Tidyverse Tools in R for Data Science and Statistical Inference

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Slides available at http://bit.ly/csp-tidy

PDF slides at http://bit.ly/csp-tidy-pdf

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Prior Installation

Make sure you have the current R, RStudio, & R packages

- Novice's Guide on ModernDive.com

- R (version 4.0.2 or greater)
- RStudio (version 1.4 or greater)

- Run this in the RStudio Console

```
pkgs <- c(
  "tidyverse", "moderndive", "dslabs",
  "infer", "janitor"
  )
install.packages(pkgs)
```

Getting started

1. Open HTML slides: https://bit.ly/csp-tidy
2. Open RStudio
3. Download course materials to your preferred location by running this in the RStudio Console:

```
usethis::use_course("bit.ly/csp-tidy")
```

4. Open the Rproj file in the folder that just opened
5. Edit Google Doc to ask and answer questions: https://bit.ly/csp-tidy-doc

R Data Types

Data types review

Vector/variable

- Type of vector (`int`, `num` or `dbl`, `chr`, `lgl`, `date`)

Data frame

- Vectors of (potentially) different types
- Each vector has the same number of rows

Data types review

```
library(tibble) # tibble is the tidyverse data.frame
library(lubridate)
ex1 <- tibble(
  vec1 = c(1980, 1990, 2000, 2010),
  vec2 = c(1L, 2L, 3L, 4L),
  vec3 = c("low", "low", "high", "high"),
  vec4 = c(TRUE, FALSE, FALSE, FALSE),
  vec5 = ymd(c("2017-05-23", "1776/07/04",
               "1983-05/31", "1908/04-01"))
)
ex1
```

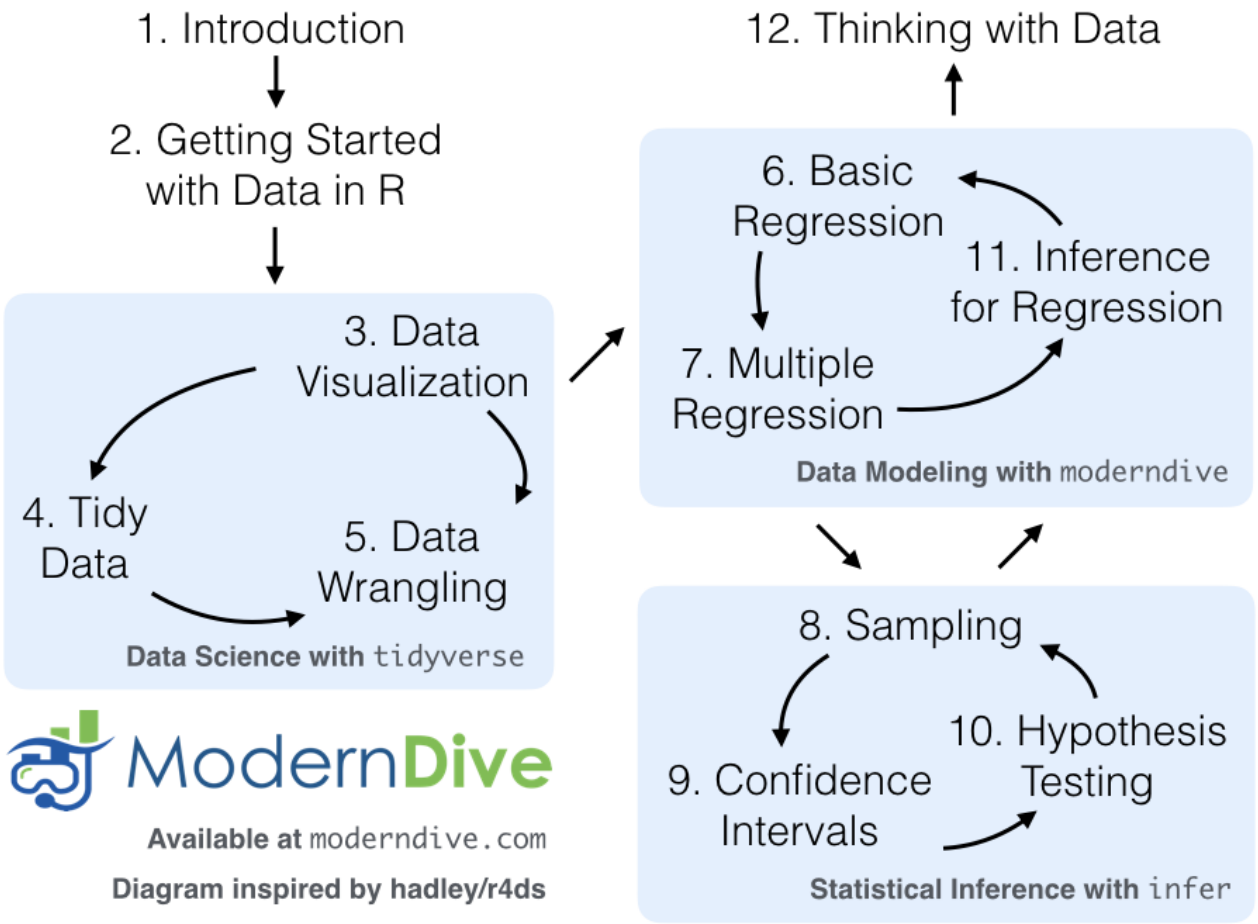
```
# A tibble: 4 x 5
   vec1  vec2 vec3  vec4  vec5
  <dbl> <int> <chr> <lgl> <date>
1  1980     1 low   TRUE  2017-05-23
2  1990     2 low   FALSE 1776-07-04
3  2000     3 high  FALSE 1983-05-31
4  2010     4 high  FALSE 1908-04-01
```

Learning objectives

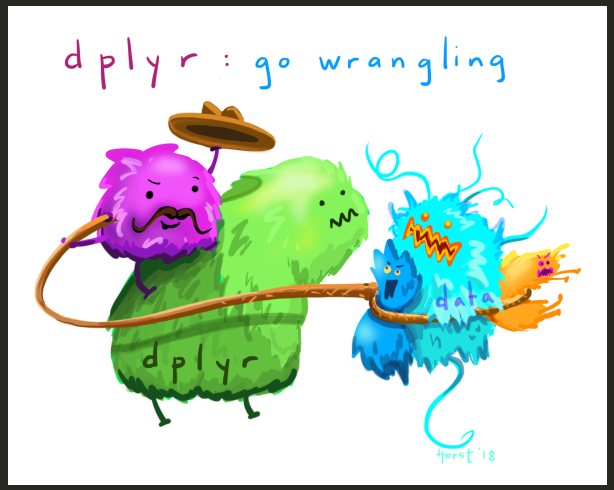
Part 1

- Distinguish between different {tidyverse} packages
- Assess different {dplyr} functions for wrangling data
- Discuss the power of "tidy data"
- Develop an intuition behind {ggplot2} plotting syntax

Shameless plug



Getting started with {dplyr}



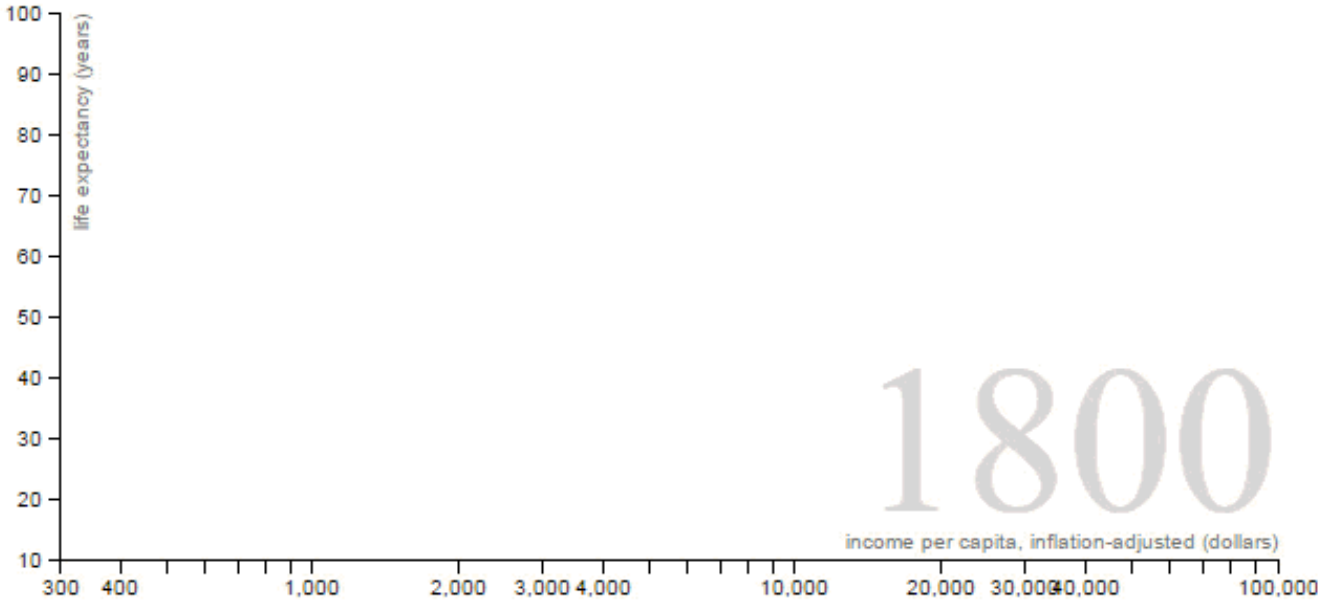
Alison Horst

dplyr package

Welcome to the tidyverse!

The {tidyverse} is a collection of R packages that share common philosophies and are designed to work together.

First motivating example for today



- Inspired by the late, great Hans Rosling

The `gapminder` data set in {dslabs}

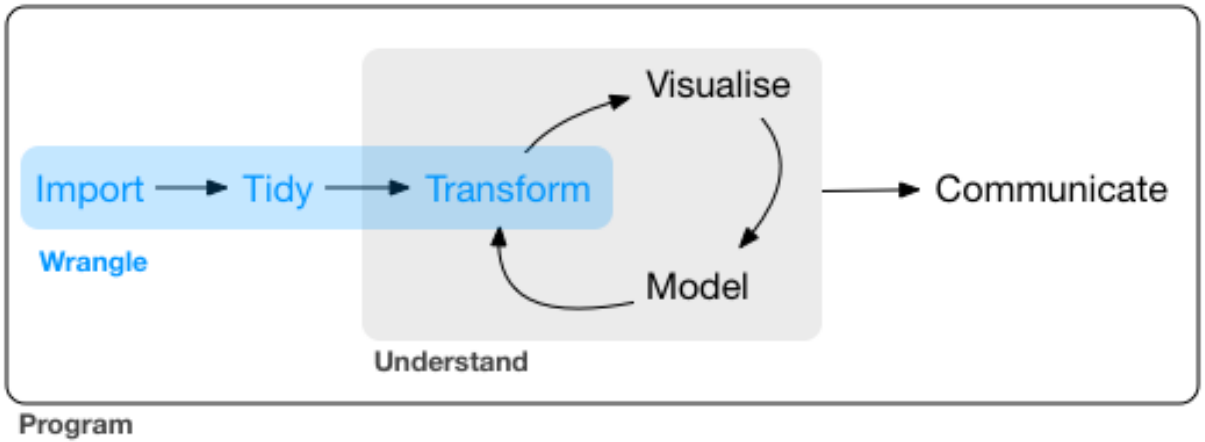
```
library(dslabs)
library(dplyr)
gapminder <- tibble(gapminder)
glimpse(gapminder)
```

```
Rows: 10,545
Columns: 9
$ country          <fct> Albania, Algeria, Angola, Antigua and…
$ year             <int> 1960, 1960, 1960, 1960, 1960, 1960, 1…
$ infant_mortality <dbl> 115.40, 148.20, 208.00, NA, 59.87, NA…
$ life_expectancy  <dbl> 62.87, 47.50, 35.98, 62.97, 65.39, 66…
$ fertility        <dbl> 6.19, 7.65, 7.32, 4.43, 3.11, 4.55, 4…
$ population       <dbl> 1636054, 11124892, 5270844, 54681, 20…
$ gdp              <dbl> NA, 1.3828e+10, NA, NA, 1.0832e+11, N…
$ continent        <fct> Europe, Africa, Africa, Americas, Ame…
$ region           <fct> Southern Europe, Northern Africa, Mid…
```

- Also check out the {gapminder} package

What is data wrangling?

