An Introduction to R and RStudio for Exploratory Data Analysis

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OCTRI Biostatistics, Epidemiology, Research & Design (BERD) Workshop

Part 1: 2020/09/16 & Part 2: 2020/09/17

slides: bit.ly/berd_intro_part2
pdf: bit.ly/berd_intro_part2_pdf

An Introduction to R and RStudio for Exploratory Data Analysis (Part 2)

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OCTRI Biostatistics, Epidemiology, Research & Design (BERD) Workshop

Do this now:

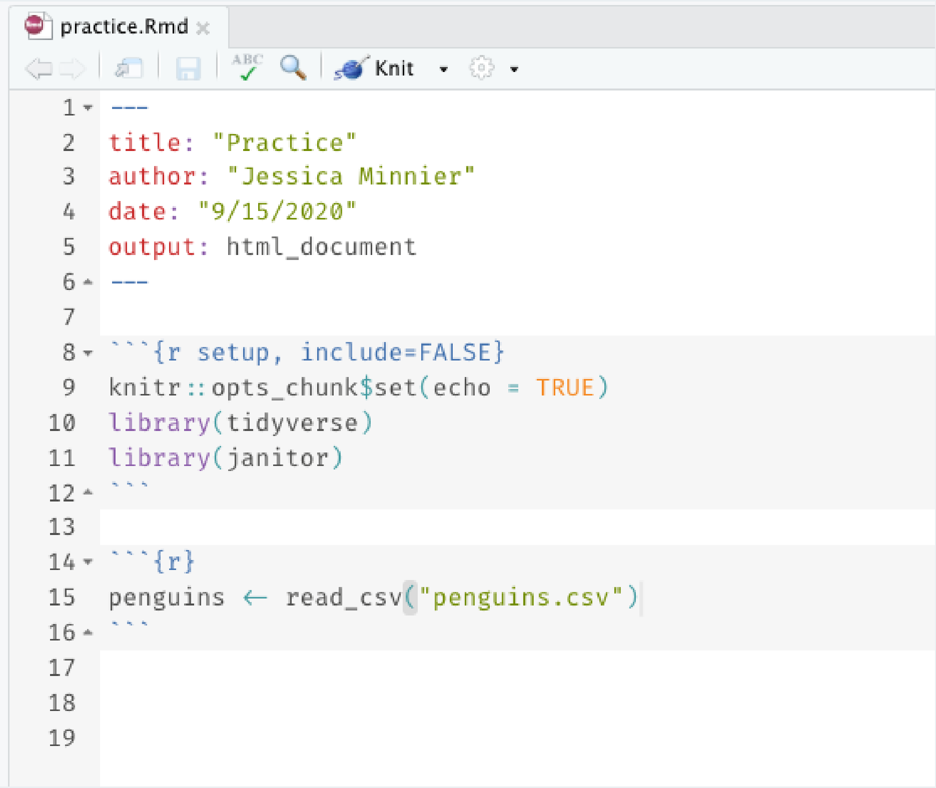
1. **Open html slides**: http://bit.ly/berd_intro_part2
2. **Download Rmd file** to follow along: bit.ly/berd_intro_rmd
3. **Open google doc** for asking questions: bit.ly/berd_doc2
    - Helpers will be monitoring this, you can ask questions, copy code or screenshots.
4. **Open Rstudio with these steps:**
    - Open the folder from yesterday
    - Double click on the `.Rproj` file.
    - All your files should be there.

Working with data, continued

- Open your old Rmd file
- If you make a new Rmd file, make sure you have this code in a code chunk at the top of the Rmd:

```
library(tidyverse)
library(janitor)
penguins <- read_csv("penguins")
```

- Remember we need to load (open) the package every time we want to use it in a new Rstudio instance *or* knit an Rmd
- When you knit an Rmd, it is blind to what you have done in the console or in the R enivronment. It starts completely from scratch.



~~~
---
title: "Practice"
author: "Jessica Minnier"
date: "9/15/2020"
output: html_document
---

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
library(tidyverse)
library(janitor)
```

```{r}
penguins <- read_csv("penguins.csv")
```
~~~

Working with data, we will use the pipe %>%

The pipe operator `%>%` is part of the tidyverse, and strings together commands to be performed sequentially

```
penguins %>% head(n=3)      # prounounce %>% as "then"
```

```
## # A tibble: 3 x 9
##      id species island bill_length_mm bill_depth_mm flipper_length_… body_mass_
##   <dbl> <chr>   <chr>           <dbl>         <dbl>            <dbl>       <dbl
## 1  1689 Adelie  Torge…           39.1          18.7              181         375
## 2  4274 Adelie  Torge…           NA            17.4              186         380
## 3  4539 Adelie  Torge…           40.3          18                195         325
## # … with 2 more variables: sex <chr>, year <dbl>
```

- Always *first list the tibble* that the commands are being applied to
- Can use **multiple pipes** to run multiple commands in sequence
    - What does the following code do?

```
penguins %>% head(n=2) %>% summary()
```

Quick tips on summarizing data

categorical data

numerical data

janitor, dplyr

Numerical data summaries: $ vs `summarize()`

We saw how to summarize a vector pulled with `$`, but there are easier ways to summarize multiple columns at once.

```
mean(penguins$body_mass_g)
```

```
## [1] 4201.754
```

```
median(penguins$body_mass_g)
```

```
## [1] 4050
```

```
penguins %>%
  summarize(mean(body_mass_g),
            median(body_mass_g))
```

```
## # A tibble: 1 x 2
##   `mean(body_mass_g)` `median(body_mass_g)`
##                 <dbl>                 <dbl>
## 1               4202.                  4050
```

`summarize()` with NA

- Don't forget `na.rm = TRUE` if you need it.
- You can also name these columns.

```
penguins %>%
  summarize(mean_mass = mean(body_mass_g),
            mean_len = mean(bill_length_mm, na.rm = TRUE))
```

```
## # A tibble: 1 x 2
##   mean_mass mean_len
##       <dbl>    <dbl>
## 1     4202.     44.0
```

By group `summarize()` (1/2)

- We can summarize data as a whole, or in groups with `group_by()`
- `group_by()` is very powerful, see data wrangling cheatsheet

```
# summary of all data as a whole
penguins %>%
  summarize(mass_mean =mean(body_mass_g),
            mass_sd = sd(body_mass_g),
            mass_cv = sd(body_mass_g)/mean(body_mass_g))
```

```
## # A tibble: 1 x 3
##   mass_mean mass_sd mass_cv
##       <dbl>   <dbl>   <dbl>
## 1     4202.    802.   0.191
```

By group `summarize()` (2/2)

- We can summarize data as a whole, or in groups with `group_by()`
- `group_by()` is very powerful, see data wrangling cheatsheet

```
# summary by group variable
penguins %>%
  group_by(species) %>%
  summarize(n_per_group = n(),
            mass_mean =mean(body_mass_g),
            mass_sd = sd(body_mass_g),
            mass_cv = sd(body_mass_g)/mean(body_mass_g))
```

```
## # A tibble: 3 x 5
##   species   n_per_group mass_mean mass_sd mass_cv
##   <chr>           <int>     <dbl>   <dbl>   <dbl>
## 1 Adelie            151     3701.    459.  0.124
## 2 Chinstrap          68     3733.    384.  0.103
## 3 Gentoo            123     5076.    504.  0.0993
```

Advanced `summarize(across())` (1/3)

- Can also use `across()` to summarize multiple variables (more examples)

```
penguins %>%
  summarize(across(c(body_mass_g, bill_depth_mm), mean))
```

```
## # A tibble: 1 x 2
##   body_mass_g bill_depth_mm
##         <dbl>         <dbl>
## 1       4202.          17.2
```

```
penguins %>%
  summarize(across(c(bill_length_mm, bill_depth_mm), mean, na.rm=TRUE))
```

```
## # A tibble: 1 x 2
##   bill_length_mm bill_depth_mm
##            <dbl>         <dbl>
## 1           44.0          17.2
```

Advanced `summarize(across())` (2/3)

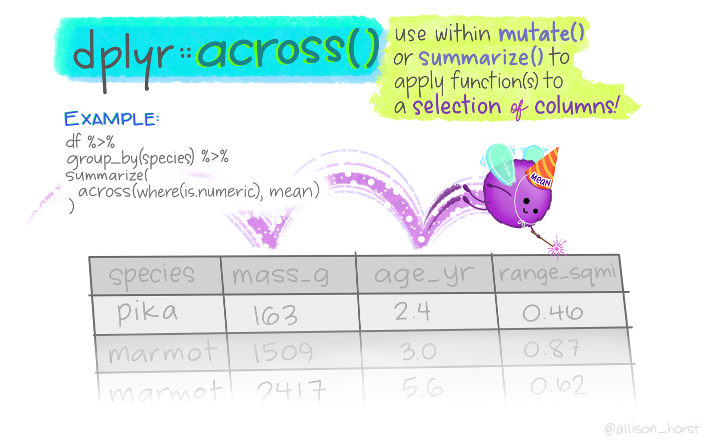
- Can also use `across()` to summarize multiple variables *and* functions (more examples)

```
penguins %>%
  summarize(across(c(body_mass_g, bill_depth_mm),
                   c(m = mean, sd = sd)))
```

```
## # A tibble: 1 x 4
##   body_mass_g_m body_mass_g_sd bill_depth_mm_m bill_depth_mm_sd
##           <dbl>          <dbl>           <dbl>            <dbl>
## 1         4202.           802.            17.2             1.97
```

Advanced `summarize(across())` (3/3)

- Can also use `across()` to summarize based on true/false conditions (more examples)



```
df %>%
group_by(species) %>%
summarize(
  across(where(is.numeric), mean)
)
```

species	mass_g	age_yr	range_sqmi
pika	163	2.4	0.46
marmot	1509	3.0	0.87
marmot	2417	5.6	0.62

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```
penguins %>%
  summarize(
    across(where(is.character),
           n_distinct))
```

```
## # A tibble: 1 x 3
##   species island   sex
##     <int>  <int> <int>
## 1       3      3     3
```

```
penguins %>%
  summarize(across(where(is.numeric),
            min, na.rm=TRUE))
```

```
## # A tibble: 1 x 6
##      id bill_length_mm bill_depth_mm flippe
##   <dbl>          <dbl>         <dbl>
## 1  1001           32.1          13.1
```

Frequency tables: simple count()

```
penguins %>% count(island)
```

```
## # A tibble: 3 x 2
##   island        n
##   <chr>     <int>
## 1 Biscoe      167
## 2 Dream       124
## 3 Torgersen    51
```

```
penguins %>% count(species, island)
```

```
## # A tibble: 5 x 3
##   species   island        n
##   <chr>     <chr>     <int>
## 1 Adelie    Biscoe       44
## 2 Adelie    Dream        56
## 3 Adelie    Torgersen    51
## 4 Chinstrap Dream        68
## 5 Gentoo    Biscoe      123
```

Fancier frequency tables: `janitor` package's `tabyl` function

```
# default table
penguins %>% tabyl(species)
```

```
##    species   n   percent
##     Adelie 151 0.4415205
##  Chinstrap  68 0.1988304
##     Gentoo 123 0.3596491
```

```
# output can be treated as tibble
penguins%>%tabyl(species)%>%select(-n)
```

```
##    species   percent
##     Adelie 0.4415205
##  Chinstrap 0.1988304
##     Gentoo 0.3596491
```

