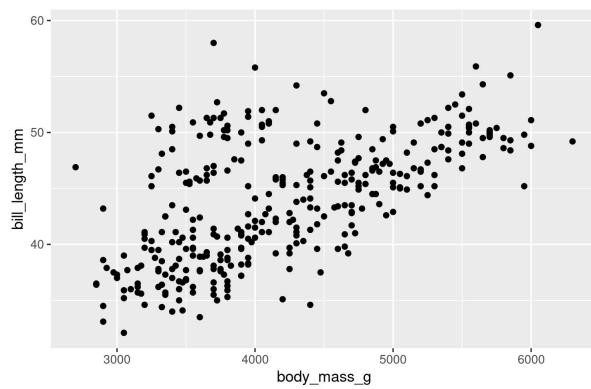


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Showing data by group

Mapping aesthetics

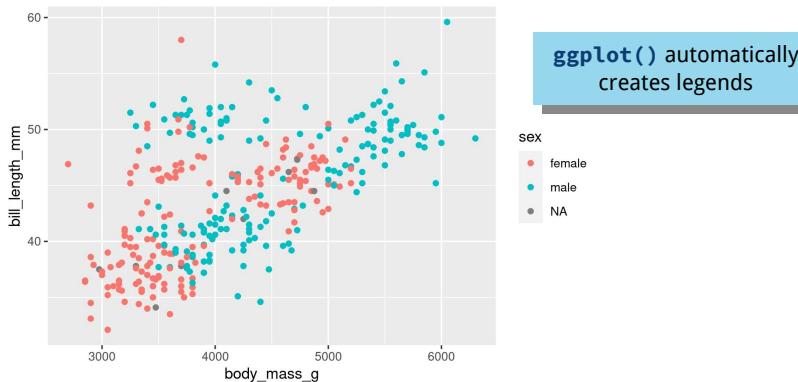
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm)) +  
  geom_point()
```



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Mapping aesthetics

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

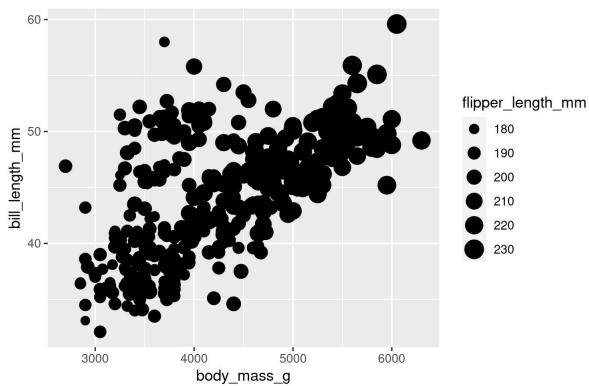


ggplot() automatically creates legends

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Mapping aesthetics

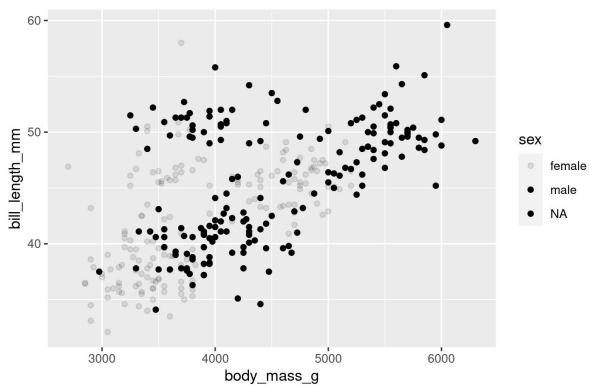
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, size = flipper_length_mm)) +  
  geom_point()
```



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Mapping aesthetics

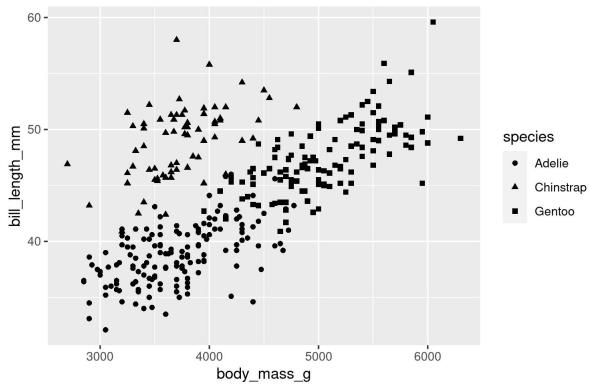
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, alpha = sex)) +  
  geom_point()
```



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Mapping aesthetics

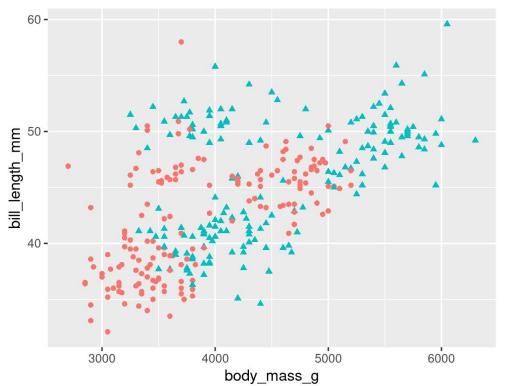
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, shape = species)) +  
  geom_point()
```