- "data janitor work"
- importing data
- cleaning data
- changing shape of data
- fixing errors and poorly formatted data elements
- transforming columns and rows
- filtering, subsetting



Base R versus the {tidyverse}

- The mean life expectancy across all years for Asia

```
# Base R
asia <- gapminder[gapminder$continent == "Asia", ]
mean(asia$life_expectancy)
```

```
[1] 65.901
```

```
library(dplyr)
gapminder %>%
  filter(continent == "Asia") %>%
  summarize(mean_exp = mean(life_expectancy))
```

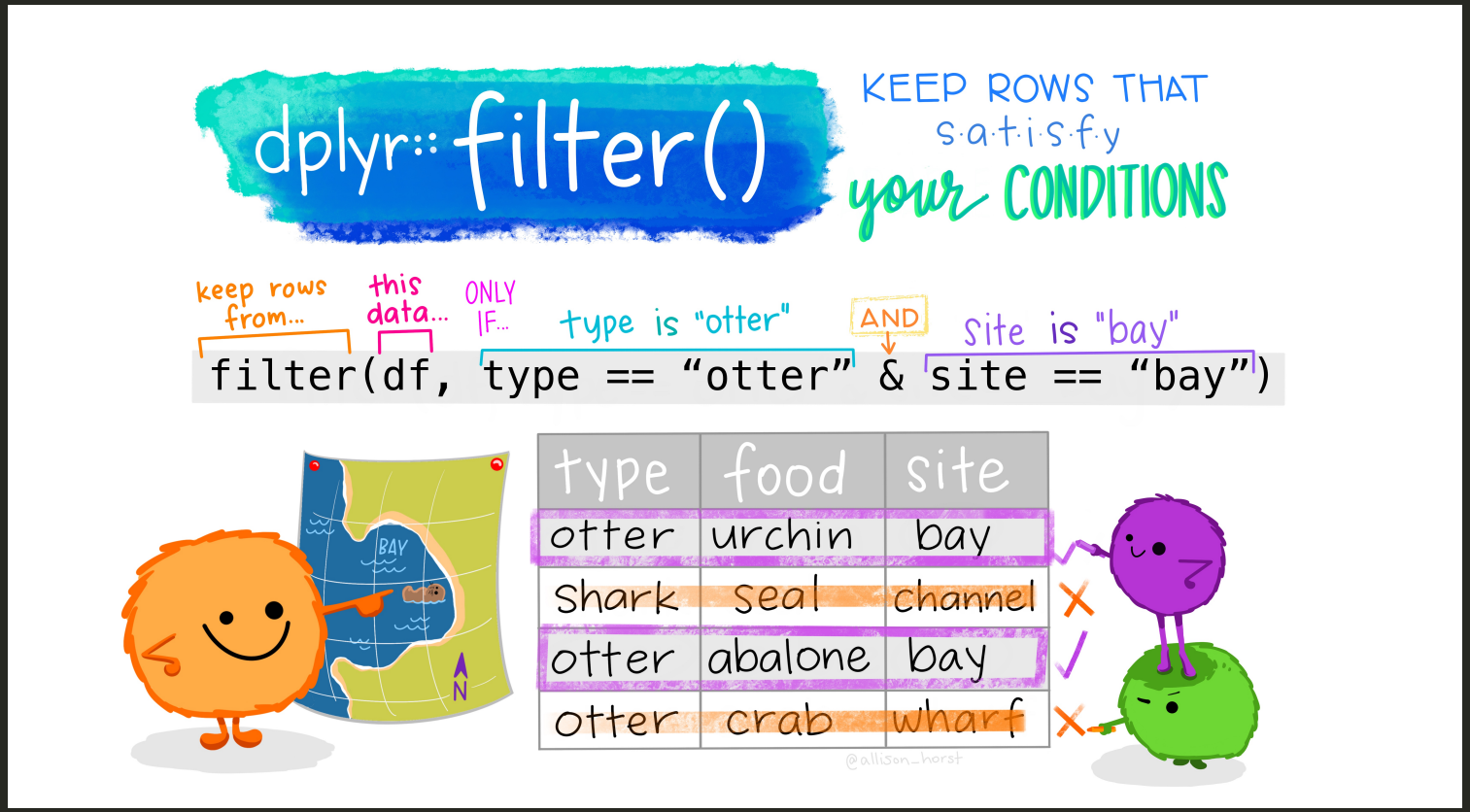
```
# A tibble: 1 x 1
  mean_exp
     <dbl>
1     65.9
```

The pipe `%>%`

- A way to chain together commands
- Can be read as "and then" when reading over code

```
library(dplyr)
gapminder %>%
  filter(continent == "Asia") %>%
  summarize(mean_exp = mean(life_expectancy))
```

`filter()` rows that satisfy specified conditions



`dplyr::filter()`

- Arguments are "filters" that you'd like to apply.

```
gap_2014 <- gapminder %>% filter(year == 2014)
gap_2014
```

```
# A tibble: 185 x 9
  country              year infant_mortality life_expectancy
  <fct>               <int>            <dbl>           <dbl>
1 Albania              2014             12.9            77.9
2 Algeria              2014             22              76.3
3 Angola               2014             98.8            59.2
4 Antigua and Barbuda  2014              6.1            76.3
5 Argentina            2014             11.5            76.3
# … with 180 more rows, and 5 more variables: fertility <dbl>,
#   population <dbl>, gdp <dbl>, continent <fct>, region <fct>
```

- Use `==` to compare a variable to a value

Logical operators

- Use `|` to check for any in multiple filters being true:

```
gapminder %>%
  filter(life_expectancy < 50 | fertility > 4) %>%
  slice_sample(n = 8)
```

```
# A tibble: 8 x 9
  country        year infant_mortality life_expectancy fertility
  <fct>         <int>            <dbl>           <dbl>     <dbl>
1 Nepal          1996             73.1            62.5      4.6 
2 Uganda         2010             49.5            57.8      6.16
3 Nicaragua      1988             54.5            71.4      4.99
4 Guinea-Bissau  1962             NA              43.6      5.67
5 Oman           1985             50.4            68.4      8.22
6 Comoros        1970            152.             48.6      7.06
7 Tajikistan     1980            100.             64.3      5.66
8 Gabon          1990             60.5            59.5      5.42
# … with 4 more variables: population <dbl>, gdp <dbl>,
#   continent <fct>, region <fct>
```

Logical operators

- Use `,` to check for all of multiple filters being true:

```
gapminder %>%
  filter(life_expectancy < 50, fertility > 4)
```

```
# A tibble: 8 x 9
  country       year infant_mortality life_expectancy fertility
  <fct>        <int>            <dbl>           <dbl>     <dbl>
1 Algeria       1960             148.            47.5      7.65
2 Angola        1960             208             36.0      7.32
3 Bangladesh    1960             176.            46.2      6.73
4 Benin         1960             187.            38.3      6.28
5 Bhutan        1960             175             35.9      6.67
6 Bolivia       1960             173.            43.8      6.7
7 Burkina Faso  1960             161.            35.2      6.29
8 Burundi       1960             145.            40.6      6.95
# … with 4 more variables: population <dbl>, gdp <dbl>,
#   continent <fct>, region <fct>
```

Logical operators

- Use `%in%` to check for any being true (shortcut to using `|` repeatedly with `==`)

```
gapminder %>%
  filter(country %in% c("Argentina", "Belgium", "Mexico"),
         year %in% c(2012, 2015))
```

```
# A tibble: 6 x 9
  country    year infant_mortality life_expectancy fertility
  <fct>     <int>            <dbl>           <dbl>     <dbl>
1 Argentina  2012             12.3            76.1      2.19
2 Belgium    2012              3.5            80.3      1.85
3 Mexico     2012             13.1            75.7      2.22
4 Argentina  2015             11.1            76.5      2.15
5 Belgium    2015              3.3            80.5      1.86
6 Mexico     2015             11.3            75.9      2.13
# … with 4 more variables: population <dbl>, gdp <dbl>,
#   continent <fct>, region <fct>
```

Your Turn

Exercise A - 5 minutes

1. Filter observations from either Europe or Africa using the `|`.
2. Filter observations from either Africa or Asia using `%in%`.
3. How many countries had life expectancy greater than 80 years in 1996?

05:00

Walk through exercise in RStudio

`summarize()`

- Any numerical summary that you want to apply to a column of a data frame is specified within `summarize()`.

```
stats_2015 <- gapminder %>%
  filter(year == 2015) %>%
  summarize(
    max_exp = max(life_expectancy),
    sd_exp = sd(life_expectancy)
  )
stats_2015
```

```
# A tibble: 1 x 2
  max_exp sd_exp
    <dbl>  <dbl>
1    83.7   7.79
```

Combining `summarize()` with `group_by()`

- When you'd like to determine a numerical summary for all levels of a different categorical variable

```
max_exp_2015_by_cont <- gapminder %>%
  filter(year == 2015) %>%
  group_by(continent) %>%
  summarize(max_exp = max(life_expectancy),
            sd_exp = sd(life_expectancy))
max_exp_2015_by_cont
```

```
# A tibble: 5 x 3
  continent max_exp sd_exp
* <fct>       <dbl>  <dbl>
1 Africa       77.6   6.52
2 Americas     81.7   3.58
3 Asia         83.7   5.12
4 Europe       83.3   3.43
5 Oceania      82.3   7.32
```

`mutate()` changes the data

`mutate()`

- Most importantly, allows you to create a new variable based on other variables

```
gapminder_plus <- gapminder %>%
  mutate(gdp_per_capita = gdp / population)
slice_sample(gapminder_plus, n = 4)
```

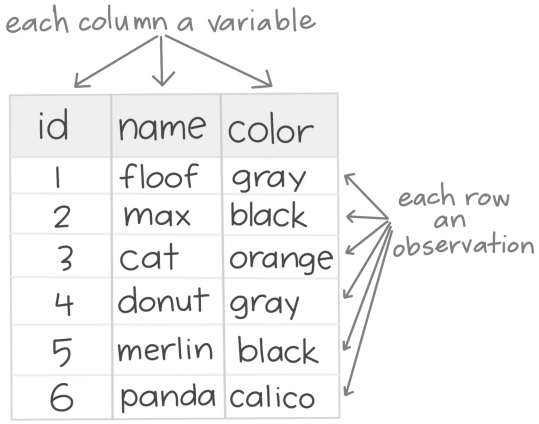
```
# A tibble: 4 x 10
  country       year infant_mortality life_expectancy fertility
  <fct>        <int>            <dbl>           <dbl>     <dbl>
1 Portugal      1972             47.6            69.2      2.88
2 Mauritius     1987             24.4            68.5      2.27
3 South Africa  1994             47.2            62.8      3.2
4 Tonga         1982             23              67.6      5.48
# … with 5 more variables: population <dbl>, gdp <dbl>,
#   continent <fct>, region <fct>, gdp_per_capita <dbl>
```

"TIDY DATA is a standard way of mapping the meaning of a dataset to its structure."