`adorn_` your table!

```
penguins %>%
  tabyl(species) %>%
  adorn_totals("row") %>%
  adorn_pct_formatting(digits=2)
```

```
##    species   n percent
##     Adelie 151  44.15%
##  Chinstrap  68  19.88%
##     Gentoo 123  35.96%
##      Total 342 100.00%
```

2x2 tabyls

```r
# default 2x2 table
penguins %>%
  tabyl(species, sex)
```

```
##     species female male NA_
##      Adelie     73   73   5
##   Chinstrap     34   34   0
##      Gentoo     58   61   4
```

What adornments does the tabyl to right have?

```r
penguins %>% tabyl(species, sex) %>%
  adorn_percentages(denominator = "col") %>%
  adorn_totals("row") %>%
  adorn_pct_formatting(digits = 1) %>%
  adorn_ns()
```

```
##     species          female             male
##      Adelie  44.2%   (73)   43.5%   (73)   55.6%
##   Chinstrap  20.6%   (34)   20.2%   (34)    0.0%
##      Gentoo  35.2%   (58)   36.3%   (61)   44.4%
##       Total 100.0% (165) 100.0% (168) 100.0%
```

- Base R has a `table` function, but it is clunkier and the output is not a data frame (or tibble).
- See the tabyl vignette for more information, adorn options, & 3-way `tabyls`

3 way tabyls are possible

```
penguins %>% tabyl(species, island, sex)
```

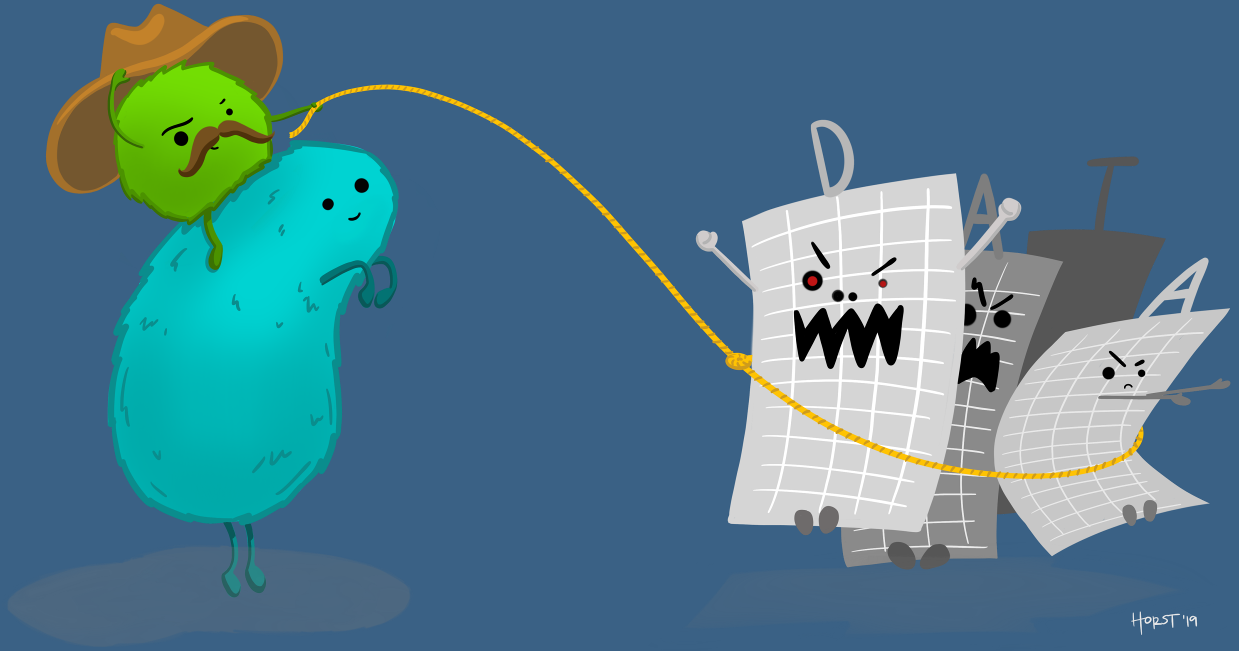
```
## $female
##    species Biscoe Dream Torgersen
##     Adelie     22    27        24
##  Chinstrap      0    34         0
##     Gentoo     58     0         0
##
## $male
##    species Biscoe Dream Torgersen
##     Adelie     22    28        23
##  Chinstrap      0    34         0
##     Gentoo     61     0         0
##
## $NA_
##    species Biscoe Dream Torgersen
##     Adelie      0     1         4
##  Chinstrap      0     0         0
##     Gentoo      4     0         0
```

Practice 3

1. Continue adding code chunks to your Rmd (or, start a new one! But remember to load the libraries and data at the top.)
2. How many different years are in the data? (Hint: use `tabyl()` or `n_distinct()`)
3. Count the number of penguins measured each year.
4. Calculate the median body mass by each species and sex subgroup. Use `summarize()` and `group_by()` to do this.
5. Create a 2x2 table of number of penguins measured in each year by each island.

- **Take a break!**

Data Wrangling



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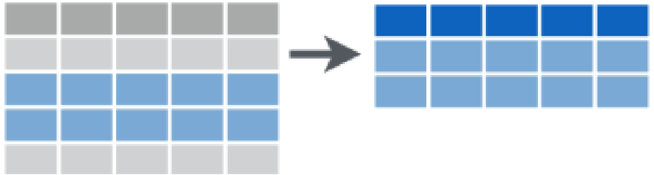
Subsetting data

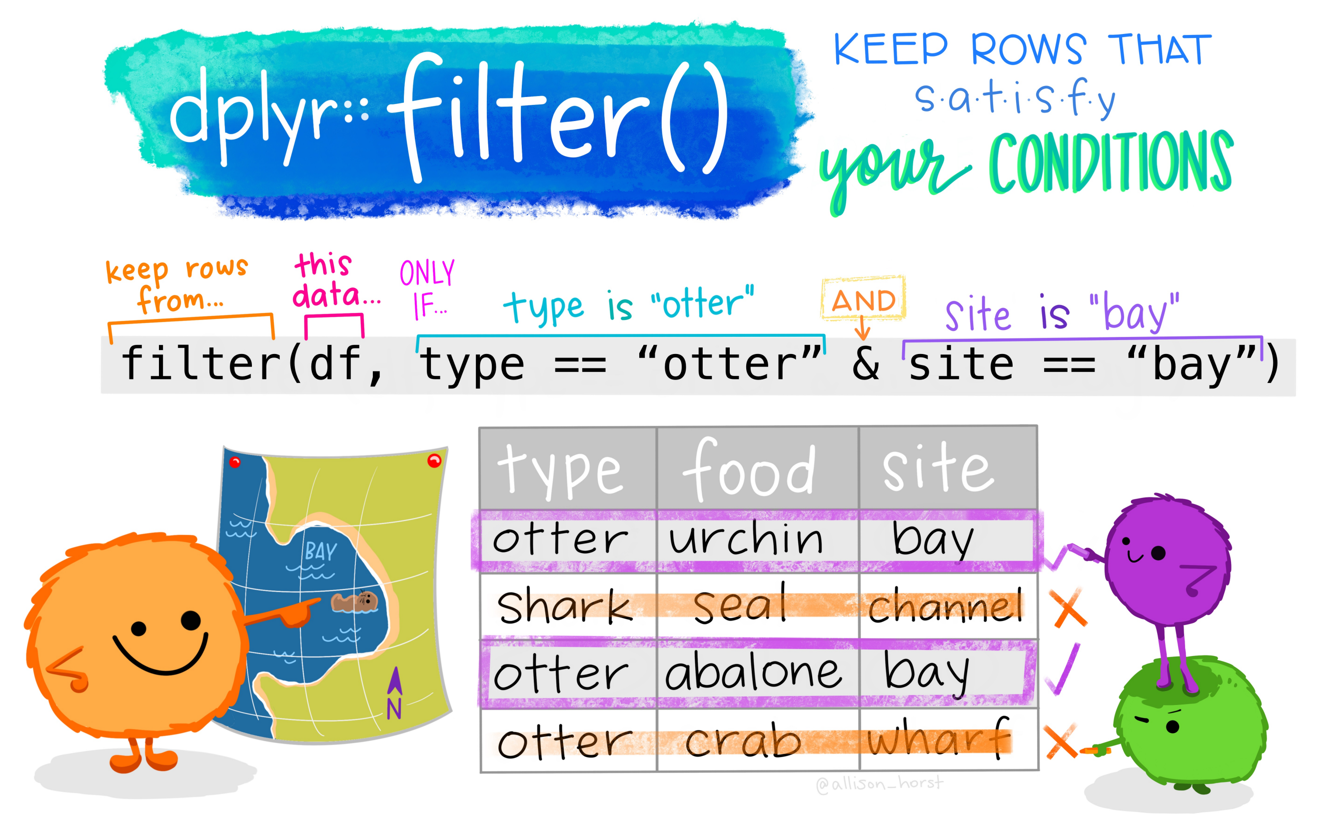
Subset Observations (Rows)



Subset Variables (Columns)

tidyverse data wrangling cheatsheet

`filter()` rows that satisfy specified conditions



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`filter()` options

Subset rows of data by specifying conditions within `filter()`

- math: >, <, >=, <=
- double = for "is equal to": ==
- & (and)
- | (or)
- != (not equal)

- `is.na()` to filter based on missing values
- `%in%` to filter based on group membership
- `!` in front negates the statement, as in
  - `!is.na(sex)`
  - `!(species %in% c("Adelie", "Gentoo"))`

```
penguins %>% filter(bill_length_mm > 55)
```

```
## # A tibble: 5 x 9
##       id species island bill_length_mm bill_depth_mm flipper_length_… body_mass_
##    <dbl> <chr>   <chr>           <dbl>         <dbl>            <dbl>      <dbl
## 1   4026 Gentoo  Biscoe           59.6          17                230        605
## 2   2415 Gentoo  Biscoe           55.9          17                228        560
## 3   4629 Gentoo  Biscoe           55.1          16                230        585
## 4   2009 Chinst… Dream            58            17.8              181        370
## 5   4452 Chinst… Dream            55.8          19.8              207        400
## # … with 2 more variables: sex <chr>, year <dbl>
```

`filter()` practice

What do these commands do? Try them out:

```r
penguins %>% filter(island == "Torgersen")
penguins %>% filter(bill_length_mm/bill_depth_mm > 3)    # can do math
penguins %>% filter((body_mass_g < 3000) | (body_mass_g > 6000))

# filter on multiple variables:
penguins %>% filter(body_mass_g < 3000, bill_depth_mm < 20, sex == "female")
penguins %>% filter(body_mass_g < 3000 & bill_depth_mm < 20 & sex == "female")
penguins %>% filter(body_mass_g < 3000 | bill_depth_mm < 20 | sex == "female")

penguins %>% filter(year == 2008)      # note the use of == instead of just =
penguins %>% filter(sex == "female")

penguins %>% filter(!(species == "Adelie"))
penguins %>% filter(species %in% c("Chinstrap", "Gentoo"))

penguins %>% filter(is.na(sex))
penguins %>% filter(!is.na(sex))
```

`select()` columns

- select columns (variables)
- no quotes needed around variable names
- can be used to rearrange columns
- syntax is flexible and has many options

```
penguins %>% select(id, island, species, body_mass_g)
```

```
## # A tibble: 342 x 4
##        id island    species body_mass_g
##     <dbl> <chr>     <chr>         <dbl>
##  1  1689 Torgersen Adelie         3750
##  2  4274 Torgersen Adelie         3800
##  3  4539 Torgersen Adelie         3250
##  4  2435 Torgersen Adelie         3450
##  5  2326 Torgersen Adelie         3650
##  6  2637 Torgersen Adelie         3625
##  7  4443 Torgersen Adelie         4675
##  8  2102 Torgersen Adelie         3475
##  9  2975 Torgersen Adelie         4250
## 10  3966 Torgersen Adelie         3300
## # … with 332 more rows
```

Column selection syntax options

There are many ways to select a set of variable names (columns):

- `var1:var20`: all columns from `var1` to `var20`
- **Removing columns**
  - `-var1`: remove the column`var1`
  - `-(var1:var20)`: remove all columns from `var1` to `var20`
- **Select by specifying text within column names**
  - `contains("mm")`, `contains("_")`: all variable names that contain the specified string
  - `starts_with("a")` or `ends_with("last")`: all variable names that start or end with the specified string

See other examples in the data wrangling cheatsheet.

