Bird Cave Workshop 2021

Creating Figures as an Intro to R

Using the **`ggplot2`** package

Steffi LaZerte

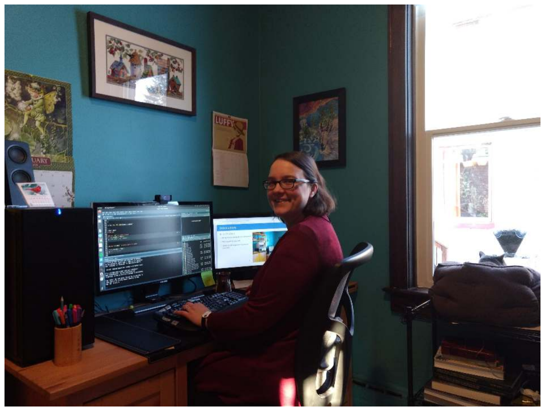
Artwork by @allison_horst

Introductions

Instructor

Dr. Steffi LaZerte

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



Introductions

Assistant

Dr. Alex Koiter

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

What about you?

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

Outline

1. A little about R

2. Creating figures with `ggplot2`

3. Combining figures with `patchwork`

4. Saving figures

Outline

1. A little about R

2. Creating figures with `ggplot2`

3. Combining figures with `patchwork`

4. Saving figures

Taken this or a similar workshop before?

During activities consider...

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

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

What is R?

R is Programming language

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

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

For example

R, what is 56 times 5.8?

```
56 * 5.8
```

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

Use code to tell R what to do

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

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

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

Use code to tell R what to do

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

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

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

R, save this value for later

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

Use code to tell R what to do

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

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

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

R, save this value for later

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

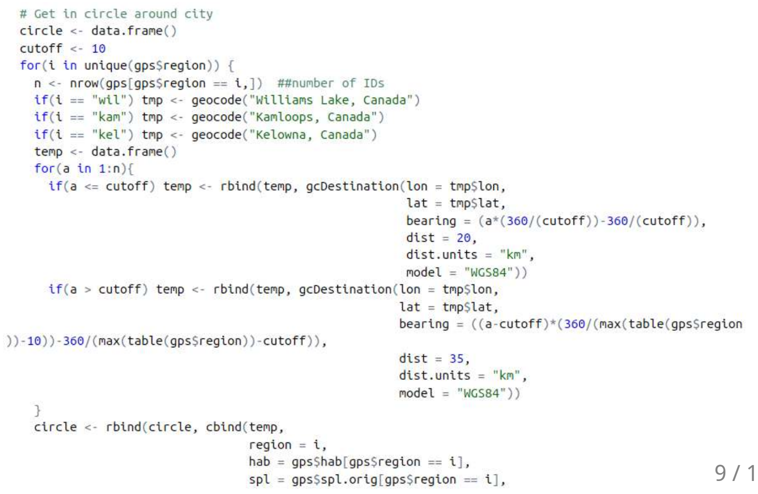
R, multiply this value by 6

```
steffis_mean * 6
```

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

Why R?

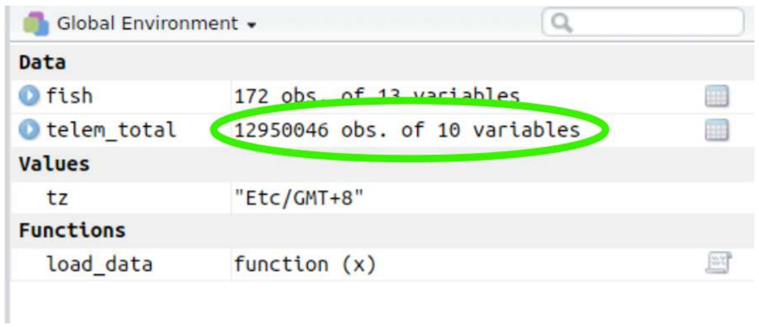
R is hard



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

Why R?

But R is powerful (and reproducible)!



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

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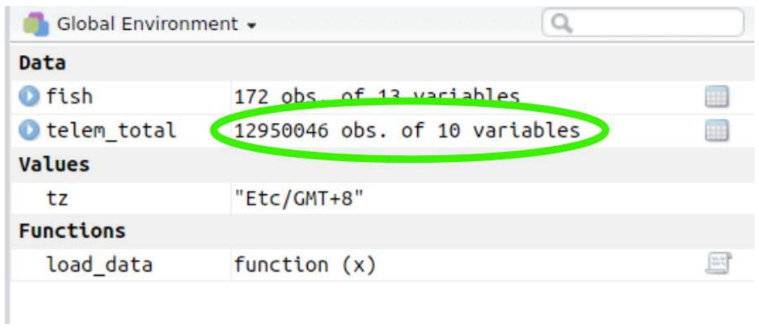

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Global Environment
Data
fish            172 obs. of 13 variables
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Values
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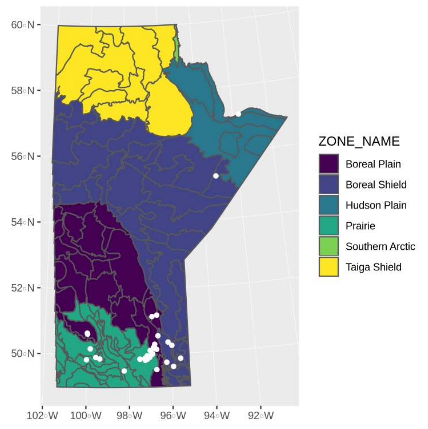
Functions
load_data       function (x)
```

(I made these slides with **R**markdown)

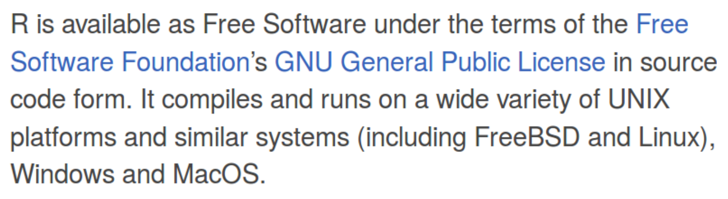
Why R?

R is also beautiful



Why R?

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



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

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ImpostR Syndrome

Impost R
Syndrome

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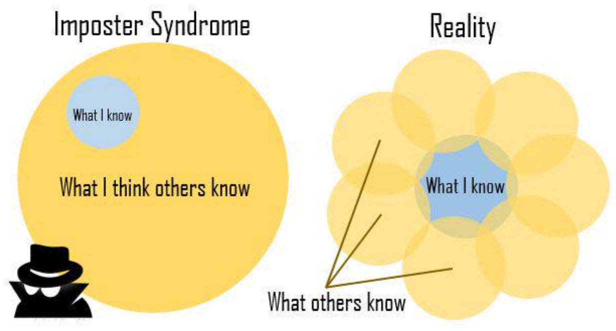
ImpostR Syndrome



David Whittaker

Impost R
Syndrome

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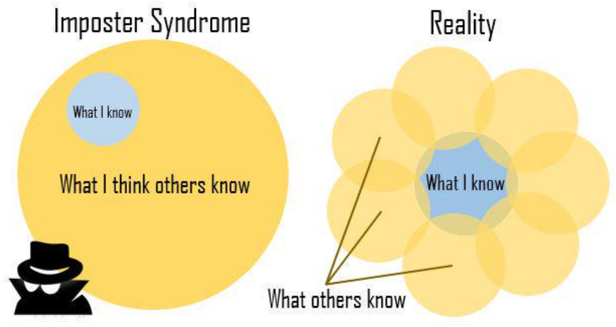
ImpostR Syndrome



David Whittaker

Impost R
Syndrome

Moral of the story?
Make friends, code in groups, learn together and don't beat yourself up

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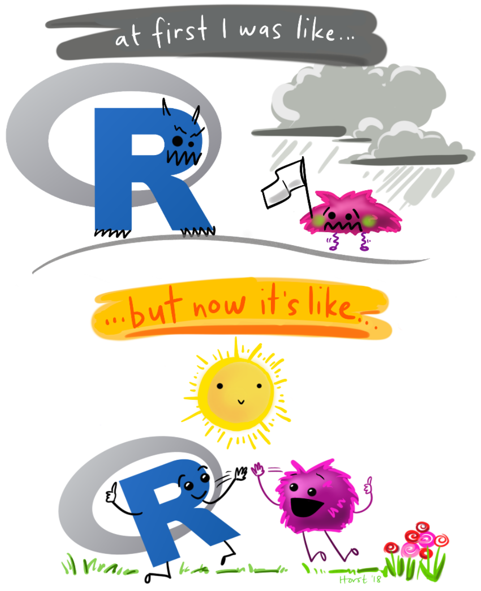

@allison_horst

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About R

Code, Output, Scripts

Code

- The actual commands

Output

- The result of running code or a script

Script

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

Code, Output, Scripts

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- The actual commands

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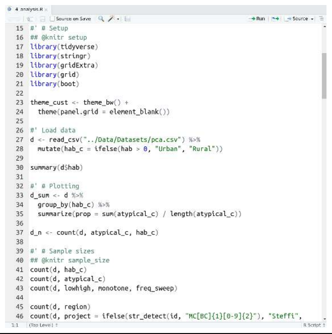
For example:

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

Code

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

Output



```
#' # Setup
## @knitr setup
library(tidyverse)
library(stringr)
library(gridExtra)
library(grid)
library(boot)

theme_cust <- theme_bw() +
  theme(panel.grid = element_blank())

#' Load data
d <- read_csv("../Data/Datasets/pca.csv") %>%
  mutate(hab_c = ifelse(hab > 0, "Urban", "Rural"))

summary(d$hab)

