NRI 7350

Data Exploration

Also **`GGally`**, **`skimr`**, **`dplyr`**, and **`moments`**

Artwork by @allison_horst

Getting started (again)

Open RStudio

Open your NRI project

Open a **new** script for today:

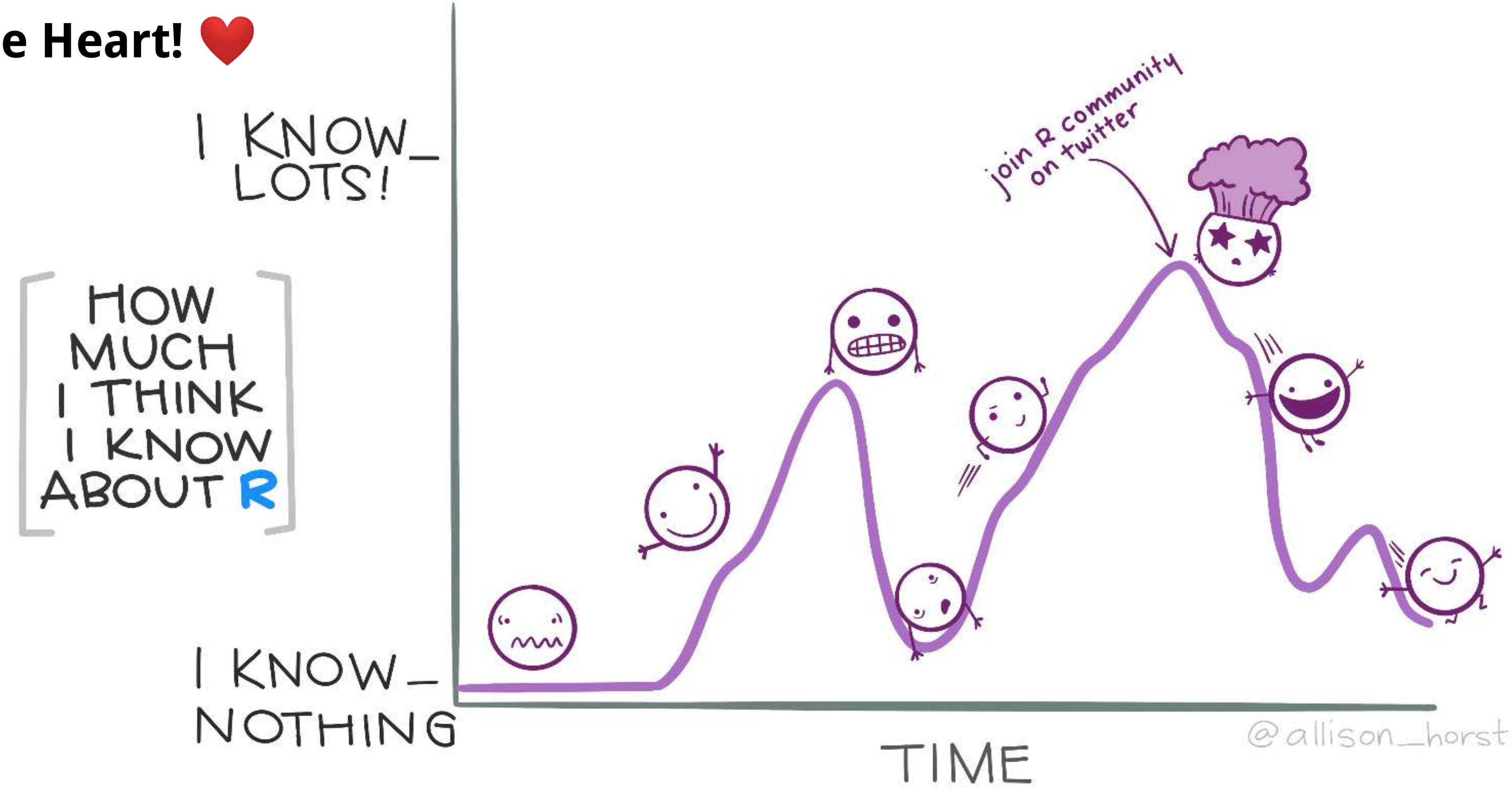
File > New File > R Script

Make sure to load packages at the top:

```
library(tidyverse)
library(palmerpenguins)
```

How Are we Doing?

Take Heart! ❤️



Artwork by @allison_horst on Twitter -- *"Knowing so little never felt so fun. #rstats"*

Exploring everything at once

Visualize with `ggpairs()`

- From **`GGally`** package

```
library(GGally)

penguins_sub <- select(penguins, -sex, -island, -year)
ggpairs(penguins_sub)
```

Side Note: `tidyverse` functions

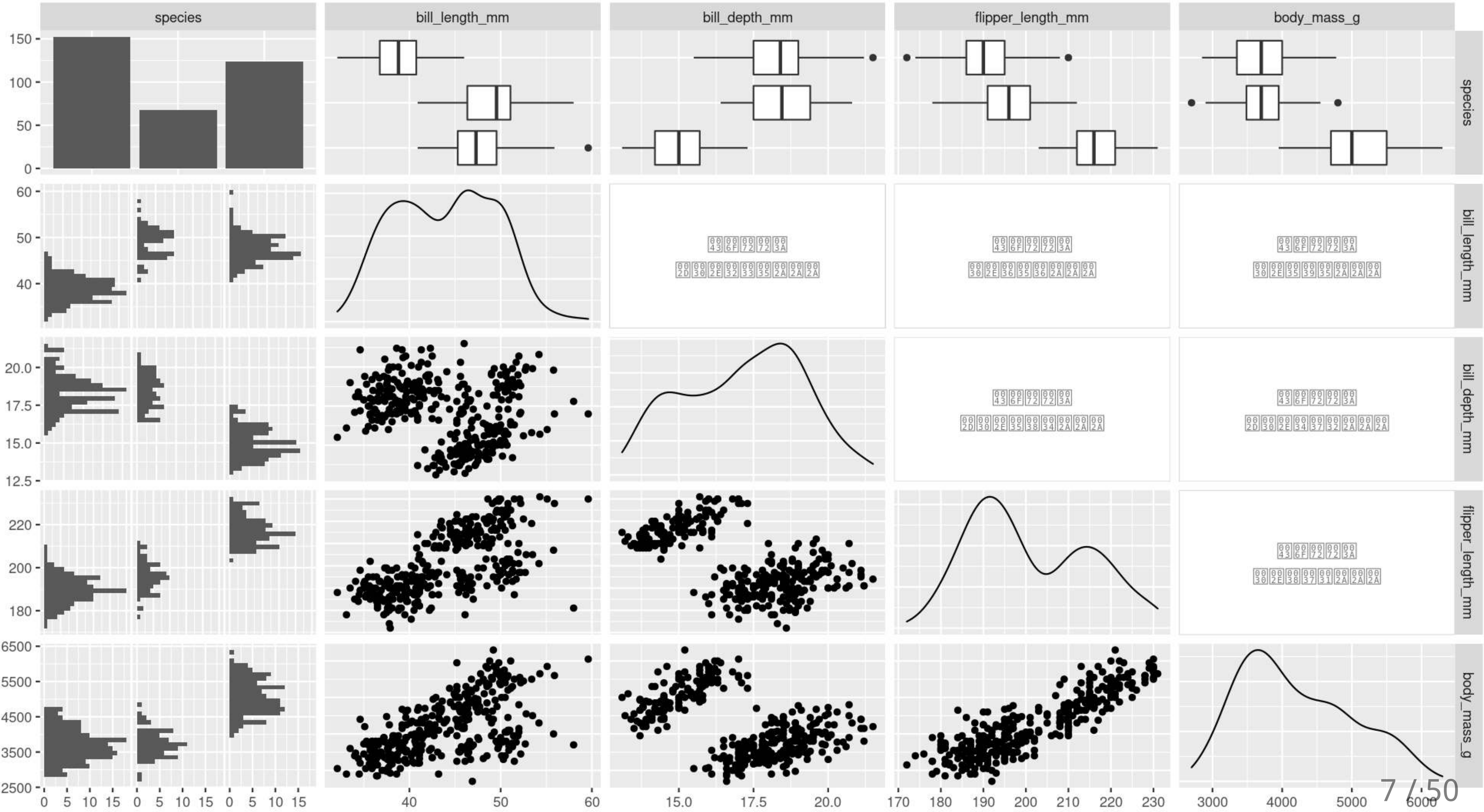
- From **`GGally`**

```r
library(GGally)

penguins_sub <- select(penguins, -sex, -island, -year)
ggpairs(penguins_sub)
```

`select()`

- **`tidyverse`** functions always start with the **data**, followed by other arguments
- you can reference any **column** from '**data**'
- **`select()`** chooses columns to keep or to remove (with **`-`**)

