

Testing Hypothesis and Measuring Confidence

Week 9

Packages needed and a Note about Icons

Please load up the following packages. Remember to first install the ones you don't have.

You may come across the following icons. The table below lists what each means.

Icon	Description
▶	Indicates that an example continues on the following slide.
■	Indicates that a section using common syntax has ended.
🔗	Indicates that there is an active hyperlink on the slide.
📗	Indicates that a section covering a concept has ended.

What is a confidence interval?

A *confidence interval* (CI) gives a range of possible values for a parameter. It depends on a specified *confidence level* with

- higher confidence levels corresponding to wider confidence intervals and
- lower confidence levels corresponding to narrower confidence intervals.

The most common confidence levels include 90%, 95%, and 99%.

Problems with how confidence intervals are taught

Not to trash your professor, but you were taught about the confidence interval in an bad way! Traditionally, the approach to finding confidence intervals for some mean is to first assume a normal curve for a population and then magic. Sure its easy enough to follow procedurally, but the process is nether intuitive nor is it fantastic for people whose strong suit isn't mathematics.

Enter a fancy term called bootstrapping (that you've already been doing)

In most studies, we simply want to if our null or alternative hypothesis is correct. More than that, the overall purpose of a hypothesis test is to answer this for an entire population, using the data we have - ergo to generalize.

We typically only have a sample of the population's data to work with^[If we had the population, there's not much of a purpose to generalize]. So working with what we have in the most efficient and useful way is essential. Recently you

1. took repeated samples from a sample data of size whatever,
2. calculate the mean for each of these samples,
3. created a new distribution of these means, and
4. hopefully recognized with enough of these sample means, you can actually estimate the population distribution.

That is what is known as **bootstrapping**

ggplot2movies

We'll look at CIs, but first let's look at the `ggplot2movies` data set...

```
head(movies)
```

```
## # A tibble: 6 x 24
##   title    year  length budget rating votes   r1   r2   r3   r4   r5
##   <chr>   <int>  <int>   <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
## 1 $      1971     121     NA     6.4    348    4.5    4.5    4.5    4.5   14.5   24
## 2 $1000... 1939      71     NA      6     20     0     14.5    4.5   24.5   14.5   14
## 3 $21 a... 1941       7     NA     8.2     5     0     0     0     0     0     0     24
## 4 $40,0... 1996      70     NA     8.2     6    14.5     0     0     0     0     0
## 5 $50,0... 1975      71     NA     3.4    17    24.5    4.5     0   14.5   14.5   4
## 6 $pent   2000      91     NA     4.3    45    4.5    4.5    4.5   14.5   14.5   14
## # ... with 12 more variables: r7 <dbl>, r8 <dbl>, r9 <dbl>, r10 <dbl>,
## #   mpaa <chr>, Action <int>, Animation <int>, Comedy <int>, Drama <int>,
## #   Documentary <int>, Romance <int>, Short <int>
```

...its size...

```
dim(movies)
```

```
## [1] 58788     24
```

That's 58,788 rows by 24 columns!

... and the names of its columns.

```
names(movies)
```

```
## [1] "title"          "year"           "length"         "budget"        "rating"  
## [6] "votes"          "r1"             "r2"             "r3"            "r4"  
## [11] "r5"             "r6"             "r7"             "r8"            "r9"  
## [16] "r10"            "mpaa"           "Action"         "Animation"     "Comedy"  
## [21] "Drama"          "Documentary"    "Romance"       "Short"
```

You can see more about the functionality by looking at its [documentation](#). For now, here's what the variables mean:

- **title**. Title of the movie.
- **year**. Year of release.
- **budget**. Total budget (if known) in US dollars
- **length**. Length in minutes.
- **rating**. Average IMDB user rating.
- **votes**. Number of IMDB users who rated this movie.
- **r1-10**. Multiplying by ten gives percentile (to nearest 10%) of users who rated this movie a 1.
- **mpaa**. MPAA rating.
- **Action, Animation, Comedy, Drama, Documentary, Romance, Short**. Binary variables representing if movie was classified as belonging to that genre.



