# summer_2021_qa

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# Class 1: Reading files and 'dplyr'

# Do now

**Do now:**

- Complete the intro poll at `bit.ly/acc_intro_poll`

**After the poll**

- Download `lab_1` from the course webpage: `harris-coding-lab.github.io`.

**Notice**

- Earlier we had a typo for the link to `lab_0` on canvas, which is now fixed. Sorry for inconvience.

# Expectations

From you:

- do the work (i.e. watch video, try basics, do lab, bring questions)
- engage in course! (i.e. work with partners, answer questions, do polls)
- have R and RStudio installed!

From us:

- prepare engaging lesson materials
- address your questions
- help you be confident for core (confident != R expert)

From everyone:

- be nice to each other and create a growth-focused environment

# Do the work

- Step 1. Videos
- Step 1a. Basics
- Step 2. QA
- Step 3. Lab

# Not an expert

We cover:

- how to work with basic data structures (tibbles, vectors)
- how to read and manipulate data
- programmer logic (if statements, loops, functions)

We won't cover in depth:

- most statistical tools
- how to join data together
- how to convert data from long to wide (pivoting)
- how to deal with very messy data
- how to work with specific data types (e.g. dates, advanced strings)
- among other things like webscrapping, package development and so forth

# Today's session

- Set up working directories
- Review some questions from QA
- Highlight key points and open up for live questions

# Setting up working directory and coding environment

1. Do you have a folder on your computer for coding lab material?
   If not, create one and make sure you know the path to the folder.
2. We recommend creating a `problem_set` folder inside your coding lab folder.
3. Make folder called `data` inside the `problem_set` folder.

# Putting your files in place

4. Create a new R script. Save your script in the `problem_set` folder. From now on, when you start a script or `Rmd` save it there.
5. Download the first data set here and put the data in your `data` folder. Find the link in the lab pdf!

# Tell R where to find files

- Local paths are like addresses on your computer. Use `getwd()` to see how your computer paths look.

```
# In lab0 we downloaded data form a URL which is an address on the inte
covid_data <-
  read_csv(
    "https://data.cdc.gov/api/views/qfhf-uhaa/rows.csv?"
    )

# Compare to a local path
wid_data <-
  read_xlsx(
    "~/coding-lab/harris-coding-lab.github.io/data/world_wealth_inequal
  )
```

6. Add a line to your script where you `setwd()` to the `data` folder.

# Working with the files

7. Finally, we are using data in an excel format. We need the package `readxl` to process data of this type. In the console, run `install.packages("readxl")`.
8. Add code to load the `tidyverse`.
9. If you followed the set-up from above, you should be able to run the following code with no error.

```
wid_data <- read_xlsx("world_wealth_inequality.xlsx")
```

# What to do when something is confusing?

- use ?
- test code in console. try to break it.
- ask teammates / try googling
- ask us!

If it's not "mission critical", you can safely move on without full understanding. (Imagine learning a language and trying to figure out all the grammar and vocabulary at the same time!)

# Question:

- What's the deal with `col_types = cols(Suppress = col_character())`?
- Do we need that "accessType=DOWNLOAD&bom=true&format=true%20target=" part?

```
covid_data <-
  read_csv(
    paste0("https://data.cdc.gov/api/views/qfhf-uhaa/rows.csv?",
           "accessType=DOWNLOAD&bom=true&format=true%20target="),
    col_types = cols(Suppress = col_character()))
```

- Note: In URLs after the `?` you send meta information about your request.

# Question: Can you explain pipes?

- Pipes %>% take the left hand side and put them into the first position on the right hand side.

```
storms %>% filter(year > 2010) %>% glimpse()

recent_storms <- filter(storms, year > 2010)
glimpse(recent_storms)
```

Notice

- `filter()` takes data in the first position and then an arbitrary number of filtering expressions.
- `glimpse()` takes data in the first position

# Lesson 0: Intro to R, RStudio and the `tidyverse`

- navigate and use Rstudio's features
  - particularly, the console, the text editor and help
- assign objects to names with `<-`
- use functions by providing inputs and learn more with `?`
- `install.packages()` (once) and then load them with `library()` (each time you restart R)

# Lesson 1: Key points: Reading files

- Tabular data is stored in a lot of different formats.
  - e.g. `.csv`, `.xlsx`, `.dta`
- Read tabular data of a given type with the proper function.
  - e.g. for `csvs` we have `read_csv()`
  - If you get a new type, Google "How to read xxx files into R tidyverse".
- We need to be aware of the file path and can `setwd()`.
- We know there are useful tools built into the `read_xxx()` functions.
  - Though we just scratched the surface.

# Lesson 1: Manipulating data with `dplyr()`

- Choose columns with `select()`.
- Choose rows based on a match criteria with `filter()`.
  - We were introduced to comparison operators like == and `%in%`.
- Make new columns with `mutate()`.
- Sort data with `arrange()` and `arrange(desc())` or `arrange(-x)`.
- Create summary statistics with `summarize()`.

# Class 2: Vectors and data types

# Course logistics:

- When should we start working on the final project?
  - Start looking for a dataset now.
  - Write code to read it into R and start investigating with `dplyr` verbs.
    - Ask simple questions that can be addressed with your current tools.

**lab 1 solutions** will be available on the course website.

# Getting started with Rmarkdown (Rmd)

- What's an Rmd?
- How to make an Rmd
- How to work with an Rmd

# Knitting: making the frustrating part less frustrating

- Install tinytex

```
install.packages("tinytex")
tinytex::install_tinytex()
```

- Knit early and often.

# When to use Rmds vs scripts?

**Rmd**

- Exploration of data
- Presentations and reports

**script**

- Projects with interrelated code (e.g. an R package)
- Working on a server that does not have Rstudio installed

# Questions from QA

**Question 1**: - Why do I need the function `summarize` in the following bit of code?

```
michigan_population_total <-
  midwest %>%
    filter(state == "MI") %>%
  summarize(total_pop = sum(poptotal))
```

- Why can't I just pipe directly into `sum`?

**Question 2**: Why do we need to use `pull()`?

# R's primary data structures: Vectors vs. tibbles

- Why do we need different data structures?
- How are vectors and tibbles related?

# Why do we need different data structures?

In theory, we can do all our work with vectors.

```
names_vec <- c("Ari", "Qiwei", "Jay", "Thomas")
surnames_vec <- c("Anisfeld", "Lin",  "Zaleski", "Whamond")
position_vec <- c("Instructor", "TA", "TA", "TA")
```

why might I want a tibble?