#' # Plotting
d_sum <- d %>%
  group_by(hab_c) %>%
  summarize(prop = sum(atypical_c) / length(atypical_c))

d_n <- count(d, atypical_c, hab_c)

#' # Sample sizes
## @knitr sample_size
count(d, hab_c)
count(d, atypical_c)
count(d, lowhigh, monotone, freq_sweep)

count(d, region)
count(d, project = ifelse(str_detect(id, "MC[BC]{1}[0-9]{2}"), "Steffi",
```

Script

RStudio vs. R

RStudio

R

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

`functions()` - Do things, Return things

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

`functions()` - Do things, Return things

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

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

`functions()` - Do things, Return things

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

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

By name:

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

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

By position:

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

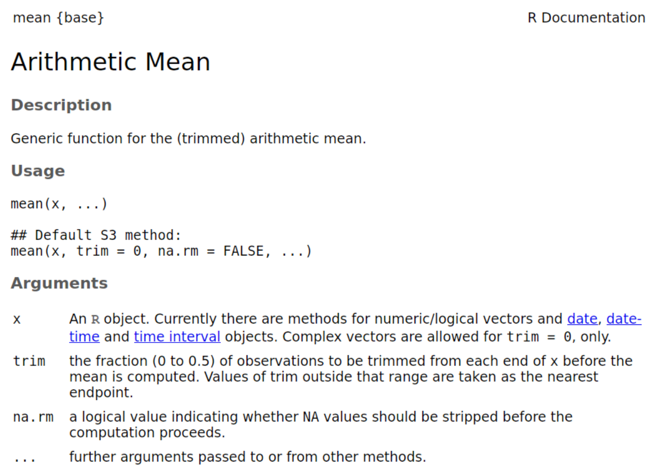
```
## [1] 5.333333
```

R documentation

```
?mean
```

R documentation

```
?mean
```



mean {base} R Documentation

Arithmetic Mean

Description

Generic function for the (trimmed) arithmetic mean.

Usage

```
mean(x, ...)

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

Arguments

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

Data

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

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

Vector (1 dimension)

```
my_data <- c("a", 100, "c")
my_data
```

```
## [1] "a"   "100" "c"
```

Data frame (2 dimensions)

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

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

rows x columns

Your first *real* code!

First Code

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

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

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

First Code

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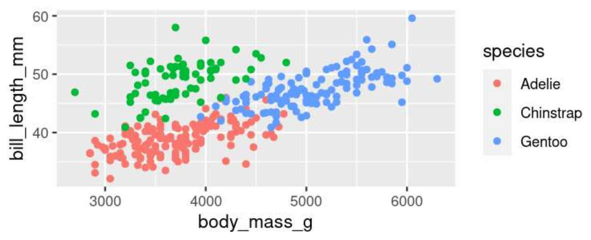
  geom_point()
```

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



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```

Packages
`ggplot2` and **`palmerpenguins`**

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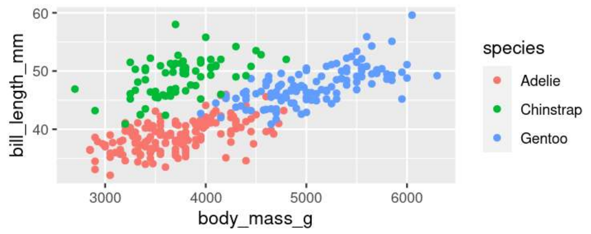

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First Code

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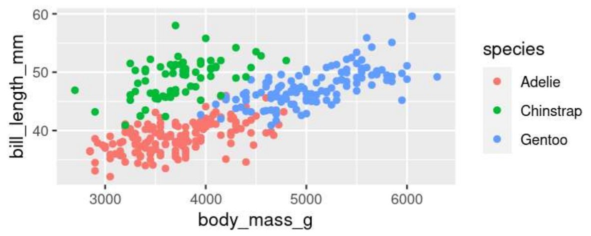
```

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

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



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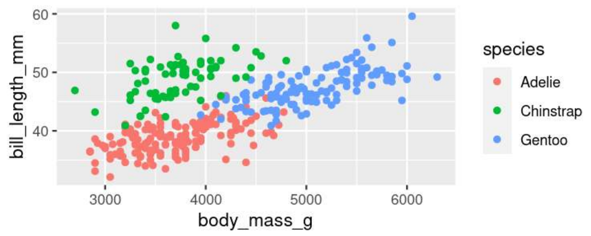
First Code

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

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

+
(Specific to **`ggplot2`**)

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



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First Code

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

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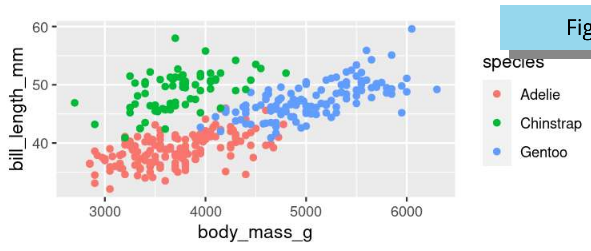
```

Figure!



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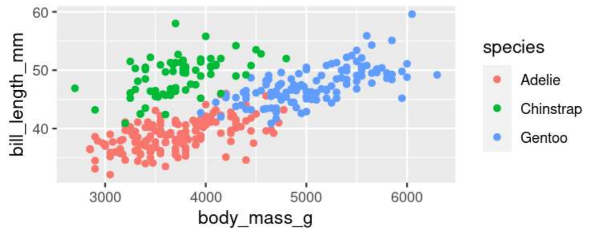
Warning

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



First Code

Comments

```
# First load the packages
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```

```
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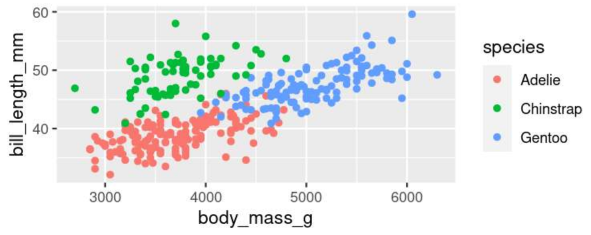
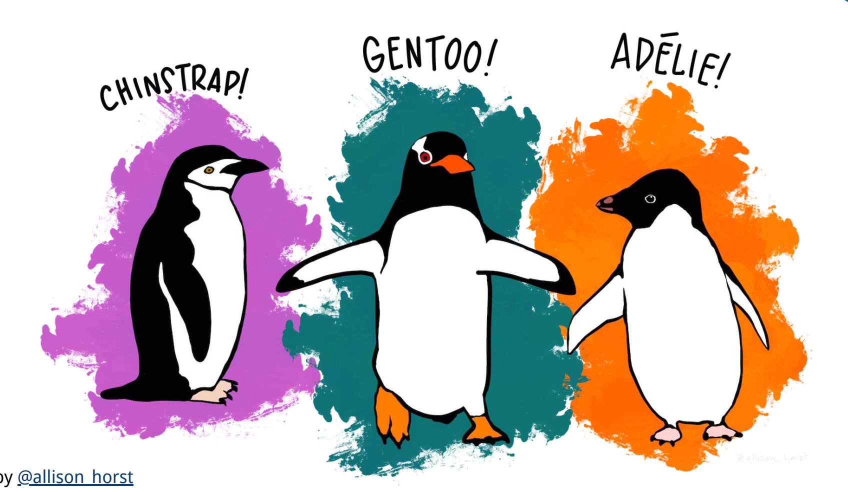


Now you know R!

Let's get started

Our data set: Palmer Penguins!

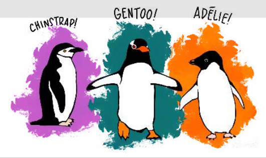


Artwork by @allison_horst

Our data set: Palmer Penguins!

```r
library(palmerpenguins)
penguins
```

```
## # A tibble: 344 x 8
##    species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>              <dbl>         <dbl>             <int>       <int> <fct>  <int>
##  1 Adelie  Torgersen           39.1          18.7               181        3750 male    2007
##  2 Adelie  Torgersen           39.5          17.4               186        3800 female  2007
##  3 Adelie  Torgersen           40.3          18                 195        3250 female  2007
##  4 Adelie  Torgersen           NA            NA                  NA          NA <NA>    2007
##  5 Adelie  Torgersen           36.7          19.3               193        3450 female  2007
##  6 Adelie  Torgersen           39.3          20.6               190        3650 male    2007
##  7 Adelie  Torgersen           38.9          17.8               181        3625 female  2007
##  8 Adelie  Torgersen           39.2          19.6               195        4675 male    2007
##  9 Adelie  Torgersen           34.1          18.1               193        3475 <NA>    2007
## 10 Adelie  Torgersen           42            20.2               190        4250 <NA>    2007
## # … with 334 more rows
```



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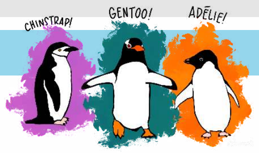
## 10 Adelie  Torgersen           42            20.2               190        4250 <NA>    2007
## # … with 334 more rows
```

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

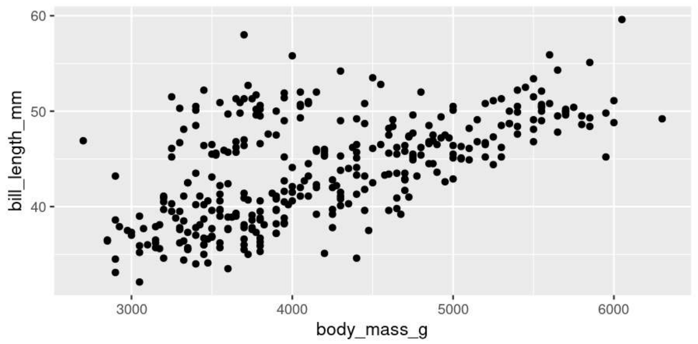


Artwork by @allison_horst

A basic plot

```r
library(palmerpenguins)
library(ggplot2)

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



Break it down