Descriptives

Let's take a look at a bar chart of the genres. But wait, those are in a bunch of columns and R likes its data in long form! To get the data set to this form, let's first select the columns we need and then use a command called `pivot_longer` which emulates a pivot table in Excel.

```
movies %>%
  select(Action, Animation, Comedy,
         Drama, Documentary, Romance, Short) %>%
  pivot_longer(
    everything(),
    names_to = "genre"
  )
```

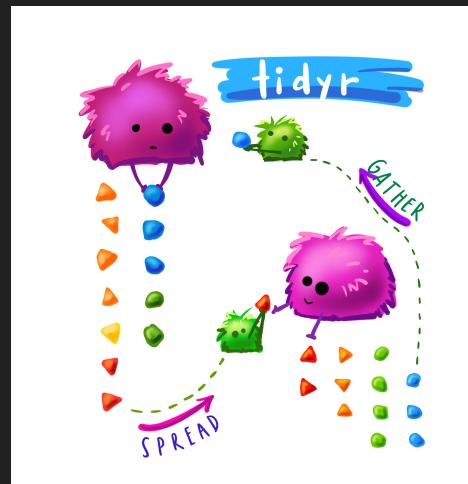


```
## # A tibble: 411,516 x 2
##   genre      value
##   <chr>     <int>
## 1 Action      0
## 2 Animation    0
## 3 Comedy       1
## 4 Drama        1
## 5 Documentary  0
## 6 Romance      0
## 7 Short        0
## 8 Action       0
## 9 Animation    0
## 10 Comedy      1
## # ... with 411,506 more rows
```

In instances where we have to go from a long to wide data set, we'd use a command called `pivot_wider`.

What Just Happened?

The previous iteration of `pivot_wider` and `pivot_longer` were given by the commands `gather` and `spread`. To see what these did, let's start out with a cartoon by the talented [Allison Horst](#) out of UC Santa Barbara.



So the commands basically took data frames from wide to long with `gather` and back again with `spread`. The `pivot_` commands do much the same but with much more flexibility. However they can be equally as confusing so we'll go over a few basics here. If you're interested in more, take a look at this fantastic overview courtesy of [R-Ladies Sydney](#). For an advanced walkthrough, the [Data Wrangling](#) site over at Stanford is a great resource.



pivot_longer

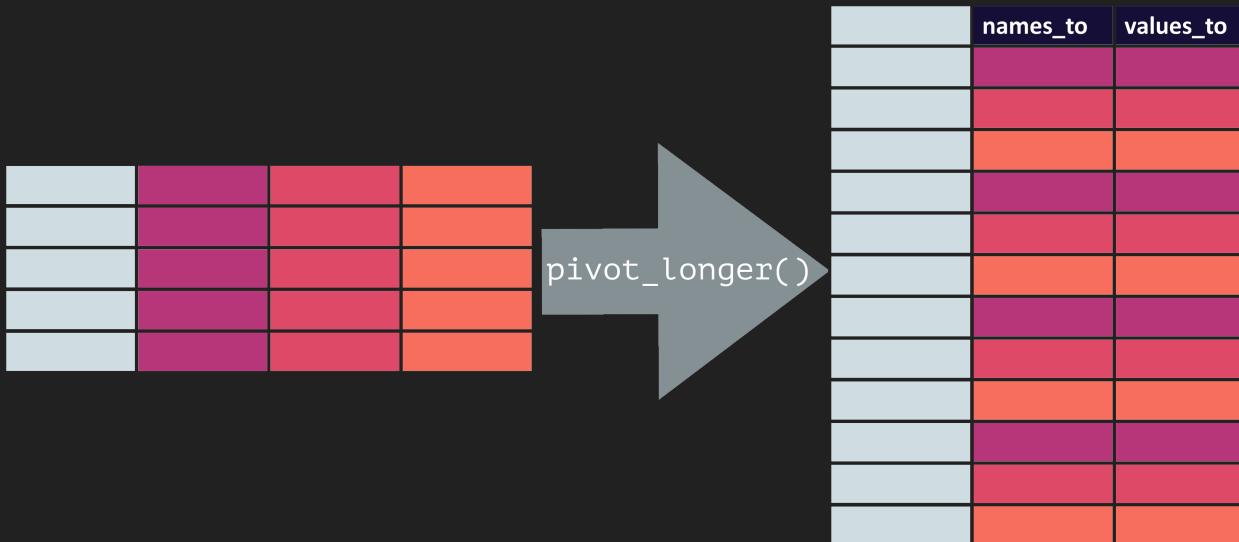
It is pretty rare that at this stage in your academic development that you need to go from long to wide so we'll be concentrating on the converse with `pivot_longer`. First note that the original graphics in this part of the walkthrough were not created by me, but by RStudio's [Allison Hill](#). I did however amend them for aesthetic purposes.

Ok let's begin!



An overview of pivot_longer

We'll concentrate one two options in `pivot_longer`: `names_to` and `values_to`.



Remember you can always run `?` in front of any command in the Console to get more information about it. For `pivot_longer`, we would simply type in

```
?pivot_longer
```

to see other options.