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Mapping aesthetics

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

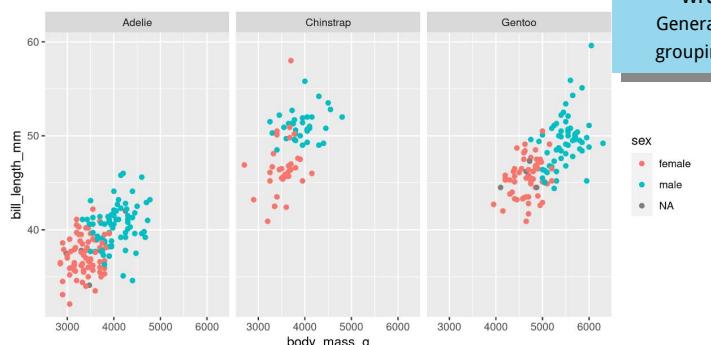


ggplot() combines
legends where it can

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Faceting: `facet_wrap()`

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



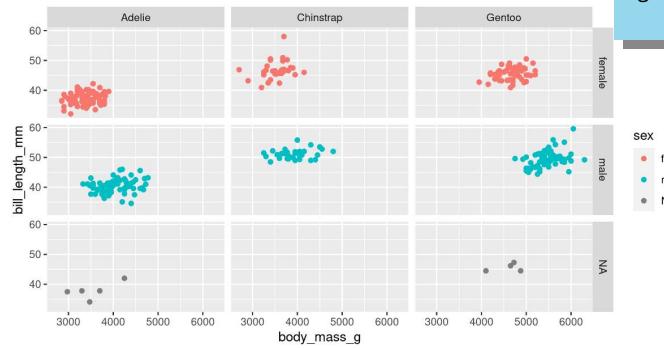
Split plots by
wrapping
Generally for one
grouping variable

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Faceting: `facet_grid()`

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

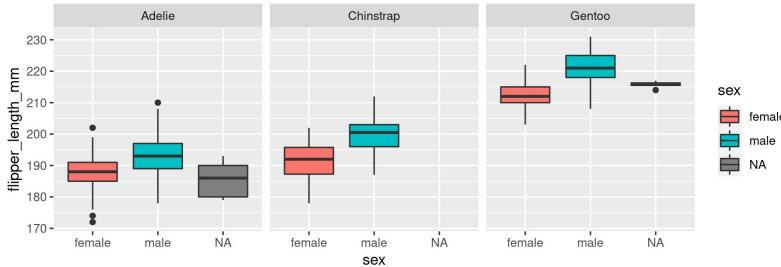
Split plots by two grouping variables on a grid



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Your Turn: Create this plot

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



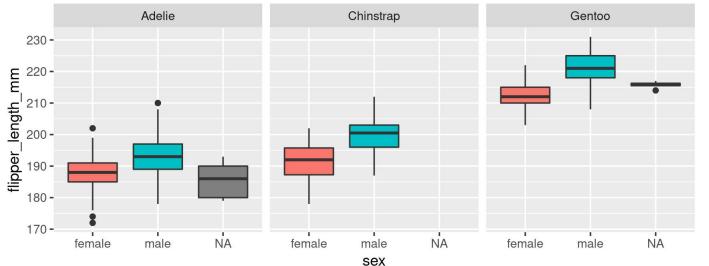
Hint: `colour` is for outlining with a colour, `fill` is for 'filling' with a colour

Extra Challenge: Split boxplots by sex and island

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Your Turn: Create this plot

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



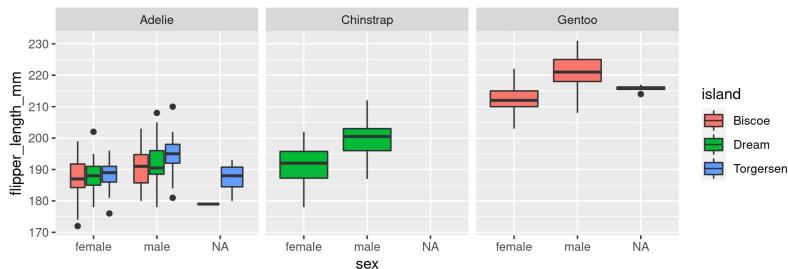
Hint: `colour` is for outlining with a colour, `fill` is for 'filling' with a colour

Extra Challenge: Split boxplots by sex and island

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Your Turn: Create this plot (Extra Challenge)

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



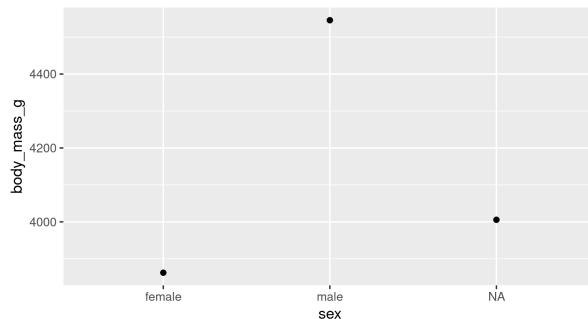
Small change (`fill = sex` to `fill = island`) results in completely different plot