—HADLEY WICKHAM

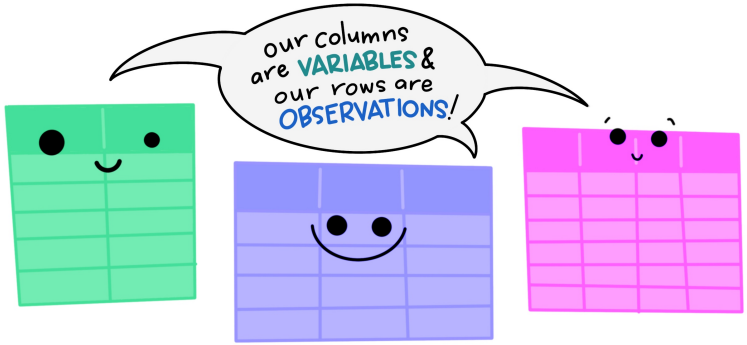
In tidy data:

- each variable forms a column
- each observation forms a row
- each cell is a single measurement



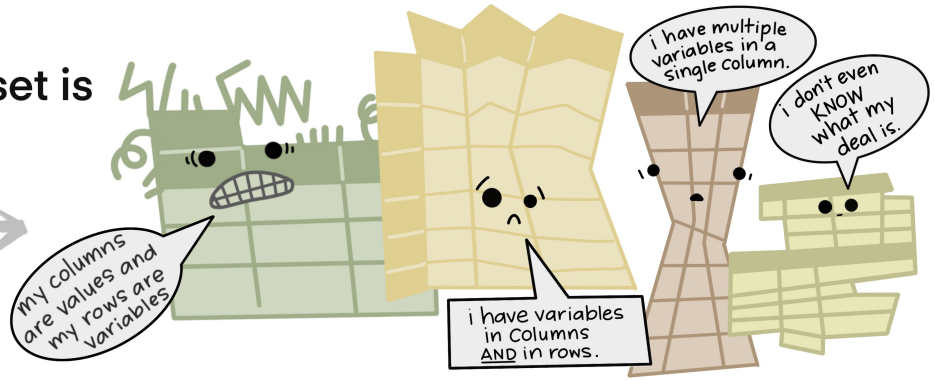
Wickham, H. (2014). Tidy Data. Journal of Statistical Software *59* (10). DOI: 10.18637/jss.v059.i10

The standard structure of tidy data means that "tidy datasets are all alike..."



"...but every messy dataset is messy in its own way."

–HADLEY WICKHAM



`arrange()`

- Reorders the rows in a data frame based on the values of one or more variables

```
gapminder_plus %>%
  arrange(year, country)
```

```
# A tibble: 10,545 x 10
  country              year infant_mortality life_expectancy
  <fct>               <int>            <dbl>           <dbl>
1 Albania              1960            115.             62.9
2 Algeria              1960            148.             47.5
3 Angola               1960            208              36.0
4 Antigua and Barbuda  1960             NA              63.0
5 Argentina            1960             59.9            65.4
# … with 10,540 more rows, and 6 more variables:
#   fertility <dbl>, population <dbl>, gdp <dbl>,
#   continent <fct>, region <fct>, gdp_per_capita <dbl>
```

`arrange()`

- Can also put into descending order

```
gapminder_plus %>%
  filter(year > 2000) %>%
  arrange(desc(life_expectancy))
```

```
# A tibble: 2,960 x 10
  country           year infant_mortality life_expectancy
  <fct>            <int>            <dbl>           <dbl>
1 Hong Kong, China  2016               NA            83.9
2 Hong Kong, China  2015               NA            83.7
3 Hong Kong, China  2014               NA            83.6
4 Hong Kong, China  2013               NA            83.4
5 Iceland           2014              1.6            83.3
# … with 2,955 more rows, and 6 more variables: fertility <dbl>,
#   population <dbl>, gdp <dbl>, continent <fct>, region <fct>,
#   gdp_per_capita <dbl>
```

Don't mix up `arrange()` and `group_by()`

- `group_by()` is used (mostly) with `summarize()` to calculate summaries over groups
- `arrange()` is used for sorting

Don't mix up `arrange()` and `group_by()`

This doesn't really do anything useful by itself

```
gapminder %>% group_by(country)
```

```
# A tibble: 10,545 x 9
# Groups:   country [185]
  country              year infant_mortality life_expectancy
  <fct>               <int>            <dbl>           <dbl>
1 Albania              1960            115.             62.9
2 Algeria              1960            148.             47.5
3 Angola               1960            208              36.0
4 Antigua and Barbuda  1960             NA              63.0
5 Argentina            1960             59.9            65.4
# … with 10,540 more rows, and 5 more variables:
#   fertility <dbl>, population <dbl>, gdp <dbl>,
#   continent <fct>, region <fct>
```

Don't mix up `arrange()` and `group_by()`

But this does

```
gapminder %>% arrange(country)
```

```
# A tibble: 10,545 x 9
  country  year infant_mortality life_expectancy fertility
  <fct>   <int>            <dbl>           <dbl>     <dbl>
1 Albania  1960            115.             62.9      6.19
2 Albania  1961            111.             63.9      6.08
3 Albania  1962            106.             64.8      5.96
4 Albania  1963            102.             65.6      5.83
5 Albania  1964             97.9            66.2      5.71
# … with 10,540 more rows, and 4 more variables:
#   population <dbl>, gdp <dbl>, continent <fct>, region <fct>
```

`select()`

- Chooses a subset of *columns* (don't mix up with `filter()`)

```
gapminder_plus %>%
  select(country, region, gdp_per_capita)
```

```
# A tibble: 10,545 x 3
  country             region          gdp_per_capita
  <fct>               <fct>                    <dbl>
1 Albania             Southern Europe             NA
2 Algeria             Northern Africa           1243.
3 Angola              Middle Africa               NA
4 Antigua and Barbuda Caribbean                   NA
5 Argentina           South America             5254.
# … with 10,540 more rows
```

Your Turn

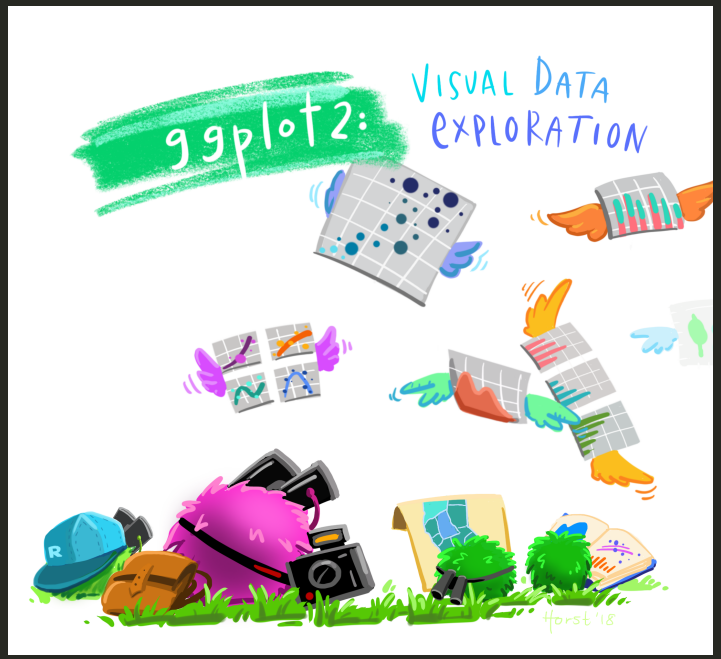
Exercise B - 5 minutes

1. Create a data frame that has the median life expectancy by year.
2. Use `arrange()` on this data frame to see the top years with the highest median life expectancy. What about the year with the lowest median life expectancy?
3. Create a new column that is median life expectancy rounded to the nearest integer, and remove the original un-rounded column with `select()`.

05:00

Walk through exercise in RStudio

Basics of {ggplot2}



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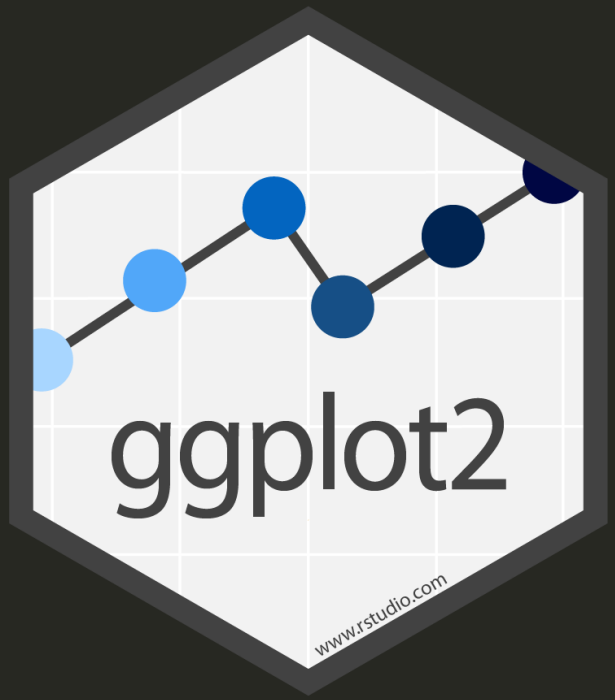


ggplot2 package

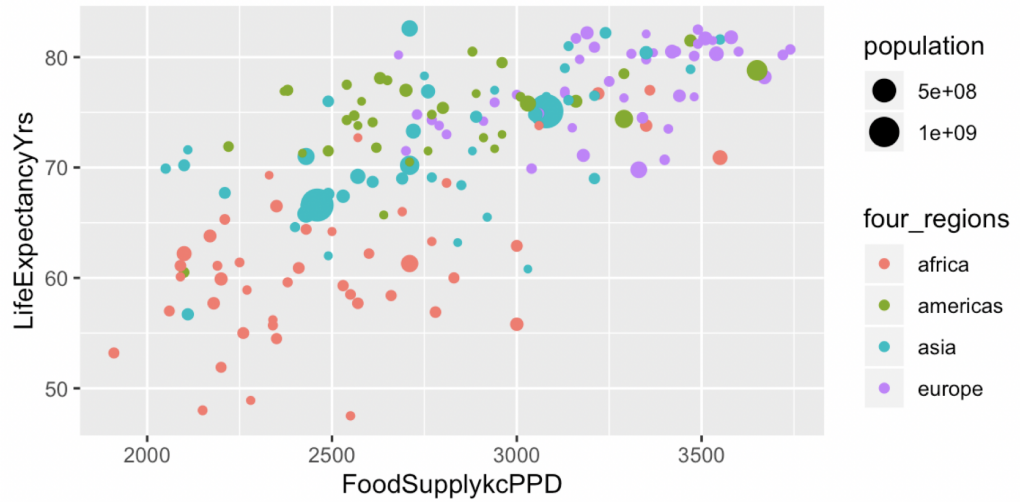
Function

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



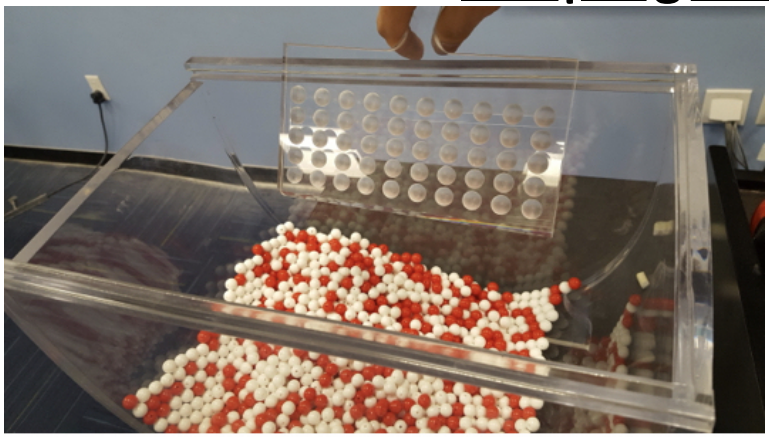
Learning objectives

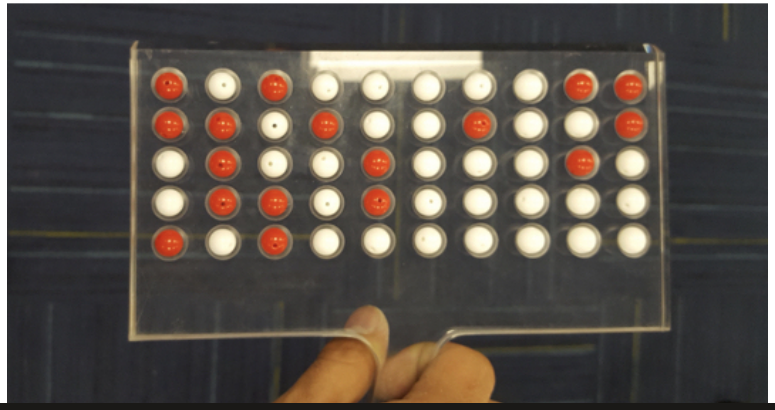
Part 2

- Build a sampling distribution by repeatedly sampling from a population using the {moderndive} package
- Compose a visualization of a sampling distribution
- Construct a bootstrap distributions for a basic confidence interval of a statistic
- Perform tidy hypothesis testing using the {infer} package

Extending this {tidyverse} knowledge to something new

- How can we now learn about sampling distributions?





```
library(moderndive)
bowl %>% slice_head(n = 15)
```

```
# A tibble: 15 x 2
   ball_ID color
     <int> <chr>
 1       1 white
 2       2 white
 3       3 white
 4       4 red
 5       5 white
 6       6 white
 7       7 red
 8       8 white
 9       9 red
10      10 white
11      11 white
12      12 white
13      13 white
14      14 white
15      15 red
```

One virtual scoop of 50 balls (one sample)

```
set.seed(8675309)
(jennys_sample <- bowl %>% slice_sample(n = 50))
```

```
# A tibble: 50 x 2
  ball_ID color
    <int> <chr>
1    2260 white
2     970 white
3    1291 white
4    1216 white
5    2217 red
# … with 45 more rows
```

Proportion that are red

```
jennys_sample %>%
  summarize(prop_red = mean(color == "red")) %>%
  pull()
```

```
[1] 0.32
```

Is this how many are in the full bowl?