If you want to follow along with the fake data set we'll be using, run the following command to build the tibble

```
juniors_multiple <- tribble(  
  ~ "baker", ~"cinnamon_1", ~"cardamom_2", ~"nutmeg_3",  
  "Emma", 1L, 0L, 1L,  
  "Harry", 1L, 1L, 1L,  
  "Ruby", 1L, 0L, 1L,  
  "Zainab", 0L, NA, 0L  
)
```

and check it just to make sure

```
juniors_multiple
```

```
## # A tibble: 4 x 4  
##   baker  cinnamon_1 cardamom_2 nutmeg_3  
##   <chr>      <int>      <int>      <int>  
## 1 Emma        1          0          1  
## 2 Harry       1          1          1  
## 3 Ruby        1          0          1  
## 4 Zainab      0         NA          0
```

Looks good! Let's convert this!



To remind you of what the `juniors_multiple` data frame looks like, we have

	baker	cinnamon_1	cardamom_2	nutmeg_3
Emma		1	0	1
Harry		1	1	1
Ruby		1	0	1
Zainab		0	NA	0

We can assign names to the eventual columns using `names_to` and `values_to`.

The diagram illustrates the flow of data through a series of arrows:

- A vertical arrow labeled "Data you have" points down to the code.
- A vertical arrow labeled "Columns you have" points down to the code.
- A horizontal arrow labeled "Cell values go to..." points up from the bottom of the code block.
- A horizontal arrow labeled "Column names go to..." points right from the "names_to" argument in the code.

```
juniors_untidy %>%
  pivot_longer(cinnamon_1:nutmeg_3,
    names_to = 'spice', ← ..... Column names go to...
    values_to = 'correct'
  )
```

Cell values go to...

Column names go to...



	baker	cinnamon_1	cardamom_2	nutmeg_3
Emma		1	0	1
Harry		1	1	1
Ruby		1	0	1
Zainab		0	NA	0

We can assign names to the eventual columns using `names_to` and `values_to`.

baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry	1	1	1
Ruby	1	0	1
Zainab	0	NA	0

baker	spice	correct
Emma	cinnamon_1	1
Emma	cardamom_2	0
Emma	nutmeg_3	1
Harry	cinnamon_1	1
Harry	cardamom_2	1
Harry	nutmeg_3	1
Ruby	cinnamon_1	1
Ruby	cardamom_2	0
Ruby	nutmeg_3	1
Zainab	cinnamon_1	0
Zainab	cardamom_2	NA
Zainab	nutmeg_3	0

```
pivot_longer(cinnamon_1:nutmeg_3,
             names_to = 'spice',
             values_to = 'correct')
```



	baker	cinnamon_1	cardamom_2	nutmeg_3
Emma		1	0	1
Harry		1	1	1
Ruby		1	0	1
Zainab		0	NA	0

Here you can see the first column `cinnamon_1` and its value `1` associated with the first row `Emma` becomes our first two values under the two columns `spice` and `correct` for our pivoted data frame.

baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry		1	1
Ruby		0	1
Zainab		NA	0

baker	spice	correct
Emma	cinnamon_1	1
Emma	cardamom_2	0
Emma	nutmeg_3	1
Harry	cinnamon_1	1
Harry	cardamom_2	1
Harry	nutmeg_3	1
Ruby	cinnamon_1	1
Ruby	cardamom_2	0
Ruby	nutmeg_3	1
Zainab	cinnamon_1	0
Zainab	cardamom_2	NA
Zainab	nutmeg_3	0

```

pivot_longer(cinnamon_1:nutmeg_3,
             names_to = 'spice',
             values_to = 'correct')
  
```



This pattern continues until a whole row is used up.

baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry		1	1
Ruby		0	1
Zainab		NA	0

baker	spice	correct
Emma	cinnamon_1	1
Emma	cardamom_2	0
Emma	nutmeg_3	1
Harry	cinnamon_1	1
Harry	cardamom_2	1
Harry	nutmeg_3	1
Ruby	cinnamon_1	1
Ruby	cardamom_2	0
Ruby	nutmeg_3	1
Zainab	cinnamon_1	1
Zainab	cardamom_2	NA
Zainab	nutmeg_3	0

```
pivot_longer(cinnamon_1:nutmeg_3,  
             names_to = 'spice',  
             values_to = 'correct')
```



Then it repeats for the next row of values...