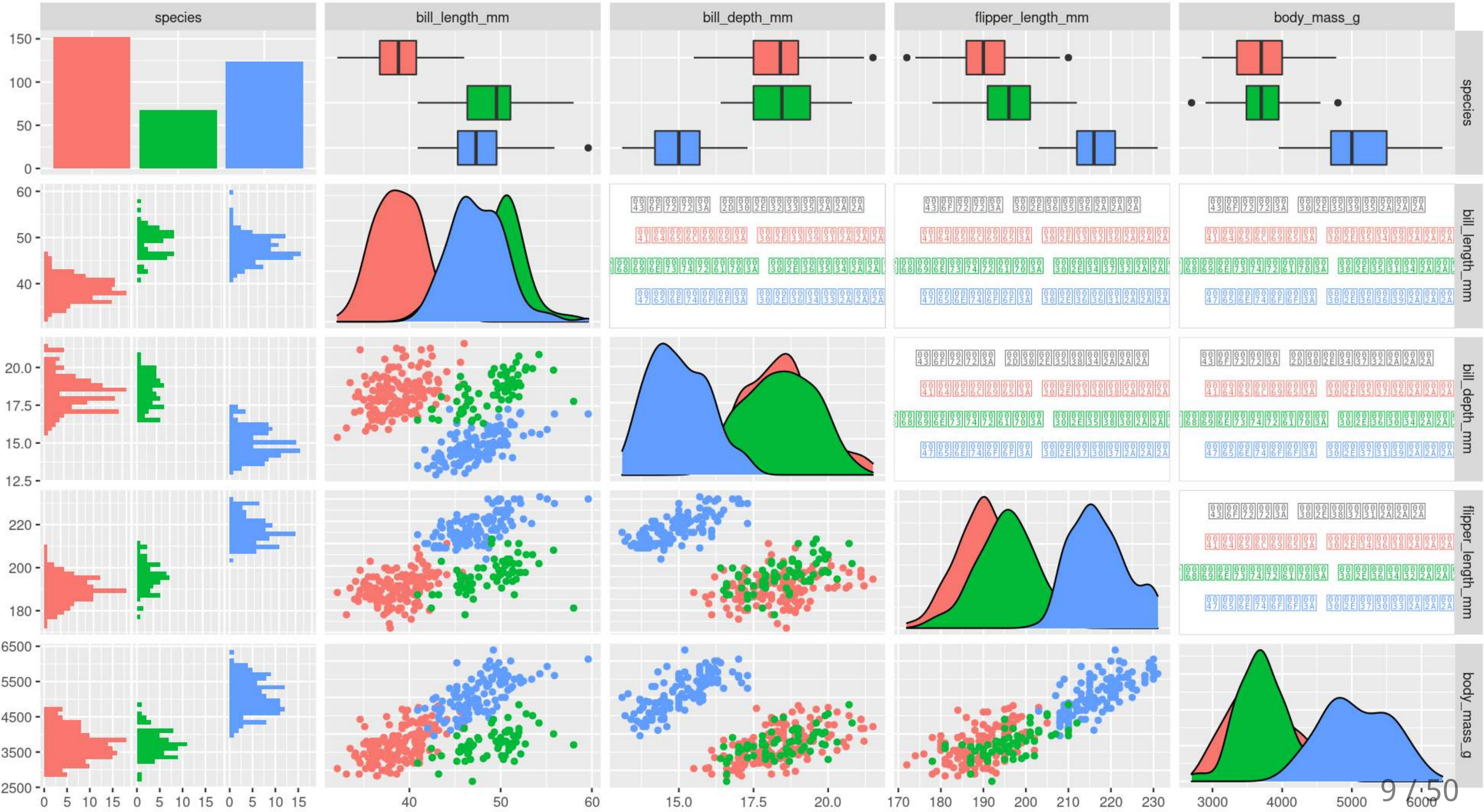

species
bill_length_mm
bill_depth_mm
flipper_length_mm
body_mass_g
150
100
50
0
60
50
40
20.0
17.5
15.0
12.5
220
200
180
6500
5500
4500
3500
2500
0 5 10 15 0 5 10 15 0 5 10 15
40
50
60
15.0
17.5
20.0
170
180
190
200
210
220
230
3000
4000
5000
6000

Visualize with `ggpairs()`

```r
library(GGally)

ggpairs(select(penguins, -sex, -island, -year), aes(colour = species))
```

> **`ggpairs()`** builds on **`ggplot()`** so we can use an **`aes()`** specification


species
bill_length_mm
bill_depth_mm
flipper_length_mm
body_mass_g
150
100
50
0
60
50
40
20.0
17.5
15.0
12.5
220
200
180
6500
5500
4500
3500
2500
0 5 10 15 0 5 10 15 0 5 10 15
40 50 60
15.0 17.5 20.0
170 180 190 200 210 220 230
3000 4000 5000 6000

Summarize with **skim()**

skim() from skimr package

```r
library(skimr)
skim(penguins)
```

```
## ── Data Summary ────────────────────────
##                            Values  
## Name                       penguins
## Number of rows             344     
## Number of columns          8       
## _______________________            
## Column type frequency:             
##   factor                   3       
##   numeric                  5       
## ________________________           
## Group variables            None    
## 
## ── Variable type: factor ──────────────────────────────────────────────────────────────────────────
##   skim_variable n_missing complete_rate ordered n_unique top_counts               
## 1 species               0         1     FALSE          3 Ade: 152, Gen: 124, Chi: 68
## 2 island                0         1     FALSE          3 Bis: 168, Dre: 124, Tor: 52
## 3 sex                  11         0.968 FALSE          2 mal: 168, fem: 165       
## 
```

Summarize with **skim()**

skim() from skimr package

```
library(skimr)
skim(penguins)
```

```
##
## ── Variable type: factor ─────────────────────────────────────────────────────────────────────
##   skim_variable n_missing complete_rate ordered n_unique top_counts
## 1 species               0             1 FALSE          3 Ade: 152, Gen: 124, Chi: 68
## 2 island                0             1 FALSE          3 Bis: 168, Dre: 124, Tor: 52
## 3 sex                  11         0.968 FALSE          2 mal: 168, fem: 165
##
## ── Variable type: numeric ────────────────────────────────────────────────────────────────────
##   skim_variable     n_missing complete_rate   mean      sd     p0   p25   p50   p75  p100 hist
## 1 bill_length_mm            2         0.994   43.9   5.46    32.1  39.2  44.4  48.5  59.6 ▃▇▇▆▁
## 2 bill_depth_mm             2         0.994   17.2   1.97    13.1  15.6  17.3  18.7  21.5 ▅▅▇▇▂
## 3 flipper_length_mm         2         0.994  201.   14.1    172   190   197   213   231   ▂▇▃▅▂
## 4 body_mass_g               2         0.994 4202.  802.    2700  3550  4050  4750  6300   ▃▇▆▃▂
## 5 year                      0         1     2008.    0.818 2007  2007  2008  2009  2009   ▇▁▇▁▇
```

Summarize with **skim()**

skim() from **skimr** package

Your Turn!

```r
library(skimr)
skim(penguins)
```

```
##
## ── Variable type: factor ────────────────────────────────────────────────────────────────────────
##   skim_variable n_missing complete_rate ordered n_unique top_counts
## 1 species               0             1 FALSE          3 Ade: 152, Gen: 124, Chi: 68
## 2 island                0             1 FALSE          3 Bis: 168, Dre: 124, Tor: 52
## 3 sex                  11         0.968 FALSE          2 mal: 168, fem: 165
##
## ── Variable type: numeric ───────────────────────────────────────────────────────────────────────
##   skim_variable     n_missing complete_rate   mean     sd    p0   p25   p50   p75  p100 hist
## 1 bill_length_mm            2         0.994   43.9   5.46  32.1  39.2  44.4  48.5  59.6 ▃▇▇▆▁
## 2 bill_depth_mm             2         0.994   17.2   1.97  13.1  15.6  17.3  18.7  21.5 ▅▅▇▇▂
## 3 flipper_length_mm         2         0.994  201.    14.1   172   190   197   213   231 ▂▇▃▅▂
## 4 body_mass_g               2         0.994 4202.   802.   2700  3550  4050  4750  6300 ▃▇▆▃▂
## 5 year                      0         1     2008.    0.818 2007  2007  2008  2009  2009 ▇▁▇▁▇
```

Summarize with **`skim()`**

- From **`skimr`** package

```
penguins_sp <- group_by(penguins, species)
skim(penguins_sp)
```

Side Note: **`tidyverse`** functions

- From **`skimr`** package

```
penguins_sp <- group_by(penguins, species)
skim(penguins_sp)
```

`group_by()`

- **`tidyverse`** functions always start with the **data**, followed by other arguments
- you can reference any **column** from '**data**'
- **`group_by()`** assigns grouping to a data frame. Here, we group **`penguins`** by species

> **Extra:**
>
> In the console look at **`penguins`** (type in **`penguins`** and hit enter), and then look at **`penguins_sp`** (type in **`penguins_sp`** and it enter).
>
> How does the output differ? (Hint very little! But there is one difference...)

Summarize with **skim()**

skim() from **skimr** package

```
penguins_sp <- group_by(penguins, species)
skim(penguins_sp)
```

```
## ── Data Summary ────────────────────────
##                            Values
## Name                       skimp
## Number of rows             344
## Number of columns          8
## _______________________
## Column type frequency:
##   factor                   2
##   numeric                  5
## ________________________
## Group variables            species
##
## ── Variable type: factor ──────────────────────────────────────────────────────────────────
##   skim_variable species   n_missing complete_rate ordered n_unique top_counts
## 1 island        Adelie            0         1     FALSE          3 Dre: 56, Tor: 52, Bis: 44
## 2 island        Chinstrap         0         1     FALSE          1 Dre: 68, Bis: 0, Tor: 0
## 3 island        Gentoo            0         1     FALSE          1 Bis: 124, Dre: 0, Tor: 0
## 4 sex           Adelie            6         0.961 FALSE          2 fem: 73, mal: 73
```

Summarize with skim()

skim() from skimr package

```
penguins_sp <- group_by(penguins, species)
skim(penguins_sp)
```

```
##
## ── Variable type: factor ──────────────────────────────────────────────────────────────────────────
##   skim_variable species   n_missing complete_rate ordered n_unique top_counts
## 1 island        Adelie            0         1     FALSE          3 Dre: 56, Tor: 52, Bis: 44
## 2 island        Chinstrap         0         1     FALSE          1 Dre: 68, Bis: 0, Tor: 0
## 3 island        Gentoo            0         1     FALSE          1 Bis: 124, Dre: 0, Tor: 0
## 4 sex           Adelie            6         0.961 FALSE          2 fem: 73, mal: 73
## 5 sex           Chinstrap         0         1     FALSE          2 fem: 34, mal: 34
## 6 sex           Gentoo            5         0.960 FALSE          2 mal: 61, fem: 58
##
## ── Variable type: numeric ─────────────────────────────────────────────────────────────────────────
##    skim_variable     species   n_missing complete_rate   mean      sd     p0    p25    p50    p75
##  1 bill_length_mm    Adelie            1         0.993   38.8   2.66    32.1   36.8   38.8   40.8
##  2 bill_length_mm    Chinstrap         0         1       48.8   3.34    40.9   46.3   49.6   51.1
##  3 bill_length_mm    Gentoo            1         0.992   47.5   3.08    40.9   45.3   47.3   49.6
##  4 bill_depth_mm     Adelie            1         0.993   18.3   1.22    15.5   17.5   18.4   19
##  5 bill_depth_mm     Chinstrap         0         1       18.4   1.14    16.4   17.5   18.4   19.4
##  6 bill_depth_mm     Gentoo            1         0.992   15.0   0.981   13.1   14.2   15     15.7
```