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Summarizing data

Add data means as points

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

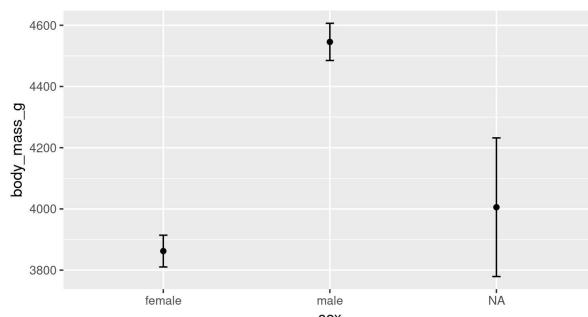


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Summarizing data

Add error bars, calculated from the data

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



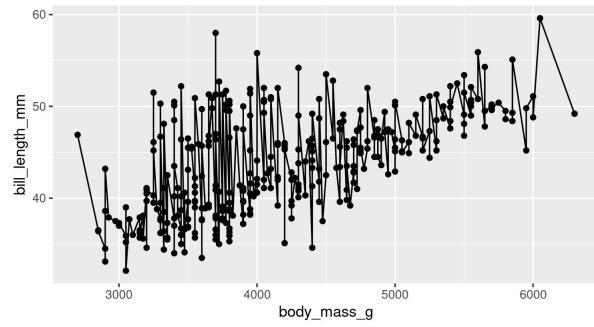
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Trendlines / Regression Lines

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()
```



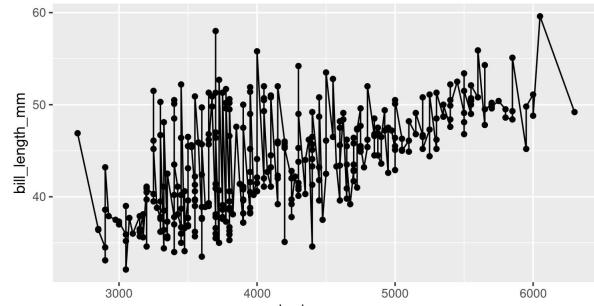
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Trendlines / Regression lines

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



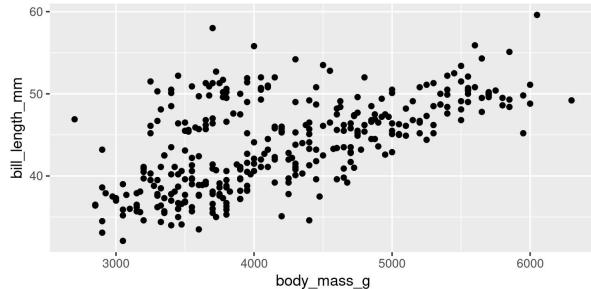
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Trendlines / Regression lines

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
```



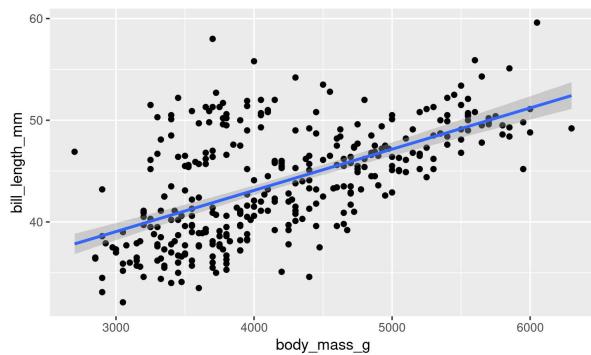
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Trendlines / Regression lines

Add the `stat_smooth()`

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

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



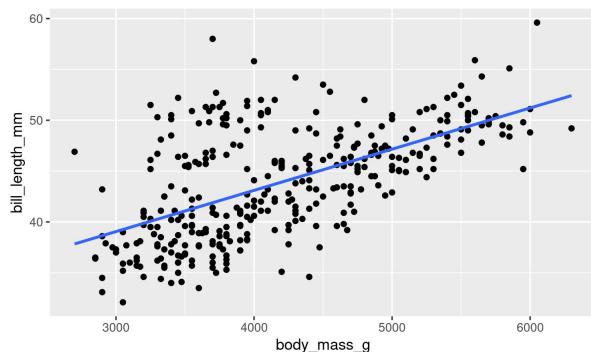
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Trendlines / Regression lines

Add the `stat_smooth()`

- remove the grey ribbon `se = FALSE`

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



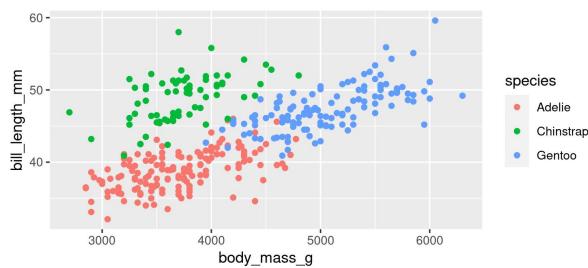
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Trendlines / Regression lines

A line for each group

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

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



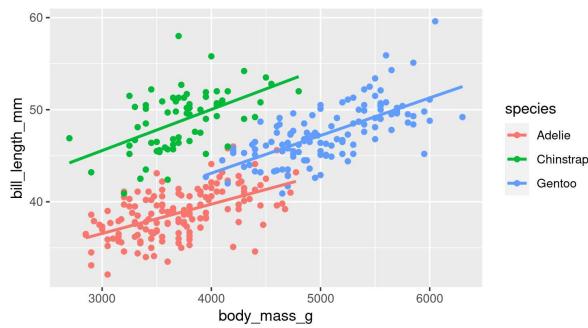
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Trendlines / Regression lines