A diagram illustrating the first step of pivoting. On the left, a table shows the initial state with columns 'baker', 'cinnamon_1', and 'nutmeg_3'. A dotted arrow points from the 'cinnamon_1' column to the right, where a new table is shown with columns 'baker', 'spice', and 'correct'. The 'cinnamon_1' column has been renamed to 'spice' and its values have been moved to the 'correct' column.

baker	cinnamon_1	nutmeg_3
Emma		
Harry	1	
Ruby		
Zoë		

baker	spice	correct
Emma		
Harry	cinnamon_1	1
Ruby		
Zoë		

pivot_longer(cinnamon_1:nutmeg_3,
names_to = 'spice',
values_to = 'correct')

A diagram illustrating the second step of pivoting. On the left, a table shows the state after the first pivot, with columns 'baker', 'cinnamon_1', 'cardamom_2', and 'nutmeg_3'. A dotted arrow points from the 'cardamom_2' column to the right, where a new table is shown with columns 'baker', 'spice', and 'correct'. The 'cardamom_2' column has been renamed to 'spice' and its value has been moved to the 'correct' column.

baker	cinnamon_1	cardamom_2	nutmeg_3
Emma			
Harry	1	1	
Ruby			
Zoë			

baker	spice	correct
Emma		
Harry	cinnamon_1	1
Harry	cardamom_2	1
Ruby		
Zoë		

pivot_longer(cinnamon_1:nutmeg_3,
names_to = 'spice',
values_to = 'correct')

A diagram illustrating the third step of pivoting. On the left, a table shows the state after the second pivot, with columns 'baker', 'cinnamon_1', 'cardamom_2', and 'nutmeg_3'. A dotted arrow points from the 'nutmeg_3' column to the right, where a new table is shown with columns 'baker', 'spice', and 'correct'. The 'nutmeg_3' column has been renamed to 'spice' and its value has been moved to the 'correct' column.

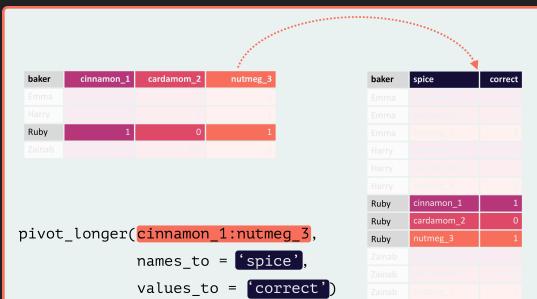
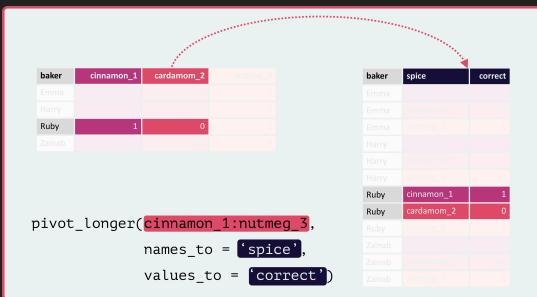
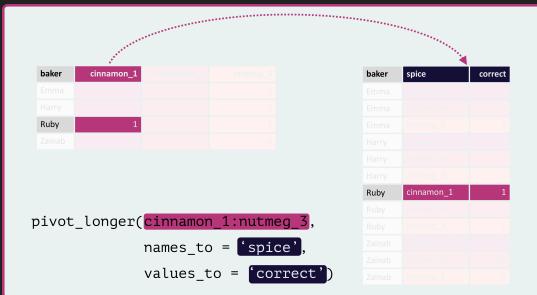
baker	cinnamon_1	cardamom_2	nutmeg_3
Emma			
Harry	1	1	1
Ruby			
Zoë			

baker	spice	correct
Emma		
Harry	cinnamon_1	1
Harry	cardamom_2	1
Harry	nutmeg_3	1
Ruby		
Zoë		

pivot_longer(cinnamon_1:nutmeg_3,
names_to = 'spice',
values_to = 'correct')



...and so forth...



...until we run out of rows...

A diagram illustrating the first step of pivoting the 'cinnamon_1' column. It shows two tables: a source table 'baker' and a target table 'spice'. The source table has columns 'baker', 'cinnamon_1', and 'nutmeg_3'. The target table has columns 'baker', 'spice', and 'correct'. A dotted arrow points from the 'cinnamon_1' column of the source table to the 'spice' column of the target table. Below the tables is the R code: `pivot_longer(cinnamon_1: nutmeg_3, names_to = 'spice', values_to = 'correct')`.

baker	cinnamon_1	nutmeg_3
Emma		
Harry		
Ruby		
Zainab	0	

baker	spice	correct
Emma		
Harry		
Ruby		
Zainab	cinnamon_1	0
Zainab		

A diagram illustrating the second step of pivoting the 'cardamom_2' column. The source table now includes the 'cardamom_2' column. A dotted arrow points from the 'cardamom_2' column of the source table to the 'spice' column of the target table. Below the tables is the R code: `pivot_longer(cinnamon_1: nutmeg_3, names_to = 'spice', values_to = 'correct')`.

baker	cinnamon_1	cardamom_2	nutmeg_3
Emma			
Harry			
Ruby			
Zainab	0	NA	

baker	spice	correct
Emma		
Harry		
Ruby		
Zainab	cinnamon_1	0
Zainab	cardamom_2	NA
Zainab		