Sampling variability

What does `rep_bowl_samples` look like?

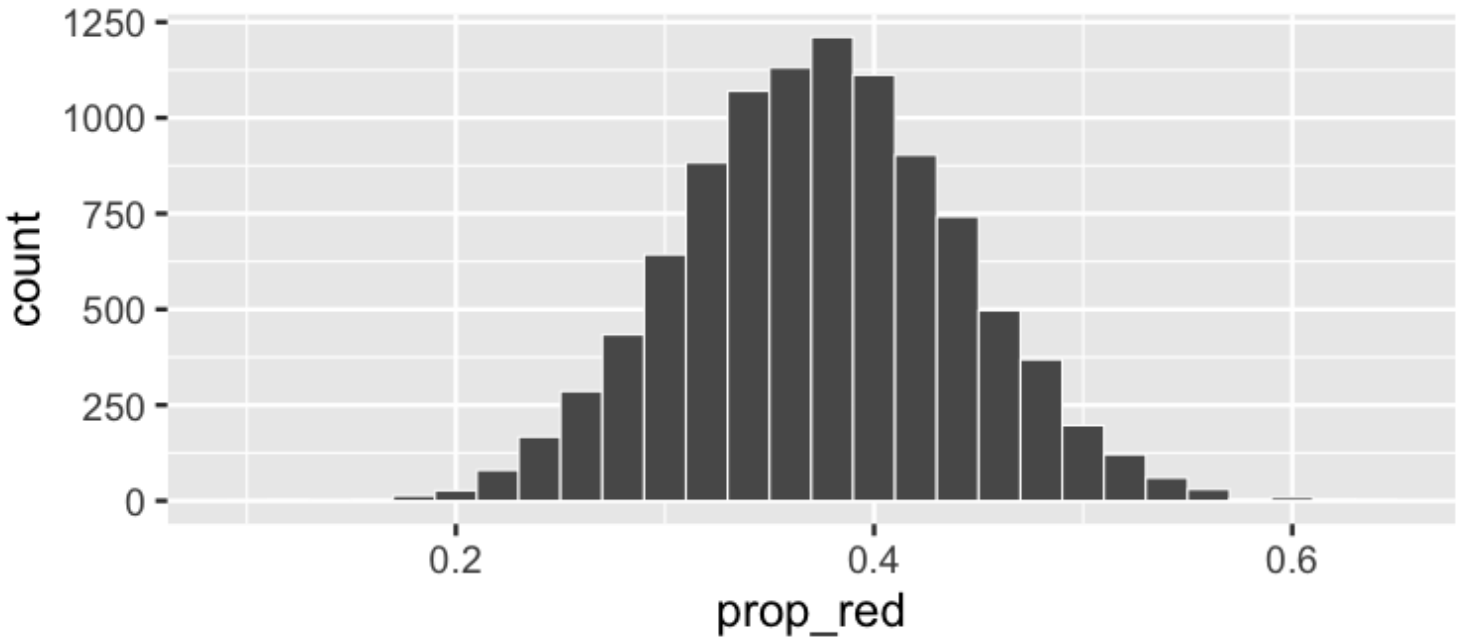
```
library(moderndive)
library(infer)
rep_bowl_samples <- bowl %>%
  rep_slice_sample(n = 50, reps = 10000)
```

How about `bowl_props`?

```
bowl_props <- rep_bowl_samples %>%
  group_by(replicate) %>%
  summarize(prop_red = mean(color == "red"))
```

The sampling distribution

```
ggplot(data = bowl_props, mapping = aes(x = prop_red)) +
  geom_histogram(binwidth = 0.02, color = "white")
```



Shifting focus

What about if all we had was the one sample of balls (not the whole bowl)?

```
jennys_sample %>% count(color)
```

```
# A tibble: 2 x 2
  color     n
* <chr> <int>
1 red      16
2 white    34
```

How could we use this sample to make a guess about the sampling variability from other samples?

Building up to statistical inference!

```
library(infer)
jennys_sample %>%
  specify(formula = color ~ NULL, success = "red")
```

```
Response: color (factor)
# A tibble: 50 x 1
  color
  <fct>
1 white
2 white
3 white
4 white
5 red
# … with 45 more rows
```

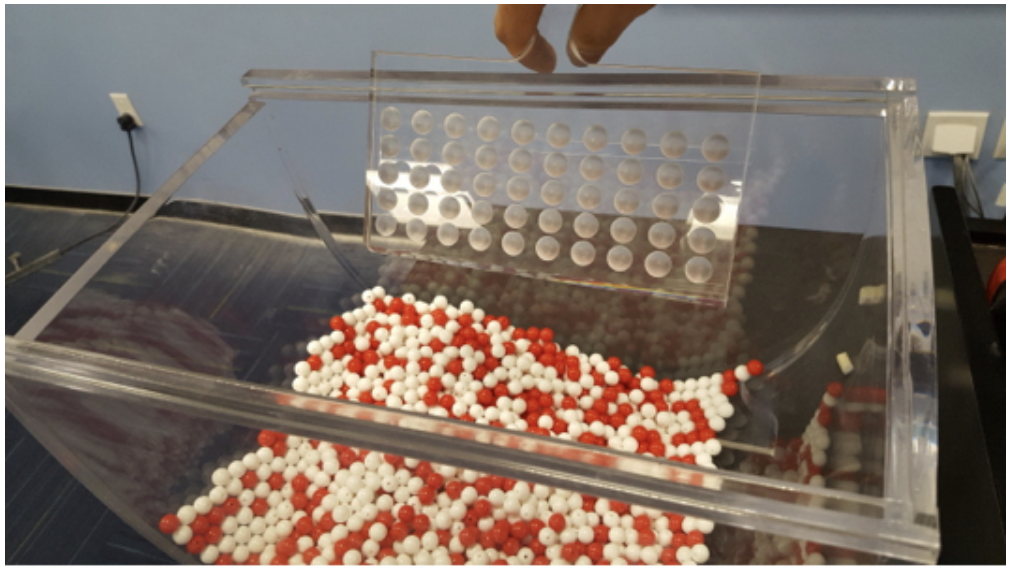
Bootstrapping?

```
library(infer)
(bootstrap_samples <- jennys_sample %>%
  specify(formula = color ~ NULL, success = "red") %>%
  generate(reps = 48, type = "bootstrap"))
```

```
Response: color (factor)
# A tibble: 2,400 x 2
# Groups:   replicate [48]
  replicate color
      <int> <fct>
1         1 red
2         1 white
3         1 white
4         1 white
5         1 white
# … with 2,395 more rows
```

What does `bootstrap_samples` represent?

- Remember we assumed that all we had was the original sample of 19 red and 31 white to start.
- Hope each selection in `bootstrap_samples` is similar to:



Bootstrap statistics

```
jennys_sample %>%
  specify(formula = color ~ NULL, success = "red") %>%
  generate(reps = 48, type = "bootstrap") %>%
  calculate(stat = "prop")
```

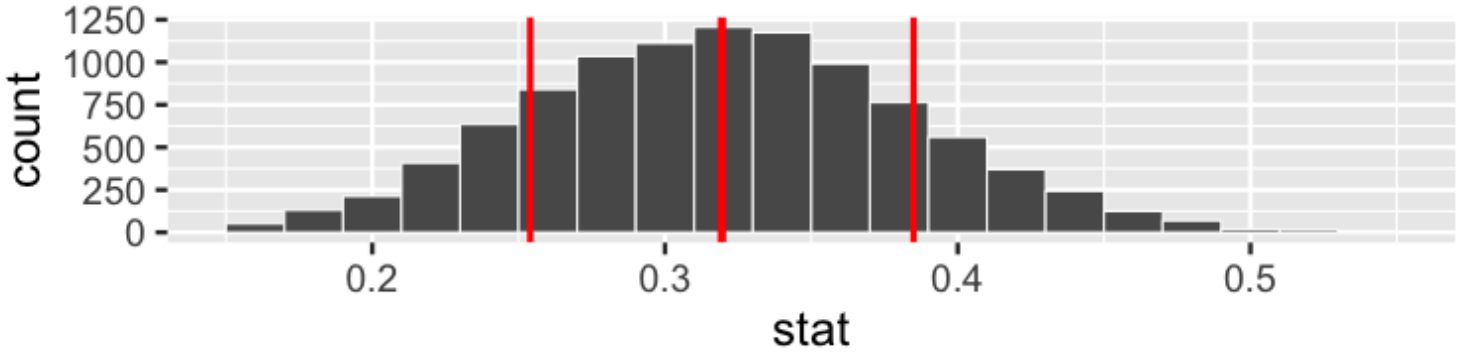
```
# A tibble: 48 x 2
  replicate  stat
*     <int> <dbl>
1         1  0.24
2         2  0.34
3         3  0.34
4         4  0.4
5         5  0.28
# … with 43 more rows
```

Do 10,000 reps to get a better sense for variability

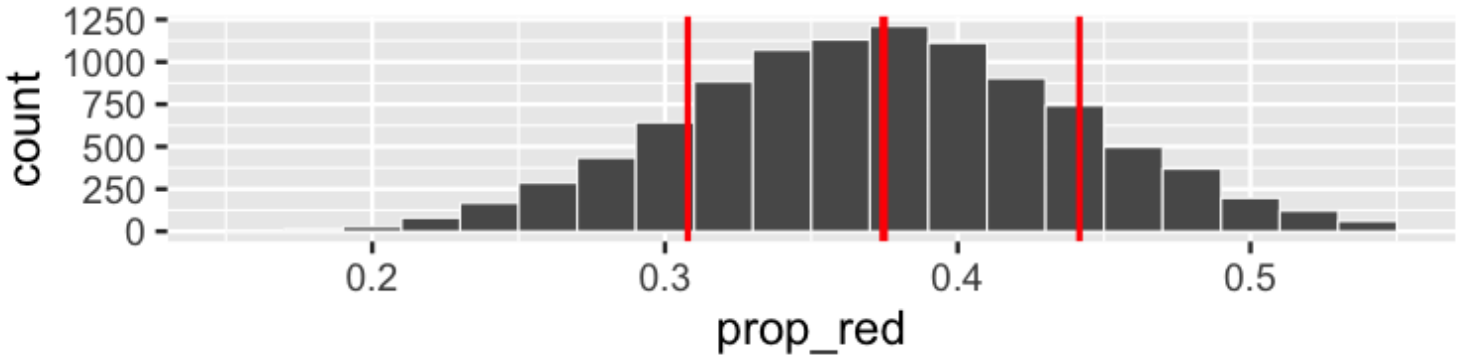
Just as we did with the sampling distribution

```
bootstrap_stats <- jennys_sample %>%
  specify(formula = color ~ NULL, success = "red") %>%
  generate(reps = 10000, type = "bootstrap") %>%
  calculate(stat = "prop")
```

The bootstrap distribution



The sampling distribution



Get a confidence interval

```
get_ci(bootstrap_stats, level = 0.95)
```

```
# A tibble: 1 x 2
  lower_ci upper_ci
     <dbl>    <dbl>
1      0.2     0.44
```