Summarize with **skim()**

skim() from **skimr** package

Your Turn!

```
penguins_sp <- group_by(penguins, species)
skim(penguins_sp)
```

```
##
## ── Variable type: factor ────────────────────────────────────────────────────────────────────────
##   skim_variable species   n_missing complete_rate ordered n_unique top_counts
## 1 island        Adelie            0         1     FALSE          3 Dre: 56, Tor: 52, Bis: 44
## 2 island        Chinstrap         0         1     FALSE          1 Dre: 68, Bis: 0, Tor: 0
## 3 island        Gentoo            0         1     FALSE          1 Bis: 124, Dre: 0, Tor: 0
## 4 sex           Adelie            6         0.961 FALSE          2 fem: 73, mal: 73
## 5 sex           Chinstrap         0         1     FALSE          2 fem: 34, mal: 34
## 6 sex           Gentoo            5         0.960 FALSE          2 mal: 61, fem: 58
##
## ── Variable type: numeric ───────────────────────────────────────────────────────────────────────
##     skim_variable     species   n_missing complete_rate   mean      sd     p0    p25    p50    p75
##  1 bill_length_mm     Adelie            1         0.993   38.8   2.66    32.1   36.8   38.8   40.8
##  2 bill_length_mm     Chinstrap         0         1       48.8   3.34    40.9   46.3   49.6   51.1
##  3 bill_length_mm     Gentoo            1         0.992   47.5   3.08    40.9   45.3   47.3   49.6
##  4 bill_depth_mm      Adelie            1         0.993   18.3   1.22    15.5   17.5   18.4   19
##  5 bill_depth_mm      Chinstrap         0         1       18.4   1.14    16.4   17.5   18.4   19.4
##  6 bill_depth_mm      Gentoo            1         0.992   15.0   0.981   13.1   14.2   15     15.7
```

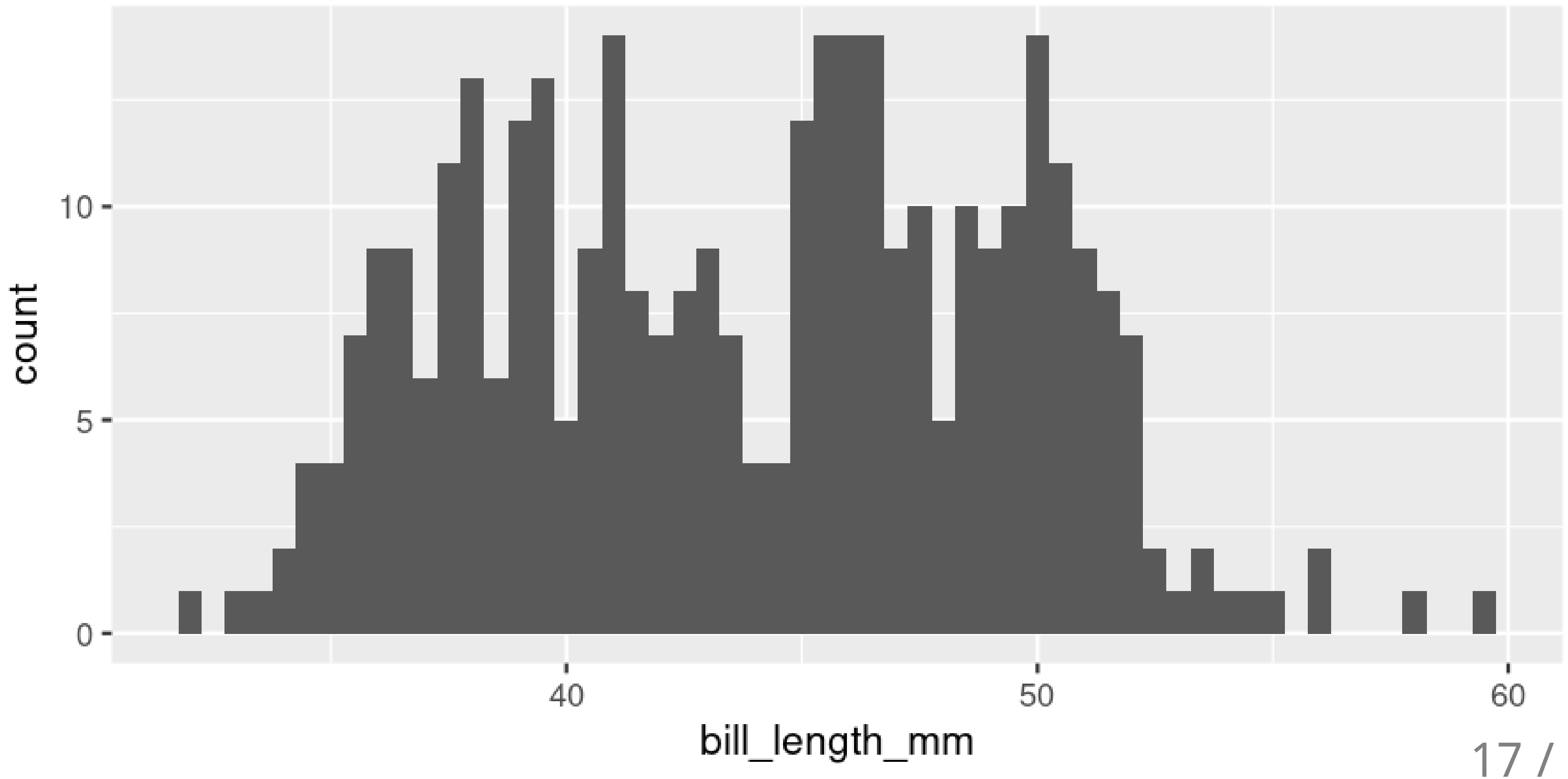
Exploring variable by variable

Visualize with **`ggplot()`**

From last week...

- Histograms

```r
ggplot(data = penguins, aes(x = bill_length_mm)) +
  geom_histogram(binwidth = 0.5)
```

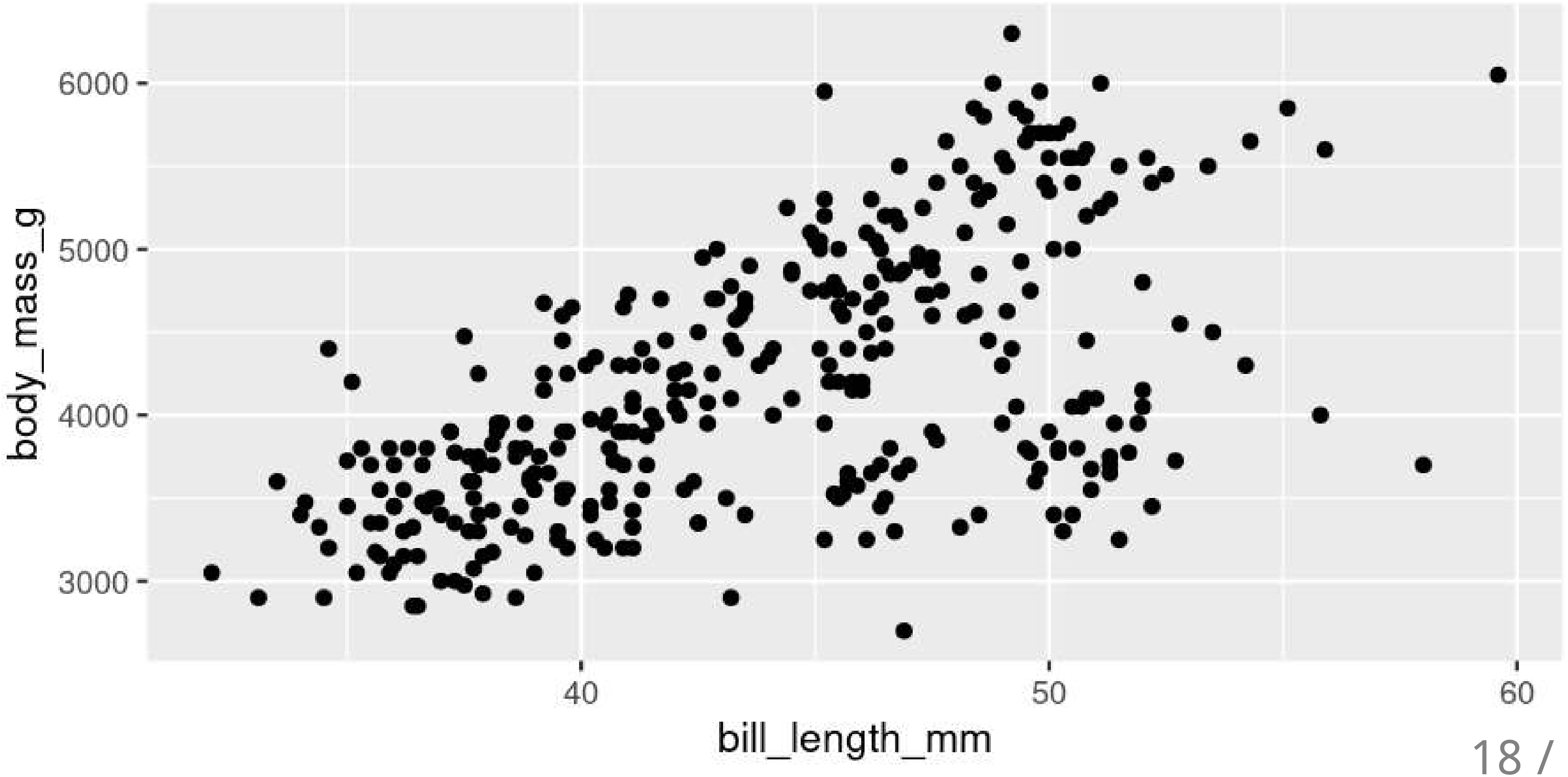


Visualize with `ggplot()`

From last week...