A diagram illustrating the final step of pivoting the 'nutmeg_3' column. The source table now includes the 'nutmeg_3' column. A dotted arrow points from the 'nutmeg_3' column of the source table to the 'spice' column of the target table. Below the tables is the R code: `pivot_longer(cinnamon_1: nutmeg_3, names_to = 'spice', values_to = 'correct')`.

baker	cinnamon_1	cardamom_2	nutmeg_3
Emma			
Harry			
Ruby			
Zainab	0	NA	0

baker	spice	correct
Emma		
Harry		
Ruby		
Zainab	cinnamon_1	0
Zainab	cardamom_2	NA
Zainab	nutmeg_3	0
Zainab		



...and get the final table of pivoted values.

baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry	1	1	1
Ruby	1	0	1
Zainab	0	NA	0

baker	spice	correct
Emma	cinnamon_1	1
Emma	cardamom_2	0
Emma	nutmeg_3	1
Harry	cinnamon_1	1
Harry	cardamom_2	1
Harry	nutmeg_3	1
Ruby	cinnamon_1	1
Ruby	cardamom_2	0
Ruby	nutmeg_3	1
Zainab	cinnamon_1	0
Zainab	cardamom_2	NA
Zainab	nutmeg_3	0

```
pivot_longer(cinnamon_1:nutmeg_3,  
             names_to = 'spice',  
             values_to = 'correct')
```



We can even amend the current command to include things like `order`!

baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry	1	1	1
Ruby	1	0	1
Zainab	0	NA	0

```
pivot_longer(cinnamon_1:nutmeg_3,  
             names_to = c('spice', 'order'),  
             names_sep = '_',  
             values_to = 'correct')
```

baker	spice	order	correct
Emma	cinnamon	1	1
Emma	cardamom	2	0
Emma	nutmeg	3	1
Harry	cinnamon	1	1
Harry	cardamom	2	1
Harry	nutmeg	3	1
Ruby	cinnamon	1	1
Ruby	cardamom	2	0
Ruby	nutmeg	3	1
Zainab	cinnamon	1	0
Zainab	cardamom	2	NA
Zainab	nutmeg	3	0



Shortcut

Rather than accounting for every column, you can just tell R not to account for columns

```
juniors_multiple %>%
  pivot_longer(-baker,
               names_to = c('spice', 'order'),
               names_sep = '_',
               values_to = 'correct')
```

```
## # A tibble: 12 x 4
##   baker   spice   order correct
##   <chr>   <chr>   <chr>   <int>
## 1 Emma    cinnamon 1        1
## 2 Emma    cardamom 2        0
## 3 Emma    nutmeg   3        1
## 4 Harry   cinnamon 1        1
## 5 Harry   cardamom 2        1
## 6 Harry   nutmeg   3        1
## 7 Ruby    cinnamon 1        1
## 8 Ruby    cardamom 2        0
## 9 Ruby    nutmeg   3        1
## 10 Zainab  cinnamon 1        0
## 11 Zainab  cardamom 2       NA
## 12 Zainab  nutmeg   3        0
```

Single column types

`pivot_wider` is great for columns of the same type. For example, if we run

```
glimpse(juniors_multiple)

## Rows: 4
## Columns: 4
## $ baker      <chr> "Emma", "Harry", "Ruby", "Zainab"
## $ cinnamon_1 <int> 1, 1, 1, 0
## $ cardamom_2 <int> 0, 1, 0, NA
## $ nutmeg_3   <int> 1, 1, 1, 0
```

all we have are integers...

Multiple column types

... but for the following

```
juniors_multiple_full <- tribble(  
  ~ "baker", ~"score_1", ~"score_2", ~"score_3",  
  ~ "guess_1", ~"guess_2", ~"guess_3",  
  "Emma", 1L, 0L, 1L, "cinnamon", "cloves", "nutmeg",  
  "Harry", 1L, 1L, 1L, "cinnamon", "cardamom", "nutmeg",  
  "Ruby", 1L, 0L, 1L, "cinnamon", "cumin", "nutmeg",  
  "Zainab", 0L, NA, 0L, "cardamom", NA_character_, "cinnamon"  
)
```

```
juniors_multiple_full
```

```
## # A tibble: 4 x 7  
##   baker  score_1  score_2  score_3  guess_1  guess_2  guess_3  
##   <chr>    <int>    <int>    <int> <chr>    <chr>    <chr>  
## 1 Emma        1        0        1 cinnamon  cloves  nutmeg  
## 2 Harry       1        1        1 cinnamon cardamom nutmeg  
## 3 Ruby        1        0        1 cinnamon cumin   nutmeg  
## 4 Zainab      0       NA        0 cardamom <NA>    cinnamon
```



```
glimpse(juniors_multiple_full)
```

```
## Rows: 4
## Columns: 7
## $ baker    <chr> "Emma", "Harry", "Ruby", "Zainab"
## $ score_1 <int> 1, 1, 1, 0
## $ score_2 <int> 0, 1, 0, NA
## $ score_3 <int> 1, 1, 1, 0
## $ guess_1 <chr> "cinnamon", "cinnamon", "cinnamon", "cardamom"
## $ guess_2 <chr> "cloves", "cardamom", "cumin", NA
## $ guess_3 <chr> "nutmeg", "nutmeg", "nutmeg", "cinnamon"
```

...we have both character and numeric vectors.