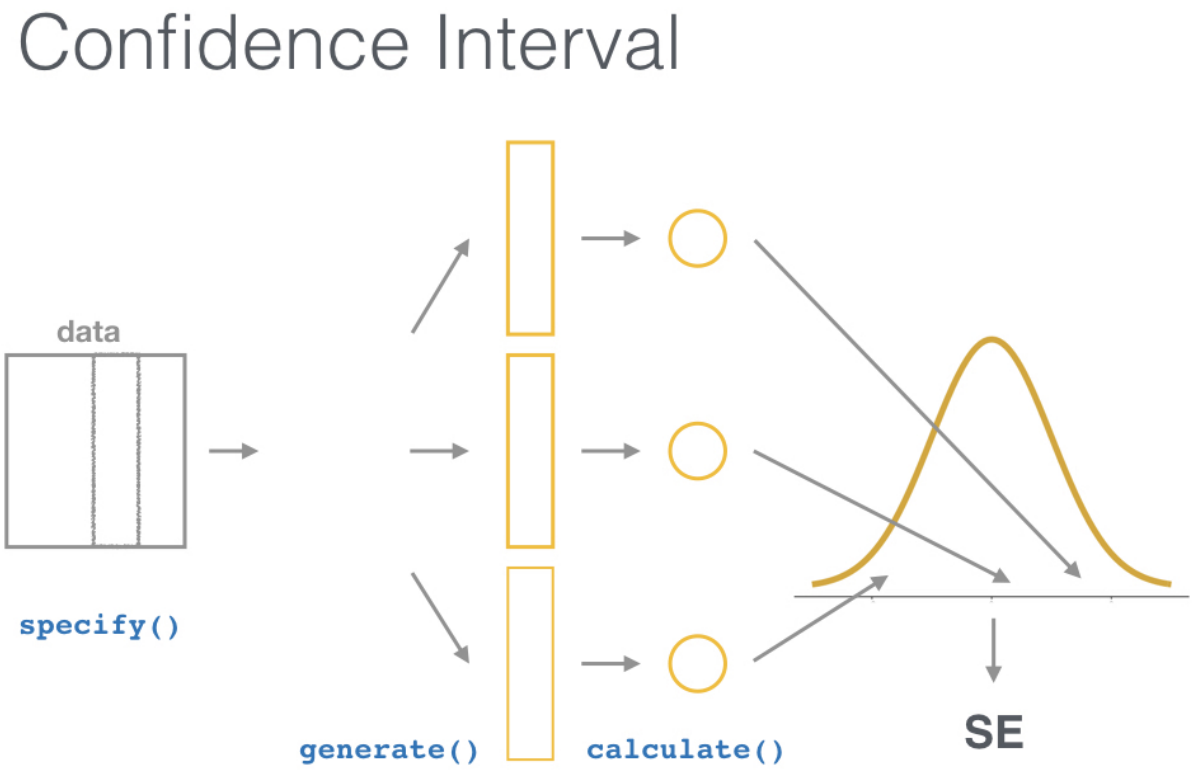
- We are 95% "confident" the true proportion of red balls in the hopper/bowl is between 0.2 and 0.44.

- In the population:

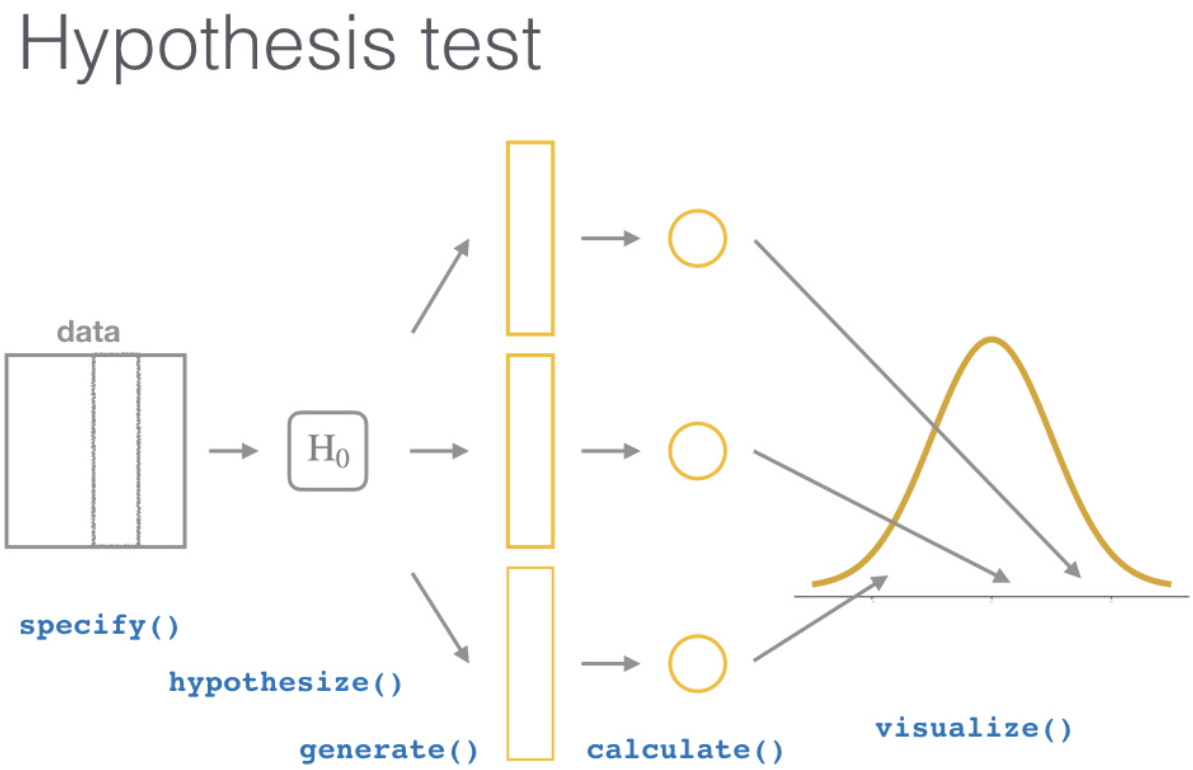
```
mean(bowl$color == "red")
```

```
[1] 0.375
```

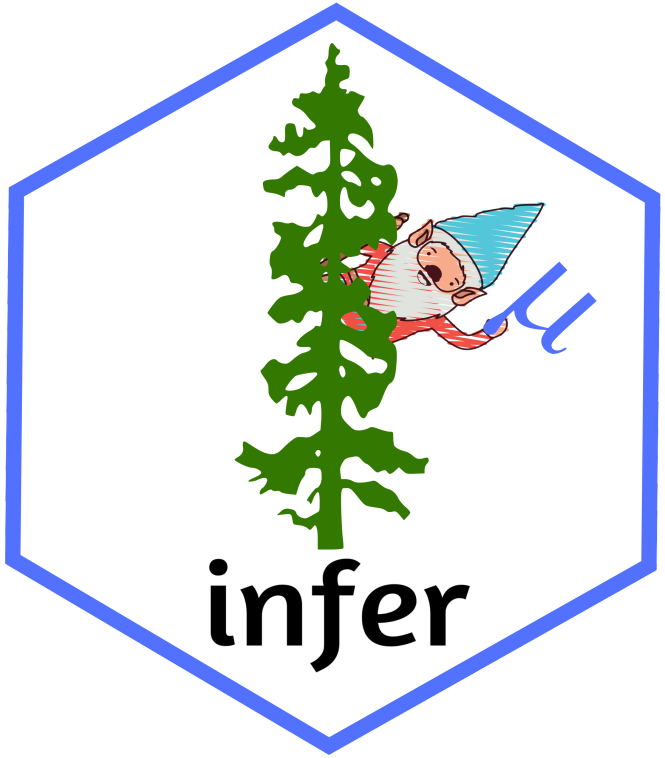
{infer} verbs



{infer} verbs


Hypothesis test
data
H_0
specify()
hypothesize()
generate()
calculate()
visualize()

Statistical Inference



{infer} hex sticker designs kindly created by Thomas Mock

Research Question

If you see someone else yawn, are you more likely to yawn? In an episode of the show *Mythbusters*, they tested the myth that yawning is contagious.

- 50 adults who thought they were being considered for an appearance on the show.
- Each participant was interviewed individually by a show recruiter ("confederate") who either yawned or did not.
- Participants then sat by themselves in a large van and were asked to wait.
- While in the van, the Mythbusters watched to see if the unaware participants yawned.

Data

- `group`
  - 34 saw the confederate yawn (`seed`)
  - 16 did not see the confederate yawn (`control`)
- `yawn`
  - `yes` - participant yawned
  - `no` - participant did not yawn

```
library(moderndive)
mythbusters_yawn %>% slice(c(1, 3, 6, 19))
```

```
# A tibble: 4 x 3
   subj group   yawn
  <int> <chr>   <chr>
1     1 seed    yes
2     3 seed    no
3     6 control no
4    19 control yes
```

Results


```
library(janitor)
mythbusters_yawn %>%
  tabyl(group, yawn) %>%
  adorn_percentages() %>%
  adorn_pct_formatting() %>%
  adorn_ns()
```

```
   group          no          yes
 control 75.0% (12) 25.0%  (4)
    seed 70.6% (24) 29.4% (10)
```

Finding: CONFIRMED

> "Though that's not an enormous increase, since they tested 50 people in the field, the gap was still wide enough for the MythBusters to confirm that yawning is indeed contagious." [1]

[1] http://www.discovery.com/tv-shows/mythbusters/mythbusters-database/yawning-contagious/

Really? Let's formally check this

- State the hypotheses

Null hypothesis:

> There is no difference between the seed and control groups in the proportion of people who yawned.

Alternative hypothesis (directional):

> More people (relatively) yawned in the seed group than in the control group.

Test the hypothesis

QUIZ: Which type of hypothesis test would you conduct here?

- A. Independent samples t-test
- B. Two proportion test
- C. Chi-square Goodness of Fit
- D. Analysis of Variance

Two proportion test

$$H_0 : p_{seed} - p_{control} = 0$$

$$H_A : p_{seed} - p_{control} > 0$$

The observed difference

```
library(infer)
obs_diff <- mythbusters_yawn %>%
  specify(yawn ~ group, success = "yes") %>%
  calculate(
    stat = "diff in props",
    order = c("seed", "control")
  )
obs_diff
```

```
# A tibble: 1 x 1
    stat
   <dbl>
1 0.0441
```

Is this difference *meaningful*?

Different question:

Is this difference *significant*?

Modeling the null hypothesis

If...

$$H_0 : p_{seed} = p_{control}$$

is true, then whether or not the participant saw someone else yawn does not matter.

In other words, there is no association between exposure and yawning.