# R's primary data structures: Vectors vs. tibbles

Tibbles encapsulate vectors

```
names_vec <- c("Ari", "Qiwei", "Jay", "Thomas")
surnames_vec <- c("Anisfeld", "Lin",  "Zaleski", "Whamond")
positions_vec <- c("Instructor", "TA", "TA", "TA")

my_tibble <- tibble(names = names_vec,
                    surnames = surnames_vec,
                    positions = positions_vec)
```

- Keep data tidy -> rows are a single observation or record.
- Keep meta-data (column names)
- Keep track of relationships between vectors
- Can hold various data types

# R's primary data structures: Vectors vs. tibbles

- vectors are simpler
- have a single data type
- some functions expect vectors or make more sense on them.

# Reviewing automatic type coercion

Type coercion is done automatically when R knows how. Usually, simpler types can be coerced to more complex types.

- `logical < integer < double < character`.

```
# paste0() is a function that combines
# two chr vectors into a single vector
paste0("str", "ing")
```

```
## [1] "string"
```

```
paste0(1L, "ing")
```

```
## [1] "1ing"
```

`1L` is an `int`, but R will coerce it into a `chr` in this context.

# Automatic coercion

Logicals are coercible to numeric or character. This is very useful!

Determine the rule for how R treats `TRUE` and `FALSE` in math.

```
TRUE + 4
FALSE + 4
sum(c(FALSE, FALSE, FALSE, FALSE))
mean(c(TRUE, TRUE, FALSE, FALSE, TRUE))
```

# Automatic coercion

```
TRUE + 4
```

```
## [1] 5
```

```
FALSE + 4
```

```
## [1] 4
```

```
sum(c(FALSE, FALSE, FALSE, FALSE))
```

```
## [1] 0
```

```
mean(c(TRUE, TRUE, FALSE, FALSE, TRUE))
```

```
## [1] 0.6
```

# Exercise

**1**: Use R to calculate the sum

$$\sum_{n=0}^{10} \frac{1}{2^n} = \frac{1}{2^0} + \frac{1}{2^1} + .. + \frac{1}{2^{10}}$$

$$\sum_{n=0}^{10} \frac{1}{2^n} = 1 + 0.5 + .. + 0.00098$$

1. Use vectorized math to create a vector with the correct numbers
2. Use a built-in function to add up all the numbers in the vector.

**Bonus** What happens to the sum as you increase `n`?

**2**: Use `paste0()` to convert `v1` and `v2` into `"hello!"`

```
v1 <- c("h","l", "o")
v2 <- c("e", "l", " !")
```

```
## [1] "h el lo  !"
```

# Key points: Class 2 vectors and data types

**vectors and vectorized coding**

- Vectors are the fundemental way to store data in R
- We can operate on vectors element-by-element without loops
  - `dplyr` verbs rely on this!
- We introduced built-in functions to build vectors and do operations on vectors.

**data types**

- (Atomic) Vectors have a single data type
  - most often: `logical`, `integer`, `double`, or `character`
- Certain operations expect a certain data type and will try to coerce the data if it can.
  - coercion can lead to unexpected behavior such as making `NA`s.

**Over weekend:** Attempt lab 2. **For Tuesday:** Watch video about control flow + try basics.

# Class 3: Control flow

# Outline

- lingering questions about Rmds
- `ifelse()` questions

# Reviewing the anatomy of an Rmd:

*Write text in the document*

```
# ^^^ start an R chunk ```{r}
# sometimes {} have meta information

# R code goes in a chunk
ex <- seq(1, 12)

# and output prints below
print(ex)
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12
```

# A meta examples: {r, echo = FALSE}

```
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12
```

# Another meta examples: {r, eval = FALSE}

```r
print(ex)
```

# Naming chunks

Chunk names help you debug

```
# code
```

Two chunks cannot have the same name

```
# If I change the name to "example" we will get an error.
```

# Quick hitters

*Q:* Why don't we get LaTex with $ in this example?

```
$$
  \sqrt{p}
$$
```

# Quick hitters

*Q:* Why don't we get LaTex with $ in this example? *A:* In a code chunk, knitr expects R code! So a dollar sign is interpreted to be referring to a named entity in an object like `data$column_name`.

So put LaTex in the "text" area of an Rmd!

$$\sqrt{p}$$

# Quick hitters

*Q:* What does this error tell you?

```r
setwd("~/Documents/coding")
```

*Error in setwd("~/Documents/coding") : cannot change working directory*

# Quick hitters

*Q:* What does this error tell you? *A:* Usually, it means your directory name is wrong somehow!

```
setwd("~/Documents/coding_lab/")
```

Note: "$\sim/$" does not work on Windows!

# An aside on relative paths

You can refer to directories **relative** to your current directory using `.` and `..`

- `.` means current directory.
- `..` means "go back" the directory path.

# an example

File structure:

- coding_lab datafile.csv
    - problem_sets my_rmd.Rmd

You could access the data with `read_csv("../datafile.csv")` in a chunk.

# What's the difference between & and &&?

- Test your hypothesis with additional examples in the console?

```
c(TRUE, TRUE) & c(TRUE, FALSE)
```

```
## [1]  TRUE FALSE
```

```
c(TRUE, TRUE) && c(TRUE, FALSE)
```

```
## [1] TRUE
```

- Which plays nicely with `ifelse()`?
- Which plays nicely with `if()`?

# What's the difference between `|` and `||`?

Similarly OR has a vectorized `|` and singleton `||` version.

- generally, you can get by with `|` and `&`!
- when you are working on code for general use (like writing a package) there will be times when you want to ensure

# Exercise

We want to make a new column called `famous_storm` that is 1 for "Katrina" and "Rita" and 0 otherwise.

This code fails.

```
# bad code :(
storms %>%
  mutate(famous_storm =
           ifelse(name == "Katrina"| "Rita", 1, 0))



storms %>%
  mutate(famous_storm =
           ifelse(name == "Katrina"| name == "Rita", 1, 0))



storms %>%
  mutate(famous_storm =
           ifelse(name %in% c("Katrina", "Rita", "Amy", "Bo
```

# Example: Creating a simulation dataset

You want to understand the impact of discrimination on gifted education.

```
discrimination_simulation <-
  tibble(group = rep(c(1, 2), 5000),
         prob_tested = runif(10000),
         iq = rnorm(10000))
```

- Students in group 1 get tested with probability 60 percent
- Students in group 2 get tested with probability 10 percent
- Students get gifted education if `iq > 1` and they're tested

# Key points: control flow with `if` and contingent column creation with `ifelse`

- Use `ifelse()` with `mutate()` to create new columns contingently.
  - `ifelse()` is vectorized so can operate on a logical vector to produce new results
- Understand how logical operators (i.e. `!`, `|`, `&`) work together with `ifelse` and conditional operators.
- Use `if()` (and `else`) to control whether an action is completed outside of a data context.