- Histograms
- Scatterplots

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

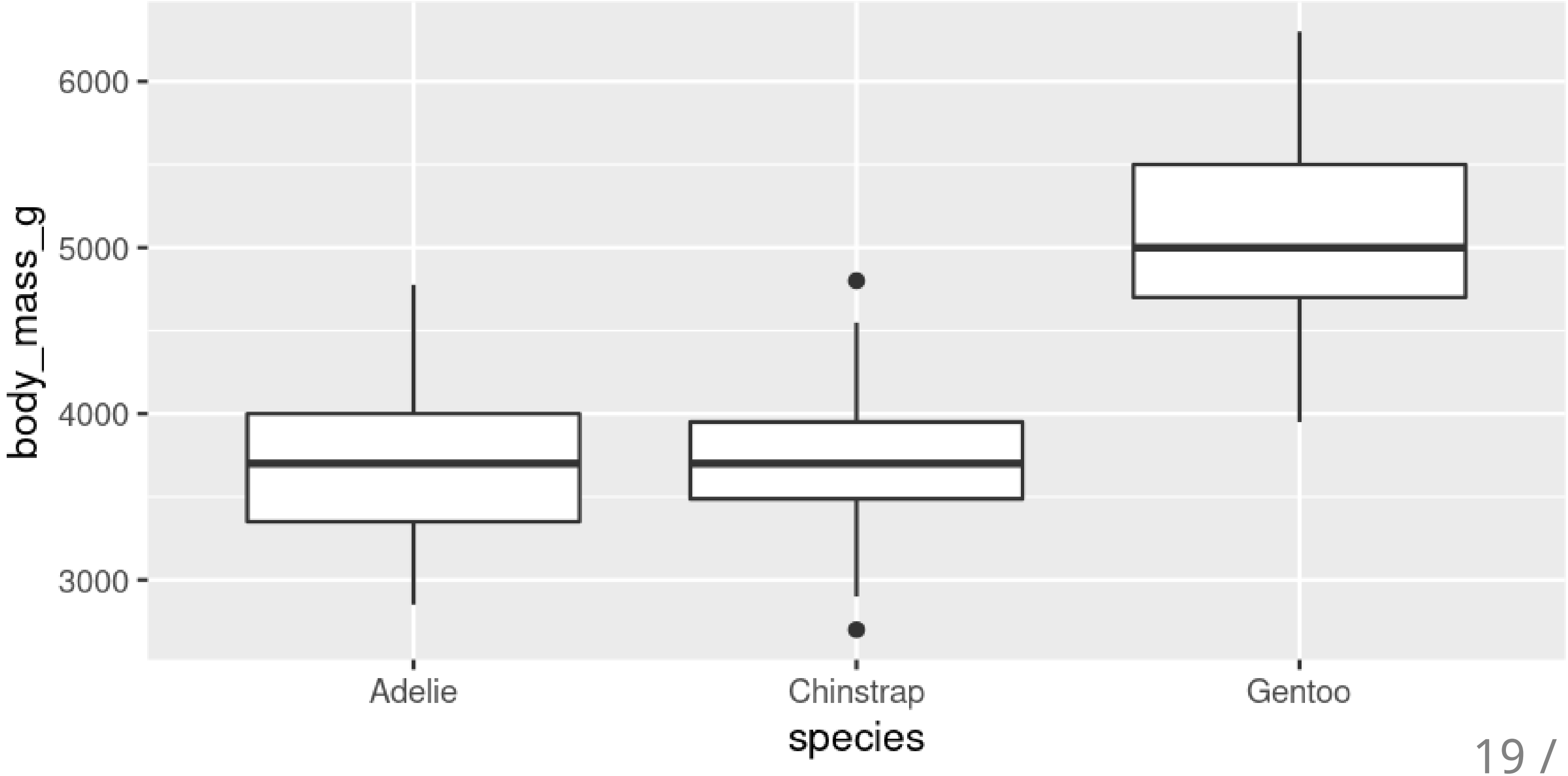


Visualize with `ggplot()`

From last week...

- Histograms
- Scatterplots
- Boxplots

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

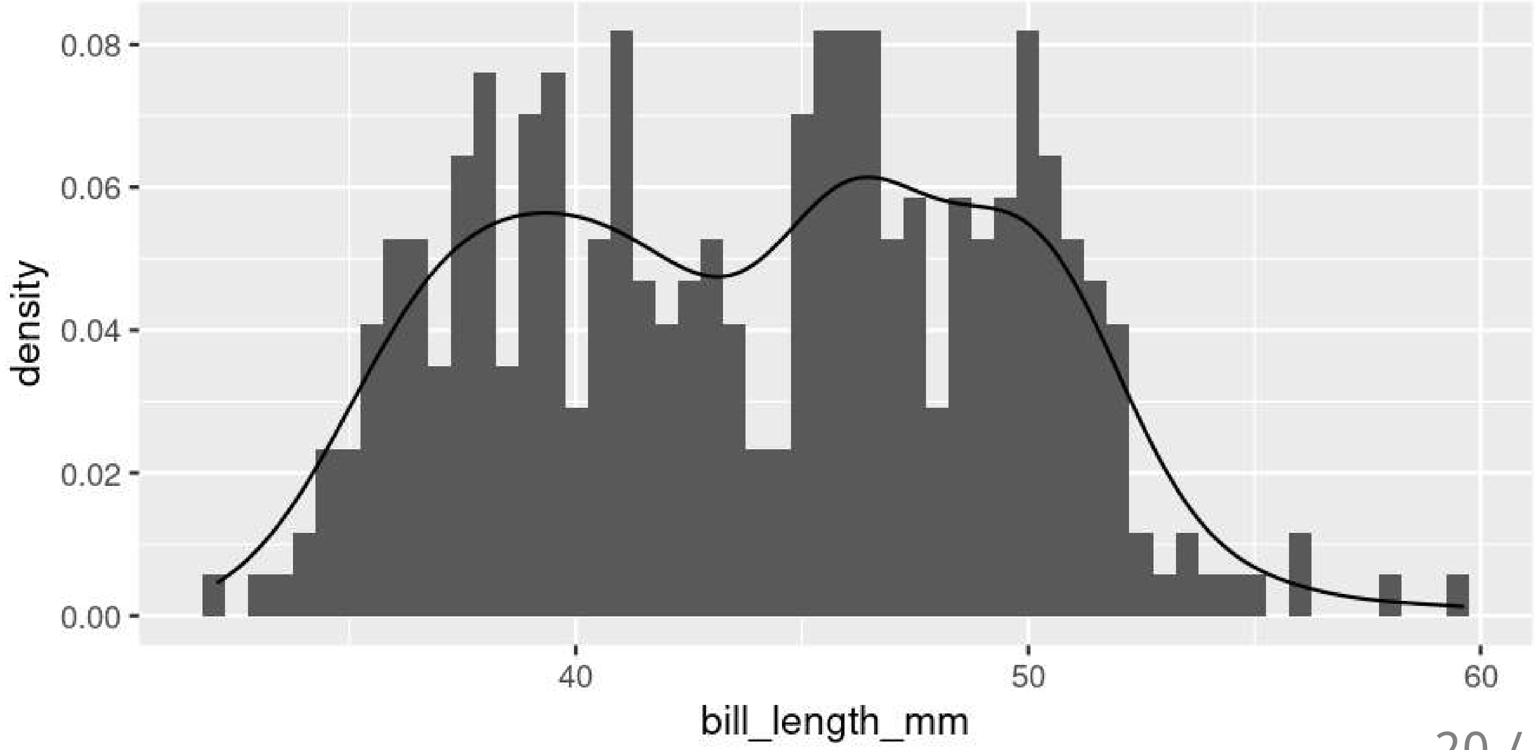


Visualize with **ggplot()**

Histogram with Density

- Default uses counts
- Here use density **`y = ..density..`**
- Same as density curve **`geom_density()`**
- Use to assess shape and distribution of data

```
ggplot(data = penguins, aes(x = bill_length_mm, y = ..density..)) +
    geom_histogram(binwidth = 0.5) +
    geom_density()
```