`select()` practice

Which columns are selected & in what order using these commands?
First guess and then try them out.

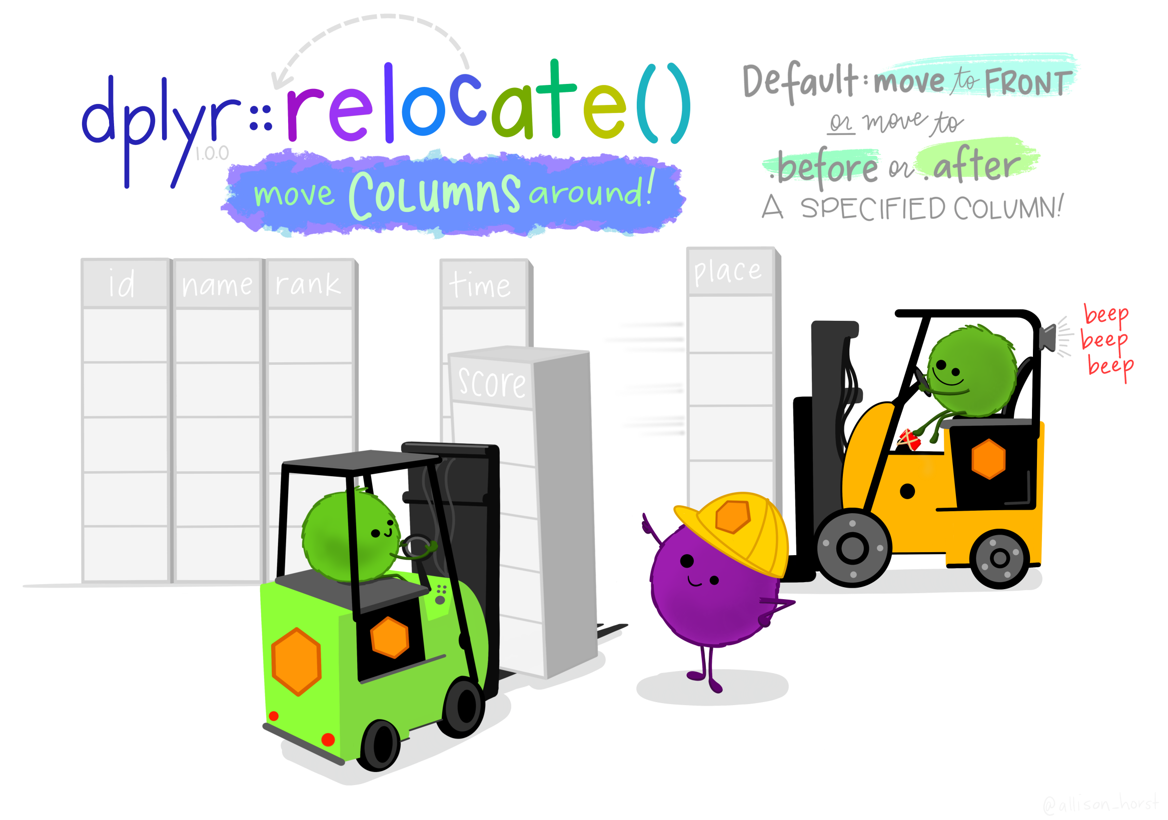
```r
penguins %>% select(id:bill_length_mm)

penguins %>% select(where(is.character))
penguins %>% select(where(is.numeric))

penguins %>% select(-id,-species)
penguins %>% select(-(id:island))

penguins %>% select(contains("bill"))
penguins %>% select(starts_with("s"))
penguins %>% select(-contains("mm"))
```

relocate() columns to move them around



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`relocate()` columns

- change the order of columns in dataset
- default action is to list specified column names first
- no quotes needed around variable names
- similar options as with `select()`, plus special ones such as `.before` and `.after`

```
penguins %>% relocate(year, body_mass_g)
```

```
## # A tibble: 342 x 9
##     year body_mass_g    id species island bill_length_mm bill_depth_mm
##    <dbl>       <dbl> <dbl> <chr>   <chr>           <dbl>         <dbl>
##  1  2007        3750  1689 Adelie  Torge…           39.1          18.7
##  2  2007        3800  4274 Adelie  Torge…           NA            17.4
##  3  2007        3250  4539 Adelie  Torge…           40.3          18
##  4  2007        3450  2435 Adelie  Torge…           36.7          19.3
##  5  2007        3650  2326 Adelie  Torge…           39.3          20.6
##  6  2007        3625  2637 Adelie  Torge…           38.9          17.8
##  7  2007        4675  4443 Adelie  Torge…           NA            19.6
##  8  2007        3475  2102 Adelie  Torge…           34.1          18.1
##  9  2007        4250  2975 Adelie  Torge…           42            20.2
## 10  2007        3300  3966 Adelie  Torge…           37.8          17.1
## # … with 332 more rows, and 2 more variables: flipper_length_mm <dbl>,
```

`relocate()` practice

What order are the columns in using these commands?
First guess and then try them out.

```
penguins %>% relocate(species:bill_length_mm)

penguins %>% relocate(where(is.character))
penguins %>% relocate(where(is.numeric))

penguins %>% relocate(flipper_length_mm,.before = bill_length_mm)
penguins %>% relocate(species, .after = island)
penguins %>% relocate(species, .after = last_col())
```

Save your modified data

- Use a new variable name and the `<-` assignment operator to save a modified data frame
- You can save the modified data using the same name, but it will replace the previous dataset

```
penguins_sub <- penguins %>% select(id:island, sex)
penguins_sub
```

```
## # A tibble: 342 x 4
##         id species island    sex
##      <dbl> <chr>   <chr>     <chr>
##  1   1689 Adelie  Torgersen male
##  2   4274 Adelie  Torgersen female
##  3   4539 Adelie  Torgersen female
##  4   2435 Adelie  Torgersen female
##  5   2326 Adelie  Torgersen male
##  6   2637 Adelie  Torgersen female
##  7   4443 Adelie  Torgersen male
##  8   2102 Adelie  Torgersen <NA>
##  9   2975 Adelie  Torgersen <NA>
## 10   3966 Adelie  Torgersen <NA>
## # … with 332 more rows
```

Make new variables

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`mutate()` the data

Use `mutate()` to add new columns to a tibble

- Many options for how to define new column of data

```
penguins <- penguins %>%
   mutate(bill_ratio = bill_length_mm / bill_depth_mm)
# use = (not <- or ==) to define new variable

penguins %>% select(bill_ratio, bill_length_mm, bill_depth_mm)
```

```
## # A tibble: 342 x 3
##    bill_ratio bill_length_mm bill_depth_mm
##         <dbl>          <dbl>         <dbl>
##  1       2.09           39.1          18.7
##  2      NA             NA             17.4
##  3       2.24           40.3          18
##  4       1.90           36.7          19.3
##  5       1.91           39.3          20.6
##  6       2.19           38.9          17.8
##  7      NA             NA             19.6
##  8       1.88           34.1          18.1
##  9       2.08           42            20.2
```

`mutate()` practice

What do the following commands do?
First guess and then try them out.

```
penguins <- penguins %>% mutate(bill_long = (bill_length_mm > 45))

penguins <- penguins %>% mutate(male = (sex == "male"))
penguins <- penguins %>% mutate(male2 = 1 * (sex == "male"))
```

`rename()` columns

- `rename(new_name = old_name)`

Code renames the column, but just prints output without saving the rename:

```
# This does not save the new name
penguins %>% rename(record = id)
```

```
## # A tibble: 342 x 10
##     record species island bill_lengt
##      <dbl> <chr>   <chr>            <
##  1    1689 Adelie  Torge…
##  2    4274 Adelie  Torge…
##  3    4539 Adelie  Torge…
##  4    2435 Adelie  Torge…
##  5    2326 Adelie  Torge…
##  6    2637 Adelie  Torge…
##  7    4443 Adelie  Torge…
##  8    2102 Adelie  Torge…
##  9    2975 Adelie  Torge…
```

Code renames the column *and* overwrites **`penguins`** with renamed column:

```
penguins2 <- penguins %>%
    rename(record = id)
penguins2
```

```
## # A tibble: 342 x 10
##     record species island bill_lengt
##      <dbl> <chr>   <chr>            <
##  1    1689 Adelie  Torge…
##  2    4274 Adelie  Torge…
##  3    4539 Adelie  Torge…
##  4    2435 Adelie  Torge…
##  5    2326 Adelie  Torge…
##  6    2637 Adelie  Torge…
##  7    4443 Adelie  Torge…
```

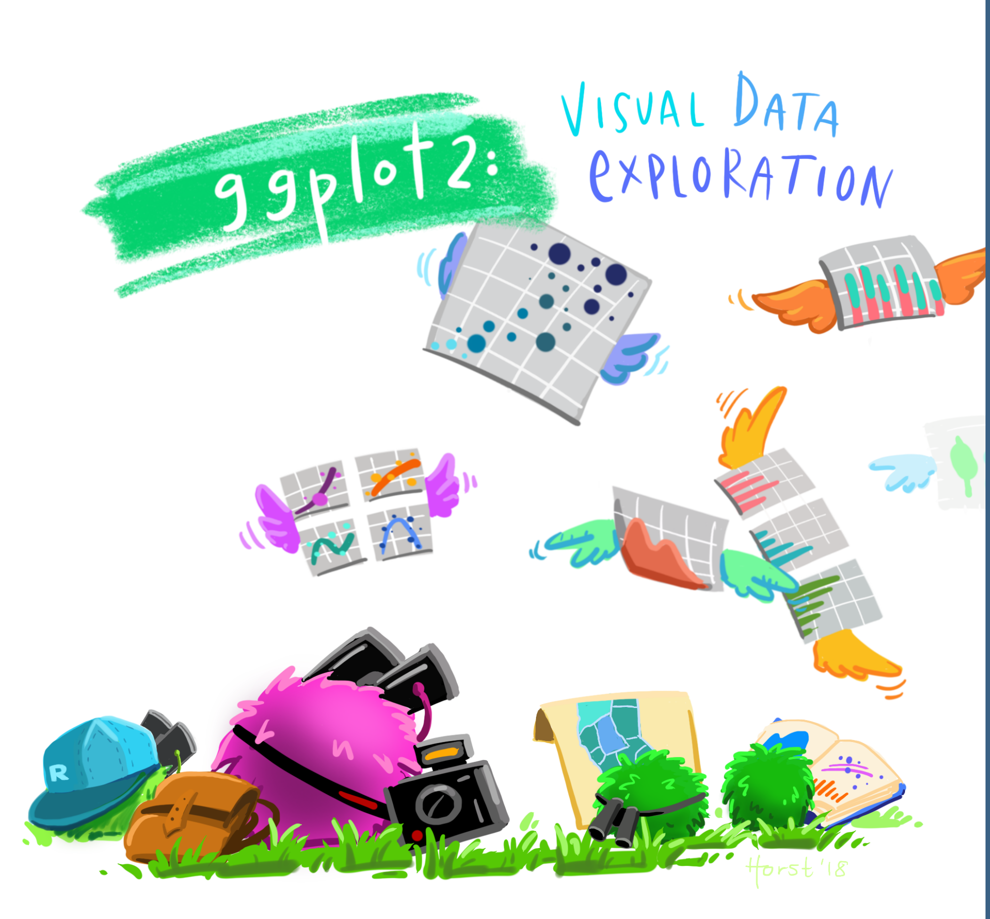
Practice 4

Create a new Rmd or continue in your current Rmd.