We also introduced `Rmds` and saw how to knit the `Rmd` to html or pdf.

**Up next:** prepare lab 3 for tomorrow. **Friday** watch video for class 4 on using `group_by` to do grouped analysis.

# Key points: `if()` versus `ifelse()`

| | `if()`/ `else()` |
|---|---|
| Used to conditionally evaluate code | yes |
| Vectorized? | no, only uses first element |
| Handles NA | no, error `missing value where T` |
| baseR | yes |

- *Takeaway:* When we are focusing on data analysis use `ifelse()` (or `if_else()`).

[1] there's a tidyverse `if_else()` that works slightly differently

# Quick hitters

**Class 2 basics**

- *Q* Why did I get double when your code shows the type is an int?

```
typeof(seq(1, 12, 1))
```

```
## [1] "double"
```

# Quick hitters

**Class 2 basics**

- *Q* Why did I get double when your code shows the type is an int?
- *A* In base R, data types are not always predictable.

```
typeof(seq(1, 12))
```

```
## [1] "integer"
```

```
typeof(seq(1, 12, 1))
```

```
## [1] "double"
```

Tidyverse functions tend to be more careful to avoid this sort of behavior.

# Horoscope game:

Make a game where you ask the user to enter their birth month and you tell them their fortune.

- Give people born in December, January or February a "cold" fortune
- Give people born in June through September a "warm" fortune
- Give people born in November a great fortune
- Give everyone else an okay fortune

e.g. `birth_month <- 2` the code should return something like `I see penguins in your forecast`.

# Class 4: Grouped analysis

# Today's class

- Review if statements and conditional expressions
- Review some base R
- Take questions about grouped analysis

**For the curious**: `"[\\r]?\\n"` is a "regular expression" which tells `separate()` to look for `"\n"` or `"\r\n"` and separate the data wherever it finds those strings within other strings.

# conditional expressions and missing data

- `NA | TRUE` returns `TRUE`. Why does `FALSE | NA` return `NA`?

Hint: Fill out this table:

| x | y | x OR y |
|---|---|---|
| `FALSE` | `FALSE` | |
| `FALSE` | `TRUE` | |
| `TRUE` | `FALSE` | |
| `TRUE` | `TRUE` | |

# conditional expressions and missing data

- `NA | TRUE` returns `TRUE`. Why does `FALSE | NA` return `NA`?

| x | y | x OR y |
|---|---|---|
| FALSE | FALSE | FALSE |
| FALSE | TRUE | |
| TRUE | FALSE | |
| TRUE | TRUE | |

# conditional expressions and missing data

- `NA | TRUE` returns `TRUE`. Why does `FALSE | NA` return `NA`?

| x | y | x OR y |
|---|---|---|
| FALSE | FALSE | FALSE |
| FALSE | TRUE | TRUE |
| TRUE | FALSE | TRUE |
| TRUE | TRUE | TRUE |

# conditional expressions and missing data

- `NA | TRUE` returns `TRUE`. Why does `FALSE | NA` return `NA`?

OR returns TRUE if **any** value is TRUE. Thus, when we have `NA | TRUE`, then we logically know that the result is `TRUE`!

`FALSE | NA` depends on the missing value, so R cannot evaluate the expression.

# conditional expressions and missing data

- `TRUE & NA` returns `NA`. Why does `FALSE & NA` return `FALSE`?

| x | y | x AND y |
|---|---|---|
| `FALSE` | `FALSE` | |
| `FALSE` | `TRUE` | |
| `TRUE` | `FALSE` | |
| `TRUE` | `TRUE` | |

# conditional expressions and missing data

- `TRUE & NA` returns `NA`. Why does `FALSE & NA` return `FALSE`?

| x | y | x AND y |
|---|---|---|
| `FALSE` | `FALSE` | `FALSE` |
| `FALSE` | `TRUE` | `FALSE` |
| `TRUE` | `FALSE` | `FALSE` |
| `TRUE` | `TRUE` | `TRUE` |

AND requires **all** `TRUE` so R knows `FALSE & NA` is `FALSE`!

# Quick hitter

*Q:* What's the difference between `ifelse()` and `if_else()`

*A:* `tidyverse::if_else()` mimics `base::ifelse()` with two major differences

# Qh: What's the difference between `ifelse()` and `if_else()`

1. `tidyverse::if_else()` has a built-in way to replace missing data.

```
ex <- c(1, NA, 0, NA, 1)
if_else(ex == 1, "Yes", "No", missing = "Eh")
```

```
## [1] "Yes" "Eh"  "No"  "Eh"  "Yes"
```

# Qh: What's the difference between `ifelse()` and `if_else()`

The same behavior requires nesting with `base::ifelse()`

```
ifelse(is.na(ex),
       "Eh",
       ifelse(ex == 1, "Yes", "No"))
```

```
## [1] "Yes" "Eh"  "No"  "Eh"  "Yes"
```

# Qh: What's the difference between `ifelse()` and `if_else()`

2. `tidyverse::if_else()` checks for type matching

```
if_else(ex == 1, 1, "No")
```

*Error: `false` must be a double vector, not a character vector.*

# Practice

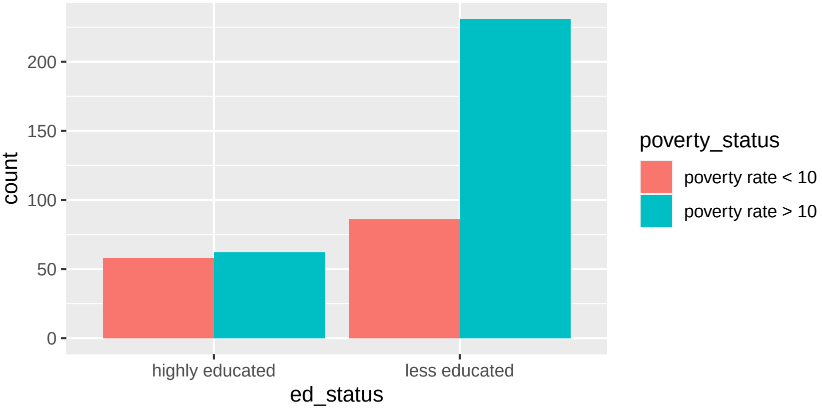
1. Use `mutate()` and `ifelse()` with `midwest` data to create binary variables

- `ed_status` = a city is "highly educated" if over 20 percent of residents have college education (`percollege`)
- `poverty_status` = distinguish between cities with poverty rates above and below 10 percent.