```r
library(palmerpenguins)
library(ggplot2)

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(ggplot2)

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

`library(ggplot2)`

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

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Break it down

```
library(palmerpenguins)
library(ggplot2)

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

`ggplot()`

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

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Break it down

```
library(palmerpenguins)
library(ggplot2)

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

`geom_point()`

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

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

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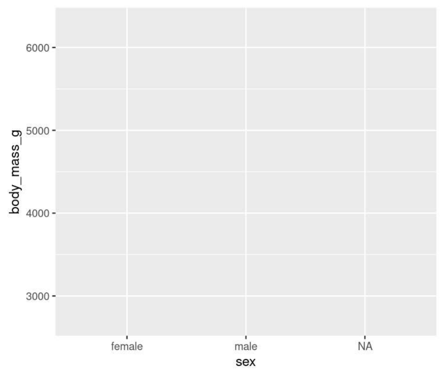
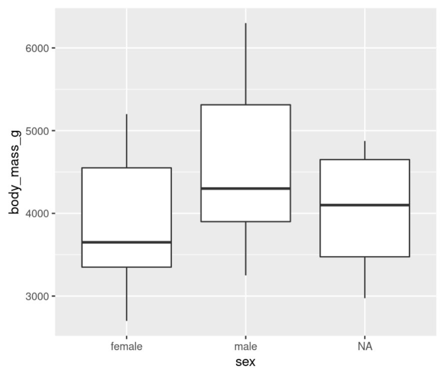
Plots are layered

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



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



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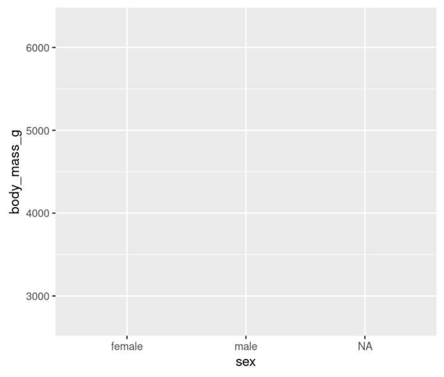
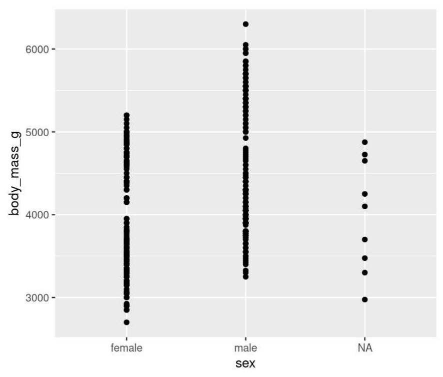
Plots are layered

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



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



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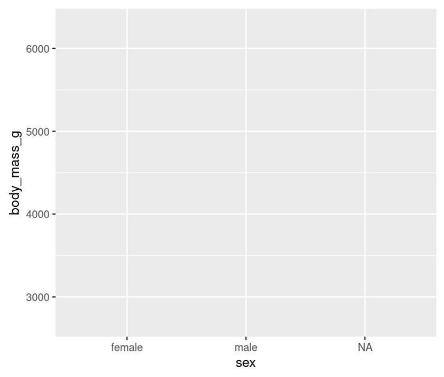
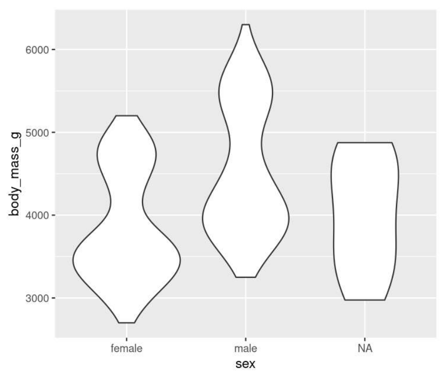
Plots are layered

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



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



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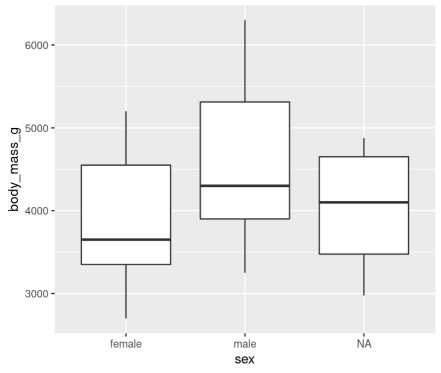
Plots are layered

You can add multiple layers

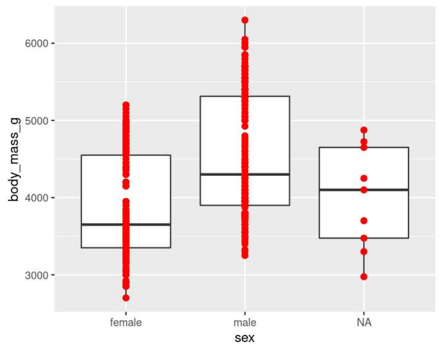
```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +
  geom_boxplot()
```



Plots are layered

You can add multiple layers

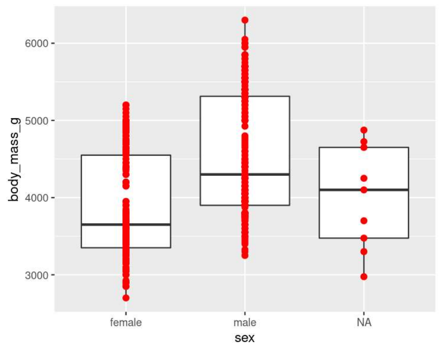
```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +
  geom_boxplot() +
  geom_point(size = 2, colour = "red")
```



Plots are layered

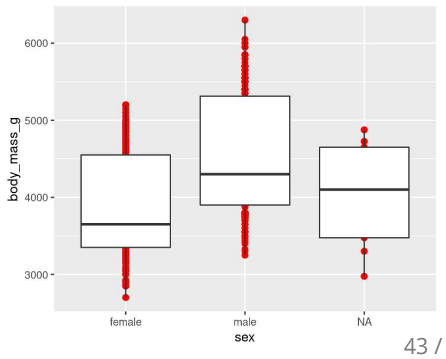
You can add multiple layers

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



Order matters

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



Plots are objects

Any ggplot can be saved as an object

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

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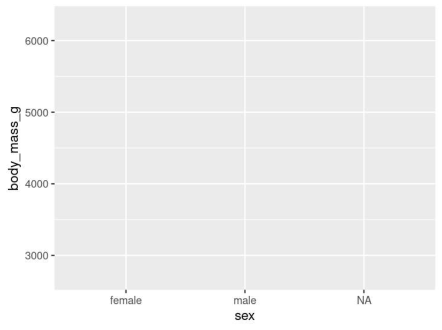
Plots are objects

Any ggplot can be saved as an object

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

```
g
```



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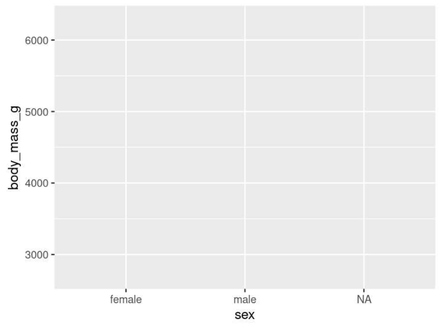
Plots are objects

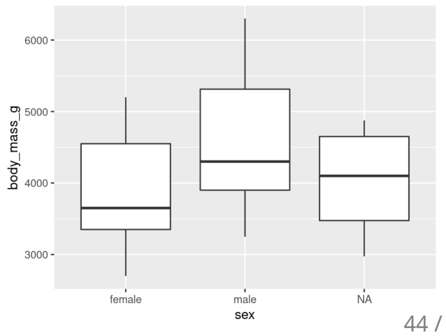
Any ggplot can be saved as an object

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

```
g
```



```
g + geom_boxplot()
```



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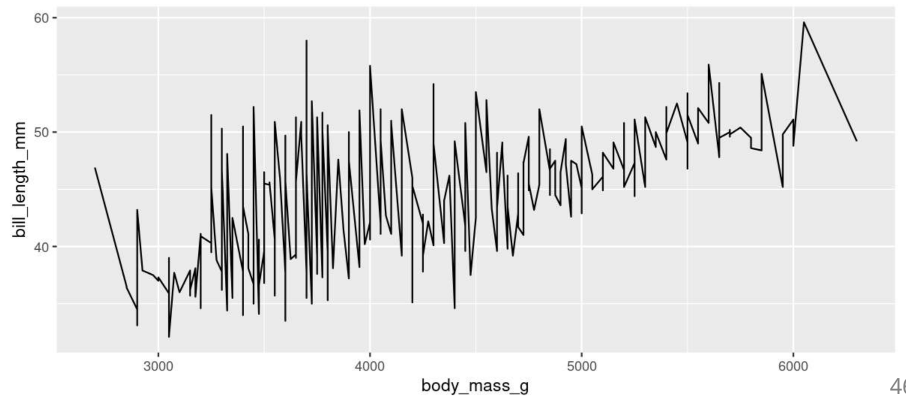
More Geoms

(Plot types)