A line for each group

- `stat_smooth()` automatically uses the same grouping

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

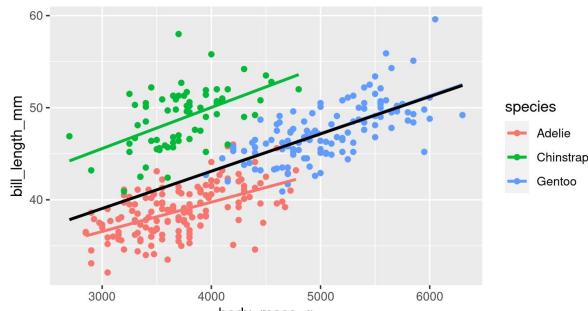


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Trendlines / Regression lines

A line for each group AND overall

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



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Your Turn: Create this plot

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

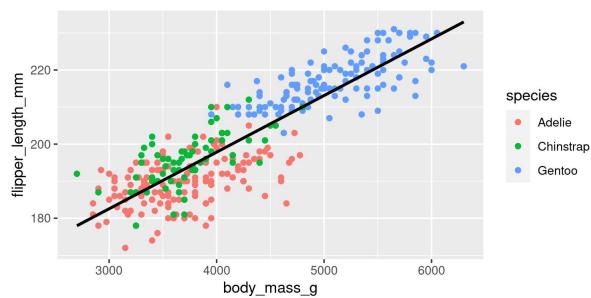
Extra Challenge: Create a separate plot for each sex as well

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Your Turn: Create this plot

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

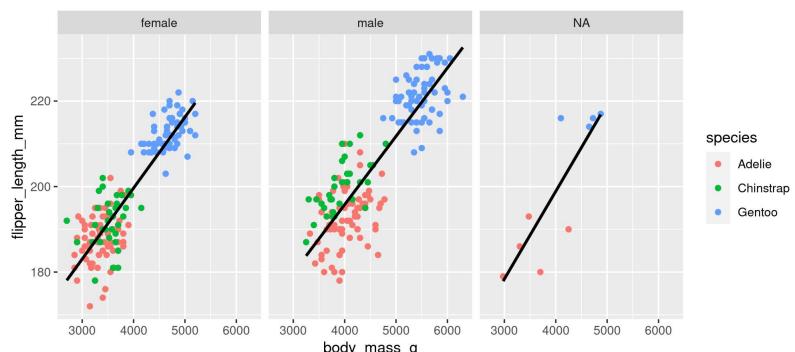
```
ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +  
  geom_point() +  
  stat_smooth(se = FALSE, colour = "black", method = "lm")
```



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Your Turn: Create this plot (Extra Challenge)

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



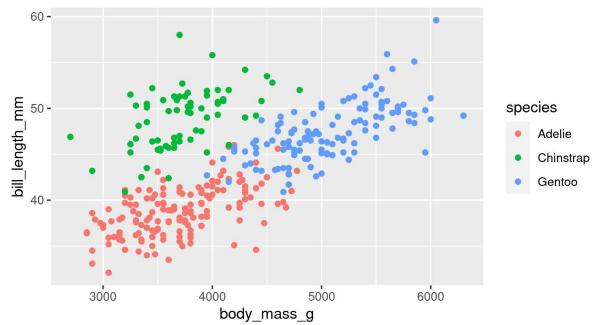
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Customizing plots

Customizing: Starting plot

Let's work with this plot

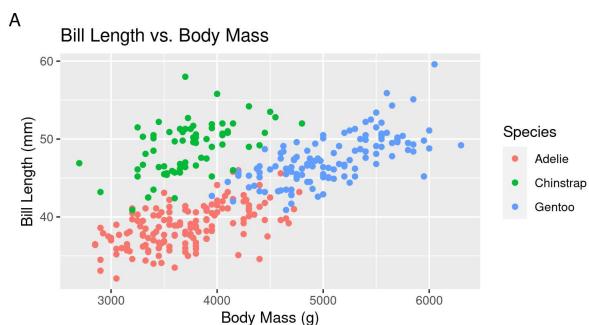
```
g <- ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = species)) +  
  geom_point()
```