Try running the following

```
juniors_multiple_full %>%
  pivot_longer(score_1:guess_3,
              names_to = c('score', 'guess'),
              names_sep = "_",
              values_to = 'correct')
```

Do you get `Error: Can't combine score_1 <integer> and guess_1 <character>.`? So what can you do?

Well since computers are stupid, you have to tell R what to look for.

Generalizing

We can actually just tell R to treat all values the same.

```
juniors_multiple_full %>%
  # Don't do anything with the baker column
  pivot_longer(-baker,
    # Treat all columns the same and order them
    names_to = c(".value", "order"),
    # Control how the column names are broken up
    names_sep = "_")
```

```
## # A tibble: 12 x 4
##   baker  order score guess
##   <chr>  <chr> <int> <chr>
## 1 Emma    1      1 cinnamon
## 2 Emma    2      0 cloves
## 3 Emma    3      1 nutmeg
## 4 Harry   1      1 cinnamon
## 5 Harry   2      1 cardamom
## 6 Harry   3      1 nutmeg
## 7 Ruby    1      1 cinnamon
## 8 Ruby    2      0 cumin
## 9 Ruby    3      1 nutmeg
## 10 Zainab 1      0 cardamom
## 11 Zainab 2     NA <NA>
## 12 Zainab 3      0 cinnamon
```

Back to the bar chart

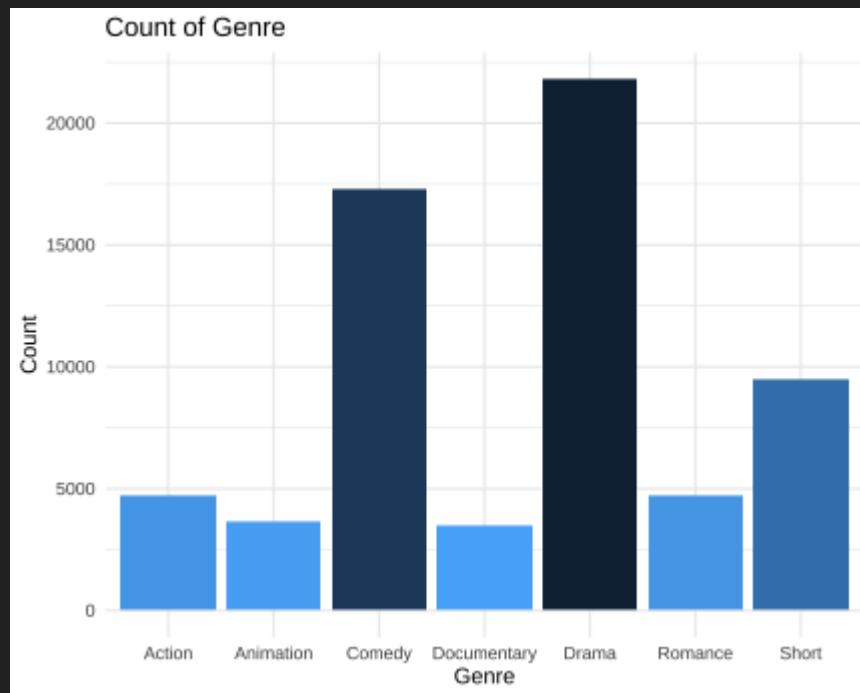
Now that we know how to pivot, we can just `group_by` genre type and then `tally`

```
movies_by_genre <- movies %>%
  select(Action, Animation, Comedy,
         Drama, Documentary, Romance, Short) %>%
  pivot_longer(everything(),
               names_to = "genre") %>%
  group_by(genre) %>%
  dplyr::tally(value)

movies_by_genre
```

```
## # A tibble: 7 x 2
##   genre      n
##   <chr>     <int>
## 1 Action     4688
## 2 Animation  3690
## 3 Comedy     17271
## 4 Documentary 3472
## 5 Drama      21811
## 6 Romance    4744
## 7 Short      9458
```

```
ggplot(movies_by_genre,
       aes(x = genre,
           y = n,
           fill = -n)) +
  geom_bar(stat='identity',
            show.legend = FALSE) +
  labs(title = "Count of Genre", x = "Genre", y = "Count") +
  theme_minimal()
```