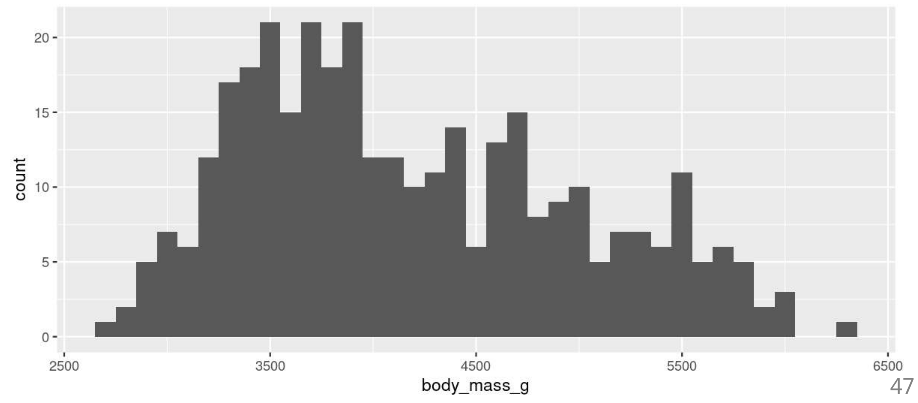
Geoms: Lines

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



Geoms: Histogram

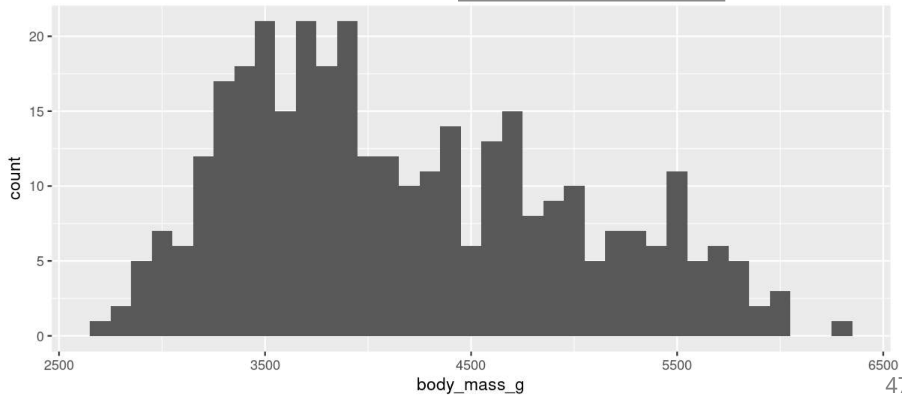
```r
ggplot(data = penguins, aes(x = body_mass_g)) +
  geom_histogram(binwidth = 100)
```



Geoms: Histogram

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

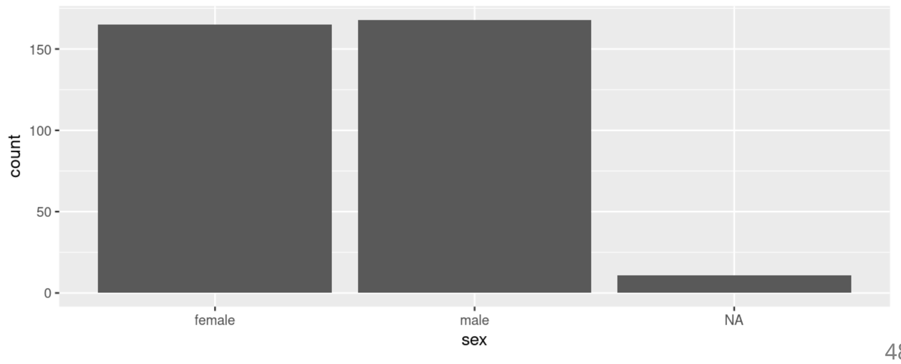
Note: We only need 1 aesthetic here (x)



Geoms: Barplots

Let `ggplot` count your data

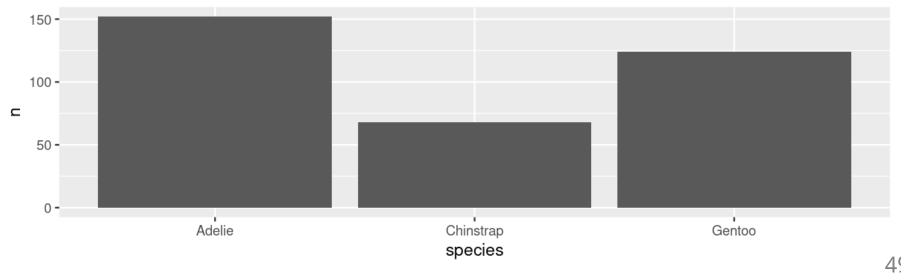
```
ggplot(data = penguins, aes(x = sex)) +
  geom_bar()
```



Geoms: Barplots

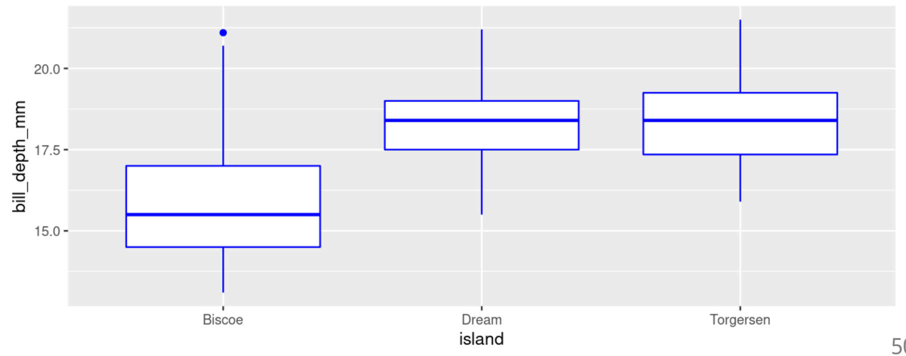
You can also provide the counts

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

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



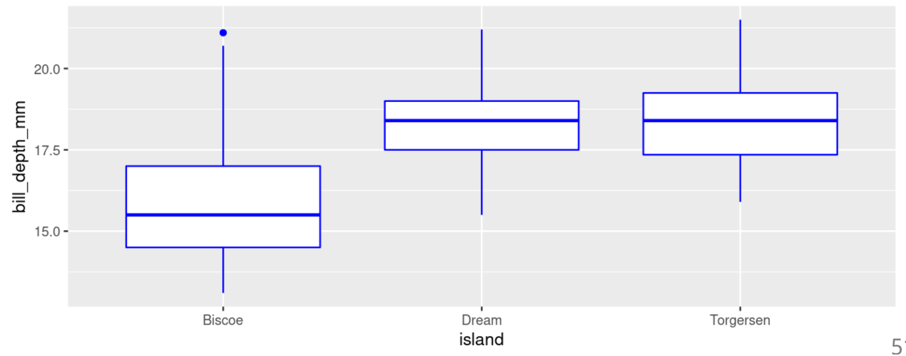
Your Turn: Create this plot

```
library(ggplot2)

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



Your Turn: Create this plot

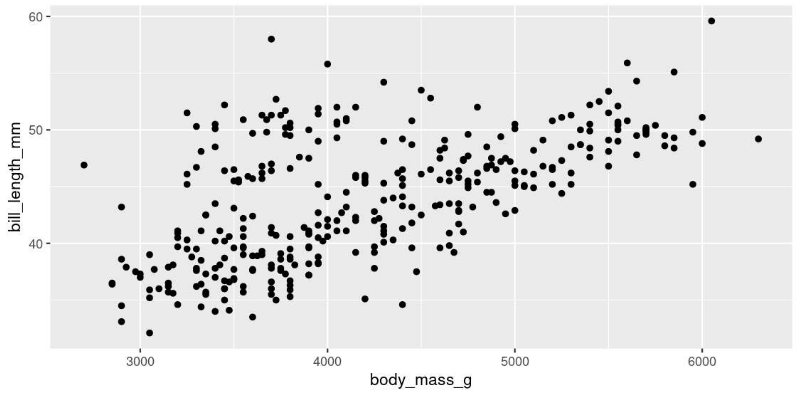
```
library(ggplot2)

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



Showing data by group

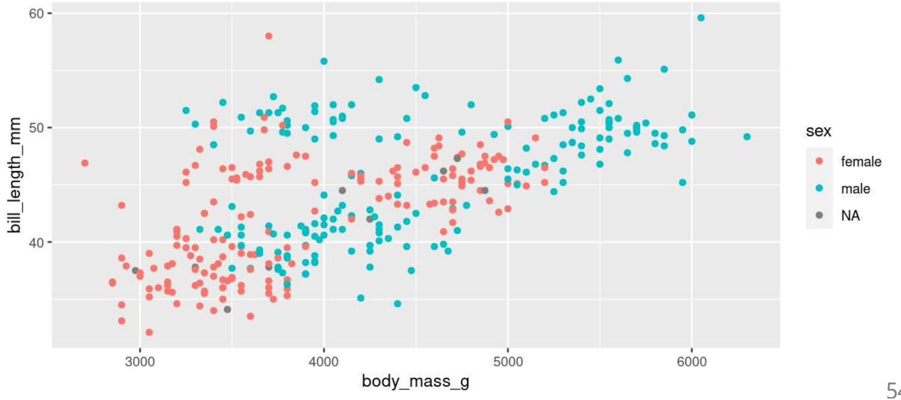
Mapping aesthetics

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



Mapping aesthetics

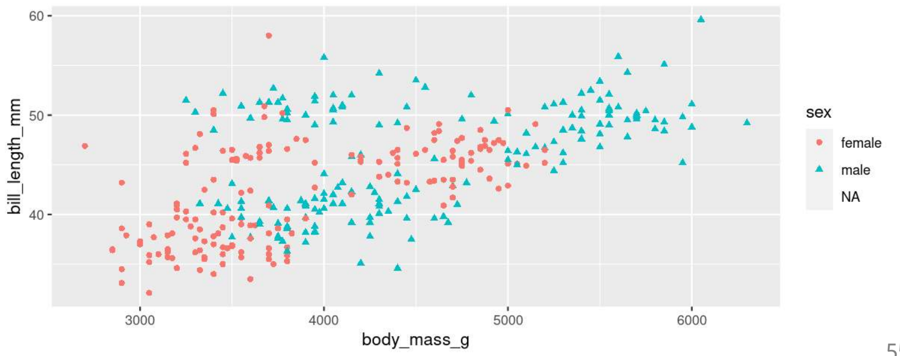
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +
  geom_point()
```



Mapping aesthetics

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

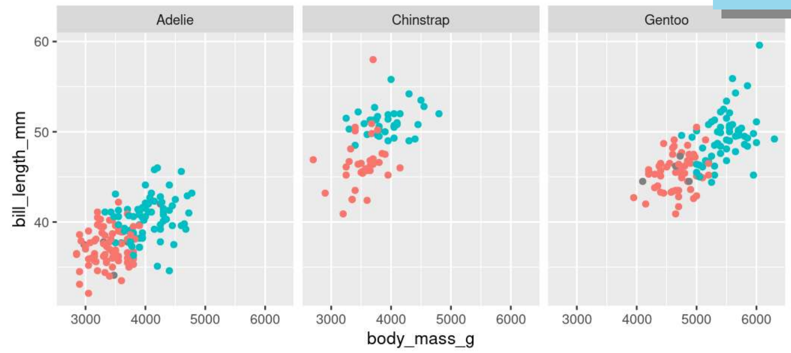
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex, shape = sex)) +
  geom_point()
```