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Customizing: Labels

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

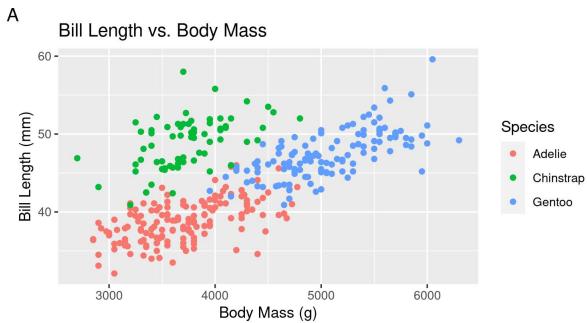


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Customizing: Labels

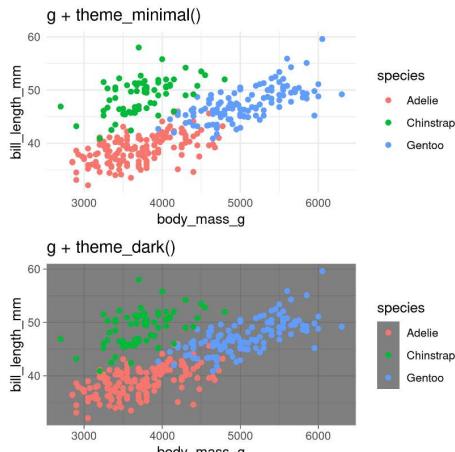
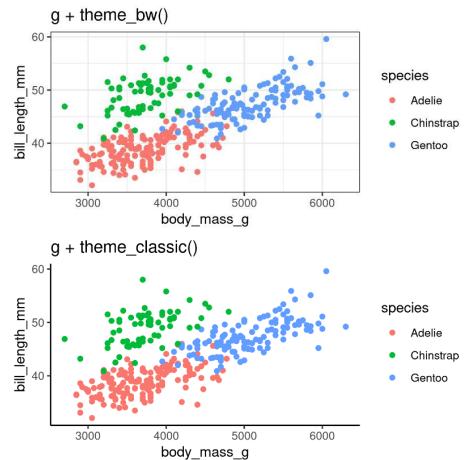
```
g + labs(title = "Bill Length vs. Body Mass",
         x = "Body Mass (g)",
         y = "Bill Length (mm)",
         colour = "Species", tag = "A")
```

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



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Customizing: Built-in themes



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Customizing: Axes

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

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

Common arguments

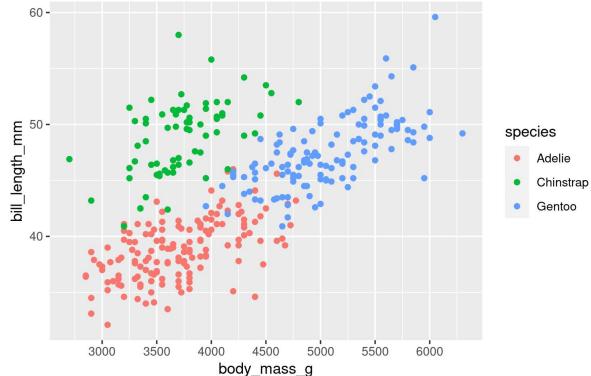
```
g + scale_x_continuous(breaks = seq(0, 20, 10)) # Tick breaks
g + scale_x_continuous(limits = c(0, 15))        # xlim() is a shortcut for this
g + scale_x_continuous(expand = c(0, 0))          # Space between axis and data
```

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Customizing: Axes

Breaks

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

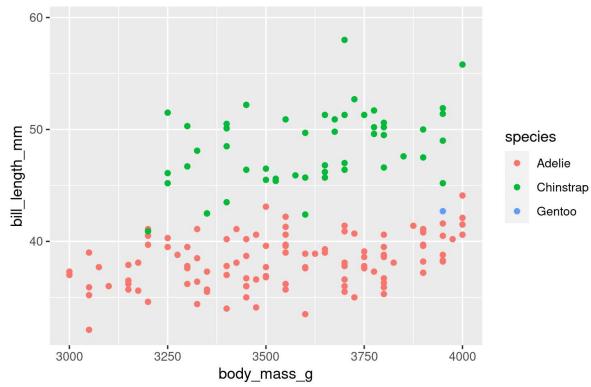


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Customizing: Axes

Limits

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

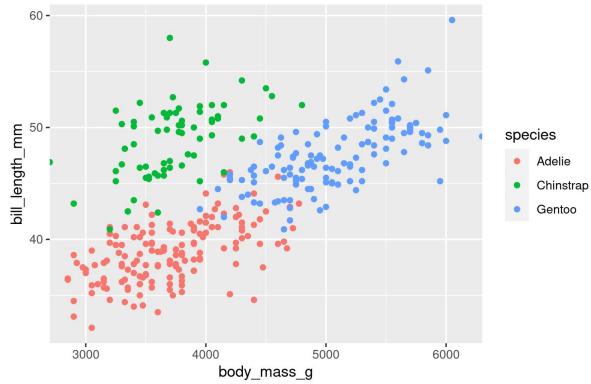


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Customizing: Axes

Space between origin and axis start

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



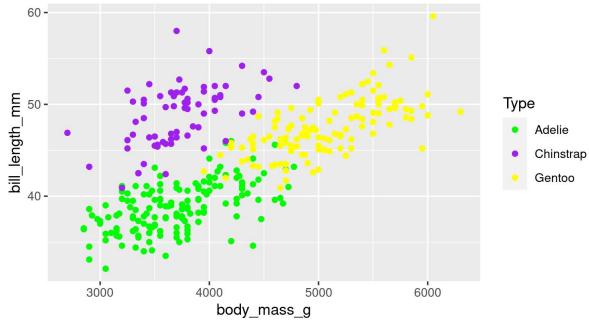
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Customizing: Aesthetics

Using scales

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

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



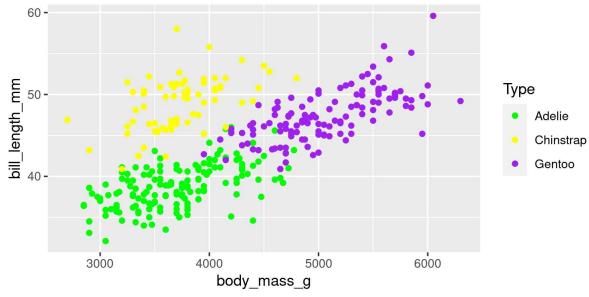
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Customizing: Aesthetics

Using scales

Or be very explicit:

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



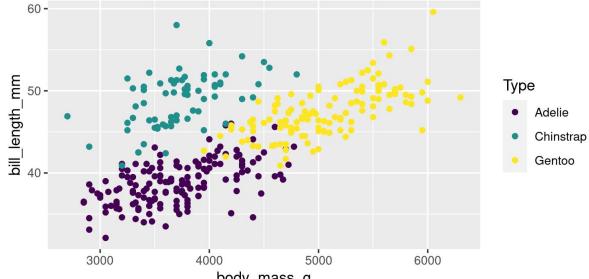
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Customizing: Aesthetics

For colours, consider colour-blind-friendly scale

`viridis_d` for "discrete" data

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



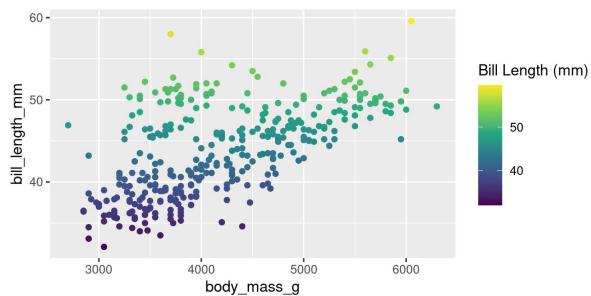
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Customizing: Aesthetics

For colours, consider colour-blind-friendly scale

`viridis_c` for "continuous" data

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



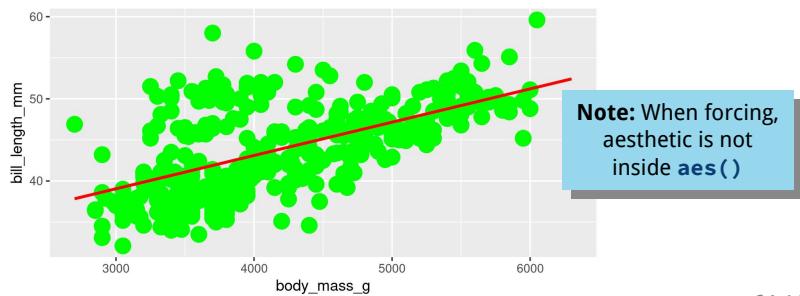
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Customizing: Aesthetics

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")
```

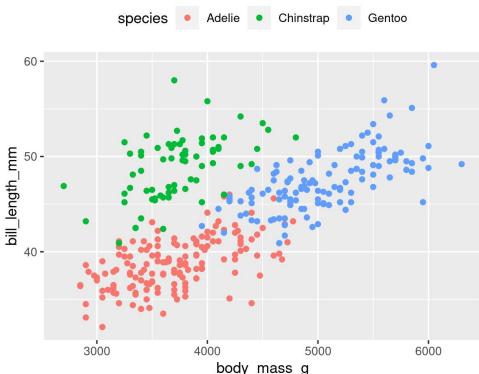


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Customizing: Legends placement

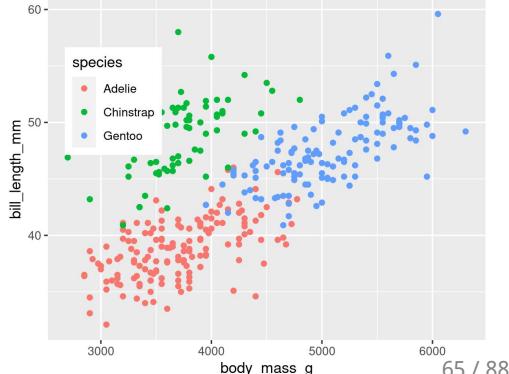
At the: top, bottom, left, right

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



Exactly here

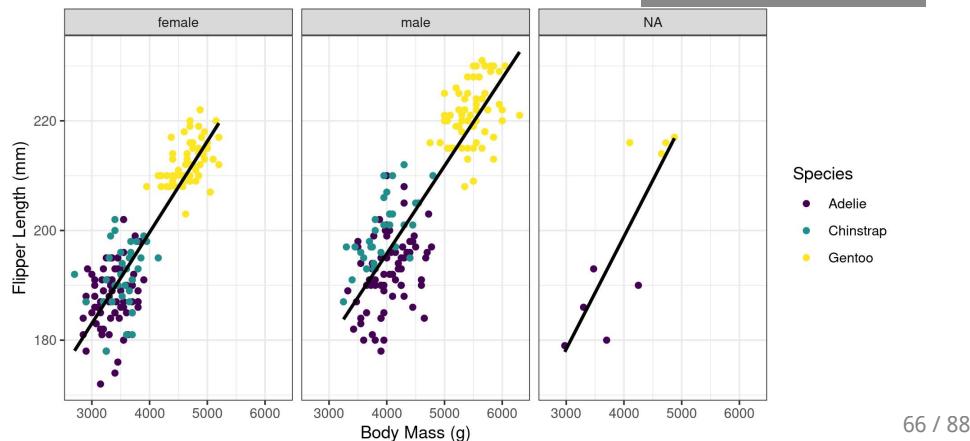
```
g + theme(legend.position = c(0.15, 0.7))
```



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Your Turn: Create this plot

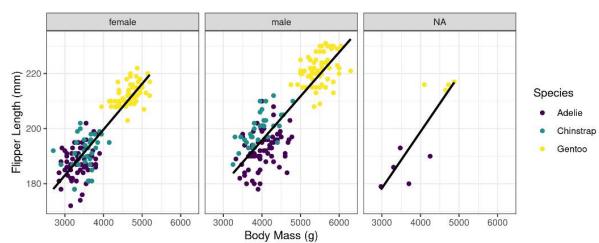
Extra Challenge:
Create a plot of your own data



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Your Turn: Create this plot

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



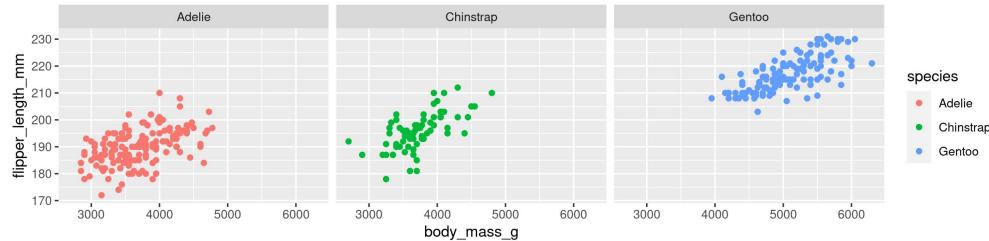
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Annotating plots

Annotating

Plot to be annotated: Let's add sample sizes

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



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Annotating

Create data to use in our annotations

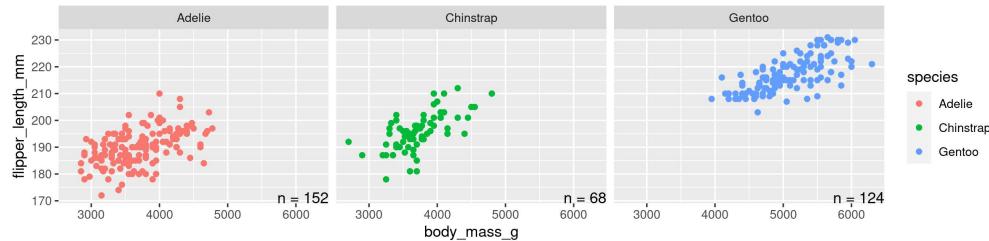
(`mutate()` is covered tomorrow!)