2. Assign your intermediate data set to a name.
3. Calculate the proportion "highly educated" and proportion "poverty rate $< 10$" for counties in Ohio.
4. Calculate the proportion "highly educated" and proportion "poverty rate $< 10$" for counties in Illinois.

# Expected output

```
midwest_binarized  %>%
  ggplot(aes(x = ed_status, fill = poverty_status)) +
    geom_bar(position = "dodge")
```



# Practice

- Calculate the proportion “highly educated” and proportion “poverty rate $< 10$” for counties in Ohio.

```
## # A tibble: 1 x 3
##   state prop_highly_educated prop_low_poverty
##   <chr>                <int>            <int>
## 1 OH                      18               29
```

- Calculate the proportion “highly educated” and proportion “poverty rate $< 10$” for counties in IL.

```
## # A tibble: 1 x 3
##   state prop_highly_educated prop_low_poverty
##   <chr>                <int>            <int>
## 1 IL                      28               27
```

## Solutions

```
midwest_binarized <-
midwest %>%
  mutate(poverty_status = ifelse(percbelowpoverty < 10, "po
         ed_status = ifelse(percollege > 20, "highly educat

midwest_binarized %>%
  filter(state == "IL") %>%
  summarize(state = first(state),
            prop_highly_educated = sum(ed_status == "highly
            prop_low_poverty = sum(percbelowpoverty < 10),
            )
```

Is there a better way? What if I want the information for all the states?

# Solutions

Use group_by() and summarize!

```
midwest_binarized %>%
  group_by(state) %>%
  summarize(
            prop_highly_educated = sum(ed_status == "highly
            prop_low_poverty = sum(percbelowpoverty < 10)
            )
```

```
## # A tibble: 5 x 3
##   state prop_highly_educated prop_low_poverty
##   <chr>                <int>            <int>
## 1 IL                      28               27
## 2 IN                      18               46
## 3 MI                      27               16
## 4 OH                      18               29
## 5 WI                      29               26
```

# Quick hitter: When do we need `ungroup()`?

Recall, `group_by()` adds information about groups "silently" without changing the data

```
midwest_grouped <-
midwest_binarized %>%
  group_by(state, ed_status, poverty_status) %>%
  select(poptotal)
```

```
## Adding missing grouping variables: `state`, `ed_status`
```

```
midwest_grouped %>%   glimpse()
```

```
## Rows: 437
## Columns: 4
## Groups: state, ed_status, poverty_status [20]
## $ state          <chr> "IL", "IL", "IL", "IL", "IL", "IL
## $ ed_status      <chr> "less educated", "less educated"
## $ poverty_status <chr> "poverty rate > 10", "poverty rat
## $ poptotal       <int> 66090, 10626, 14991, 30806, 5836
```

# Quick hitter: When do we need ungroup()?

If we want to do analysis where groups get in the way, we need ungroup().

```
midwest_grouped %>%
  ungroup() %>%
  glimpse()
```

```
## Rows: 437
## Columns: 4
## $ state          <chr> "IL", "IL", "IL", "IL", "IL", "II
## $ ed_status      <chr> "less educated", "less educated",
## $ poverty_status <chr> "poverty rate > 10", "poverty rat
## $ poptotal       <int> 66090, 10626, 14991, 30806, 5836,
```

# Quick hitter: When do we need ungroup()?

If we want to do analysis where groups get in the way, we need ungroup().

```
midwest_grouped %>%
  summarize(biggest_county = max(poptotal))
```

```
## `summarise()` has grouped output by 'state', 'ed_status

## # A tibble: 20 x 4
## # Groups:   state, ed_status [10]
##    state ed_status        poverty_status    biggest_count
##    <chr> <chr>            <chr>                       <int
##  1 IL    highly educated poverty rate < 10          78166
##  2 IL    highly educated poverty rate > 10         510506
##  3 IL    less educated   poverty rate < 10           4805
##  4 IL    less educated   poverty rate > 10          24923
##  5 IN    highly educated poverty rate < 10          30083
##  6 IN    highly educated poverty rate > 10          79715
##  7 IN    less educated   poverty rate < 10          15619
```

# Quick hitter: When do we need `ungroup()`?

If we want to do analysis where groups get in the way, we need `ungroup()`.

```
midwest_grouped %>%
  ungroup() %>%
  summarize(biggest_county = max(poptotal))
```

```
## # A tibble: 1 x 1
##   biggest_county
##            <int>
## 1        5105067
```

# Sure, but why would I group that data in the first place?

Perhaps you did a `group_by() + summarize()` with multiple groups.

- The default is to strip the "last" grouping variable

```
midwest_grouped %>%
  summarize(avg_pop = mean(poptotal)) %>%
  glimpse()
```

```
## `summarise()` has grouped output by 'state', 'ed_status
## Rows: 20
## Columns: 4
## Groups: state, ed_status [10]
## $ state          <chr> "IL", "IL", "IL", "IL", "IN", "IN
## $ ed_status      <chr> "highly educated", "highly educat
## $ poverty_status <chr> "poverty rate < 10", "poverty rat
## $ avg_pop        <dbl> 234318.64, 390871.41, 25303.62, 3
```

# BaseR: what's the deal with subsetting?

How many ways can you pull out the even numbers from `vec`?

```
vec <- 1:10
```

# BaseR: what's the deal with subsetting?

How many ways can you pull out the even numbers from vec?

```
vec <- 1:10
vec[c(2, 4, 6, 8, 10)]
```

```
## [1]  2  4  6  8 10
```

```
vec[rep(c(FALSE, TRUE), 5)]
```

```
## [1]  2  4  6  8 10
```

```
vec[seq(2, 10, 2)]
```

```
## [1]  2  4  6  8 10
```

```
vec[vec %% 2 == 0]
```

```
## [1]  2  4  6  8 10
```

Notice `filter()` works like the final option!

# BaseR: what's the deal with subsetting?

Now what if vec is a column in a tibble?

```
data <- tibble(vec_col = 1:10, random_col = "A")
```

# BaseR: what's the deal with subsetting?

Now what if vec is a column in a tibble?

```
data <- tibble(vec_col = 1:10, random_col = "A")

# equivalent to pull() (with filter)
data$vec_col[data$vec_col %% 2 == 0] # nicest way
data[["vec_col"]][c(2, 4, 6, 8, 10)]
data[rep(c(FALSE, TRUE), 5), ][["vec_col"]]

#equivalent to select() (with filter)
data[rep(c(FALSE, TRUE), 5), "vec_col" ]
data[seq(2, 10, 2), "vec_col"]

data %>%
  filter(vec_col %% 2 == 0) %>%
  select(vec_col)
```

# BaseR: what's the deal with subsetting?

Using `[` with vectors is natural.