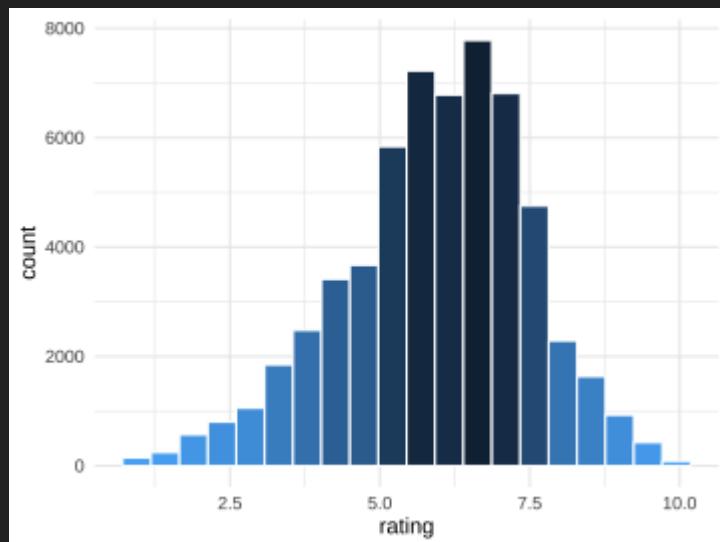


Back to the movies

Let's take a look at the ratings

```
pop <- movies %>%
  ggplot(aes(x = rating, fill = -..count..)) +
  geom_histogram(color = "white",
                 bins = 20,
                 show.legend = FALSE) +
  theme_minimal()

pop
```



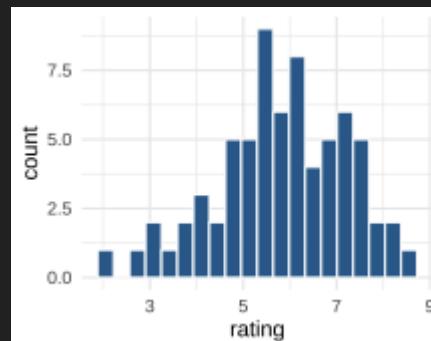
Purpose

We would like to produce a confidence interval for the population mean rating. Let's first pretend we had to take a sample of $n = 70$ from the $N = 58788$ movies. To do this, we'll use the `sample_n` command from the `dplyr` package.

```
set.seed(999) # Random number generator
movies_sample <- movies %>%
  sample_n(70)
```

Let's see what this looks like

```
ggplot(data = movies_sample, aes(x = rating,
                                   fill = n)) +
  geom_histogram(color = "white", bins = 20, show.legend = FALSE) +
  theme_minimal()
```



Population Estimation

We can think of the histogram as an estimate of our population distribution histogram that we plotted earlier so a population mean rating will provide a good estimate. To estimate a plausible range of values, we can start by using the mean of the sample. A good way to do this is to add parentheses around a variable declaration like so

```
(movies_sample_mean <- movies_sample %>%
  summarize(mean = mean(rating)))
```

```
## # A tibble: 1 x 1
##       mean
##   <dbl>
## 1  5.81
```

This value is only a single estimation. What you did earlier was to keep sampling from the population, or what is known as **sampling with replacement**.



Sampling with Replacement

To do this, we can use the `resample` command from the `mosaic` package. Let's see one instance of this.

```
resample(movies_sample) %>%
  arrange(orig.id) %>%
  summarize(mean = mean(rating))
```

```
## # A tibble: 1 x 1
##       mean
##     <dbl>
## 1  5.75
```

But again, this is only one sample mean.

To do a whole bunch we can run a do command with parentheses like so

```
do(10) *  
  (resample(movies_sample) %>%  
    summarize(mean = mean(rating)))
```

```
##          mean  
## 1  5.842857  
## 2  6.090000  
## 3  5.572857  
## 4  5.777143  
## 5  5.408571  
## 6  5.815714  
## 7  6.010000  
## 8  5.738571  
## 9  5.547143  
## 10 5.640000
```