```
library(tidyverse)  
n <- count(penguins, species)  
n <- mutate(n, text = paste0("n = ", n))  
n  
  
## # A tibble: 3 x 3  
##   species      n text  
##   <fct>     <int> <chr>  
## 1 Adelie      152 n = 152  
## 2 Chinstrap    68 n = 68  
## 3 Gentoo      124 n = 124
```

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Annotating

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



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Combining plots

Combining plots with **patchwork**

Setup

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

```
library(patchwork)

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

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

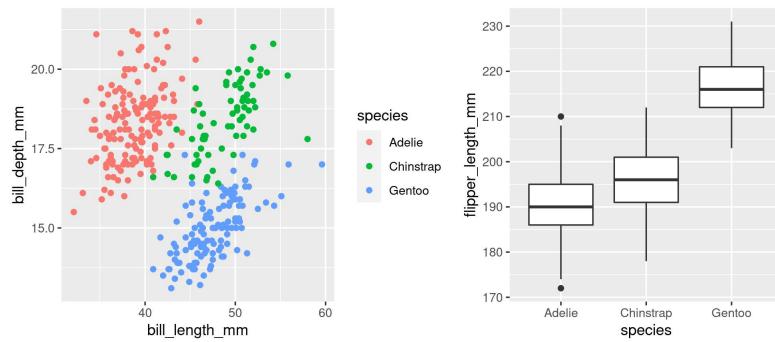
g3 <- ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g, colour = species)) +
  geom_point()
```

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Combining plots with **patchwork**

Side-by-Side 2 plots