- you can extract based on
  - indices
  - a vector of booleans (of equal length)
  - and names (if there are names)

When working with data, use tidyverse verbs to extract data.

- easier to remember words
- help avoid syntax errors and confusion between `[` `[[` and `$`

When googling for help add "in R tidyverse" to your query. If you start doing numerical computing, look for a review of `[` and `[[`.

# Wait did you say names for a vector?

Yep, we can have a named vector.

```
x <- c("a" = 1, "b"= 2)
x["a"]
```

```
## a
## 1
```

# Named vectors are not, Lists

Notice this is distinct from a list.

- The key difference is that lists can accept different data types as entries.

```
c("a" = c(1, 2), "b"= 2)
```

```
## a1 a2  b
##  1  2  2
```

```
list("a" = c(1, 2), "b"= 2)
```

```
## $a
## [1] 1 2
##
## $b
## [1] 2
```

# Tibbles are built on lists

- but tibbles enforce all entries to be the same length vectors.

```
my_tib <- tibble(a = c(1, 2),
       b = "A")

my_list <- list(a = c(1, 2),
       b = c("A", "A"))

# e.g.
my_tib[["b"]]
```

```
## [1] "A" "A"
```

```
my_list[["b"]]
```

```
## [1] "A" "A"
```

# Key points: Grouped analysis with `group_by()`

- *groups* are a set of rows that belong together.
  - `group_by()` adds information about groups “silently” without changing the data
- Use `group_by()` with `summarize()` to create summary tables at group-level.
  - Use with functions that *reduce* data from a vector to a single value per group.
  - Expected output: a table with one row per group and one column per summary statistic (and one column per grouping column.)

# Key points: Grouped analysis with `group_by()`

- we can also use `group_by()` to do grouped analysis with `mutate()`
  - you can use a "window function" like `lag()`
  - or add summary statistics to your main data set for futher analysis
- `group_by()` also can impact `arrange()` and `filter()`

**Up next:** Grouping() watch video for class 5 on using `loops`.

# Discussion

How do we make the data for this graph?

- What "groups" are required for the visualization?

# Exercise

A student came during office hours and asked why `mean(percentile=="p90p100")` doesn't calculate the average wealth shares (`value`) for the top 10 percentile group.

```
wid_data %>%
  filter(country %in% c("China", "India", "USA")) %>%
  group_by(country) %>%
  summarize(p90_mean = mean(percentile == "p90p100",
                            na.rm = TRUE))
```

# Class 5: Loops

# Feedback

Thank you for filling out the feedback form (we have 30 so far!)

- "Would be great if you could post solutions to the labs at the end of each week." **These are on the course website**
- "Please share qa code". **These are (newly) on the course website**

# Today's class

- `case_when()` question
- Review a few grouped analysis concepts
- Practice using loops

# Quicker hitter

**Q** Why do you end `case_when()` with `TRUE ~ ...`?

```
x <- 1:35
case_when(
  x %% 35 == 0 ~ "fizz buzz",
  x %% 5 == 0 ~ "fizz",
  x %% 7 == 0 ~ "buzz",
  TRUE ~ as.character(x)
)
```

```
##  [1] "1"         "2"         "3"         "4"         "f
##  [7] "buzz"      "8"         "9"         "fizz"      "1
## [13] "13"        "buzz"      "fizz"      "16"        "1
## [19] "19"        "fizz"      "buzz"      "22"        "2
## [25] "fizz"      "26"        "27"        "buzz"      "2
## [31] "31"        "32"        "33"        "34"        "f
```

# Quicker hitter

**A** If no cases match, NA is returned.

```
x <- 1:35
case_when(
  x %% 35 == 0 ~ "fizz buzz",
  x %% 5 == 0 ~ "fizz",
  x %% 7 == 0 ~ "buzz"
)
```

```
##  [1] NA          NA          NA          NA          "f
##  [7] "buzz"      NA          NA          "fizz"      NA
## [13] NA          "buzz"      "fizz"      NA          NA
## [19] NA          "fizz"      "buzz"      NA          NA
## [25] "fizz"      NA          NA          "buzz"      NA
## [31] NA          NA          NA          NA          "f
```

# Q: What does `group_by()` do?

The following command runs without error, but I'm not seeing any change in `grouped_data` compared to `traffic_data`.

- Both still have 4478 jobs of 9 variables.

Am I missing something?

```
grouped_data <-
 traffic_data %>%
   group_by(Race, Gender)
```

# Two questions on grouped mutates.

Recall:

- `group_by() + summarize()` **collapses** the data to a row with summary values per group.
- `group_by() + mutate()` maintains the data set, but adds columns that may depend on group membership
  - e.g. `lag()`, `row_number()`

# How does `lag()` work?

Find the “previous” (lag()) or “next” (lead()) values in a vector.

```r
lag(c(1, 2, 3))
```

```
## [1] NA  1  2
```

# How does `lag()` work?

Useful for comparing values behind of or ahead of the current values.

```
x <- 1:5
tibble(behind = lag(x), x, ahead = lead(x))
```

```
## # A tibble: 5 x 3
##   behind     x ahead
##    <int> <int> <int>
## 1     NA     1     2
## 2      1     2     3
## 3      2     3     4
## 4      3     4     5
## 5      4     5    NA
```

# How does lag() work with grouped data?

- Why is this wrong?

```
x <- c(2, 3, 30, 20)
group <- c("A", "A", "B", "B")
time <- c(1, 2, 2, 1)
tibble(group, time,  x) %>%
  mutate(previous = lag(x))
```

```
## # A tibble: 4 x 4
##   group  time     x previous
##   <chr> <dbl> <dbl>    <dbl>
## 1 A         1     2       NA
## 2 A         2     3        2
## 3 B         2    30        3
## 4 B         1    20       30
```

# How does lag() work with grouped data?

You need to have the data in the correct

- order
- group

```
tibble(time, group,  x) %>%
  group_by(group) %>%
  arrange(time) %>%
  mutate(previous = lag(x))
```

```
## # A tibble: 4 x 4
## # Groups:   group [2]
##    time group     x previous
##   <dbl> <chr> <dbl>    <dbl>
## 1     1 A         2       NA
## 2     1 B        20       NA
## 3     2 A         3        2
## 4     2 B        30       20
```

# Practice

Use `txhousing`, a tidyverse dataset.

- Calculate the monthly change in number of `sales` for each `city`.
  - hint: use `lag()` in a grouped mutate!
- Calculate the annual change in total `sales` for each `city`.