1. Create a dataset for just the Torgersen island penguins that are female.
2. Restrict the data to just Torgersen female penguins that weigh more than 3500 g.
3. Restrict the dataset from the previous step to include just the columns with the original body measurements.
4. Add a column for the difference in the flipper and bill lengths, and call it `flipper_bill_diff`.
5. How many rows and columns does your final dataset have?

- **Take a break!**

Making prettier plots



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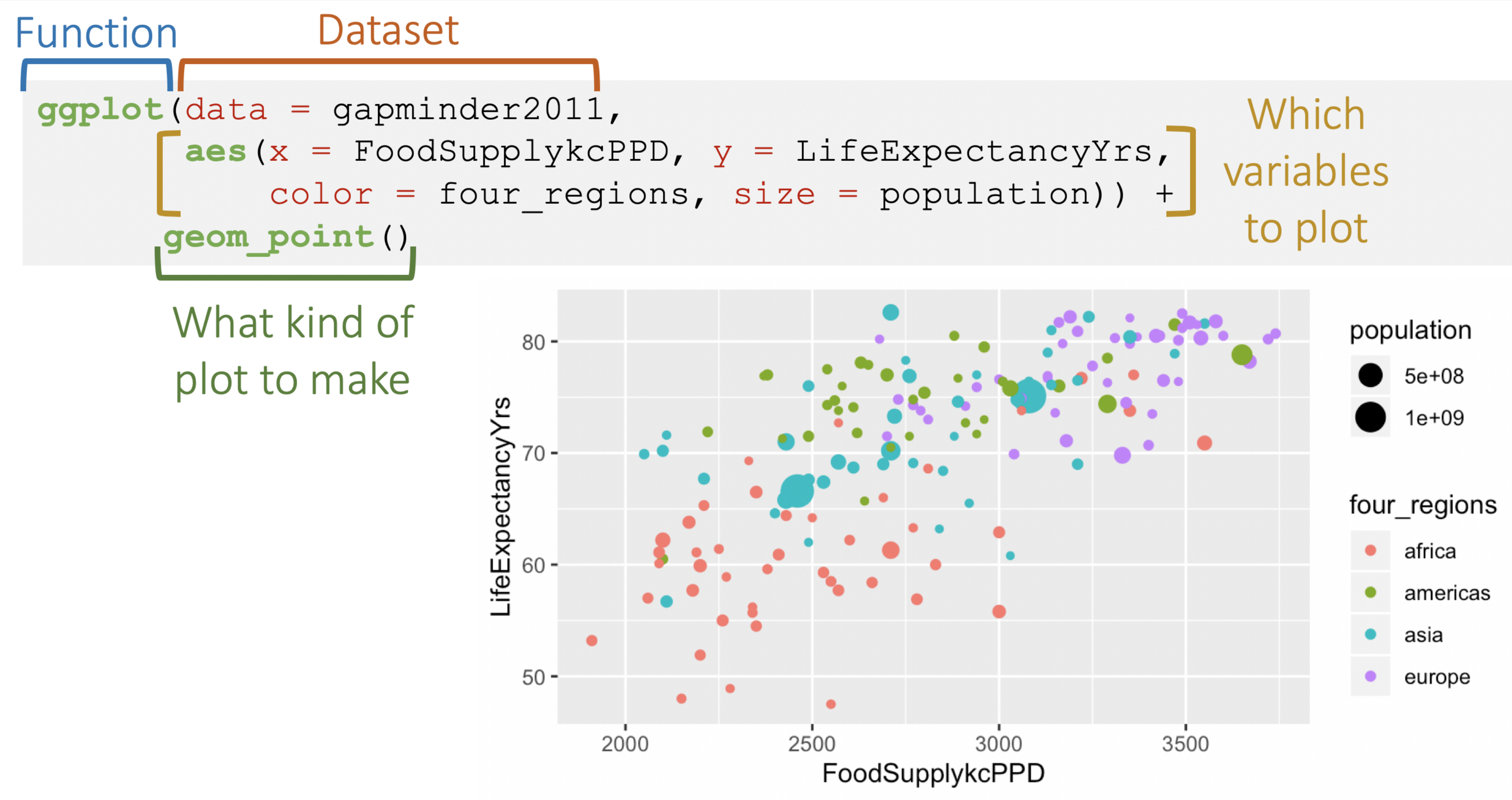
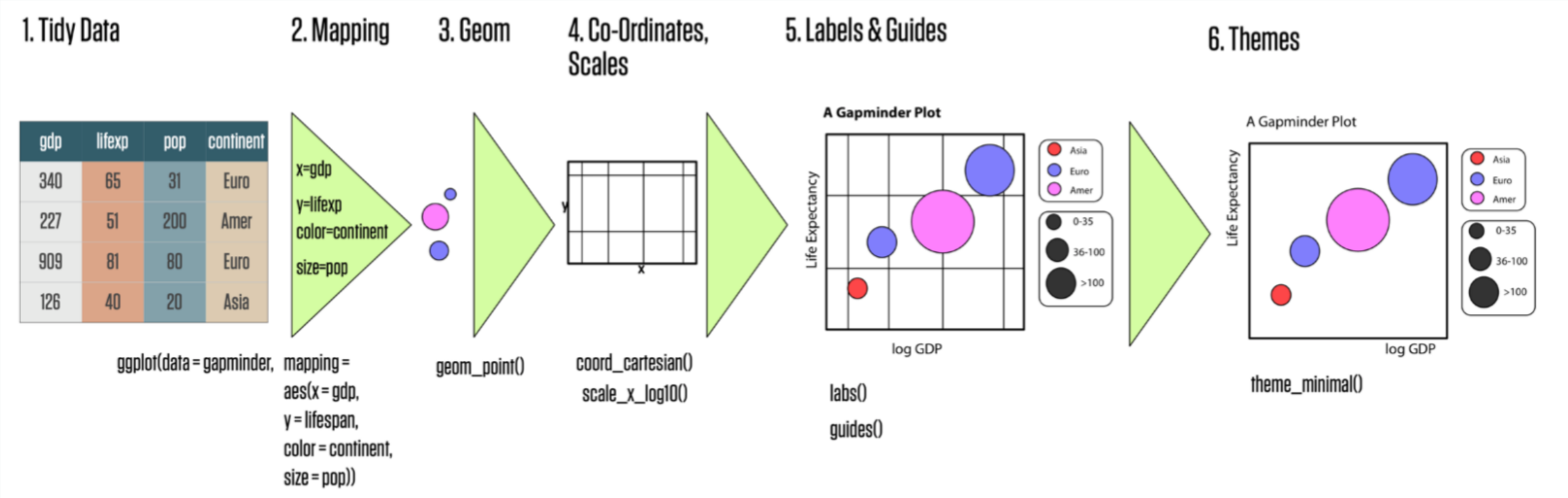
Basics of ggplot

- For a full treatment, watch our BERD workshop "Data Visualization with R and ggplot2"



```
ggplot(data = gapminder2011,
       aes(x = FoodSupplykcPPD, y = LifeExpectancyYrs,
           color = four_regions, size = population)) +
      geom_point()
```

Grammar of ggplot2



gdp	lifexp	pop	continent
340	65	31	Euro
227	51	200	Amer
909	81	80	Euro
126	40	20	Asia

```
ggplot(data = gapminder, mapping =
aes(x = gdp,
y = lifespan,
color = continent,
size = pop))
```

```
geom_point()
```

```
coord_cartesian()
scale_x_log10()
```

```
labs()
guides()
```

```
theme_minimal()
```

Kieran Healy

Back to ggplot code

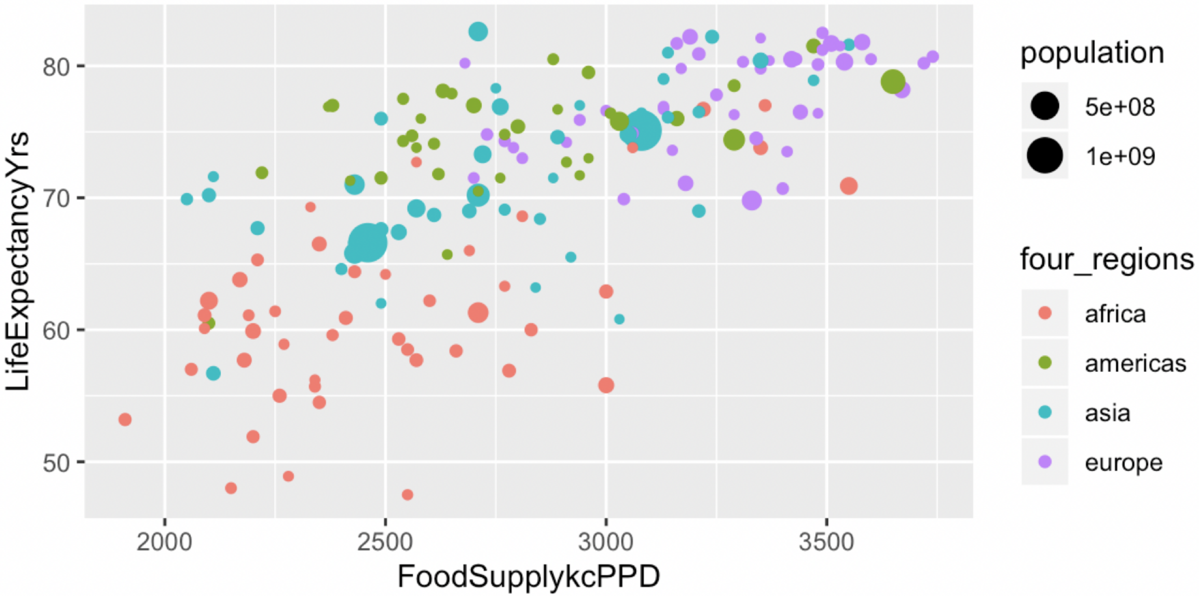
Function

Dataset

```
ggplot(data = gapminder2011,
       aes(x = FoodSupplykcPPD, y = LifeExpectancyYrs,
           color = four_regions, size = population)) +
       geom_point()
```