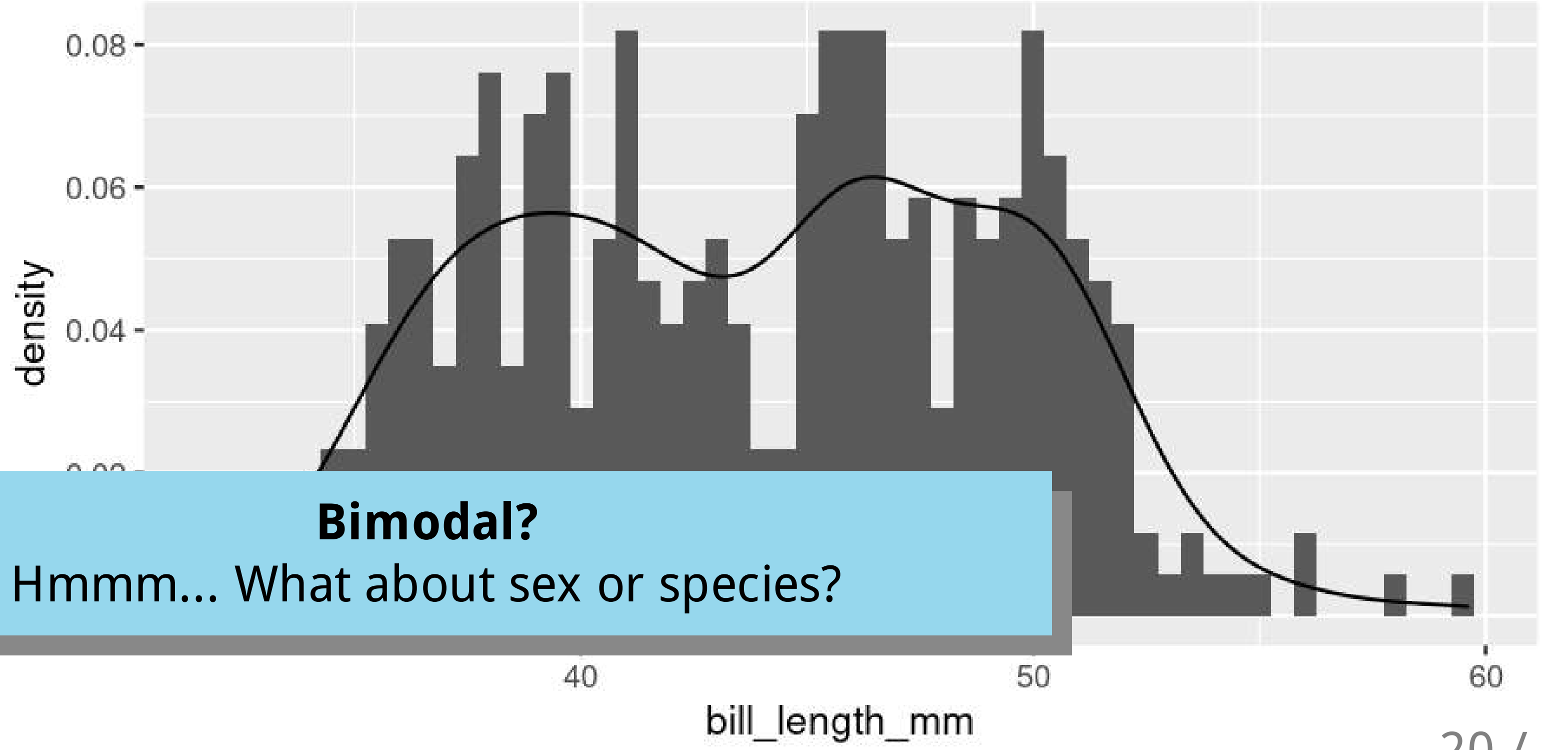


Visualize with **ggplot()**

Histogram with Density

- Default uses counts
- Here use density **`y = ..density..`**
- Same as density curve **`geom_density()`**
- Use to assess shape and distribution of data

```
ggplot(data = penguins, aes(x = bill_length_mm, y = ..density..)) +
    geom_histogram(binwidth = 0.5) +
    geom_density()
```



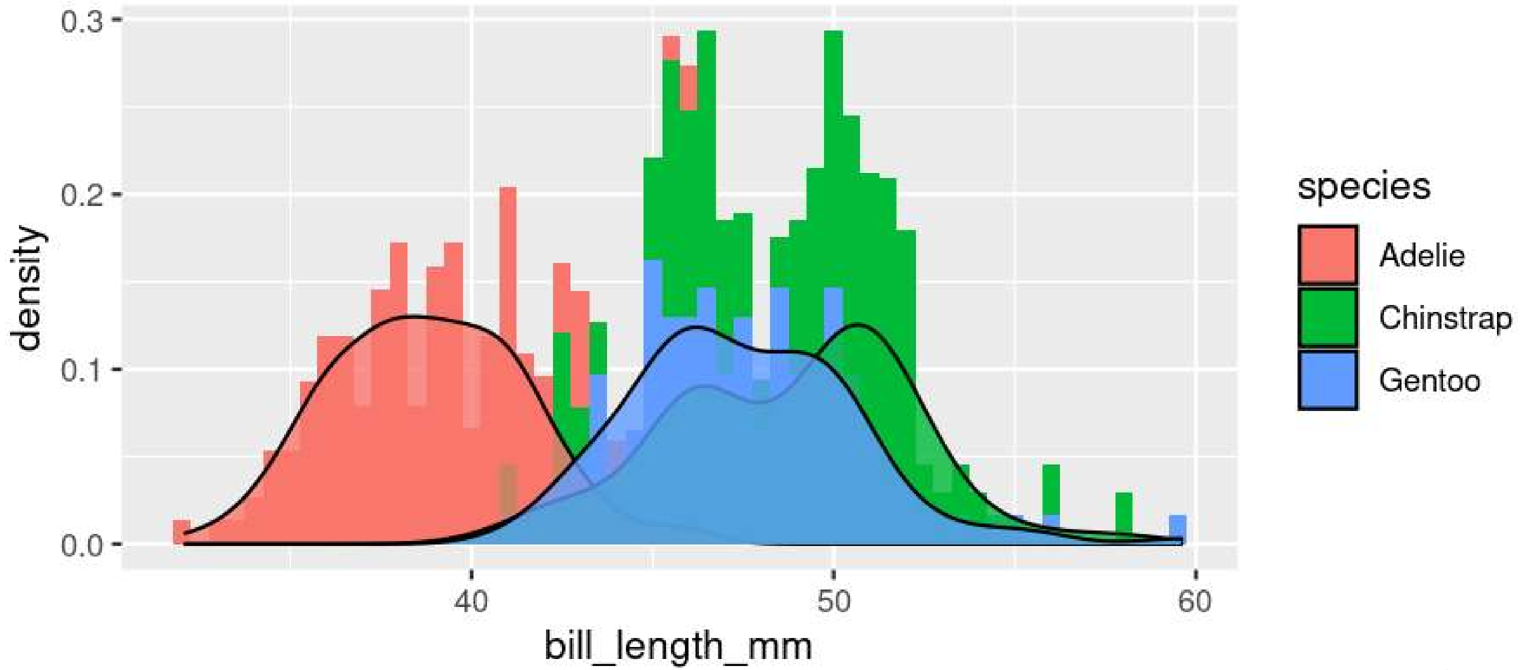
Bimodal?
Hmmm... What about sex or species?

Visualize with `ggplot()`

Histogram with Density

- Default uses counts
- Here use density **`y = ..density..`**
- Same as density curve **`geom_density()`**
- Use to assess shape and distribution of data

```
ggplot(data = penguins, aes(x = bill_length_mm, y = ..density..,
                            fill = species)) +
    geom_histogram(binwidth = 0.5) +
    geom_density(alpha = 0.8)
```

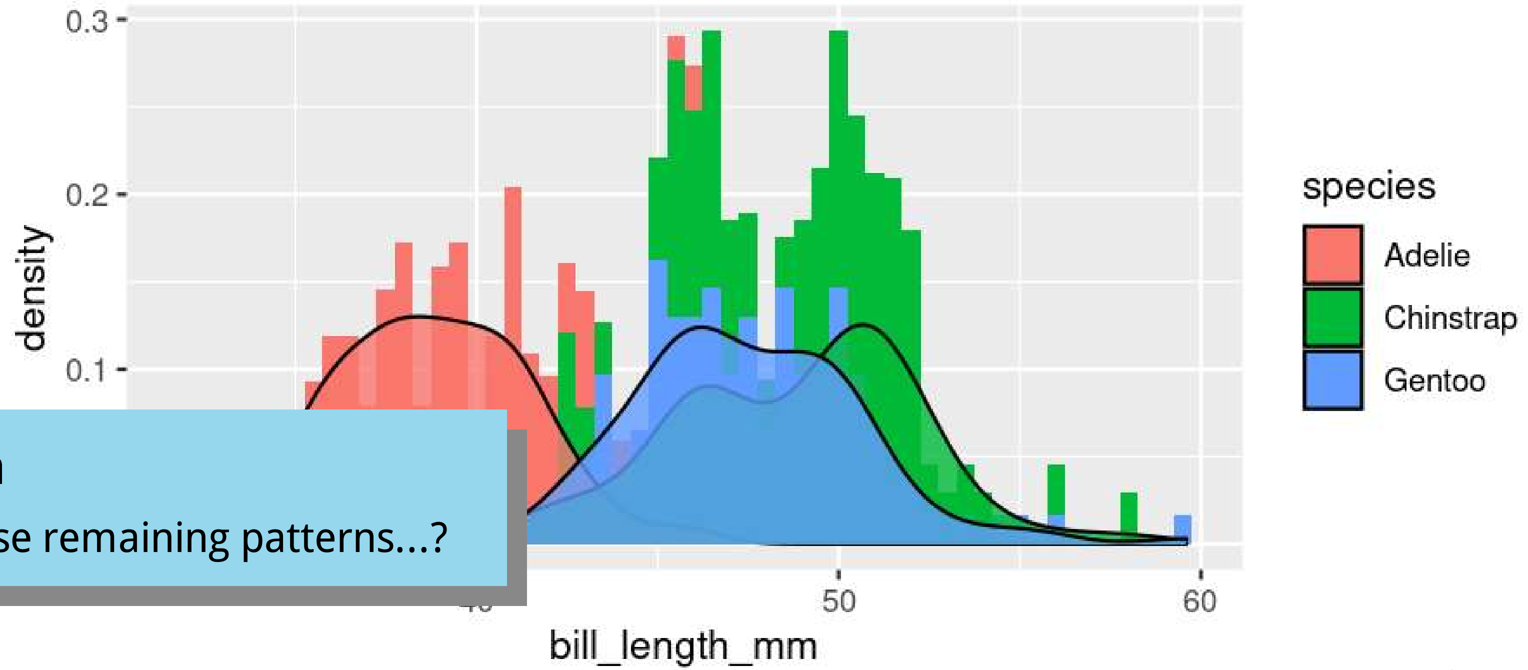


Visualize with **`ggplot()`**

Histogram with Density

- Default uses counts
- Here use density **`y = ..density..`**
- Same as density curve **`geom_density()`**
- Use to assess shape and distribution of data

```
ggplot(data = penguins, aes(x = bill_length_mm, y = ..density..,
                            fill = species)) +
    geom_histogram(binwidth = 0.5) +
    geom_density(alpha = 0.8)
```