Faceting: `facet_wrap()`

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

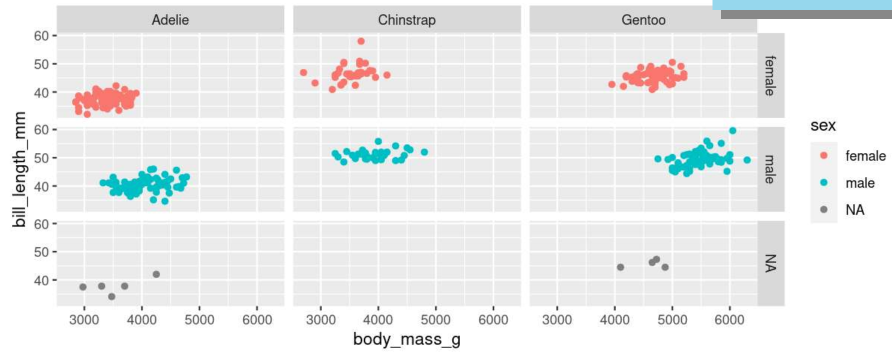
Split plots by **one** grouping variable



Faceting: `facet_grid()`

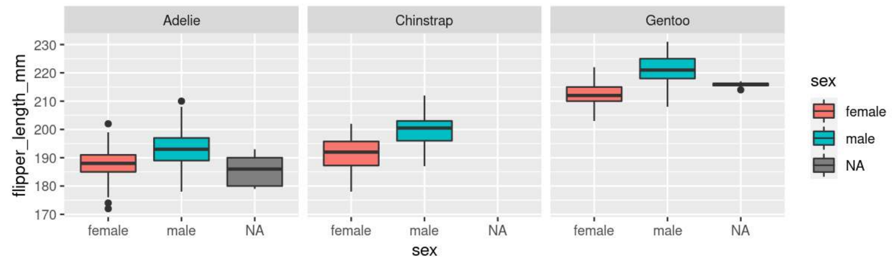
```
ggplot(data = penguins, aes(x = body_mass_g, y = bill_length_mm, colour = sex)) +
  geom_point() +
  facet_grid(sex ~ species)
```

Split plots by **two** grouping variables



Your Turn: Create this plot

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

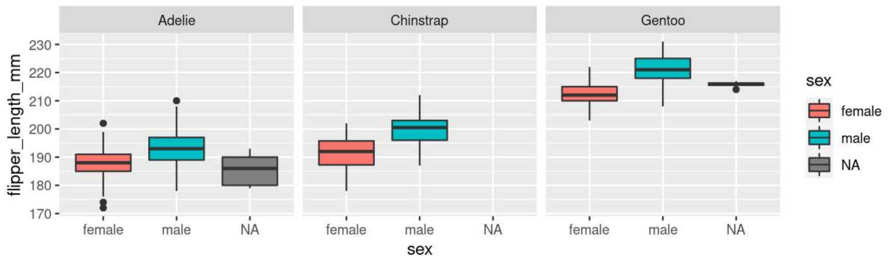


Hint: **`colour`** is for outlining with a colour, **`fill`** is for 'filling' with a colour

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

Your Turn: Create this plot

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



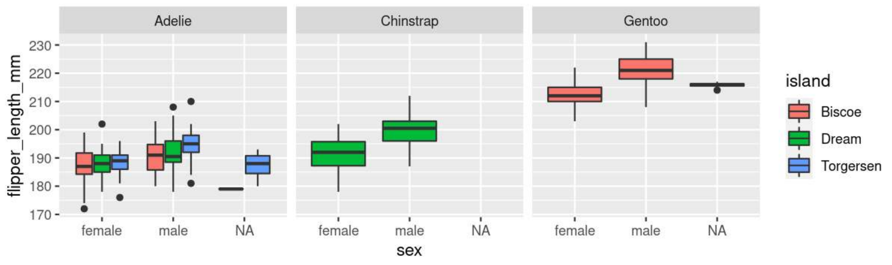
Hint: **`colour`** is for outlining with a colour, **`fill`** is for 'filling' with a colour

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

Your Turn: Create this plot

Too Easy?

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



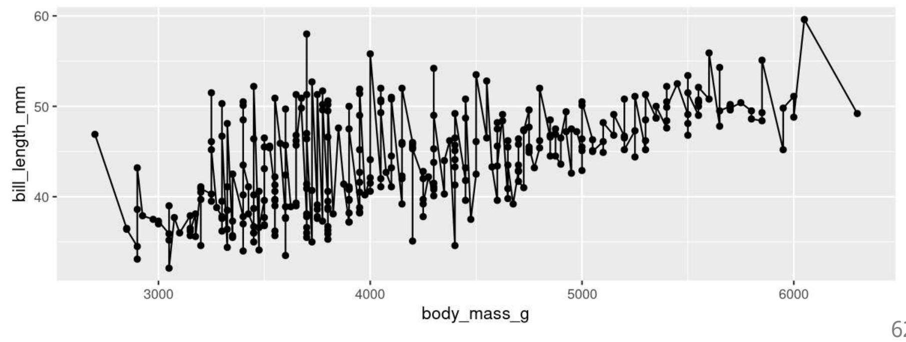
Small change (**`fill = sex`** to **`fill = island`**) results in completely different plot

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()
```

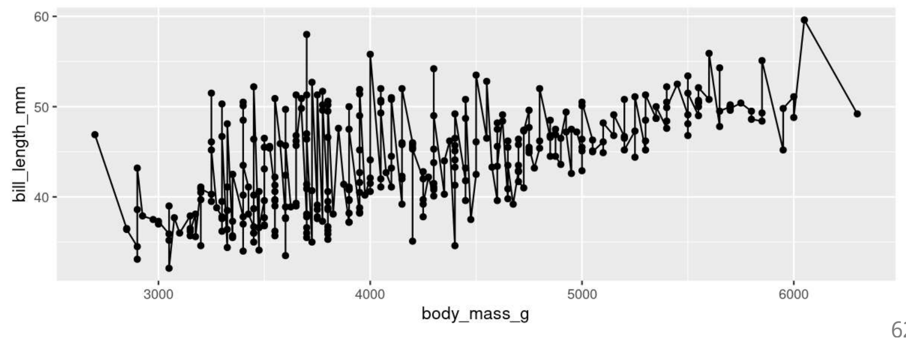


Trendlines / Regression lines

`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

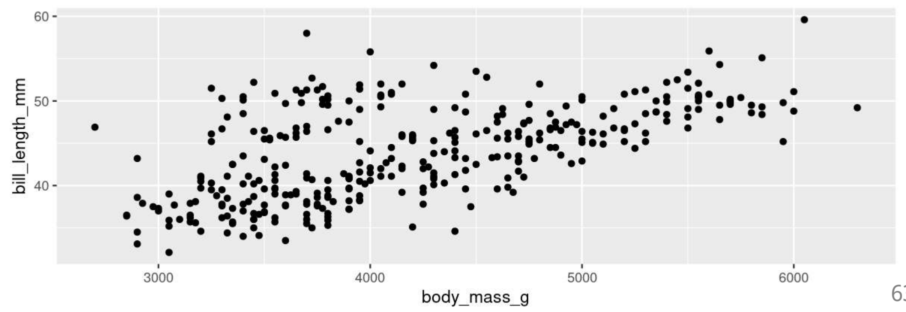


Trendlines / Regression lines

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
```