Which variables to plot

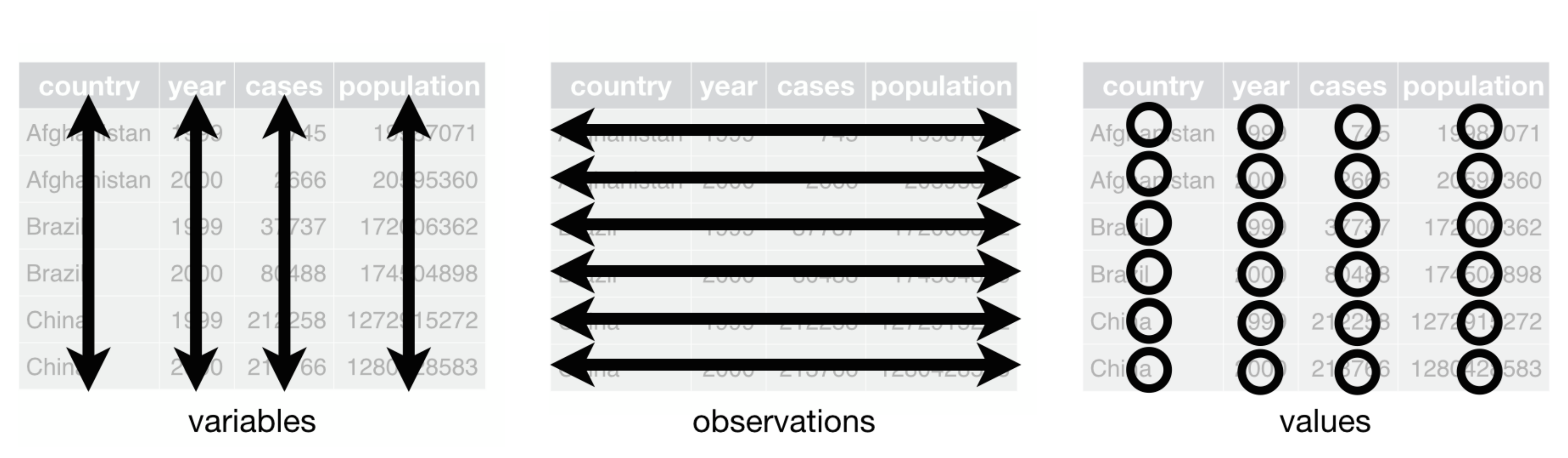
What kind of plot to make



Ggplot needs tidy data

What are **tidy** data?

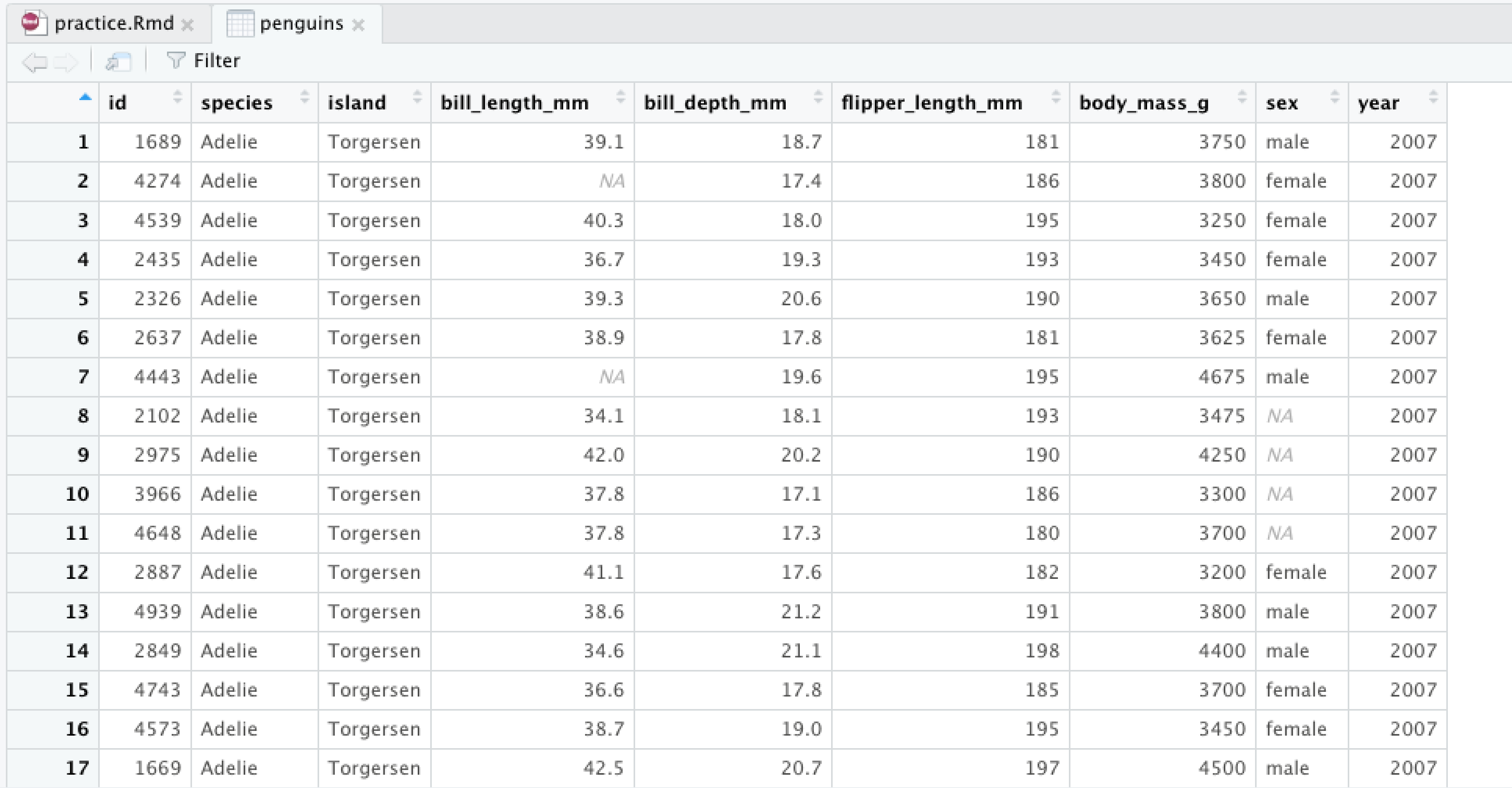
1. Each variable forms a column
2. Each observation forms a row
3. Each value has its own cell



G. Grolemond & H. Wickham's R for Data Science

See BERD workshop Data Wrangling Part 1 slides for more info.

Is our data tidy?

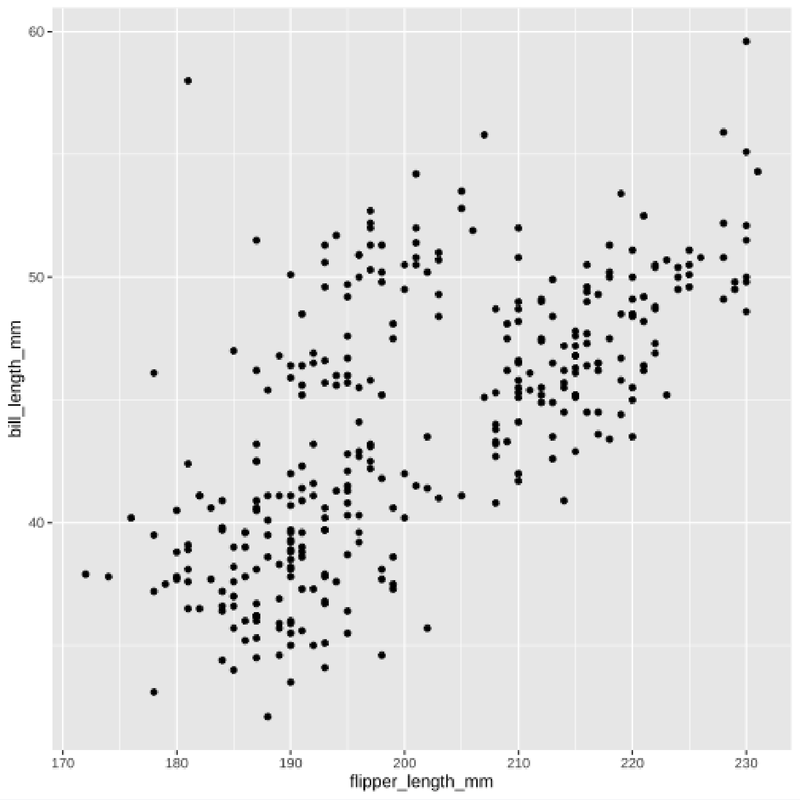


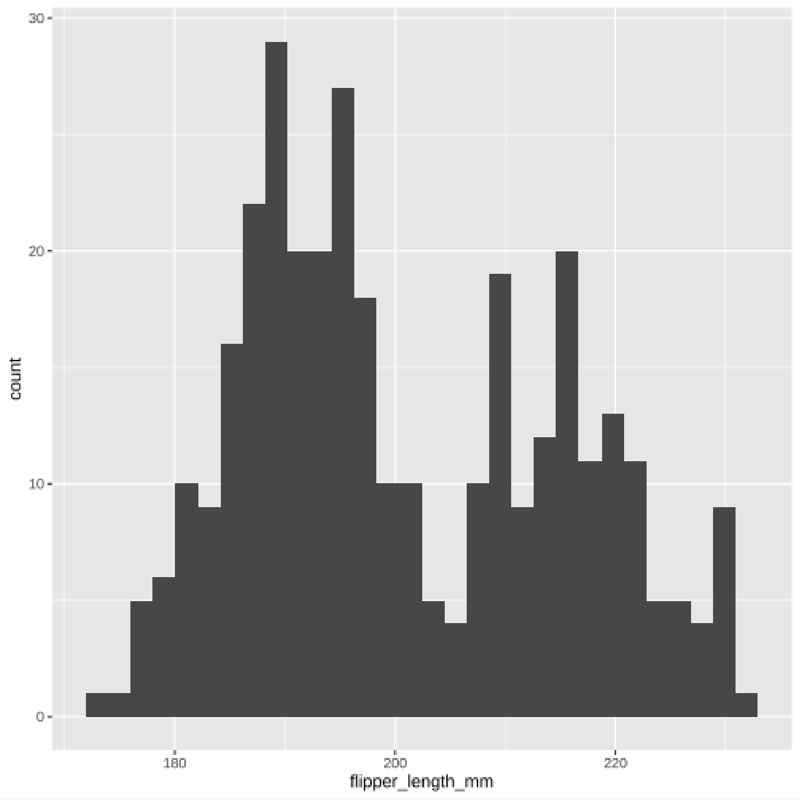
	id	species	island	bill_length_mm	bill_depth_mm	flipper_length_mm	body_mass_g	sex	year
1	1689	Adelie	Torgersen	39.1	18.7	181	3750	male	2007
2	4274	Adelie	Torgersen	NA	17.4	186	3800	female	2007
3	4539	Adelie	Torgersen	40.3	18.0	195	3250	female	2007
4	2435	Adelie	Torgersen	36.7	19.3	193	3450	female	2007
5	2326	Adelie	Torgersen	39.3	20.6	190	3650	male	2007
6	2637	Adelie	Torgersen	38.9	17.8	181	3625	female	2007
7	4443	Adelie	Torgersen	NA	19.6	195	4675	male	2007
8	2102	Adelie	Torgersen	34.1	18.1	193	3475	NA	2007
9	2975	Adelie	Torgersen	42.0	20.2	190	4250	NA	2007
10	3966	Adelie	Torgersen	37.8	17.1	186	3300	NA	2007
11	4648	Adelie	Torgersen	37.8	17.3	180	3700	NA	2007
12	2887	Adelie	Torgersen	41.1	17.6	182	3200	female	2007
13	4939	Adelie	Torgersen	38.6	21.2	191	3800	male	2007
14	2849	Adelie	Torgersen	34.6	21.1	198	4400	male	2007
15	4743	Adelie	Torgersen	36.6	17.8	185	3700	female	2007
16	4573	Adelie	Torgersen	38.7	19.0	195	3450	female	2007
17	1669	Adelie	Torgersen	42.5	20.7	197	4500	male	2007