Original universe

subj	group	yawn
1	seed	yes
2	control	yes
3	seed	no
4	seed	yes
5	seed	no
6	control	no
15	seed	no
16	seed	no
17	seed	no
18	seed	no
19	control	yes
20	seed	no

```
   group no yes Total
control 12   4    16
   seed 24  10    34
  Total 36  14    50
```

Parallel universe

subj	group	alt_yawn
1	seed	no
2	control	no
3	seed	no
4	seed	no
5	seed	no
6	control	no
15	seed	no
16	seed	yes
17	seed	no
18	seed	yes
19	control	no
20	seed	yes

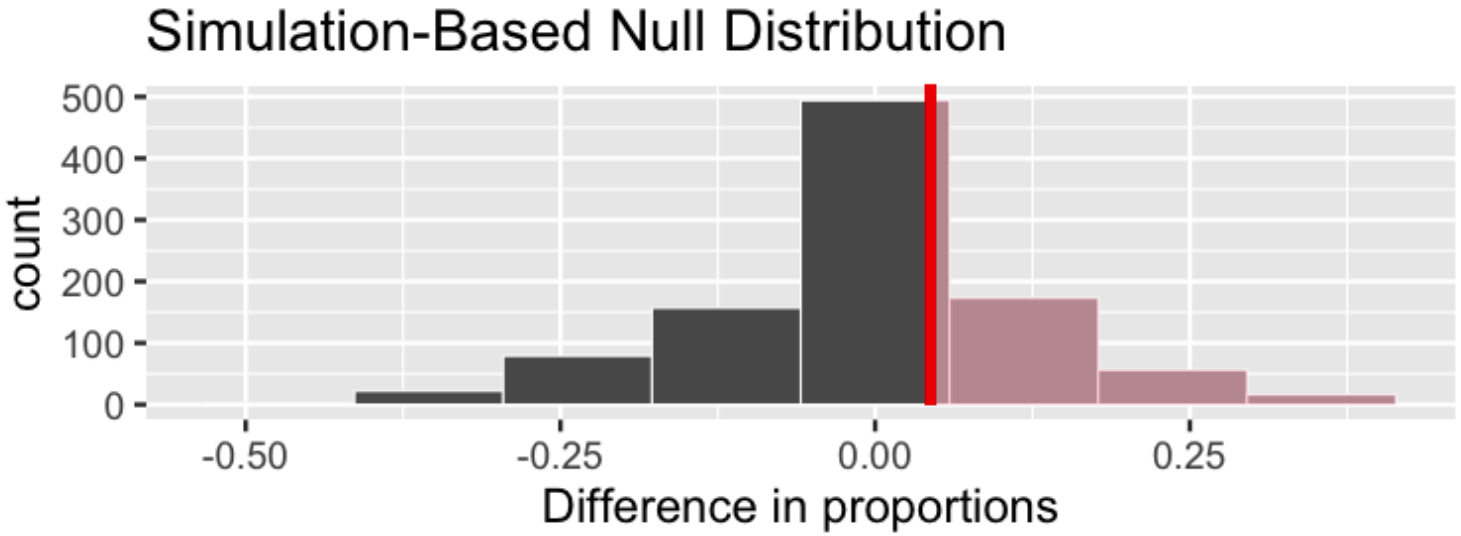
```
   group no yes Total
control 12   4    16
   seed 24  10    34
  Total 36  14    50
```

1000 parallel universes

replicate	stat
1	0.22794
2	0.41176
3	0.04412
4	0.04412
5	-0.04779
6	0.13603
7	-0.23162
8	0.22794
9	-0.04779
10	0.04412
11	0.13603
12	0.04412
13	0.04412
14	-0.04779
15	-0.13971

replicate	stat
986	0.04412
987	-0.13971
988	0.04412
989	-0.23162
990	-0.04779
991	-0.13971
992	-0.13971
993	-0.13971
994	0.04412
995	-0.13971
996	-0.23162
997	0.13603
998	-0.04779
999	0.04412
1000	0.04412

The parallel universe distribution



The distribution of 1000 differences in proportions, if the null hypothesis were *true* and yawning was not contagious.

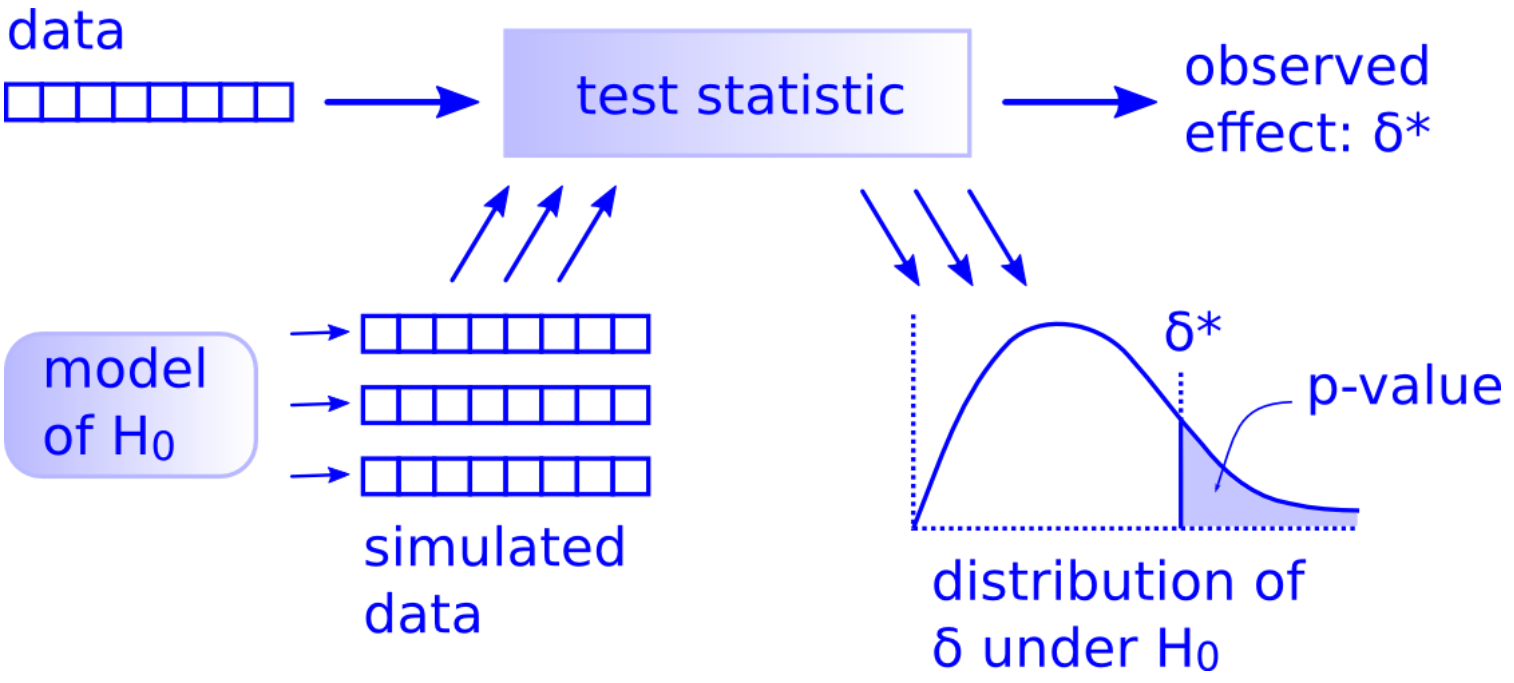
Calculating the p-value

The shaded proportion is the p-value!

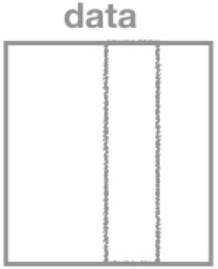
```
null_distn %>%
  get_p_value(obs_stat = obs_diff, direction = "right")
```

```
# A tibble: 1 x 1
  p_value
    <dbl>
1   0.493
```

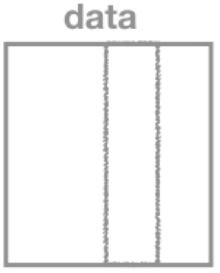
There is Only One Test!



Hypothesis test

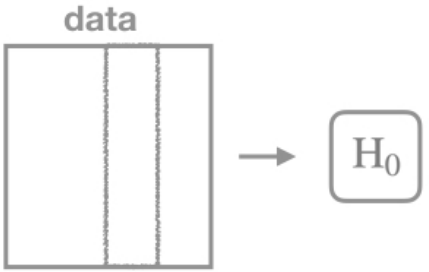


Hypothesis test



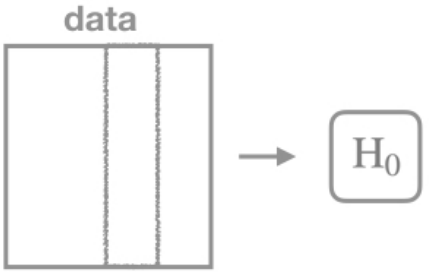

```
specify()
```

Hypothesis test




```
specify()
```

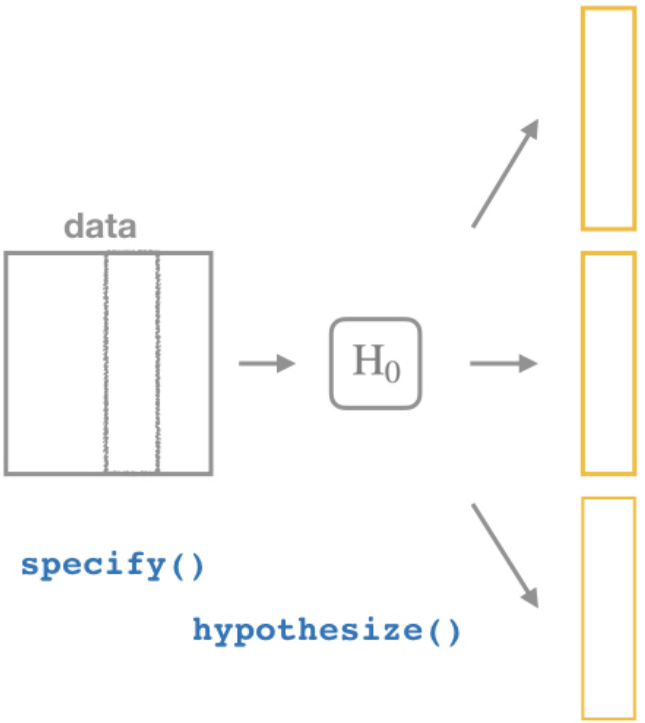
Hypothesis test



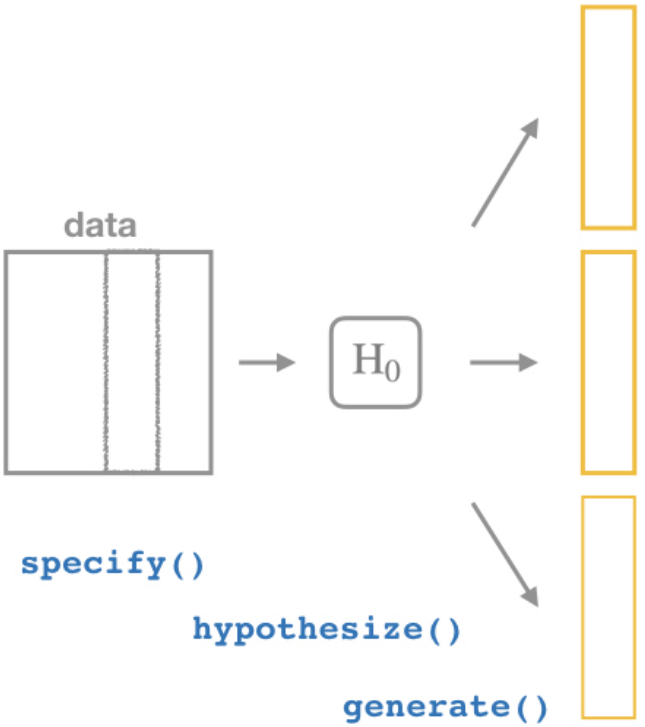

```
specify()
```

```
hypothesize()
```