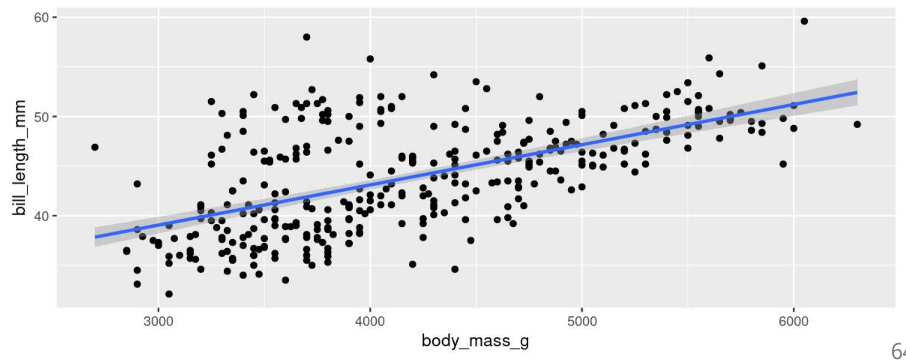


Trendlines / Regression lines

Add the `stat_smooth()`

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

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

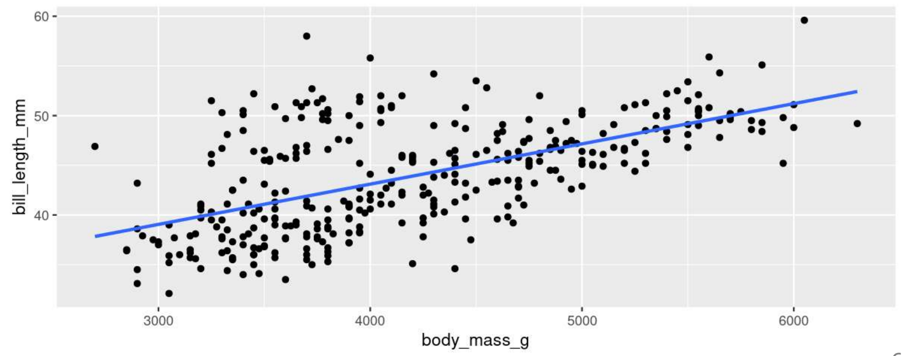


Trendlines / Regression lines

Add the `stat_smooth()`

- remove the grey ribbon `se = FALSE`

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

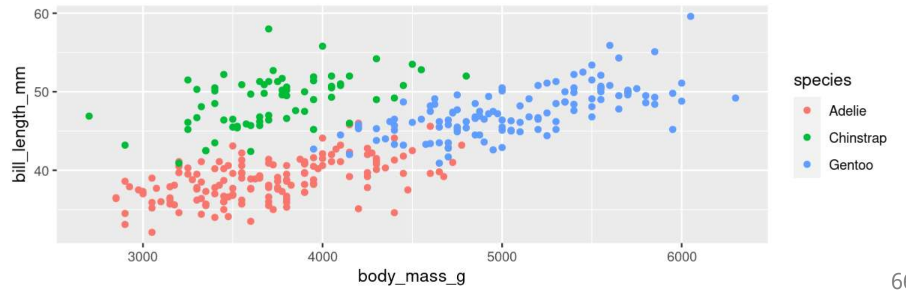


Trendlines / Regression lines

A line for each group

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

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

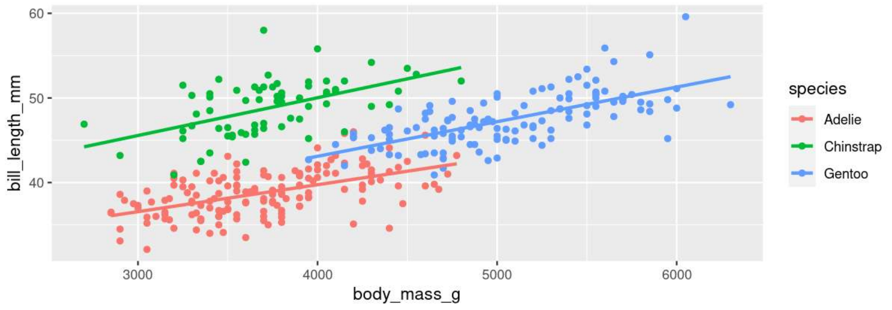


Trendlines / Regression lines

A line for each group

- `stat_smooth()` automatically uses the same grouping

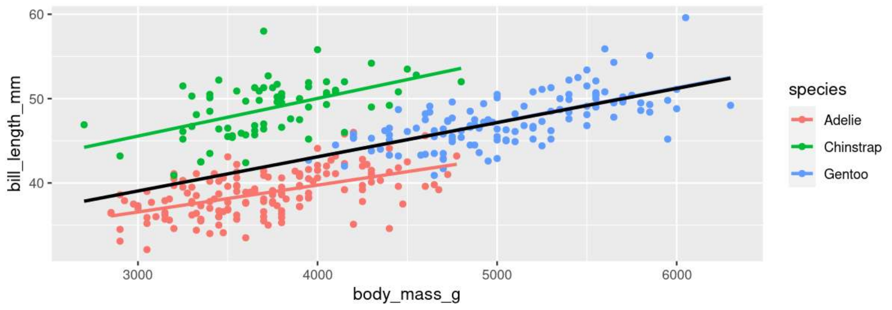
```
g + stat_smooth(method = "lm", se = FALSE)
```



Trendlines / Regression lines

A line for each group AND overall

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



Your Turn: Create this plot

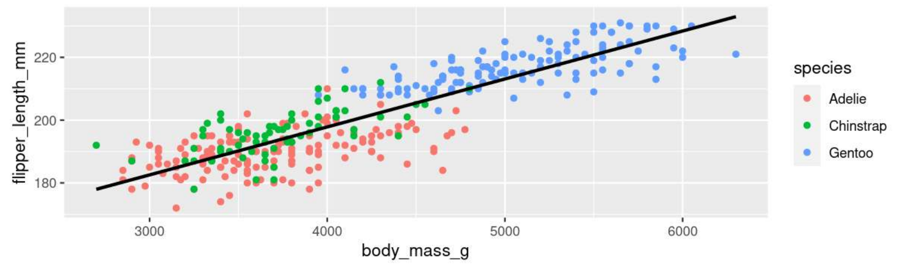
- A scatter plot: Flipper Length by Body Mass grouped by Species
- With *a single regression line for the overall trend*

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

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*

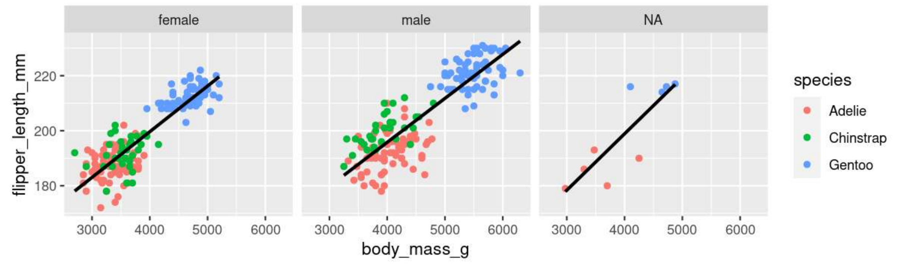
```r
ggplot(data = penguins, aes(x = body_mass_g, y = flipper_length_mm, colour = species)) +
  geom_point() +
  stat_smooth(se = FALSE, colour = "black", method = "lm")
```



Your Turn: Create this plot

Too Easy?

```r
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)
```

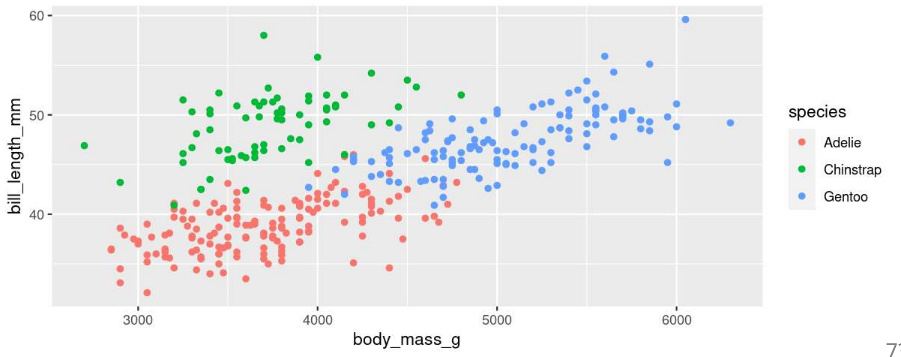


Customizing plots

Customizing: Starting plot

Let's work with this plot

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



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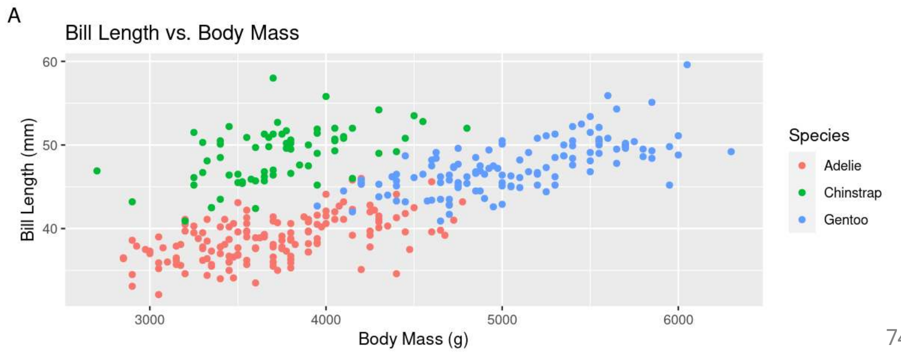
Customizing: Labels