Simple plots

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

```
ggplot(data = penguins,
       aes(x = flipper_length_mm)) +
  geom_histogram()
```



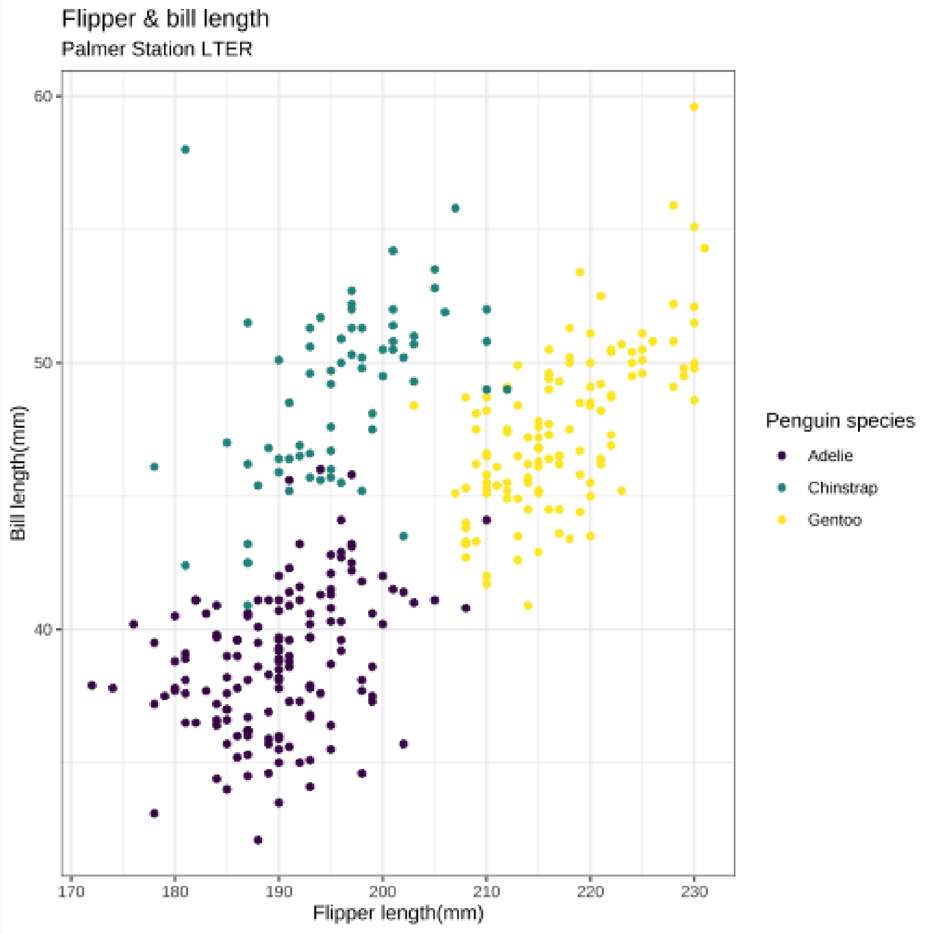


Improved plots - tips

- **Start with simple**, slowly add in additions/colors/etc
- You are building a plot layer by layer! ++++++
- At the beginning, **just copy and paste examples** that you want to edit until you understand what each function does
- It will take some trial and error!
- **Watch BERD ggplot video** for more instruction, and many customizations

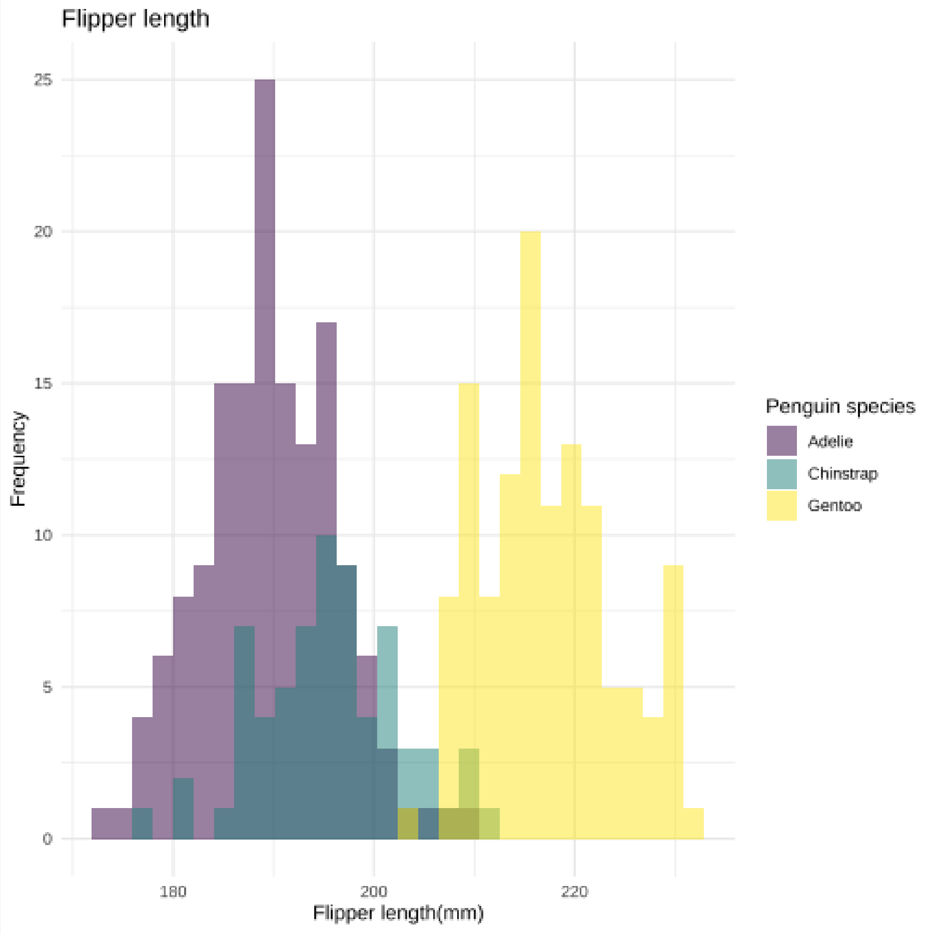
Improved scatterplot

```r
ggplot(data = penguins,
       aes(x = flipper_length_mm,
           y = bill_length_mm,
           color = species)) +
  geom_point()+
  labs(
    title = "Flipper & bill length",
    subtitle = "Palmer Station LTER",
    x = "Flipper length(mm)",
    y = "Bill length(mm)") +
  scale_color_viridis_d(
    name = "Penguin species") +
  theme_bw()
```



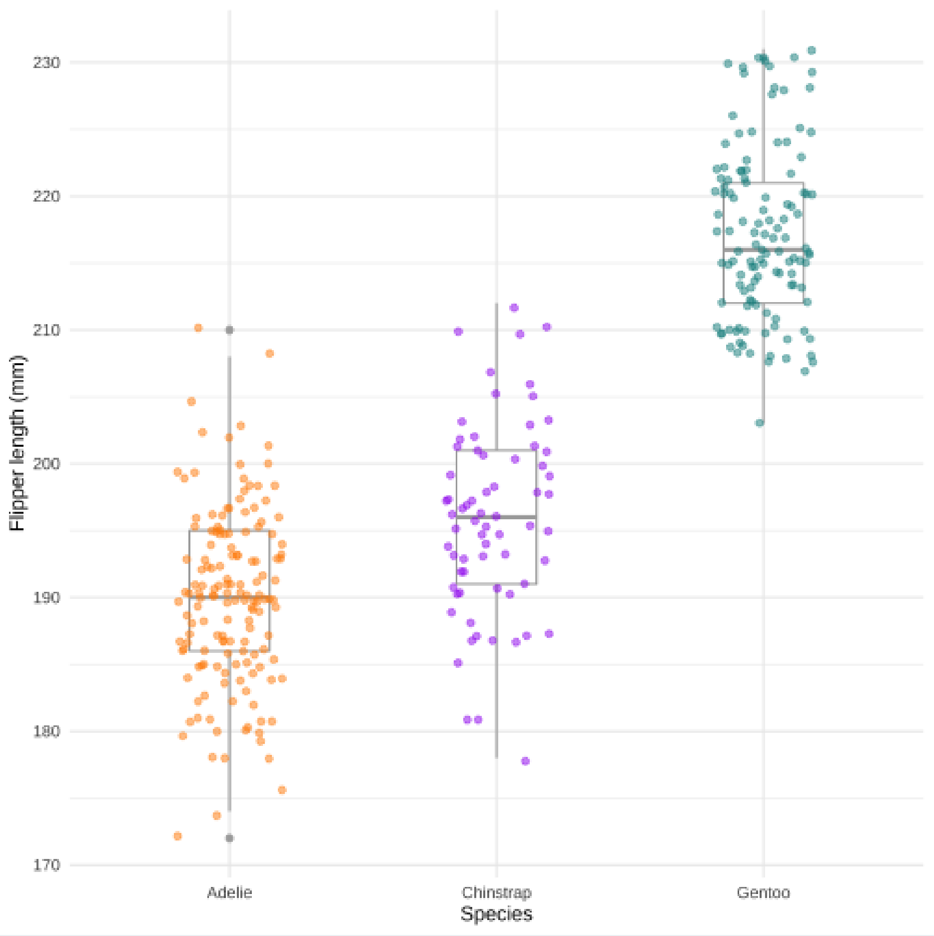
Improved histogram

```
ggplot(data = penguins,
       aes(x = flipper_length_mm,
           fill = species)) +
  geom_histogram(
    alpha = 0.5,
    position = "identity") +
  labs(
    title = "Flipper length",
    x = "Flipper length(mm)",
    y = "Frequency") +
  scale_fill_viridis_d(
    name = "Penguin species") +
  theme_minimal()
```



Boxplot + jitter

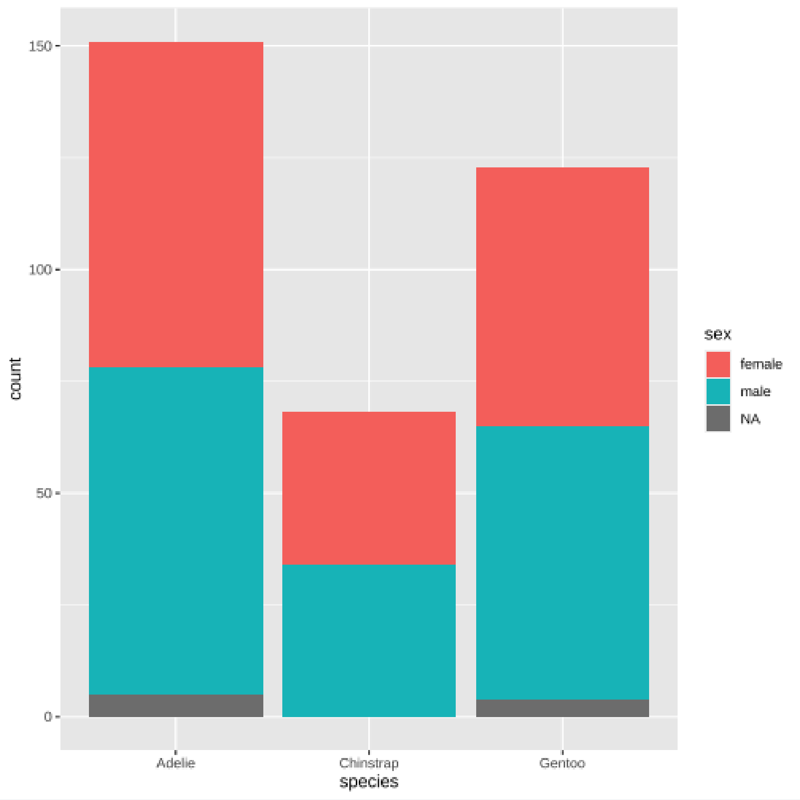
```
ggplot(data = penguins,
       aes(x = species,
           y = flipper_length_mm)) +
  geom_boxplot(color="darkgrey",
               width = 0.3,
               show.legend = FALSE) +
  geom_jitter(
    aes(color = species),
    alpha = 0.5,
    show.legend = FALSE,
    position = position_jitter(
      width = 0.2, seed = 0)) +
  scale_color_manual(
    values = c("darkorange","purple",
               "cyan4")) +
  theme_minimal() +
  labs(x = "Species",
       y = "Flipper length (mm)")
```