**Q.**

Explain the `rank()` function(s). How is it different than `order()` and `sort()`?

```
x <- c(10, 0, 1, 2, 3, NA)

rank(x)
```

```
## [1] 5 1 2 3 4 6
```

```
order(x)
```

```
## [1] 2 3 4 5 1 6
```

```
sort(x)
```

```
## [1]  0  1  2  3 10
```

```
row_number(x)
```

```
## [1]  5  1  2  3  4 NA
```

## A. Sort puts the data in order.

```
x
```

```
## [1] 10  0  1  2  3 NA
```

```
(the_order <- order(x))
```

```
## [1] 2 3 4 5 1 6
```

```
x[the_order]
```

```
## [1]  0  1  2  3 10 NA
```

```
sort(x, na.last = TRUE)
```

```
## [1]  0  1  2  3 10 NA
```

## **A**. Rank ranks the data in place.

```
x
```

```
## [1] 10  0  1  2  3 NA
```

```
(the_rank <- rank(x))
```

```
## [1] 5 1 2 3 4 6
```

```
the_order
```

```
## [1] 2 3 4 5 1 6
```

# `tidyverse` provides 6 ranking functions

```
# the help shows all 6!
?row_number()
```

Explain how the ranking functions interact with a `group_by() + mutate()`.

# For loops and iteration

- Iteration is useful when we are repeatedly calling the same block of code or function while changing one (or two) inputs.
- but if you can, use vectorized operations!

# For loops

Compare and contrast the two code blocks

```r
# block a
x <- -10:10
y <- integer(length = length(x))

for (i in seq_along(x)) {
  y[[i]] <- x[[i]]^2 + x[[i]] + 1
}
```

and

```r
# block b
x <- -10:10
y <- c()

for (item in x) {
  y <- c(y, item^2 + item + 1)
}
```

# loops

| | block a | block b |
|---|---|---|
| iterates over | indexes | items |
| preallocates space? | yes | no |
| vectorized? | no | no |

# Vectorized? No.

Can you vectorize the code?

```
# block b
x <- -10:10
y <- c()

for (item in x) {
  y <- c(y, item^2 + item + 1)
}
```

# Vectorized? yes.

```r
x <- -10:10
y <- x^2 + x + 1
```

# Is preallocation a big deal?

I encapsulated our code into functions for testing.

```
preallocate_loop <- function(x){
  y <- integer(length = length(x))
  for (i in seq_along(x)) {
    y[[i]] <- x[[i]]^2 + x[[i]] + 1
  }
  y
}
```

```
build_loop <- function(x){
    y <- c()
    for (item in x) {
      y <- c(y, item^2 + item + 1)
    }
    y
  }
```

# For tiny data sets, it's not a huge deal.

```
x <- -10:10
bench::mark(preallocate_loop(x), build_loop(x)) %>%
  select(expression, min, median, mem_alloc)
```

```
## # A tibble: 2 x 4
##   expression                min   median mem_alloc
##   <bch:expr>           <bch:tm> <bch:tm> <bch:byt>
## 1 preallocate_loop(x)    5.33us   7.71us    41.6KB
## 2 build_loop(x)          7.54us  21.98us    29.5KB
```

# For big data sets, it increasingly becomes a big deal.

```r
# warning this test takes a while!
x <- -1e4:1e4
bench::mark(preallocate_loop(x), build_loop(x)) %>%
  select(expression, min, median, mem_alloc)
```

```
## Warning: Some expressions had a GC in every iteration; s
```

```
## # A tibble: 2 x 4
##   expression                min   median mem_alloc
##   <bch:expr>           <bch:tm> <bch:tm> <bch:byt>
## 1 preallocate_loop(x)    2.76ms    3.2ms  234.48KB
## 2 build_loop(x)           2.52s    2.52s    1.49GB
```

# vectorized option

```
vectorized_code <- function(x) {
  x^2 + x + 1
}
```

# vectorized option performs favorably

```
x <- -1e6:1e6
bench::mark(preallocate_loop(x),
            vectorized_code(x)) %>%
  select(expression, min, median, mem_alloc)
```

```
## Warning: Some expressions had a GC in every iteration; s
```

```
## # A tibble: 2 x 4
##   expression                 min   median mem_alloc
##   <bch:expr>            <bch:tm> <bch:tm> <bch:byt>
## 1 preallocate_loop(x)  669.9ms  669.9ms    22.9MB
## 2 vectorized_code(x)    20.1ms   56.2ms    22.9MB
```

# mea culpa: the case for `[[`

Last class, I encouraged you to not use `[[` for subsetting / indexing.

- But we need these when indexing into lists!

# lists

lists are a **data structure** that can store different data types in the same object.

```r
list(c(12, 1), 4, "f")
```

```
## [[1]]
## [1] 12  1
##
## [[2]]
## [1] 4
##
## [[3]]
## [1] "f"
```

# lists

- tibbles/data.frames are built on lists

```
(x <- list('int' = c(12L, 1L),
      'dbl' = c(4.02, pi),
      'char' = c("f", "f")))
```

```
## $int
## [1] 12  1
##
## $dbl
## [1] 4.020000 3.141593
##
## $char
## [1] "f" "f"
```

# Why [[

[[ pulls out the whatever is in the ith position of the list while [ pulls out a subset of the list.

```
x[1]
```

```
## $int
## [1] 12  1
```

```
x[[1]]
```

```
## [1] 12  1
```

# Why [[

When setting the ith stuff in a list we use [[ so we can place any given object into the list.

```
# create an empty list
output <- vector("list", 2)
(output[1] <- c(1, 2))
```

```
## Warning in output[1] <- c(1, 2): number of items to repl
## replacement length
```

```
## [1] 1 2
```

```
(output[[1]] <- c(1, 2))
```

```
## [1] 1 2
```

# Key points: for-loops

- If you can't vectorize, for loops work for iteration
  - Clearly define what you will iterate over (values or indicies)
  - Preallocate space for your output (if you can)
  - The body of the for-loop has parametrized code based on thing your iterating over
  - Debug as you code by testing your understanding of what the for-loop should be doing (e.g. using `print()`)

Learn more in chapter 21 of r for data science:
https://r4ds.had.co.nz/iteration.html

# Class 6: Functions

# Today's class

- loop questions
- functions writing concepts
- primer for lab 6

**Reminder:** Please turn in your final projects on gradescope.

- Suggested deadline Sept 17 (tomorrow)
- Final deadline Sept 24.