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



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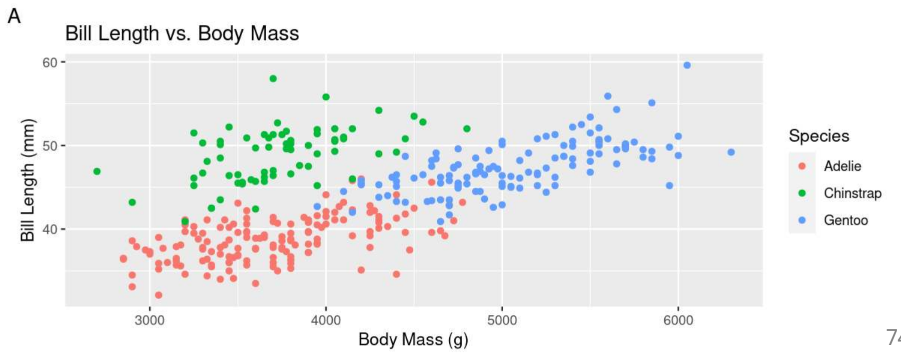
Customizing: Labels

```r
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



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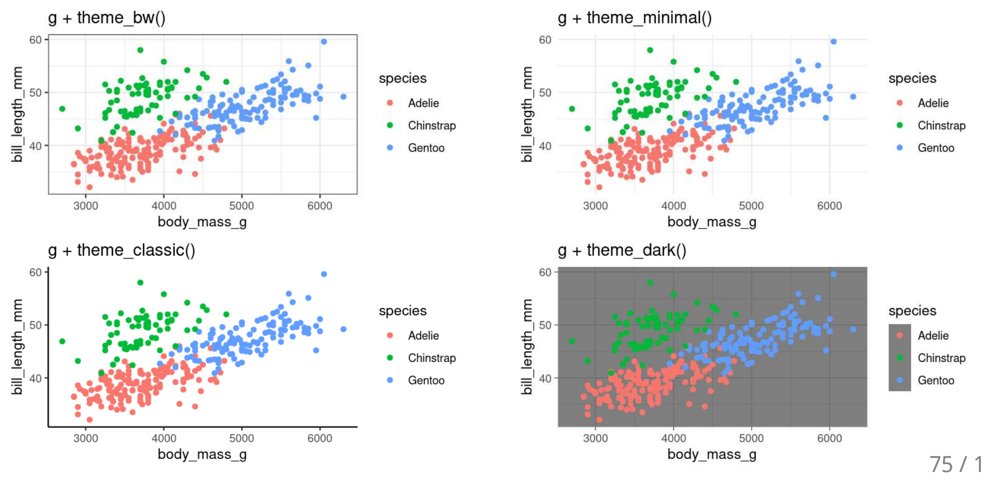
Customizing: Built-in themes



Customizing: Axes

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

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

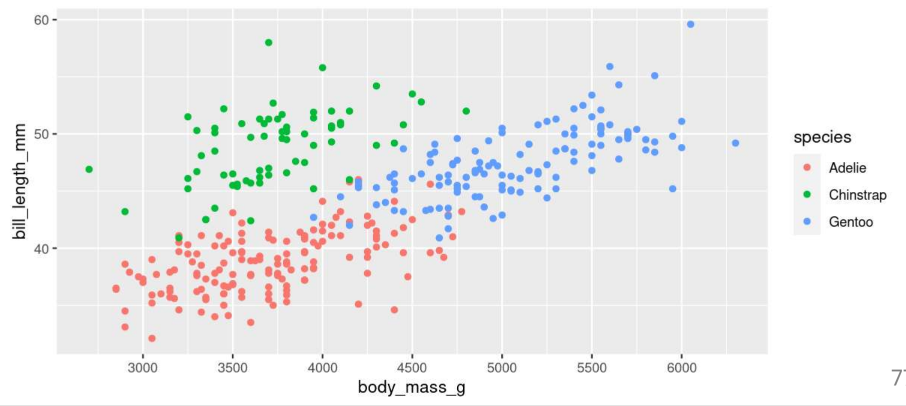
Common arguments

```
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

Breaks

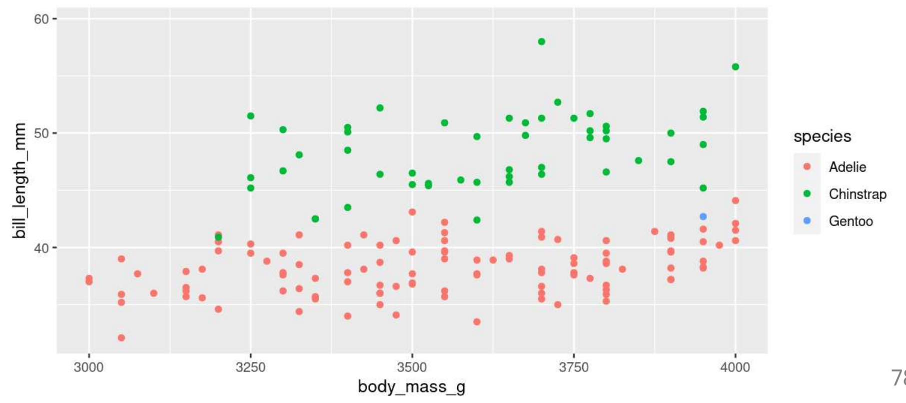
```
g + scale_x_continuous(breaks = seq(2500, 6500, 500))
```



Customizing: Axes

Limits

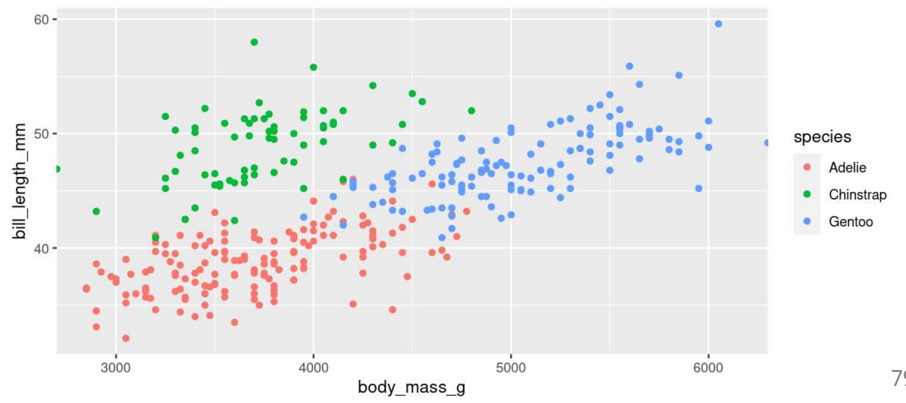
```
g + scale_x_continuous(limits = c(3000, 4000))
```



Customizing: Axes

Space between origin and axis start

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

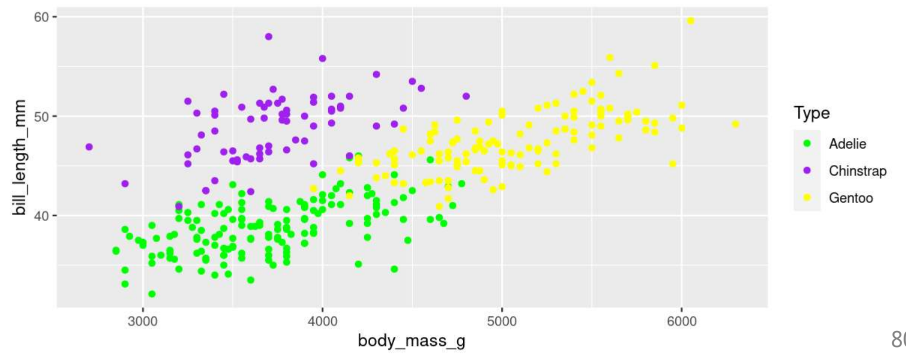


Customizing: Aesthetics

Using scales

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

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

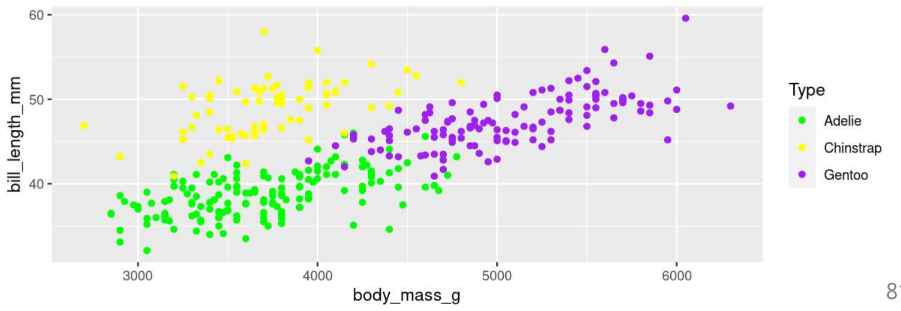


Customizing: Aesthetics

Using scales

Or be very explicit:

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

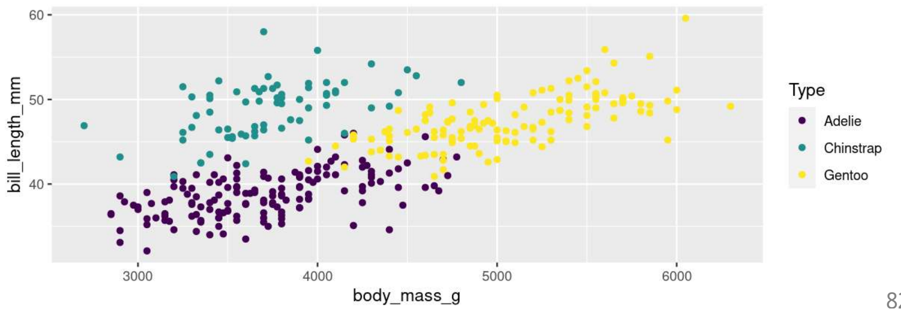


Customizing: Aesthetics

For colours, consider colour-blind-friendly 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")
```

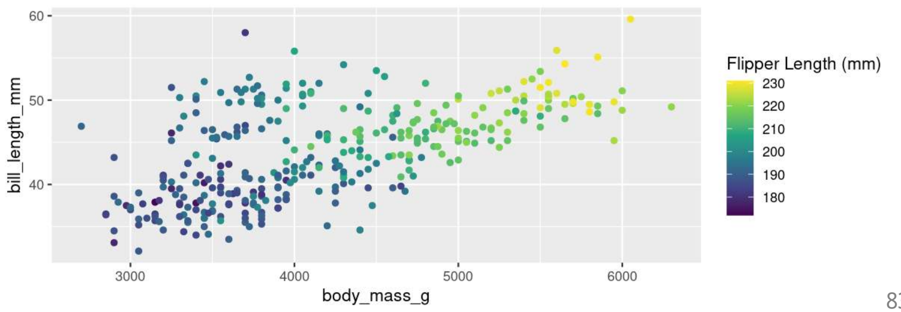


Customizing: Aesthetics

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 = flipper_length_mm)) +
  geom_point() +
  scale_colour_viridis_c(name = "Flipper Length (mm)")
```