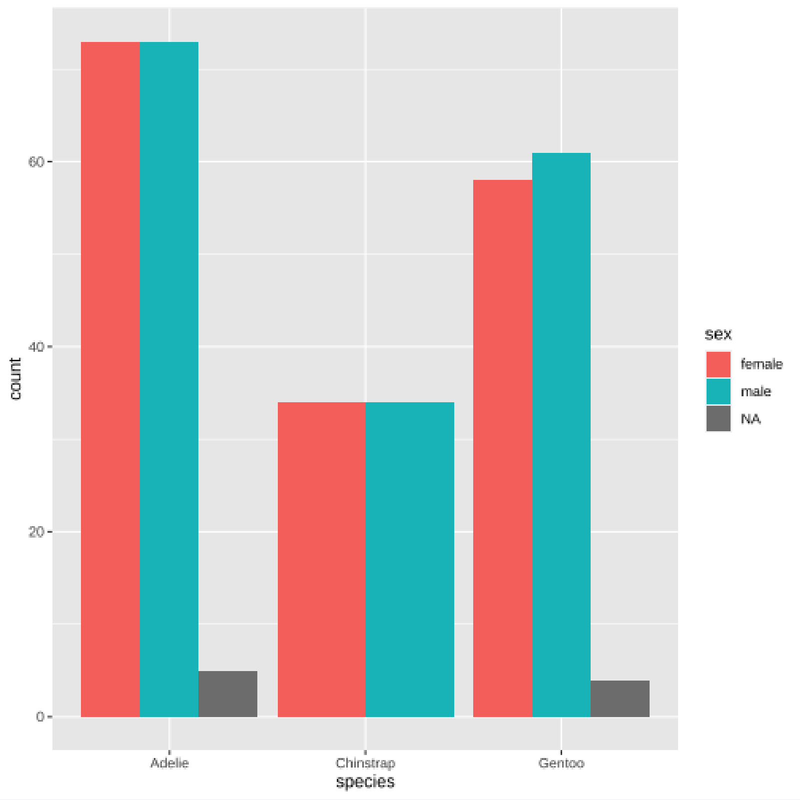


Bar plots - counts

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

```
ggplot(data = penguins,
       aes(x = species,
           fill = sex)) +
  geom_bar(position = "dodge")
```



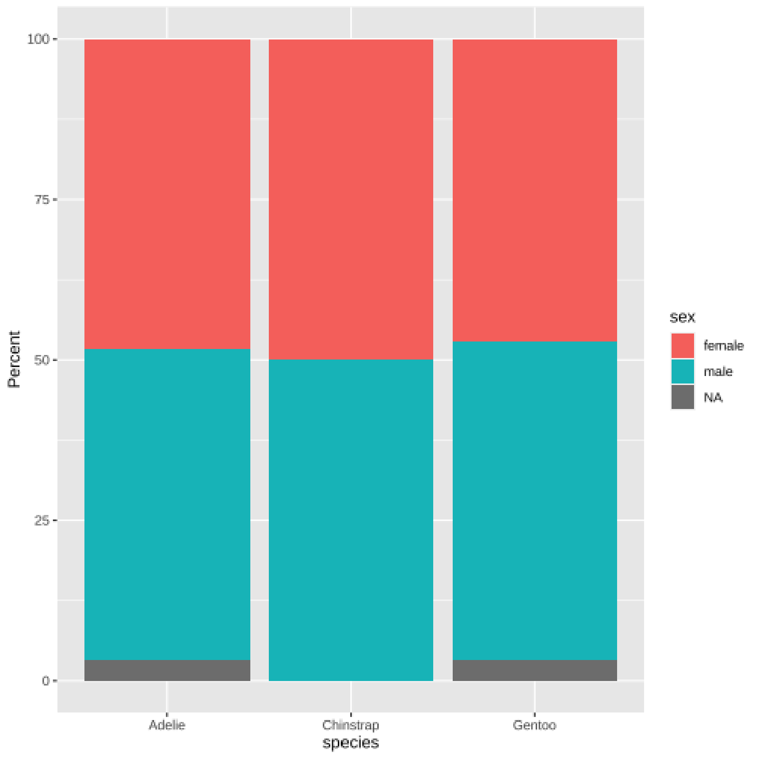


Bar plots - percentages

```
pct_data <- penguins %>%
  count(species, sex) %>%
  # filter(!is.na(sex)) %>%
  group_by(species) %>%
  mutate(pct = 100*n/sum(n))
pct_data
```

```
## # A tibble: 8 x 4
## # Groups:   species [3]
##   species   sex        n   pct
##   <chr>     <chr>  <int> <dbl>
## 1 Adelie    female    73 48.3
## 2 Adelie    male      73 48.3
## 3 Adelie    <NA>       5  3.31
## 4 Chinstrap female    34 50
## 5 Chinstrap male      34 50
## 6 Gentoo    female    58 47.2
## 7 Gentoo    male      61 49.6
## 8 Gentoo    <NA>       4  3.25
```

```
ggplot(data = pct_data,
       aes(x = species, y = pct,
           fill = sex)) +
  geom_col()+
  ylab("Percent")
```

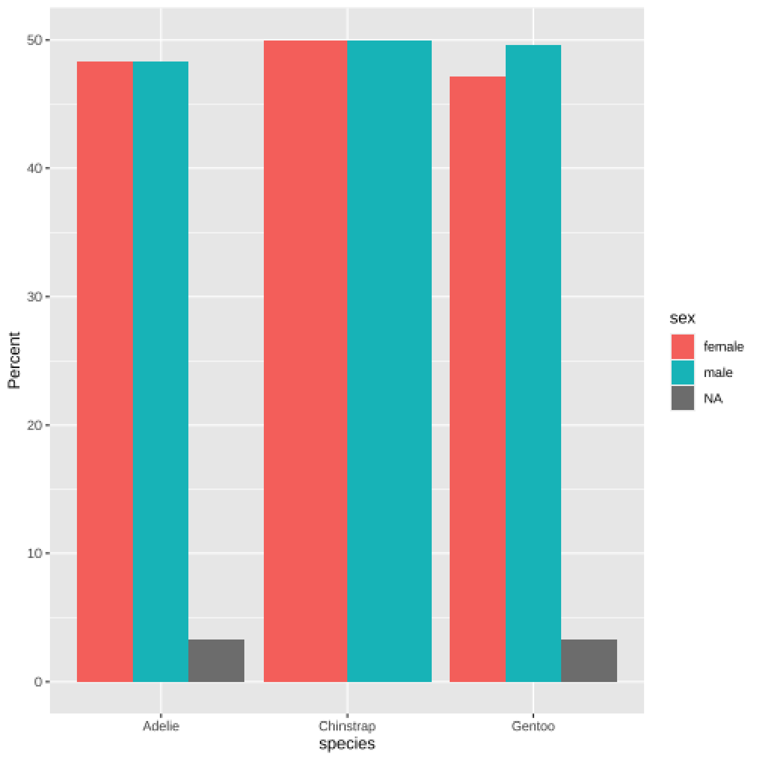


Bar plots - percentages

```r
pct_data <- penguins %>%
  count(species, sex) %>%
  # filter(!is.na(sex)) %>%
  group_by(species) %>%
  mutate(pct = 100*n/sum(n))
pct_data
```

```
## # A tibble: 8 x 4
## # Groups:   species [3]
##   species   sex        n   pct
##   <chr>     <chr>  <int> <dbl>
## 1 Adelie    female    73 48.3
## 2 Adelie    male      73 48.3
## 3 Adelie    <NA>       5  3.31
## 4 Chinstrap female    34 50
## 5 Chinstrap male      34 50
## 6 Gentoo    female    58 47.2
## 7 Gentoo    male      61 49.6
## 8 Gentoo    <NA>       4  3.25
```

```r
ggplot(data = pct_data,
       aes(x = species, y = pct,
           fill = sex)) +
  geom_col(position = "dodge") +
  ylab("Percent")
```



Practice 5

1. Continue adding code chunks to your Rmd (or, start a new one! But remember to load the libraries and data at the top.)

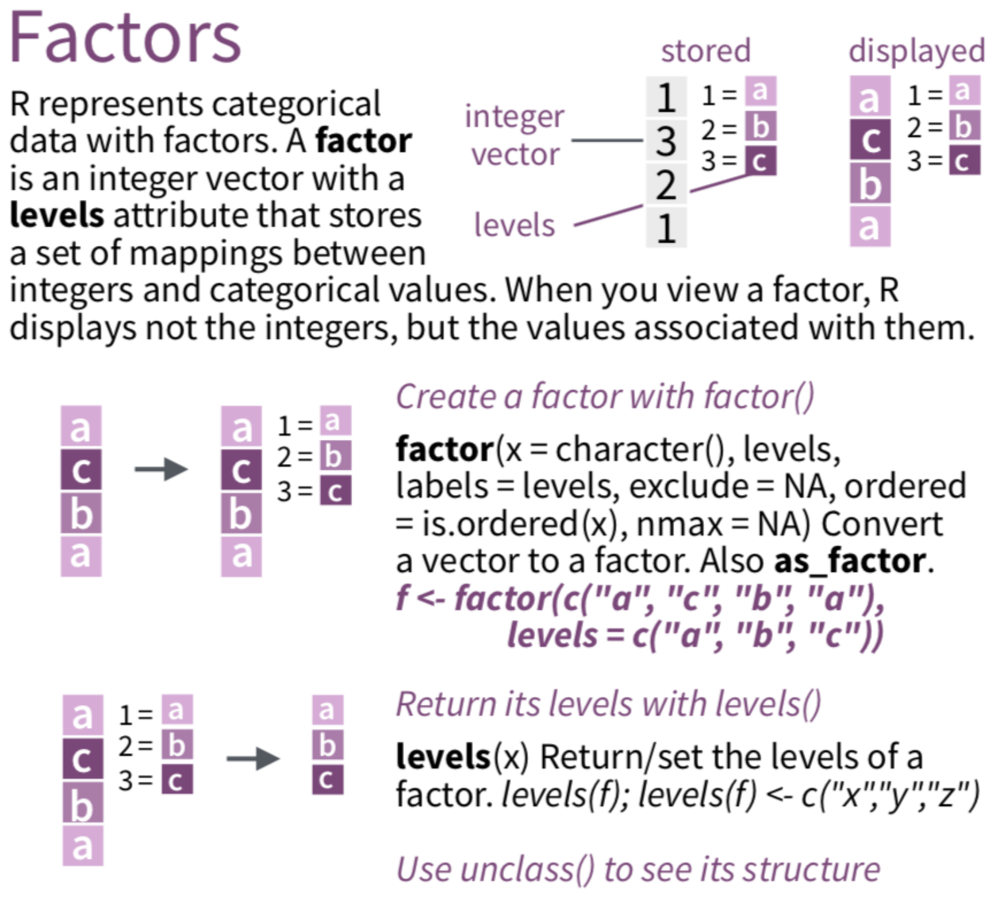
2. Make a scatter plot of bill depth vs bill length.