## Q Can I pipe a for-loop into `ggplot()`?

```
# psuedo-code
for (i in seq_along(x)) {
  results[[i]] <- some_function(x[[i]])
} %>%
  ggplot(aes(x = x, y = y))  + ...
```

## **Reframe Q** What is the output of a for-loop? Can it be a tibble?

- Each iteration there's an "intermediate output" which is the final line of code in the loop. (like a function).

```
x <- c(0, 1, 2)
result <- integer(length(x))

output <- for (i in seq_along(x)) {
  result[[i]] <- x[[i]]^2
  "last line inside loop"
} %>% print()
```

```
## [1] "last line inside loop"
## [1] "last line inside loop"
## [1] "last line inside loop"
```

- The "final output" is NULL

```
print(output)
```

```
## NULL
```

## Q Can I pipe a for-loop into `ggplot()`?

If the last line inside the loop is a tibble, then yes (kind of).

- R doesn't display the output
- But we can assign it to a name

```
my_plot <- vector("list", 3)

for ( i in 1:3) {
  # do stuff
  # ...
  # end with
  txhousing
} %>%
  ggplot(aes(x = sales, y = volume)) +
  geom_point() -> my_plot[[i]]

my_plot[[3]]
```

- *Don't do it!* More natural to call ggplot w/i the loop or after collecting a dataset.

# Q How to preallocate space for a tibble?

```
estimates <- tibble(n = integer(), sample_mean = double())

for (n in sample_sizes) {
  sample_mean <- mean(rnorm(n, mean = 0, sd = 5))
  estimates <- bind_rows(estimates,
              c(n = n, sample_mean = sample_mean))
}
estimates
```

# Named vectors behave like “rows” with a single data type

```r
row_1 <- c(a = 1, b = "dog")
row_2 <- c(a = 2, b = "cat")

bind_rows(row_1, row_2)
```

```
## # A tibble: 2 x 2
##   a     b
##   <chr> <chr>
## 1 1     dog
## 2 2     cat
```

# Named lists behave like “rows” with a various data type

```r
row_1 <- list(a = 1, b = "dog")
row_2 <- list(a = 2, b = "cat")

bind_rows(row_1, row_2)
```

```
## # A tibble: 2 x 2
##       a b
##   <dbl> <chr>
## 1     1 dog
## 2     2 cat
```

# We could also create one row tibbles

```
tibble_1 <- tibble(a = 1, b = "dog")
tibble_2 <- tibble(a = 2, b = "cat")

bind_rows(tibble_1, tibble_2)
```

```
## # A tibble: 2 x 2
##       a b
##   <dbl> <chr>
## 1     1 dog
## 2     2 cat
```

# “rows” can be bound together with bind_rows()

```
row_3 <- list(a = 3, b = "dog")
data <- bind_rows(row_1, row_2)
(data <- bind_rows(data, row_3))
```

```
## # A tibble: 3 x 2
##       a b
##   <dbl> <chr>
## 1     1 dog
## 2     2 cat
## 3     3 dog
```

# “rows” can be bound together with `bind_rows()`

```
our_rows <- list(row_1, row_2, row_3)
(data <- bind_rows(our_rows))
```

```
## # A tibble: 3 x 2
##       a b
##   <dbl> <chr>
## 1     1 dog
## 2     2 cat
## 3     3 dog
```

# Q How to preallocate space for a tibble?

The previous slide suggest we preallocate a `list` with one slot for each row.

```
sample_sizes <- seq(2, 10, 2) # c(2, 4, 6, 8, 10)
estimates <- vector("list", length(sample_sizes))
```

# Q How to preallocate space for a tibble?

Then in the body of the loop we assign a "row" to the ith entry of `estimates`

```
for (i in seq_along(sample_sizes)) {
  n <- sample_sizes[[i]]
  sample_mean <- mean(rnorm(n, mean = 0, sd = 5))
  estimates[[i]] <- c(n = n, sample_mean = sample_mean)
}

# estimates is a list of vectors until bind_rows(.)!
estimates <- bind_rows(estimates)
```

notice this is the **only time** in coding lab we advocate using lists.

- use vectorized code / use tidyverse code

# another loop example

Compute the mean of every column in `midwest`

# another ~~loop~~ example

Compute the mean of every column in `midwest`.

- use `across()` (we won't cover this in detail)

```
midwest %>%
  summarize(across(.fns = mean))
```

```
## # A tibble: 1 x 28
##     PID county state   area poptotal popdensity popwhite
##   <dbl>  <dbl> <dbl>  <dbl>    <dbl>      <dbl>    <dbl
## 1 1437.     NA    NA 0.0332   96130.      3098.   81840.
## # ... with 19 more variables: popasian <dbl>, popother <
## #   percblack <dbl>, percamerindan <dbl>, percasian <dbl
## #   popadults <dbl>, perchsd <dbl>, percollege <dbl>, pe
## #   poppovertyknown <dbl>, percpovertyknown <dbl>, perc
## #   percchildbelowpovert <dbl>, percadultpoverty <dbl>,
## #   percelderlypoverty <dbl>, inmetro <dbl>, category <
```

# another loop example

Compute the mean of every column in `midwest`

- What should we loop over?
- How do we calculate what we're looking for?

# another loop example

**Compute the mean of every column in `midwest`**

```
mean(midwest[["area"]])
```

```
## [1] 0.03316934
```

```
# or
midwest %>%
  pull(area) %>%
  mean()
```

```
## [1] 0.03316934
```

```
# or
midwest %>%
  summarise(area = mean(area))
```

```
## # A tibble: 1 x 1
##      area
##     <dbl>
```

# another loop example

```
# preallocate output
col_names <- names(midwest)
midwest_means <- vector("double", ncol(midwest))

# determine what to loop over
for (i in seq_along(col_names)) {
  #  body
  col_name <- col_names[[i]]
  midwest_means[[i]] <- mean(midwest[[col_name]])
}

tibble(names = col_names, means = midwest_means)
```

```
## # A tibble: 28 x 2
##    names                  means
##    <chr>                  <dbl>
##  1 PID                1437.
##  2 county               NA
```

# function writing concept

- A function maps an input to an output.
  "A user logs into our website. You respond with a greeting."