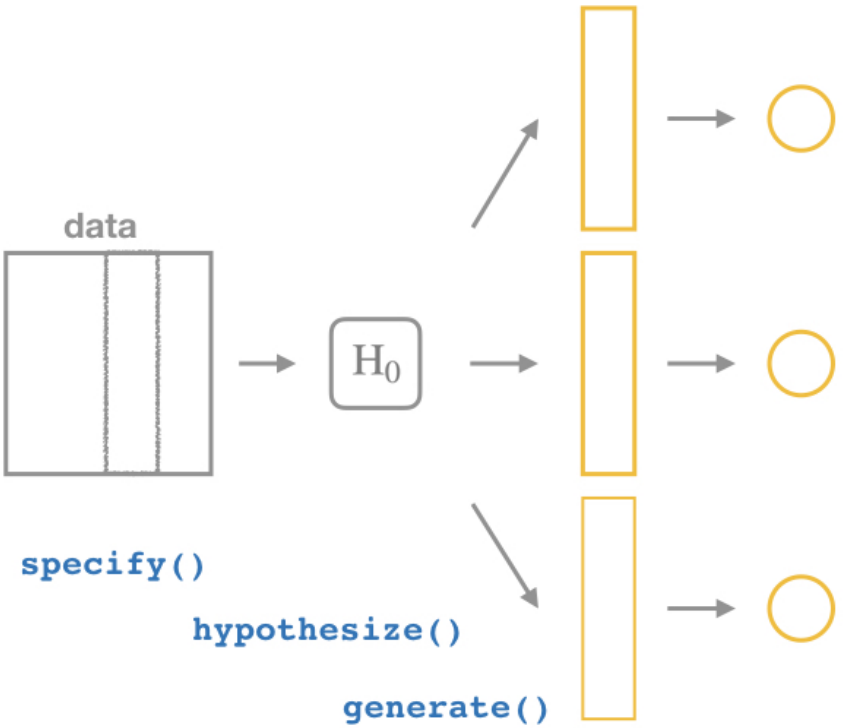
Hypothesis test



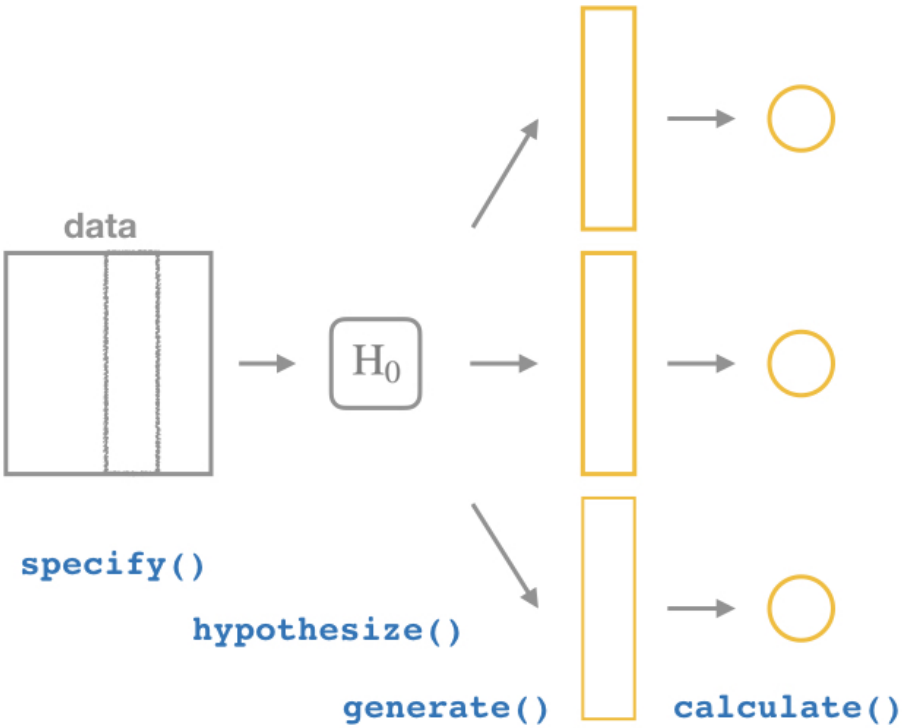
Hypothesis test



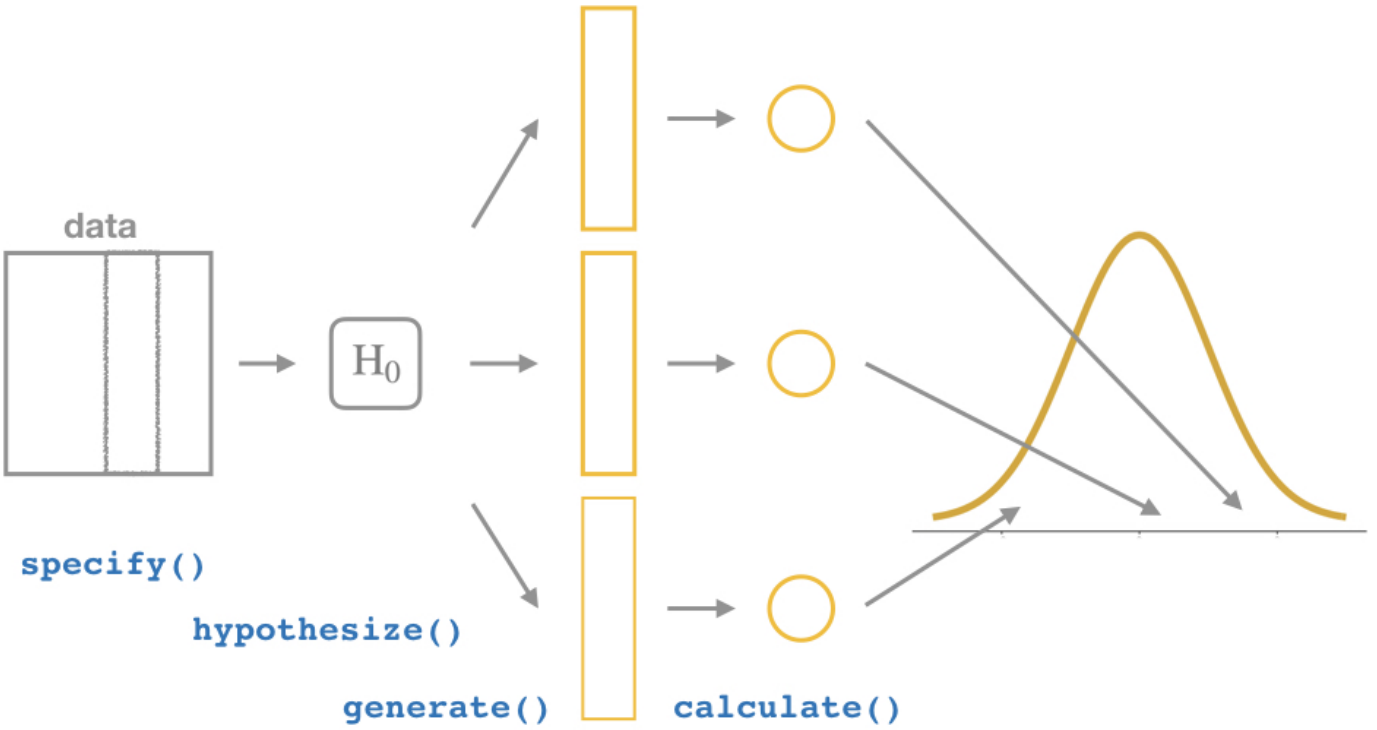
Hypothesis test



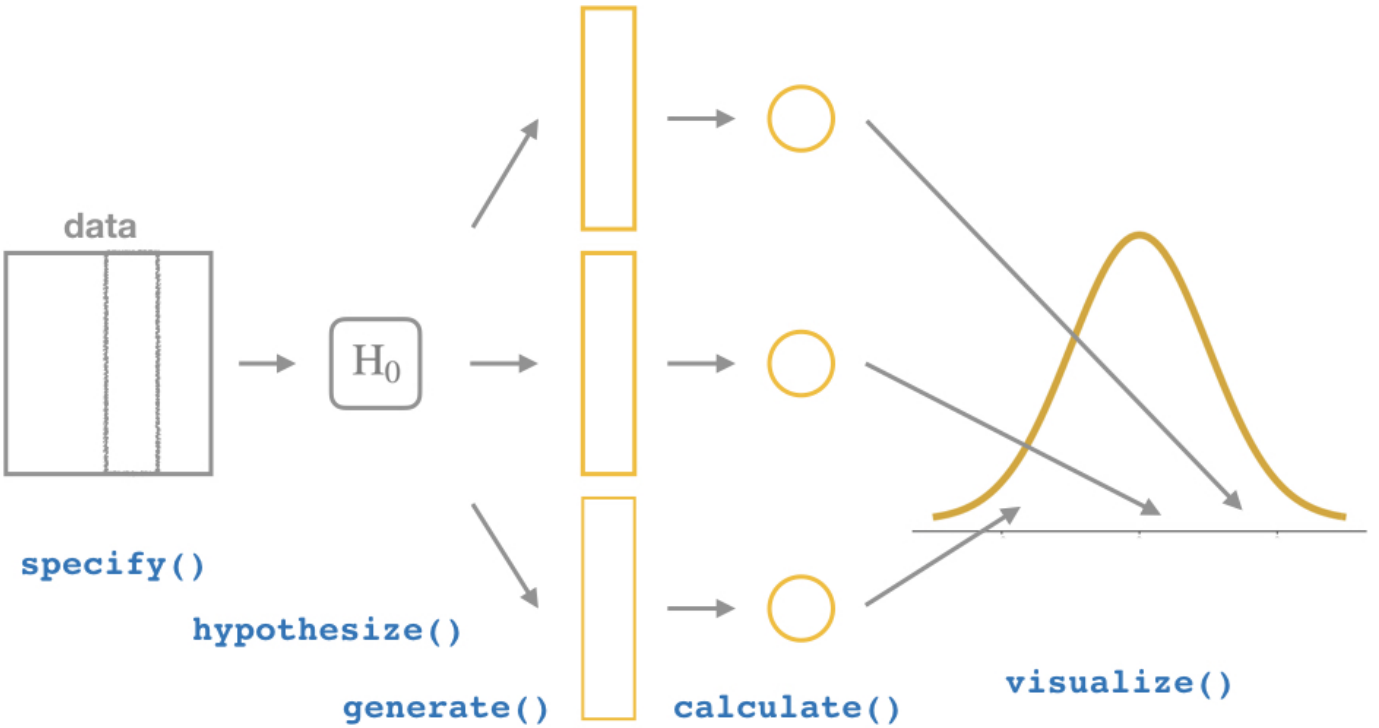
Hypothesis test



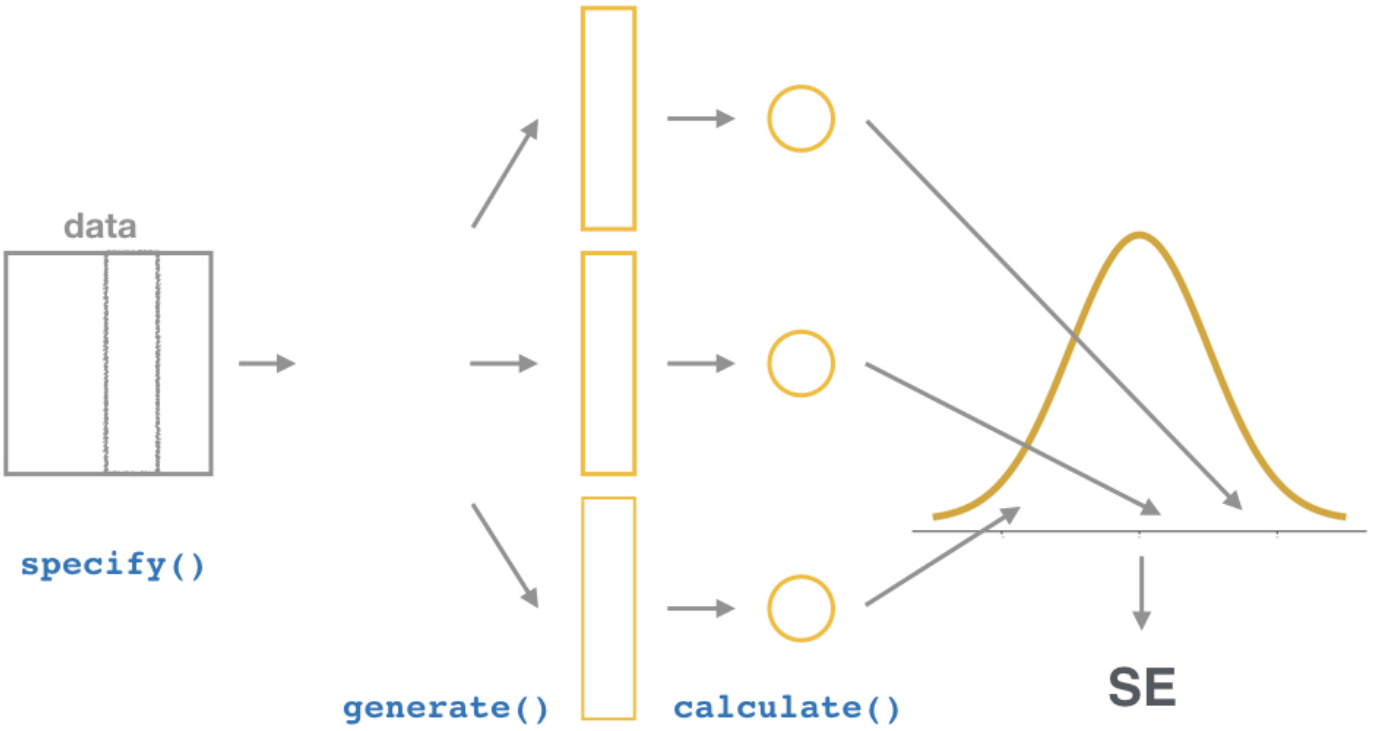
Hypothesis test



Hypothesis test



Confidence Interval



{infer}

Five main functions:

- `specify()`
- `hypothesize()`
- `generate()`
- `calculate()`
- `visualize()`

{infer}

- `specify()` the response and explanatory variables (`y ~ x`)
- `hypothesize()` what the null hypothesis is (here, `independence` of `y` and `x`)
- `generate()` new samples from parallel universes under the null hypothesis model:
    - Resample from our original data without replacement, each time shuffling the `group` (`type = "permute"`)
    - Do this a ton of times (`reps = 1000`)
- `calculate()` the statistic (`stat = "diff in props"`) for each of the `reps`

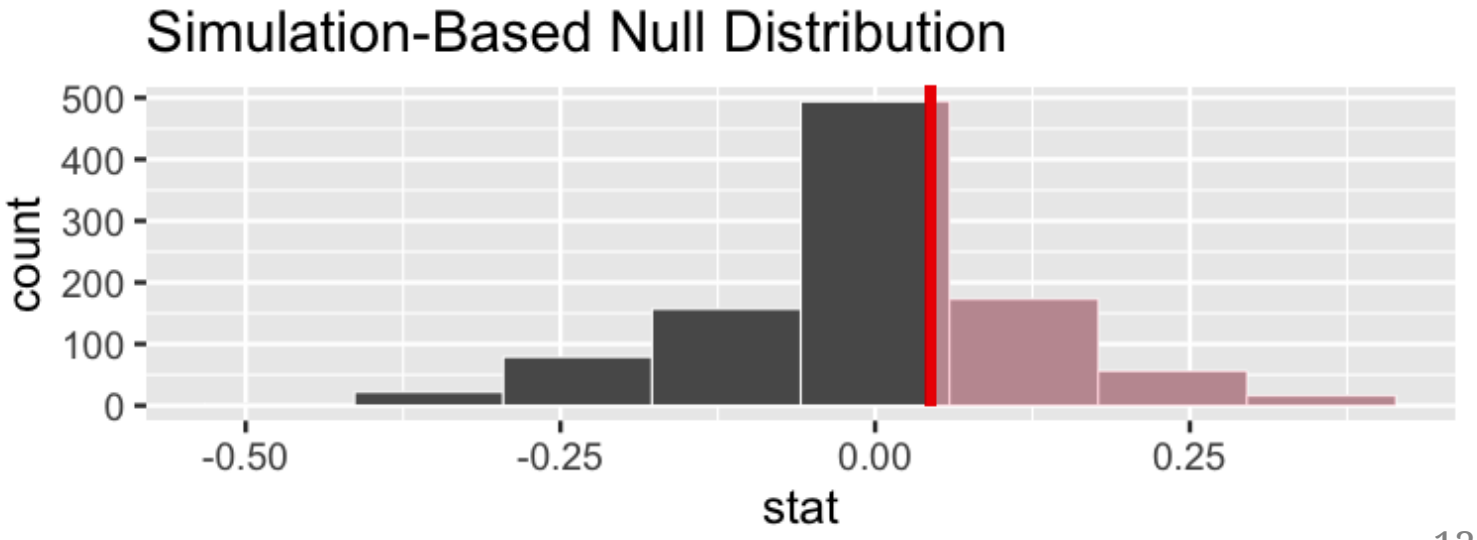
{infer} example

```
set.seed(8)
null_distn <- mythbusters_yawn %>%
  specify(
    formula = yawn ~ group,
    success = "yes"
  ) %>%
  hypothesize(null = "independence") %>%
  generate(reps = 1000, type = "permute") %>%
  calculate(
    stat = "diff in props",
    order = c("seed", "control")
  )
```

Visualize the null distribution

- `visualize()` the distribution of the `stat` (here, `diff in props`)

```
null_distn %>%
  visualize(bins = 8) +
  shade_p_value(obs_stat = obs_diff, direction = "right")
```



Classical inference

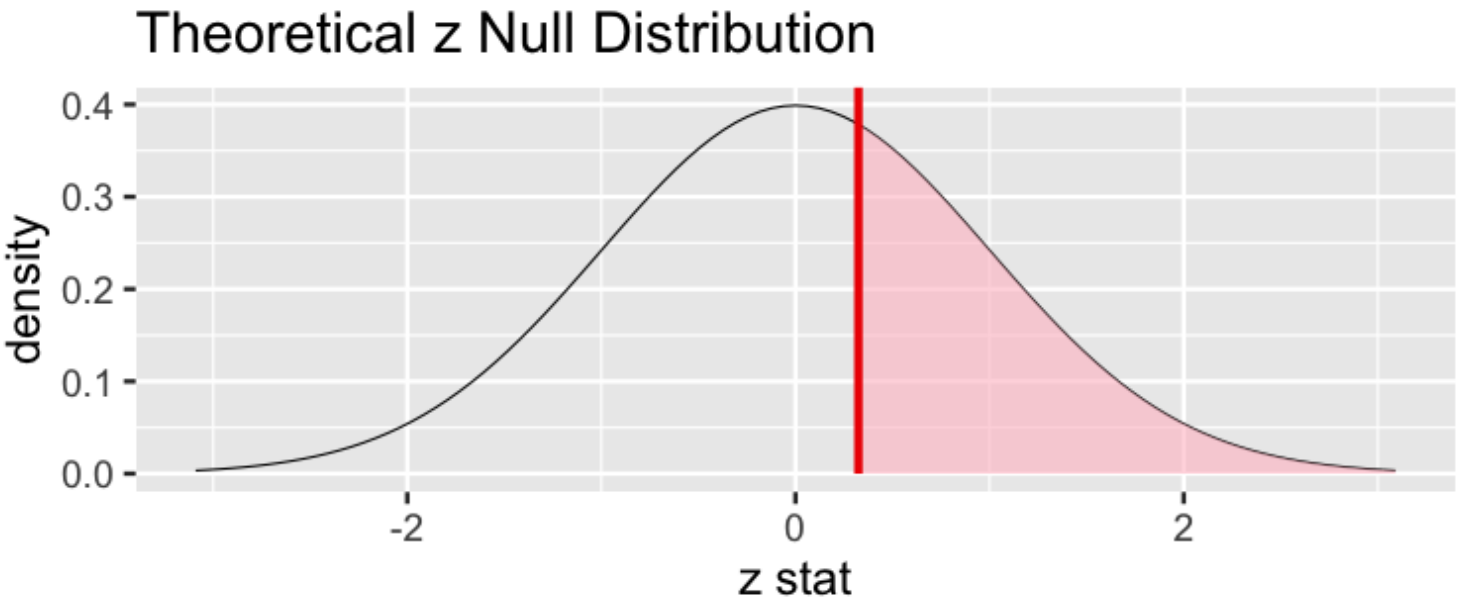
Rely on theory to tell us what the null distribution looks like.

```
obs_z <- mythbusters_yawn %>%
  specify(yawn ~ group, success = "yes") %>%
  calculate(stat = "z", order = c("seed", "control"))

mythbusters_yawn %>%
  specify(yawn ~ group, success = "yes") %>%
  hypothesize(null = "independence") %>%
  # generate() is not needed since we are not simulating
  calculate(stat = "z", order = c("seed", "control")) %>%
  visualize(method = "theoretical")
  shade_p_value(obs_stat = obs_z, direction = "right")
```

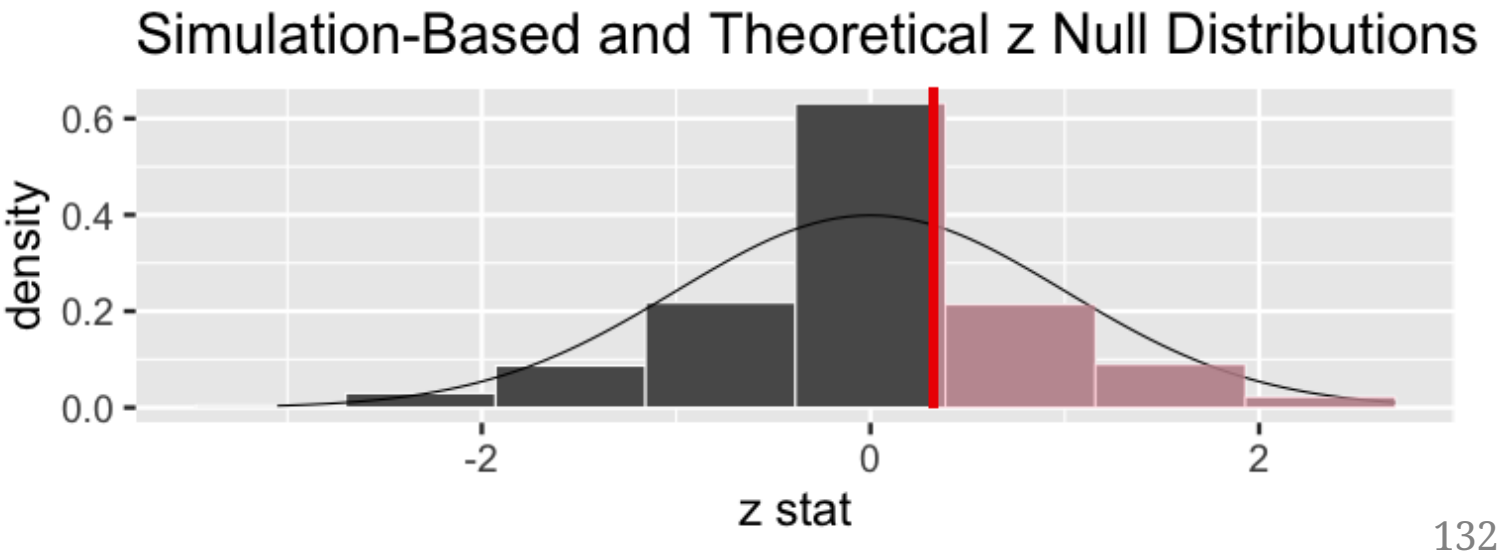
Classical inference

```
Warning: Check to make sure the conditions have been met for the
theoretical method. {infer} currently does not check these for
you.
```



Simulation-based vs Classical (`stat = "z"`)

```
mythbusters_yawn %>%
  specify(yawn ~ group, success = "yes") %>%
  hypothesize(null = "independence") %>%
  generate(reps = 1000, type = "permute") %>%
  calculate(stat = "z", order = c("seed", "control")) %>%
  visualize(method = "both", bins = 8) +
  shade_p_value(obs_stat = obs_z, direction = "right")
```



More info and resources

- https://infer.tidymodels.org/
  - Many examples under Articles
  - Discussed in www.ModernDive.com
    - Sign up to the mailing list for updates
- Learn the tidyverse

Any questions?

- Slides created via the R package xaringan by Yihui Xie
- Slides' source code at https://github.com/ismayc/talks/
- R code from throughout the slides as an R script here

Thanks!

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Appendix

Freely available information

ModernDive

Statistical Inference via Data Science
A ModernDive into R and the Tidyverse

- Webpage: https://moderndive.com
- Developmental version: https://moderndive.netlify.app
- GitHub Repo
- Please signup for our mailing list!

Good practices in RStudio

Use projects (read this)

- Create an RStudio project for each data analysis project
- A project is associated with a directory folder
  - Keep data files there
  - Keep scripts there; edit them, run them in bits or as a whole
  - Save your outputs (plots and cleaned data) there
- Only use relative paths, never absolute paths
  - relative (good): `read_csv("data/mydata.csv")`
  - absolute (bad):

```
read_csv("/home/yourname/Documents/stuff/mydata.csv")
```

Advantages of using RStudio projects

- standardize file paths
- keep everything together
- a whole folder can be shared and run on another computer

Useful keyboard shortcuts

action	mac	windows/linux
run code in script	cmd + enter	ctrl + enter
`<-`	option + -	alt + -
`%>%`	cmd + shift + m	ctrl + shift + m

Try typing (with shortcut) and running

```
y <- 5
y
```

Now, in the console, press the up arrow.

Other keyboard shortcuts: (see full list)

action	mac	windows/linux
interrupt currently executing command	esc	esc
in console, go to previously run code	up/down	up/down
keyboard shortcut help	option + shift + k	alt + shift + k