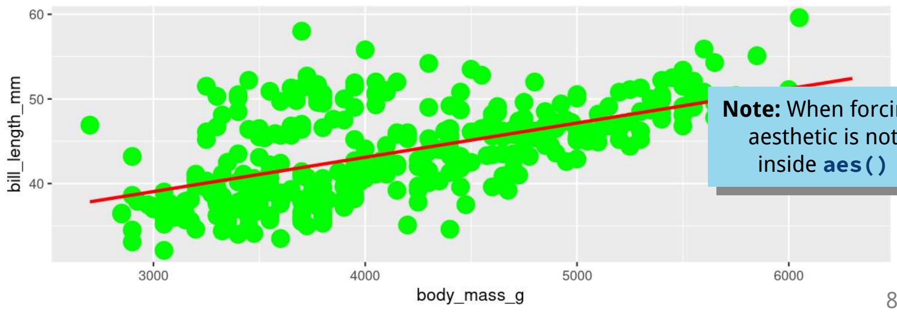


Customizing: Aesthetics

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()`**

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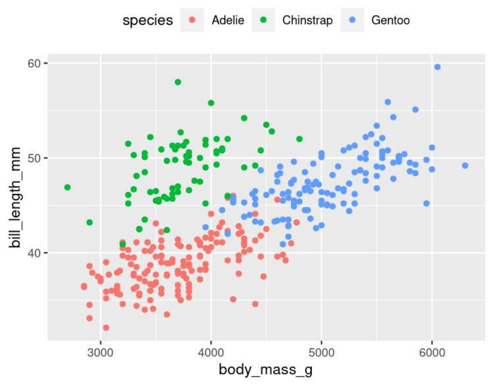
Customizing: Legends placement

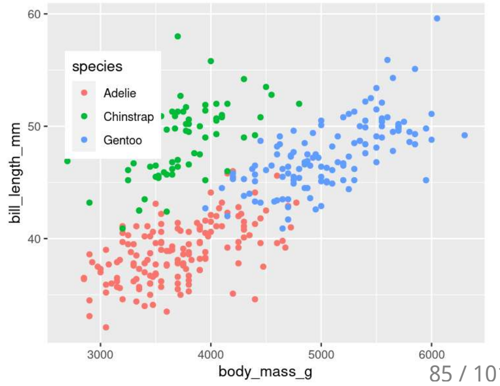
At the: top, bottom, left, right

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



Exactly here

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



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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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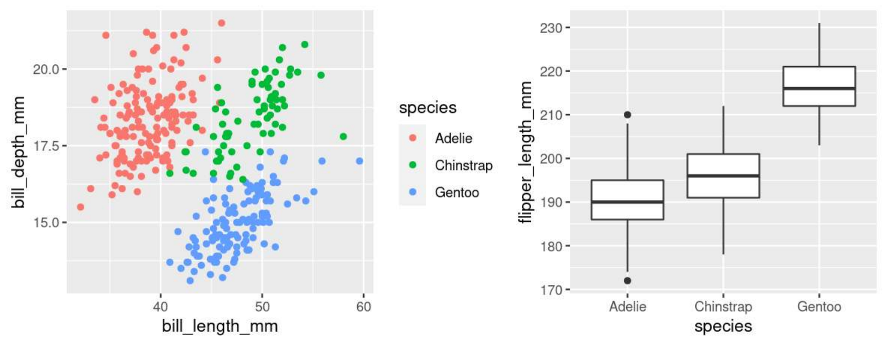
Combining plots with **`patchwork`**

Side-by-Side 2 plots

```
g1 + g2
```



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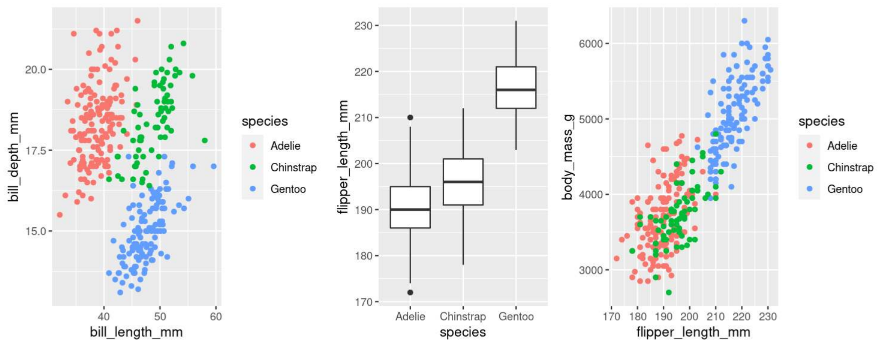
Combining plots with **`patchwork`**

Side-by-Side 3 plots

```
g1 + g2 + g3
```



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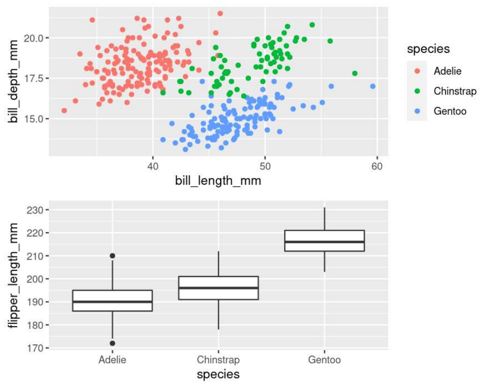
Combining plots with **patchwork**

Stacked 2 plots

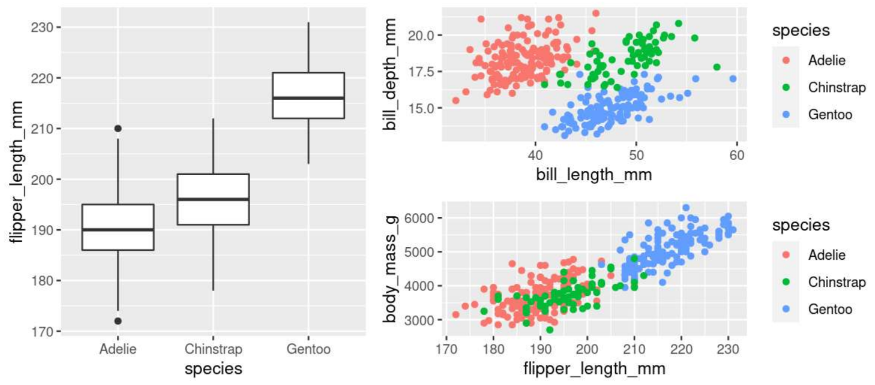
```
g1 / g2
```



Combining plots with **patchwork**

More complex arrangements

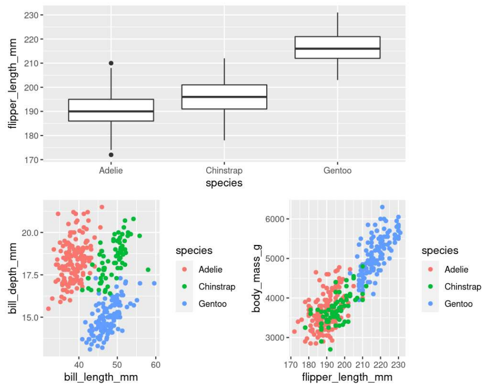
```
g2 + (g1 / g3)
```



Combining plots with **patchwork**

More complex arrangements

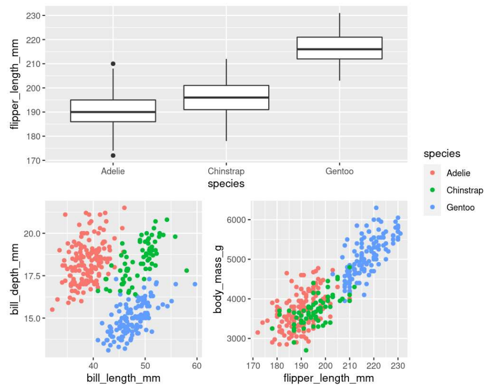
```
g2 / (g1 + g3)
```



Combining plots with **`patchwork`**

"collect" common legends

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



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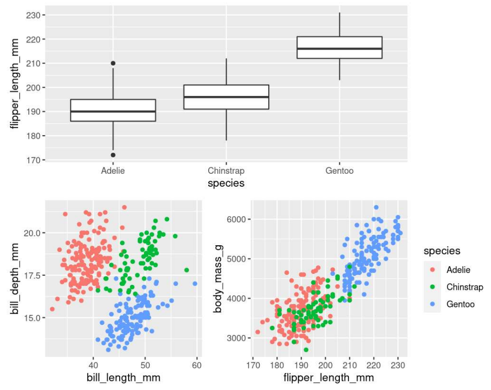
Combining plots with **`patchwork`**

"collect" common legends

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



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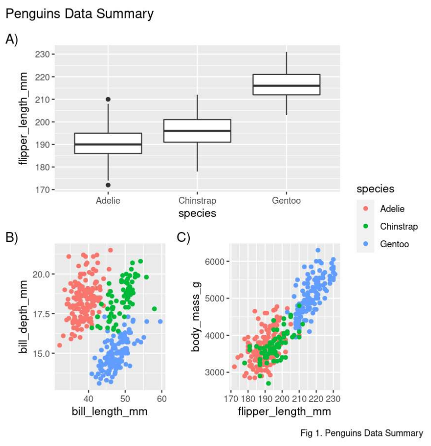
Combining plots with **`patchwork`**

Annotate

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

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

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Your Turn!

Create a figure with...

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

:D

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

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