Extra

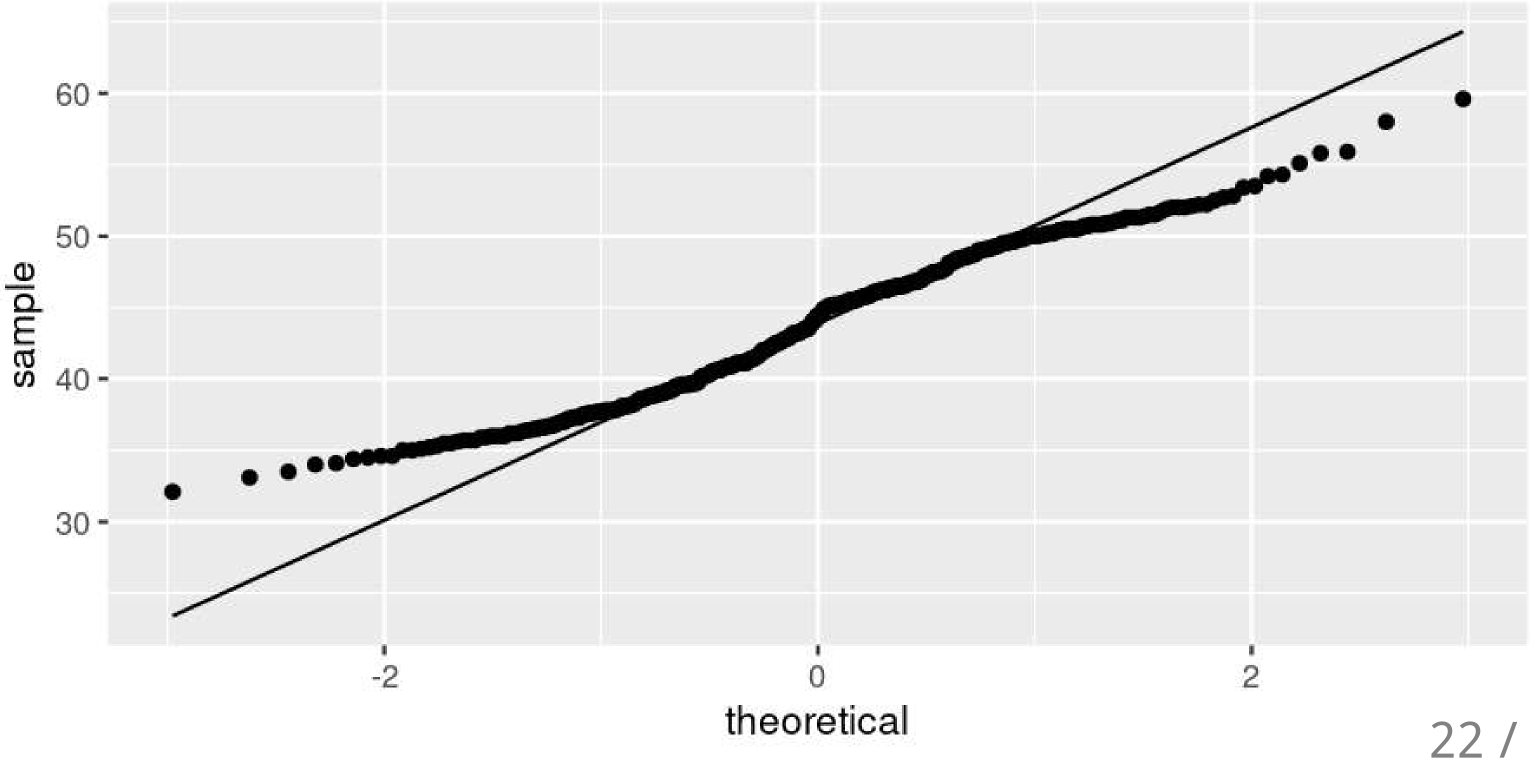
Perhaps sex plays a role in those remaining patterns...?

Visualize with **`ggplot()`**

QQ Norm plots

- Assess whether data follows normal distribution

```
ggplot(data = penguins, aes(sample = bill_length_mm)) +
  stat_qq() +     # Add the points
  stat_qq_line() # Add the line
```



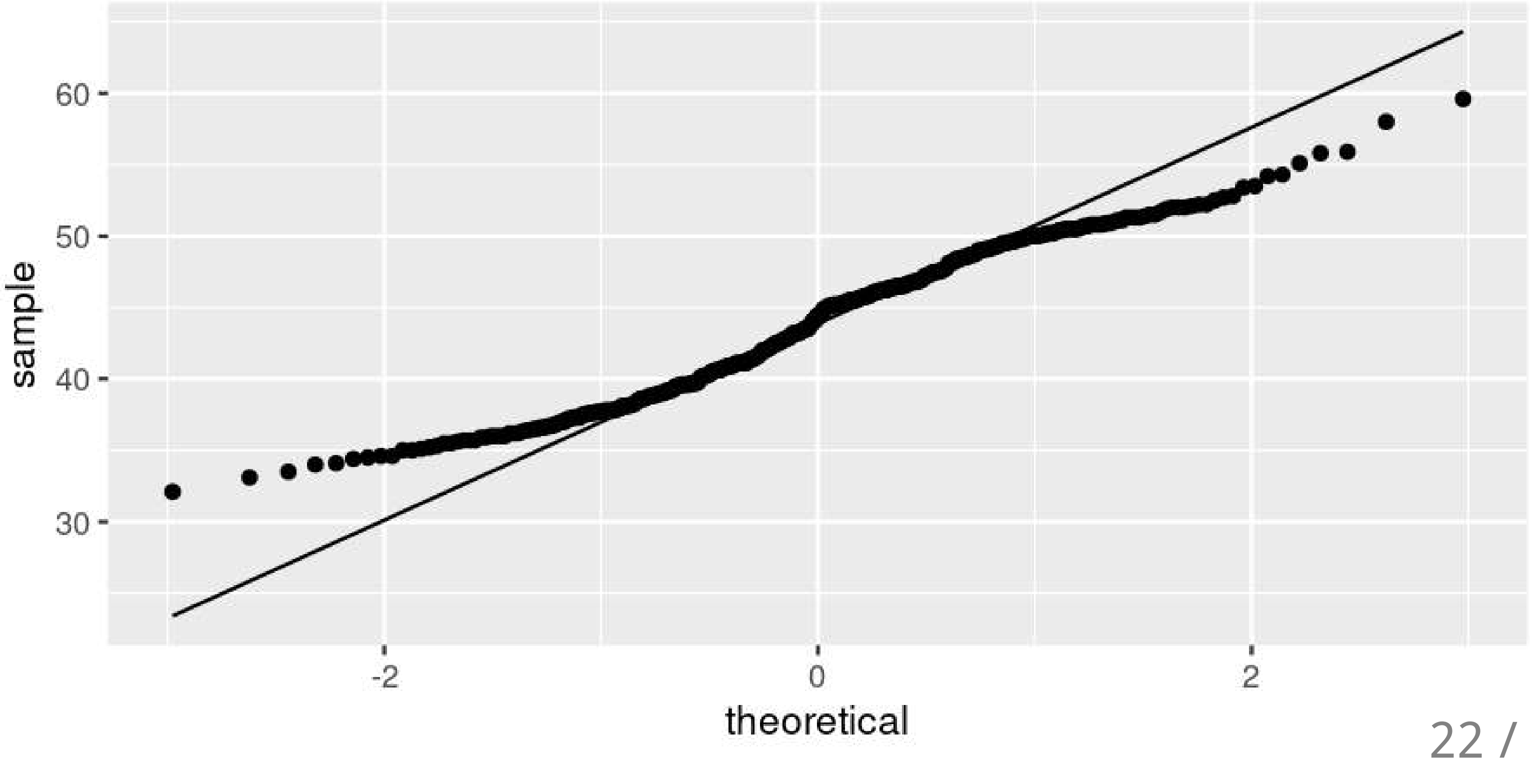
Visualize with `ggplot()`

QQ Norm plots

- Asses
  follow
  distribution

Here we are **NOT** assessing assumptions of normality for a model

That involves model residuals: Stay tuned for next week!



Summarize with **`summarize()`** Ha!

- From **`dplyr`** package (part of **`tidyverse`**)

```
summarize(penguins,
          mean_mass = mean(body_mass_g),
          sd_mass = sd(body_mass_g),
          median_mass = median(body_mass_g))
```

Side Note: `tidyverse` functions

- From **`dplyr`** package (part of **`tidyverse`**)

```r
summarize(penguins,
          mean_mass = mean(body_mass_g),
          sd_mass = sd(body_mass_g),
          median_mass = median(body_mass_g))
```

`summarize()`

- **`tidyverse`** functions always start with the **data**, followed by **other arguments**
- you can reference any **column** from '**data**'
- **`summarize()`** creates a data frame with **new columns** (summarizes your data)

Summarize with **summarize()**

- From **dplyr** package (part of **tidyverse**)

```
summarize(penguins,
          mean_mass = mean(body_mass_g),
          sd_mass = sd(body_mass_g),
          median_mass = median(body_mass_g))
```

```
## # A tibble: 1 x 3
##   mean_mass sd_mass median_mass
##       <dbl>   <dbl>       <int>
## 1        NA      NA          NA
```

Summarize with **summarize()**

- From **dplyr** package (part of **tidyverse**)

```
summarize(penguins,
          mean_mass = mean(body_mass_g),
          sd_mass = sd(body_mass_g),
          median_mass = median(body_mass_g))
```

```
## # A tibble: 1 x 3
##   mean_mass sd_mass median_mass
##       <dbl>   <dbl>       <int>
## 1        NA      NA          NA
```

> Why all **NA**s?