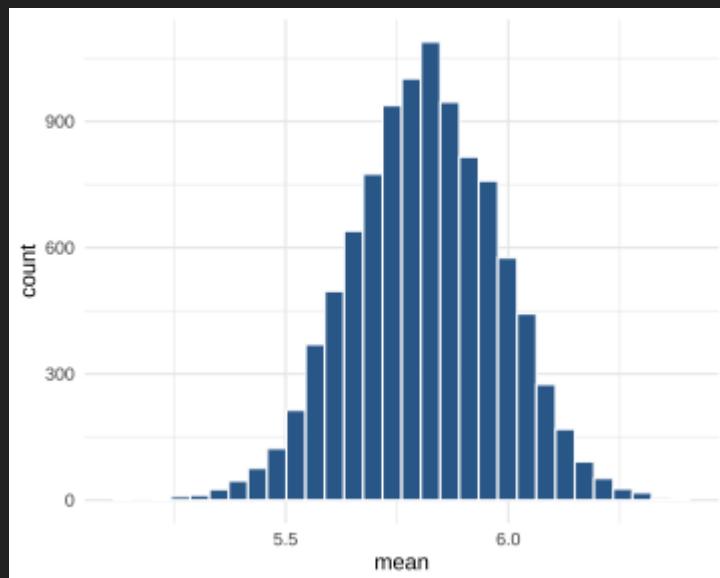


But a sample of 10 is so lame. Let's think big and try 10000!

```
not_lame <- do(10000) * summarize(resample(movies_sample),  
                                     mean = mean(rating))
```

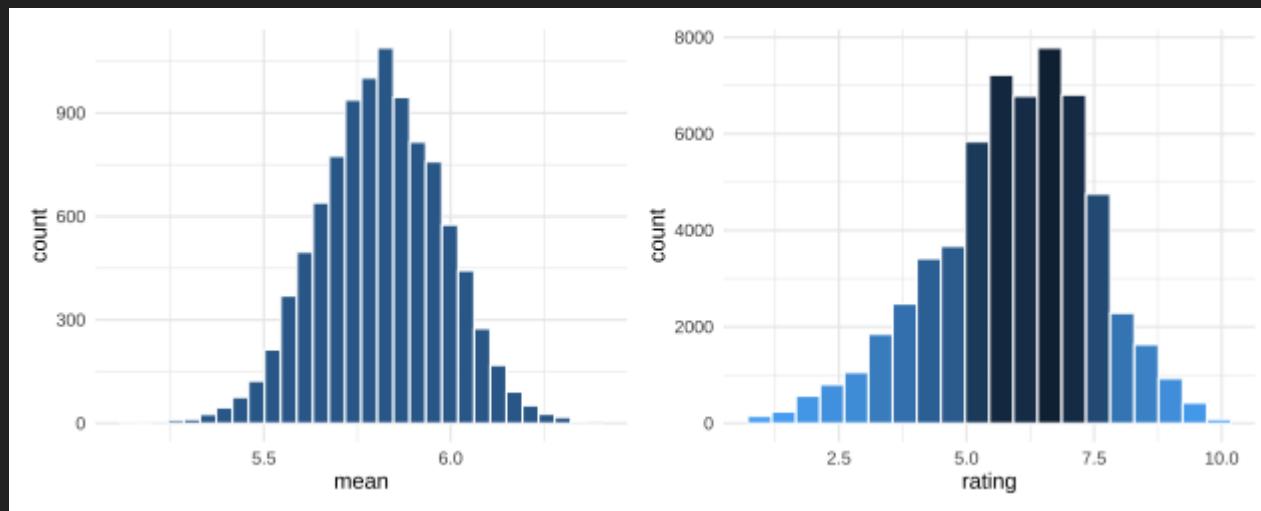
Estimating the population

```
samp <- ggplot(data = not_lame ,  
                 mapping = aes(x = mean,  
                               fill = n)) +  
  geom_histogram(bins = 30,  
                 color = "white",  
                 show.legend = FALSE) +  
  theme_minimal()  
  
samp
```



Comparison

On the left is our sample distribution while on the right is the original population distribution.



I'd say that the distribution of the sample means estimates the population pretty well!

Confidence using quantiles

We can now calculate a confidence interval using many options. Let's first isolate the middle 95% of values which corresponds to a 95% confidence interval for the population mean rating.

```
(ci95_mean <- confint(not_lame,  
                      level = 0.95,  
                      method = "quantile"))
```

```
##   name lower      upper level    method estimate  
## 1 mean  5.49  6.134286  0.95 percentile  5.814286
```

Based on the sample data and bootstrapping techniques, we can be 95% confident that the true mean rating of ALL IMDB ratings is between 5.49 and about 6.13.

Confidence using the standard error

Recall that the **standard error** is the standard deviation of the sampling distribution and is approximated by the bootstrap distribution or the null distribution depending on the context. To do this we can use the same function as before but only by changing the method

```
(ci95_mean <- confint(not_lame,
                        level = 0.95,
                        method = "stderr"))

## Warning: confint: Using df = Inf.

##   name      lower      upper level method estimate margin.of.error
## 1 mean 5.488224 6.139428  0.95  stderr 5.814286      0.3256022
```

The interpretation is virtually the same here.

Thats it!