# fwc: input-output

Write the function!

input: `name` output: `greeting`

Recall

```
#psuedo code for a function
function_name <- function(inputs) {
    body
}
```

# fwc: input-output

```r
greet_user <- function(name) {
  paste0("Hello ", name, "!")
}

greet_user("Qiwei")
```

```
## [1] "Hello Qiwei!"
```

# fwc: when to write a function?

- If you repeat very similar code more than twice
- You can easily parameterize the similar code

```
txhousing %>%
  filter(city == "Austin") %>%
  mutate(date = year + month / 12) %>%
  ggplot(aes(x = date, y = sales)) +
  geom_line() +
  labs(title = "Austin's sales volume")
```

# fwc: don't repeat yourself

```r
sales_trends <- function(city_name){
  txhousing %>%
    filter(city == city_name) %>%
    mutate(date = year + month / 12) %>%
    ggplot(aes(x = date, y = sales)) +
    geom_line() +
    labs(title = str_c(city_name, "'s sales volume"))
  }
```

# fwc: don't repeat yourself

```
sales_trends("Austin")
sales_trends("Houston")
```

# fwc: don't repeat yourself (Advanced)

Extra slick: can we parameterize the `y` variable.

# fwc: test your code as you write it

```r
trends <- function(city_name, var){
txhousing %>%
  filter(city == city_name) %>%
  mutate(date = year + month / 12) %>%
  ggplot(aes(x = date, y = var)) +
  geom_line() +
  labs(title = str_c(city_name, "'s ", var))
}

trends("Austin", sales, "sales volume")
```

# fwc: don't repeat yourself (Advanced)

Extra slick: can we parameterize the y variable.

```
trends <- function(city_name, var, var_description){
txhousing %>%
  filter(city == city_name) %>%
  mutate(date = year + month / 12) %>%
  ggplot(aes(x = date, y = {{ var }})) +
  geom_line() +
  labs(title = str_c(city_name,
                     "'s ",
                     var_description))
}

trends("Austin", sales, "sales volume")
```

# `{{ }}`?

`{{ }}` "forwards" the name `var` from your global environment (where it's undefined) to the tibble's environment (where it's a column name).

- The ideas here are somewhat advanced for coding camp

# fwc: break big ideas into small ideas

- **problem** encapsulating 100s of lines of data analysis in a single function is a recipe for disaster.
- **solution** break the 100s of lines of analysis into coherent chunks (think high level about input-output!)

This is the heart of lab 6.

# Background for the lab

# Concepts: `r/q/p/d` functions

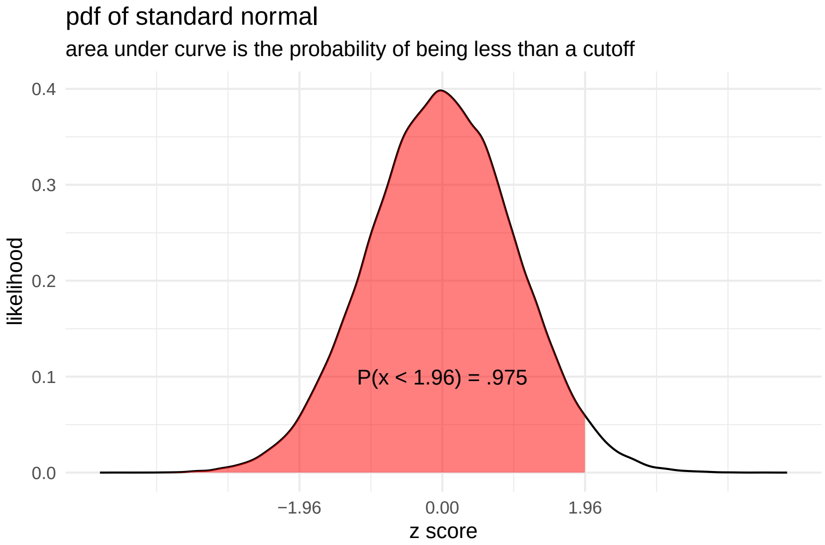
R has built-in functions for working with distributions.

| | example | what it does? |
|---|---|---|
| r | `rnorm(n)` | generates a random sample of size n |
| p | `pnorm(q)` | returns CDF value at q |
| q | `qnorm(p)` | returns inverse CDF (the quantile) for a given probability |
| d | `dnorm(x)` | returns pdf value at x |

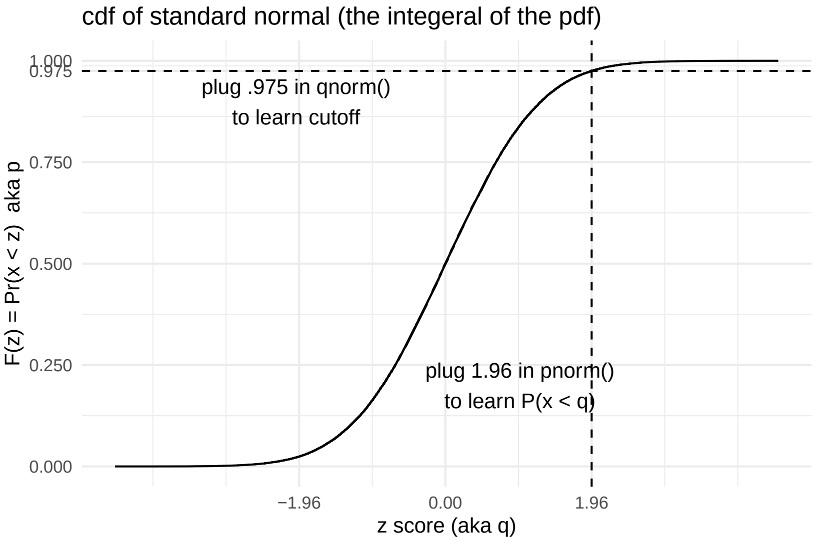
We should already be familiar with `r` functions like `rnorm()` and `runif()`.

- These concepts will be taught in stats. We don't expect you to learn them here. We can help you reason through the material enough to do the coding.

# What are p and q?



# What are p and q?



# What are p and q?

**pnorm** returns the probability we observe a value less than or equal to some value q.

```
pnorm(1.96)
```

```
## [1] 0.9750021
```

```
pnorm(0)
```

```
## [1] 0.5
```

**qnorm** returns the inverse of `pnorm`. Plug in the probability and get the cutoff.

```
qnorm(.975)
```

```
## [1] 1.959964
```

```
qnorm(.5)
```

```
## [1] 0
```

# Monte Carlo experiments

Monte Carlo is a world gambling hub.

- Gamblers know that roulette wheels are not made perfectly.
- If you watch the wheel long enough and take notes you can figure out the empirical probability

# Monte Carlo experiments

Statisticians use the same idea.

Esp. if we're not sure how to calculate something exactly, but have a model

- complicated interacting systems
- integrals or other objects without a closed form solution (or a difficult to compute closed form)

# How to do a Monte Carlo Simulation

1. Generate random samples of data using a known process (e.g. `rnorm()`).
2. Make calculations based on the random sample.
3. Aggregate the results.

You will do this in the functions lab!

# Thank you

It has been a blast.