Summarize with **summarize()**

- **mean()**, **sd()**, **median()**

Need to tell summary statistic functions to remove missing values **na.rm = TRUE**

```
summarize(penguins,
          mean_mass = mean(body_mass_g, na.rm = TRUE),
          sd_mass = sd(body_mass_g, na.rm = TRUE),
          median_mass = median(body_mass_g, na.rm = TRUE))
```

```
## # A tibble: 1 x 3
##   mean_mass sd_mass median_mass
##       <dbl>   <dbl>       <dbl>
## 1     4202.    802.        4050
```

Summarize with **summarize()**

- **mean()**, **sd()**, **median()**, **quantile()**, **n()***

```r
summarize(penguins,
          mean_mass = mean(body_mass_g, na.rm = TRUE),
          sd_mass = sd(body_mass_g, na.rm = TRUE),
          median_mass = median(body_mass_g, na.rm = TRUE),
          q25_mass = quantile(body_mass_g, probs = 0.25, na.rm = TRUE),
          n = n(),                                                       # Sample size
          n_no_missing = sum(!is.na(body_mass_g)))                       # Non-missing sample size
```

```
## # A tibble: 1 x 6
##   mean_mass sd_mass median_mass q25_mass     n n_no_missing
##       <dbl>   <dbl>       <dbl>    <dbl> <int>        <int>
## 1     4202.    802.        4050     3550   344          342
```

* **n()** only works *inside* **summarize()**/**mutate()**

Your Turn: **`summarize()`**

Calculate summary statistics for **Bill Length**

```
summarize(penguins,
                                  bill_length_mm               ,
                              bill_length_mm               ,
                                      bill_length_mm               ,
                                     bill_length_mm                             ,
                      ,
                                         bill_length_mm  )
```

Side Note: Removing `NA`s

- With arguments
  - `na.rm = TRUE` (summary stats i.e. `mean()`, `sd()`)
  - `na.action = na.exclude` (models i.e., `lm()`, `lmer()`)
- You can remove all `NA`s from your data (`drop_na()`)
- You can selectively remove `NA`s from your data (`filter()`)

Side Note: Removing **NAs**

Remove all NAs

- This removes **every** row that has an **NA** in **any** column
- **drop_na()** function from **tidyr** package (part of **tidyverse**)

```
penguins_no_na <- drop_na(penguins)
```

- Consider removing columns with lots of **NA**s first (assuming you don't need them)

```
penguins_no_na <- select(penguins, -sex)
penguins_no_na <- drop_na(penguins_no_na)
```

Side Side Note: `tidyverse` functions

- From **`tidyr`** package (part of **`tidyverse`**)

```
penguins_no_na <- drop_na(penguins)
```

`drop_na()`

- **`tidyverse`** functions always start with the **data**, followed by other arguments
- here, there are no other arguments

Side Note: Removing **NAs**

Selective remove `NA`s with `filter()`

- From **`dplyr`** package (part of tidyverse)

```
filter(penguins, !is.na(body_mass_g))
```

- `is.na()` checks if there is an `NA` and returns `TRUE` if so
- `!` turns a `TRUE` into a `FALSE`
- `filter()` only keeps rows that are `TRUE`
- **Thus** any row with an `NA` in `body_mass_g` is removed

Side Side Note: **`tidyverse`** functions

- From **`dplyr`** package (part of **`tidyverse`**)

```
filter(penguins, !is.na(body_mass_g))
```

`filter()`

- **`tidyverse`** functions always start with the **data**, followed by other arguments
- you can reference any **column** from '**data**'
- **`filter()`** keeps only rows that return **TRUE** to the logical statements

Summarize with **summarize()** (and **group_by()**)

- Can also use **group_by()** to calculate summaries by groups

```
penguins_sp <- group_by(penguins, species)
summarize(penguins_sp,
          mean_mass = mean(body_mass_g, na.rm = TRUE),
          sd_mass = sd(body_mass_g, na.rm = TRUE),
          median_mass = median(body_mass_g, na.rm = TRUE))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 3 x 4
##   species   mean_mass sd_mass median_mass
##   <fct>         <dbl>   <dbl>       <dbl>
## 1 Adelie        3701.    459.        3700
## 2 Chinstrap     3733.    384.        3700
## 3 Gentoo        5076.    504.        5000
```

Summarize with **`summarize()`** (and **`group_by()`**)

- Can also use **`group_by()`** to calculate summaries by groups

```
penguins_sp_sex <- group_by(penguins, species, sex)
summarize(penguins_sp_sex,
          mean_mass = mean(body_mass_g, na.rm = TRUE),
          sd_mass = sd(body_mass_g, na.rm = TRUE),
          median_mass = median(body_mass_g, na.rm = TRUE))
```

```
## # A tibble: 8 x 5
## # Groups:   species [3]
##   species   sex    mean_mass sd_mass median_mass
##   <fct>     <fct>      <dbl>   <dbl>       <dbl>
## 1 Adelie    female     3369.    269.        3400
## 2 Adelie    male       4043.    347.        4000
## 3 Adelie    <NA>       3540     477.        3475
## 4 Chinstrap female     3527.    285.        3550
## 5 Chinstrap male       3939.    362.        3950
## 6 Gentoo    female     4680.    282.        4700
## 7 Gentoo    male       5485.    313.        5500
## 8 Gentoo    <NA>       4588.    338.        4688.
```

Summarize with **summarize()** (and **group_by()**)

- Can also use **group_by()** to calculate summaries by groups

```
penguins_sp_sex <- group_by(penguins, species, sex)
summarize(penguins_sp_sex,
          mean_mass = mean(body_mass_g, na.rm = TRUE),
          sd_mass = sd(body_mass_g, na.rm = TRUE),
          median_mass = median(body_mass_g, na.rm = TRUE))
```

```
## # A tibble: 8 x 5
## # Groups:   species
##   species   sex    mean_mass sd_mass median_mass
##   <fct>     <fct>      <dbl>   <dbl>       <dbl>
## 1 Adelie    female     3369.    269.        3400
## 2 Adelie    male       4043.    347.        4000
## 3 Adelie    <NA>       3540     477.        3475
## 4 Chinstrap female     3527.    285.        3550
## 5 Chinstrap male       3939.    362.        3950
## 6 Gentoo    female     4680.    282.        4700
## 7 Gentoo    male       5485.    313.        5500
## 8 Gentoo    <NA>       4588.    338.        4688.
```

Where are the decimal points?

Side Note: Where are the decimal points?

- **`tibble`** hides them for easy viewing

```r
penguins_sum <- summarize(penguins_sp_sex,
                          mean_mass = mean(body_mass_g, na.rm = TRUE),
                          sd_mass = sd(body_mass_g, na.rm = TRUE),
                          median_mass = median(body_mass_g, na.rm = TRUE))
penguins_sum
```

```
## # A tibble: 8 x 5
## # Groups:   species [3]
##   species   sex    mean_mass sd_mass median_mass
##   <fct>     <fct>      <dbl>   <dbl>       <dbl>
## 1 Adelie    female     3369.    269.        3400
## 2 Adelie    male       4043.    347.        4000
## 3 Adelie    <NA>       3540     477.        3475
## 4 Chinstrap female     3527.    285.        3550
## 5 Chinstrap male       3939.    362.        3950
## 6 Gentoo    female     4680.    282.        4700
## 7 Gentoo    male       5485.    313.        5500
## 8 Gentoo    <NA>       4588.    338.        4688.
```

Side Note: Where are the decimal points?

- **`tibble`** hides them for easy viewing

```r
penguins_sum <- summarize(penguins_sp_sex,
                          mean_mass = mean(body_mass_g, na.rm = TRUE),
                          sd_mass = sd(body_mass_g, na.rm = TRUE),
                          median_mass = median(body_mass_g, na.rm = TRUE))
penguins_sum
```

```
## # A tibble: 8 x 5
## # Groups:   species [3]
##   species   sex    mean_mass sd_mass median_mass
##   <fct>     <fct>      <dbl>   <dbl>       <dbl>
## 1 Adelie    female     3369.    269.        3400
## 2 Adelie    male       4043.    347.        4000
## 3 Adelie    <NA>       3540     477.        3475
## 4 Chinstrap female     3527.    285.        3550
## 5 Chinstrap male       3939.    362.        3950
## 6 Gentoo    female     4680.    282.        4700
## 7 Gentoo    male       5485.    313.        5500
## 8 Gentoo    <NA>       4588.    338.        4688.
```

Note

If you want to keep the output, you need to assign (**`<-`**) it to an object.

Here, **`penguins_sum`**

Side Note: Where are the decimal points?