```
g1 + g2
```

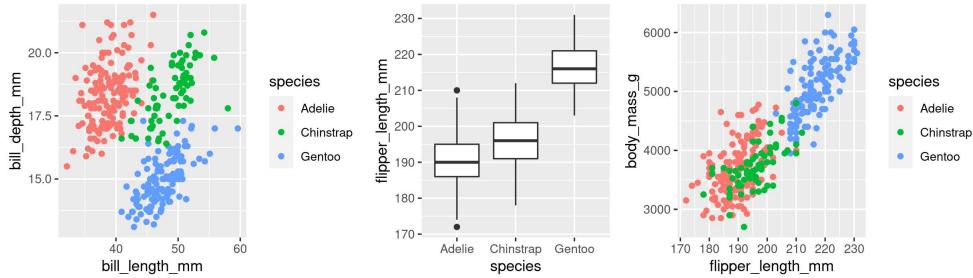


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Combining plots with **patchwork**

Side-by-Side 3 plots

`g1 + g2 + g3`

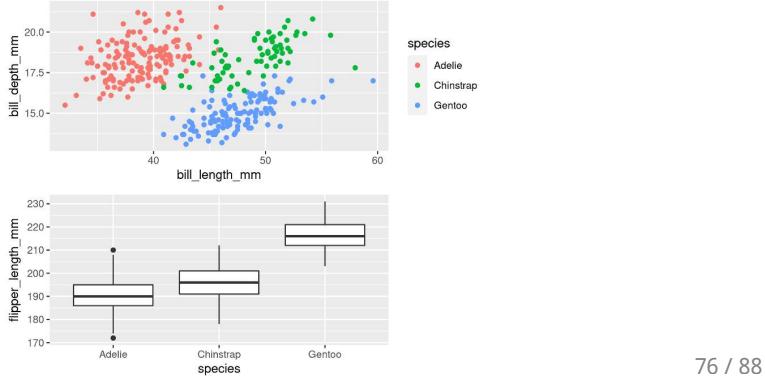


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Combining plots with **patchwork**

Stacked 2 plots

`g1 / g2`

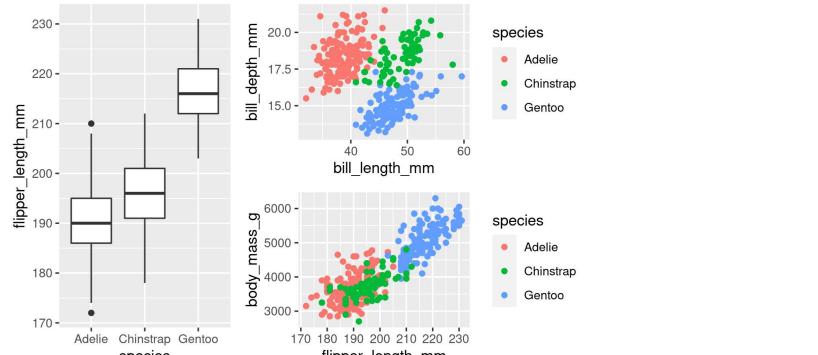


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Combining plots with **patchwork**

More complex arrangements

`g2 + (g1 / g3)`

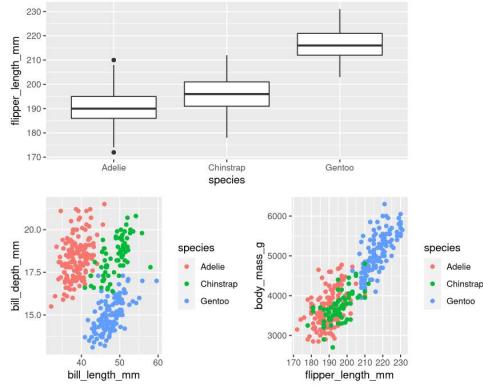


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Combining plots with **patchwork**

More complex arrangements

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

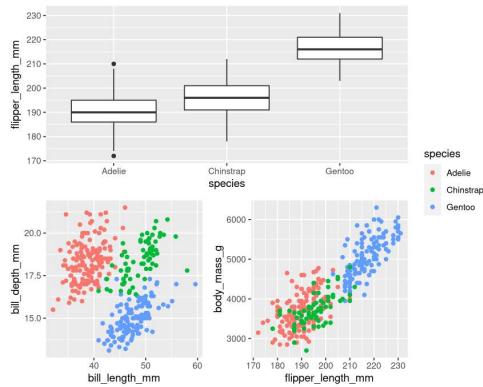


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Combining plots with **patchwork**

"collect" common legends

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

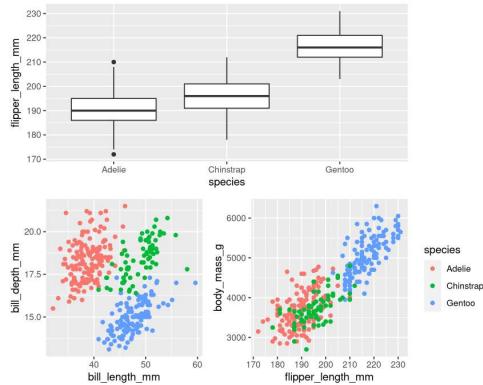


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Combining plots with **patchwork**

"collect" common legends

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

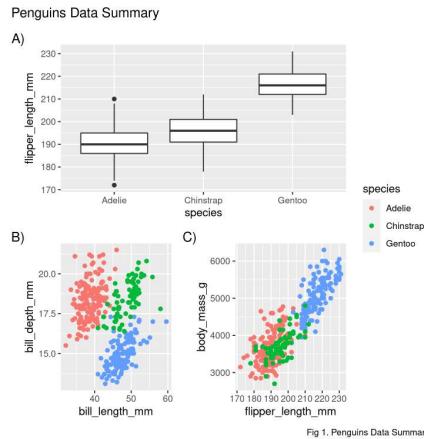


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Combining plots with **patchwork**

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 = ")")
```



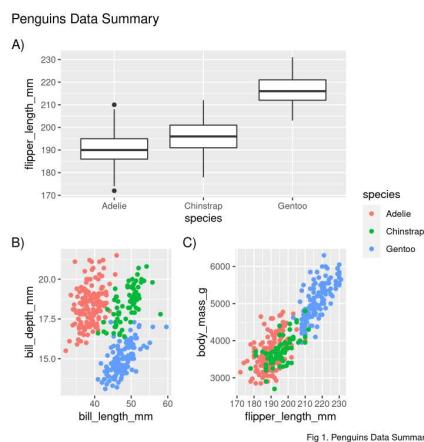
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Combining plots with **patchwork**

Annotate

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

Your Turn: Combine any 3 figures



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Saving plots

Saving plots

RStudio Export

Demo

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Saving plots

RStudio Export

Demo

`ggsave()`

```
g <- ggplot(penguins, aes(x = sex, y = bill_length_mm, fill = year)) +  
  geom_boxplot()  
  
ggsave(filename = "penguins_mass.png", plot = g)  
  
## Saving 6 x 3.9 in image
```

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Saving plots

Publication quality plots

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

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

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Wrapping up: Common mistakes

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

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Wrapping up: Common mistakes

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

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

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

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

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

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Wrapping up: Common mistakes

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

Either move the aesthetic...

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

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

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

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Wrapping up: Further reading (all **Free!**)

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

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