3. Add `+ geom_smooth(method="lm")` to the plot. What is this saying about the association between bill depth and length?

4. Now add `color = species` to the aesthetic `aes()`. Keep `geom_smooth`. How do the associations look now?

Factors for categorical data

- `factor` is a data type that saves character variables as categories (factor levels)
- Using factor data types are useful for making plots and necessary for some statistical modeling functions
- We recommend using commands from the `forcats` package to work with factor data
- See `forcats` cheatsheet and `forcats` vignette



Factors

R represents categorical data with factors. A **factor** is an integer vector with a **levels** attribute that stores a set of mappings between integers and categorical values. When you view a factor, R displays not the integers, but the values associated with them.

Create a factor with factor()

factor(x = character(), levels, labels = levels, exclude = NA, ordered = is.ordered(x), nmax = NA) Convert a vector to a factor. Also **as_factor**.

f <- factor(c("a", "c", "b", "a"), levels = c("a", "b", "c"))

Return its levels with levels()

levels(x) Return/set the levels of a factor. *levels(f); levels(f) <- c("x","y","z")*

Use unclass() to see its structure

Create a factor variable using factor()

```
penguins <- penguins %>%
  mutate(sex_fac = factor(sex))
levels(penguins$sex_fac)  # factor levels are in alphanumeric order by default
```

```
## [1] "female" "male"
```

```
penguins %>% select(sex, sex_fac) %>% summary()  # character vs. factor types
```

```
##      sex                sex_fac   
##  Length:342         female:165  
##  Class :character   male  :168  
##  Mode  :character   NA's  :  9
```

```
penguins %>% select(sex, sex_fac) %>% str()  # str for structure
```

```
## tibble [342 × 2] (S3: tbl_df/tbl/data.frame)
##  $ sex    : chr [1:342] "male" "female" "female" "female" ...
##  $ sex_fac: Factor w/ 2 levels "female","male": 2 1 1 1 2 1 2 NA NA NA ...
```

Specify order of factor levels: `fct_relevel()`

```r
penguins <- penguins %>%
  mutate(species_fac = factor(species))

summary(penguins$species_fac)  # levels are in alphanumeric order by default
```

```
##    Adelie Chinstrap    Gentoo
##       151        68       123
```

```r
penguins <- penguins %>%
  mutate(species_fac = fct_relevel(species_fac,
                                   c("Adelie", "Gentoo", "Chinstrap")))

summary(penguins$species_fac)  # levels are specified order
```

```
##    Adelie    Gentoo Chinstrap
##       151       123        68
```

Collapse factor levels

```
penguins <- penguins %>%
  mutate(species_fac2 = fct_collapse(species_fac, # collapse levels
                                    Adelie = c("Adelie"),
                                    Other = c("Gentoo", "Chinstrap"))
         )

penguins %>% select(species_fac, species_fac2) %>% summary()
```

```
##     species_fac  species_fac2
##  Adelie   :151   Adelie:151  
##  Gentoo   :123   Other :191  
##  Chinstrap: 68               
```

```
penguins %>% tabyl(species_fac, species_fac2)
```

```
##  species_fac Adelie Other
##       Adelie    151     0
##       Gentoo      0   123
##    Chinstrap      0    68
```

The more you know

Save data frame

- Save **.RData** file: the standard R format, which is recommended if saving data for future use in R

```
save(penguins, file = "penguins.RData")  # saving mydata within the data folder
```

You can load .RData files using the load() command:

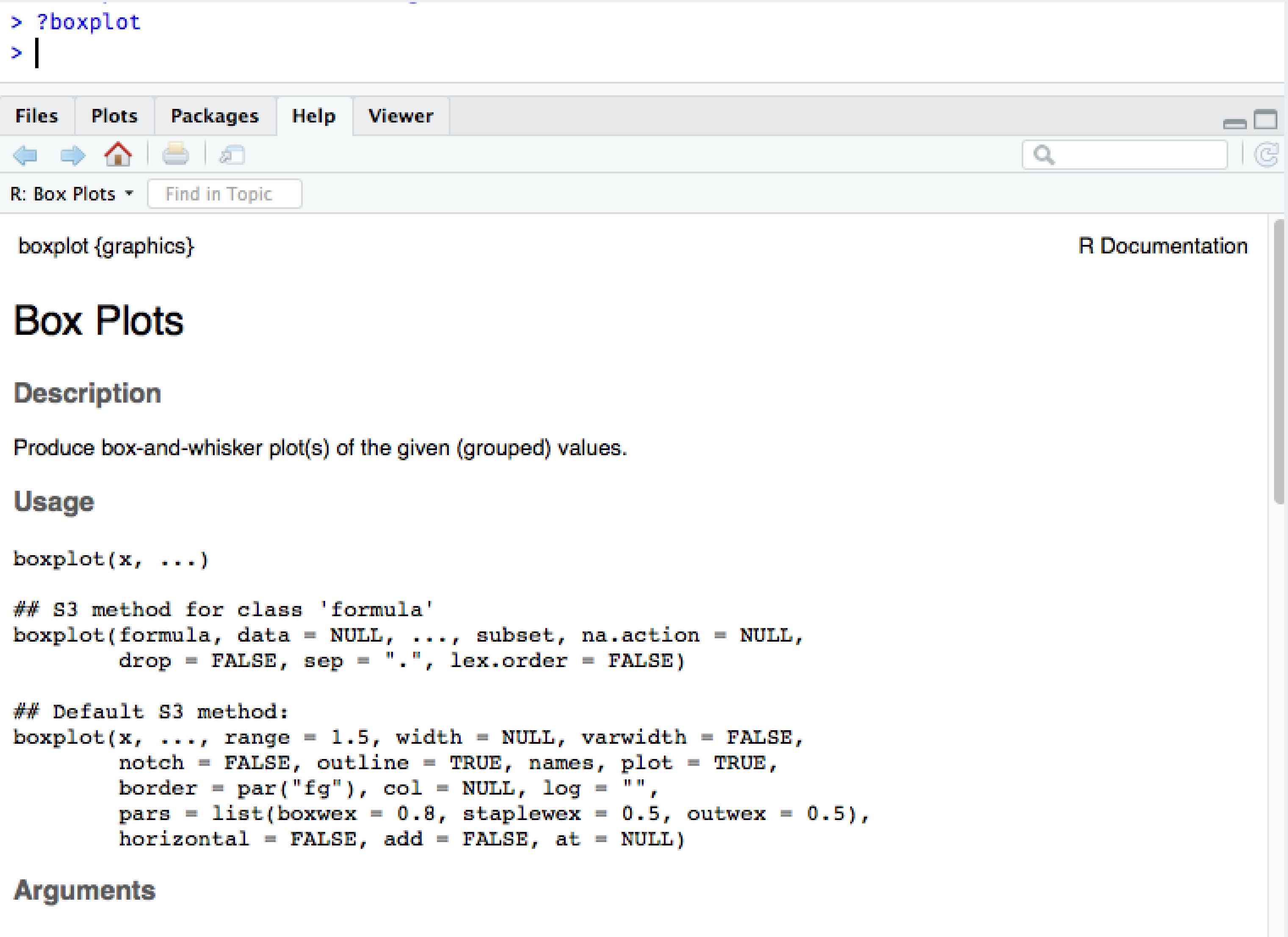
```
load("penguins.RData")
```

- Save **csv** file: comma-separated values

```
write_csv(penguins, path = "my_penguin_data.csv")
```

How to get help (1/2)

Use ? in front of function name in console. Try this:



```
> ?boxplot
>
```

boxplot {graphics}　R Documentation

Box Plots

Description

Produce box-and-whisker plot(s) of the given (grouped) values.

Usage

```
boxplot(x, ...)

## S3 method for class 'formula'
boxplot(formula, data = NULL, ..., subset, na.action = NULL,
        drop = FALSE, sep = ".", lex.order = FALSE)

## Default S3 method:
boxplot(x, ..., range = 1.5, width = NULL, varwidth = FALSE,
        notch = FALSE, outline = TRUE, names, plot = TRUE,
        border = par("fg"), col = NULL, log = "",
        pars = list(boxwex = 0.8, staplewex = 0.5, outwex = 0.5),
        horizontal = FALSE, add = FALSE, at = NULL)
```

Arguments

How to get help (2/2)

- Use `??` (i.e `??dplyr` or `??read_csv`) for searching all documentation in installed packages (including unloaded packages)
- search Stack Overflow #r tag
- googlequestion + rcran or + r (i.e. "make a boxplot rcran" "make a boxplot r")
- google error in quotes (i.e. `"Evaluation error: invalid type (closure) for variable '***'"`)
- search github for your function name (to see examples) or error
- Rstudio community
- twitter #rstats

Resources

- Click on this *LONG LIST* of resources for learning R
- Watch recordings of our other workshops with **all slides/materials at github.com/jminnier/berd_r_courses**

Recommended viewing order of BERD workshops:

- *Either* this workshop, or the older version: *Getting Started with R and Rstudio* (September 24, 2019, 3 hour version)
    - no tidyverse, just base R introduction; The new version we are doing now is hopefully better!
- *Data Wrangling in R, Part 1A and 1B* (April 18, 2019, 2 hours)
    - more data wrangling, tidy data, removing missing data, arranging data
- *Data Wrangling in R, Part 2* (April 25, 2019, 2 hours)
    - even more data wrangling, adding columns, summarizing, joining/merging two or more data sets together, reshaping data from wide to long format or vice versa, more methods for dealing with NAs, working with dates and factors, cleaning up messy column names
- *Data Visualization with R and ggplot2* (May 20, 2020, 2.5 hours)
    - additional ggplot examples, many more ways to customize your ggplots!

Other Resources

Getting started:

- Again, check out this *LONG LIST* of resources for learning R
- R Bootcamp - by Ted Laderas and Jessica Minnier
- Rstudio primers
- Teacup Giraffes for learning stats & R

Basic help with installation and using Rstudio

- RStudio IDE Cheatsheet
- Install R/RStudio help video
- Basic Basics

Some of this is drawn from materials in online books/lessons:

- Intro to R/RStudio by Emma Rand
- Modern Dive - An Introduction to Statistical and Data Sciences via R by Chester Ismay & Albert Kim
- R for Data Science - Hadley Wickham & Garrett Grolemund
- Cookbook for R by Winston Chang

Local resources

- OHSU's BioData club + active slack channel
- Portland's R user meetup group + active slack channel
- R-ladies PDX meetup group
- Cascadia R Conf - click on Years for old videos

Allison Horst

Contact info:

Jessica Minnier: *minnier@ohsu.edu*

Meike Niederhausen: *niederha@ohsu.edu*

This workshop info:

- Code for these slides on github: jminnier/berd_r_courses
- Link to html: part 1 & part 2
- all the R code in an R script: part 1 & part 2
- answers to practice problems can be found here: part 1 & part 2