- **as.data.frame()** to see the raw data

```
as.data.frame(penguins_sum)
```

```
##     species    sex mean_mass  sd_mass median_mass
## 1    Adelie female  3368.836 269.3801      3400.0
## 2    Adelie   male  4043.493 346.8116      4000.0
## 3    Adelie   <NA>  3540.000 477.1661      3475.0
## 4 Chinstrap female  3527.206 285.3339      3550.0
## 5 Chinstrap   male  3938.971 362.1376      3950.0
## 6    Gentoo female  4679.741 281.5783      4700.0
## 7    Gentoo   male  5484.836 313.1586      5500.0
## 8    Gentoo   <NA>  4587.500 338.1937      4687.5
```

- Or click on the name in the Environment pane

Side Note: Where are all my data?

```
penguins
```

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

... with 334 more rows, and 2 more variables: sex <fct>, year <int>

Side Note: Where are all my data?

```
print(penguins, n = Inf)
```

```
## # A tibble: 344 x 8
##      species island bill_length_mm bill_depth_mm flipper_length_… body_mass_g
##      <fct>   <fct>           <dbl>         <dbl>            <int>       <int>
##    1 Adelie  Torge…           39.1          18.7              181        3750
##    2 Adelie  Torge…           39.5          17.4              186        3800
##    3 Adelie  Torge…           40.3          18                195        3250
##    4 Adelie  Torge…           NA            NA                 NA          NA
##    5 Adelie  Torge…           36.7          19.3              193        3450
##    6 Adelie  Torge…           39.3          20.6              190        3650
##    7 Adelie  Torge…           38.9          17.8              181        3625
##    8 Adelie  Torge…           39.2          19.6              195        4675
##    9 Adelie  Torge…           34.1          18.1              193        3475
##   10 Adelie  Torge…           42            20.2              190        4250
##   11 Adelie  Torge…           37.8          17.1              186        3300
##   12 Adelie  Torge…           37.8          17.3              180        3700
##   13 Adelie  Torge…           41.1          17.6              182        3200
##   14 Adelie  Torge…           38.6          21.2              191        3800
##   15 Adelie  Torge…           34.6          21.1              198        4400
```

Side Note: Where are all my data?

```
as.data.frame(penguins)
```

```
##         species    island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g    sex year
## 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          18.0               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           42.0          20.2               190        4250   <NA> 2007
## 11       Adelie Torgersen           37.8          17.1               186        3300   <NA> 2007
## 12       Adelie Torgersen           37.8          17.3               180        3700   <NA> 2007
## 13       Adelie Torgersen           41.1          17.6               182        3200 female 2007
## 14       Adelie Torgersen           38.6          21.2               191        3800   male 2007
## 15       Adelie Torgersen           34.6          21.1               198        4400   male 2007
## 16       Adelie Torgersen           36.6          17.8               185        3700 female 2007
## 17       Adelie Torgersen           38.7          19.0               195        3450 female 2007
```

Summarize with **`summarize()`**

`skewness()`, `kurtosis()`

- From **`moments`** package

```r
library(moments)

summarize(penguins,
          skew_mass = skewness(body_mass_g, na.rm = TRUE),
          kurt_mass = kurtosis(body_mass_g, na.rm = TRUE))
```

```
## # A tibble: 1 x 2
##   skew_mass kurt_mass
##       <dbl>     <dbl>
## 1     0.468      2.27
```

1. Normal distribution, skew = 0, kurtosis = 3*
2. Remember that it's best to evaluate the distribution **both** visually and statistically

* ***Excess* kurtosis** would be 0 for a normal distribution, but this functions measures **kurtosis**

Summarize with **summarize()**

Confidence Intervals

- By hand!
- 95% Confidence interval ranges from [mean - (1.96 *SE)] to [mean + (1.96* SE)]
- You can also express this interval as: mean +/- (1.96 * SE)
- Standard Errors (SE) can be calculated by SD / sqrt(n)

```
summarize(penguins,
          mean_mass = mean(body_mass_g, na.rm = TRUE),
          sd_mass = sd(body_mass_g, na.rm = TRUE),
          n = n(),
          se_mass = sd_mass / sqrt(n),        # Calculate Standard Error
          ci_mass = 1.96 * se_mass,           # CI margin of error
          ci_low_mass = mean_mass - ci_mass,  # The lower range
          ci_high_mass = mean_mass + ci_mass) # The upper range
```

Summarize with **summarize()**

Confidence Intervals

- By hand!
- 95% Confidence interval ranges from [mean - (1.96 *SE)] to [mean + (1.96* SE)]
- You can also express this interval as: mean +/- (1.96 * SE)
- Standard Errors (SE) can be calculated by SD / sqrt(n)

```
## # A tibble: 1 x 7
##   mean_mass sd_mass     n se_mass ci_mass ci_low_mass ci_high_mass
##       <dbl>   <dbl> <int>   <dbl>   <dbl>       <dbl>        <dbl>
## 1     4202.    802.   344    43.2    84.7       4117.        4287.
```

Put it All Together

```
penguins_sp <- group_by(penguins, species)
summarize(penguins_sp,
          mean_mass = mean(body_mass_g, na.rm = TRUE),
          sd_mass = sd(body_mass_g, na.rm = TRUE),
          q25_mass = quantile(body_mass_g, probs = 0.25, na.rm = TRUE),
          median_mass = median(body_mass_g, na.rm = TRUE),
          q75_mass = quantile(body_mass_g, probs = 0.25, na.rm = TRUE),
          n = n(),
          n_no_missing = sum(!is.na(body_mass_g)),
          skew_mass = skewness(body_mass_g, na.rm = TRUE),
          kurt_mass = kurtosis(body_mass_g, na.rm = TRUE),
          se_mass = sd_mass / sqrt(n),
          ci_mass = 1.96 * se_mass,
          ci_low_mass = mean_mass - ci_mass,
          ci_high_mass = mean_mass + ci_mass)
```

Put it All Together

```
##     species mean_mass  sd_mass q25_mass median_mass q75_mass   n n_no_missing  skew_mass kurt_mass
## 1    Adelie  3700.662 458.5661   3350.0        3700   3350.0 152          151 0.28249381  2.405611
## 2 Chinstrap  3733.088 384.3351   3487.5        3700   3487.5  68           68 0.24194125  3.463681
## 3    Gentoo  5076.016 504.1162   4700.0        5000   4700.0 124          123 0.06878276  2.257871
##    se_mass  ci_mass ci_low_mass ci_high_mass
## 1 37.19462 72.90146    3627.761     3773.564
## 2 46.60747 91.35065    3641.738     3824.439
## 3 45.27097 88.73111    4987.285     5164.747
```

Put it All Together (Advanced!)

pivot_longer() transposes data

- from tidyr package (part of tidyverse)

```
penguins_long <- pivot_longer(penguins,
                              cols = c(bill_length_mm, bill_depth_mm, flipper_length_mm, 
body_mass_g),
                              names_to = "measurement", values_to = "values")

penguins_long
```

```
## # A tibble: 1,376 x 6
##    species island    sex     year measurement       values
##    <fct>   <fct>     <fct>  <int> <chr>              <dbl>
##  1 Adelie  Torgersen male    2007 bill_length_mm      39.1
##  2 Adelie  Torgersen male    2007 bill_depth_mm       18.7
##  3 Adelie  Torgersen male    2007 flipper_length_mm  181  
##  4 Adelie  Torgersen male    2007 body_mass_g       3750  
##  5 Adelie  Torgersen female  2007 bill_length_mm      39.5
##  6 Adelie  Torgersen female  2007 bill_depth_mm       17.4
##  7 Adelie  Torgersen female  2007 flipper_length_mm  186  
```

Put it All Together **(Advanced!)**

`pivot_longer()` transposes data

- from **`tidyr`** package (part of **`tidyverse`**)

```
penguins_long <- pivot_longer(penguins,
                              cols = c(bill_length_mm, bill_depth_mm, flipper_length_mm,
body_mass_g),
                              names_to = "measurement", values_to = "values")

penguins_long
```

```
## # A tibble: 1,376 x 6
##    species island    sex     year measurement       values
##    <fct>   <fct>     <fct>  <int> <chr>              <dbl>
##  1 Adelie  Torgersen male    2007 bill_length_mm      39.1
##  2 Adelie  Torgersen male    2007 bill_depth_mm       18.7
##  3 Adelie  Torgersen male    2007 flipper_length_mm  181  
##  4 Adelie  Torgersen male    2007 body_mass_g       3750  
##  5 Adelie  Torgersen female  2007 bill_length_mm      39.5
##  6 Adelie  Torgersen female  2007 bill_depth_mm       17.4
##  7 Adelie  Torgersen female  2007 flipper_length_mm  186  
```

Extra

Compare **`penguins`** to **`penguins_long`**. Can you see what the **`pivot_longer()`** function is doing?

Put it All Together **(Advanced!)**

```
penguins_long_sp <- group_by(penguins_long, species, measurement)

summarize(penguins_long_sp,
          mean = mean(values, na.rm = TRUE),
          sd = sd(values, na.rm = TRUE),
          q25 = quantile(values, probs = 0.25, na.rm = TRUE),
          median = median(values, na.rm = TRUE),
          q75 = quantile(values, probs = 0.25, na.rm = TRUE),
          n = n(),
          n_no_missing = sum(!is.na(values)),
          skew = skewness(values, na.rm = TRUE),
          kurt = kurtosis(values, na.rm = TRUE))
```

Put it All Together (Advanced!)

```
## `summarise()` regrouping output by 'species' (override with `.groups` argument)
```

```
## # A tibble: 12 x 11
## # Groups:   species [3]
##    species   measurement         mean      sd    q25 median    q75     n n_no_missing     skew
kurt
##    <fct>     <chr>              <dbl>   <dbl>  <dbl>  <dbl>  <dbl> <int>        <int>    <dbl>
<dbl>
##  1 Adelie    bill_depth_mm       18.3   1.22    17.5   18.4   17.5   152          151  0.318
2.90
##  2 Adelie    bill_length_mm      38.8   2.66    36.8   38.8   36.8   152          151  0.160
2.81
##  3 Adelie    body_mass_g       3701.  459.    3350   3700   3350     152          151  0.282
2.41
##  4 Adelie    flipper_length_mm  190.    6.54   186    190    186     152          151  0.0865
3.28
##  5 Chinstrap bill_depth_mm       18.4   1.14    17.5   18.4   17.5    68           68  0.00673
2.10
##  6 Chinstrap bill_length_mm      48.8   3.34    46.3   49.6   46.3    68           68 -0.0886
2.95
```

All Data vs. Variable by Variable

Depends on what you need

- `ggpairs()` and `skim()`
  - Lots of data quickly summarized and examined
  - Less easily customized

- `ggplot()` and `summarize()`
  - Take a bit longer to write out
  - Very customizable
  - Can easily include stats not available in `ggpairs()` and `skim()`

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

- RStudio > Help > Cheatsheets > Data Transformation with dplyr
- R for Data Science
  - Data transformation
  - Exploratory Data Analysis