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>  <int>  <dbl> <int> <dbl> <dbl> <dbl> <dbl> <dbl> <db
## 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    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.

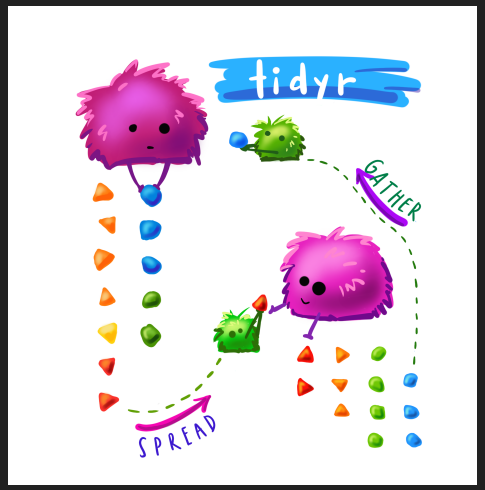
```
movies %>%
  select(Action, Animation, Comedy,
         Drama, Documentary, Romance, Short) %>%
  pivot_longer(
    everything(),
    names_to = "genre"
  )
```

```
## # 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.

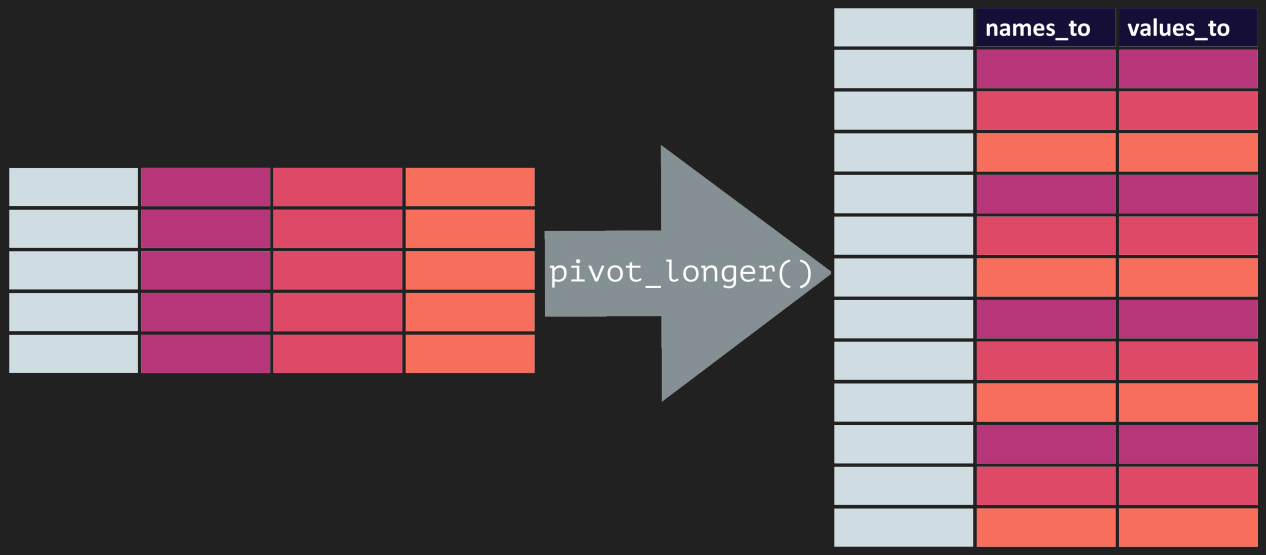
pivot_longer

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
```

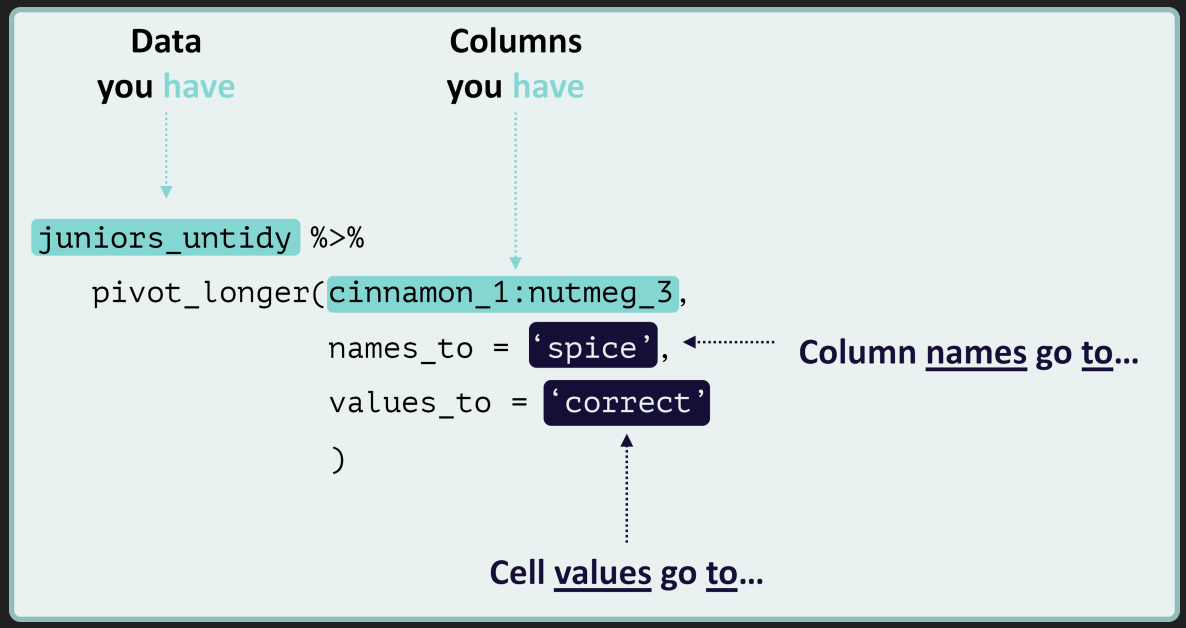
```
## # A tibble: 4 x 4
##   baker  cinnamon_1 cardamom_2 nutmeg_3
##   <chr>       <int>      <int>    <int>
## 1 Emma            1          0        1
## 2 Harry           1          1        1
## 3 Ruby            1          0        1
## 4 Zainab          0         NA        0
```

Looks good! Let's convert this!

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

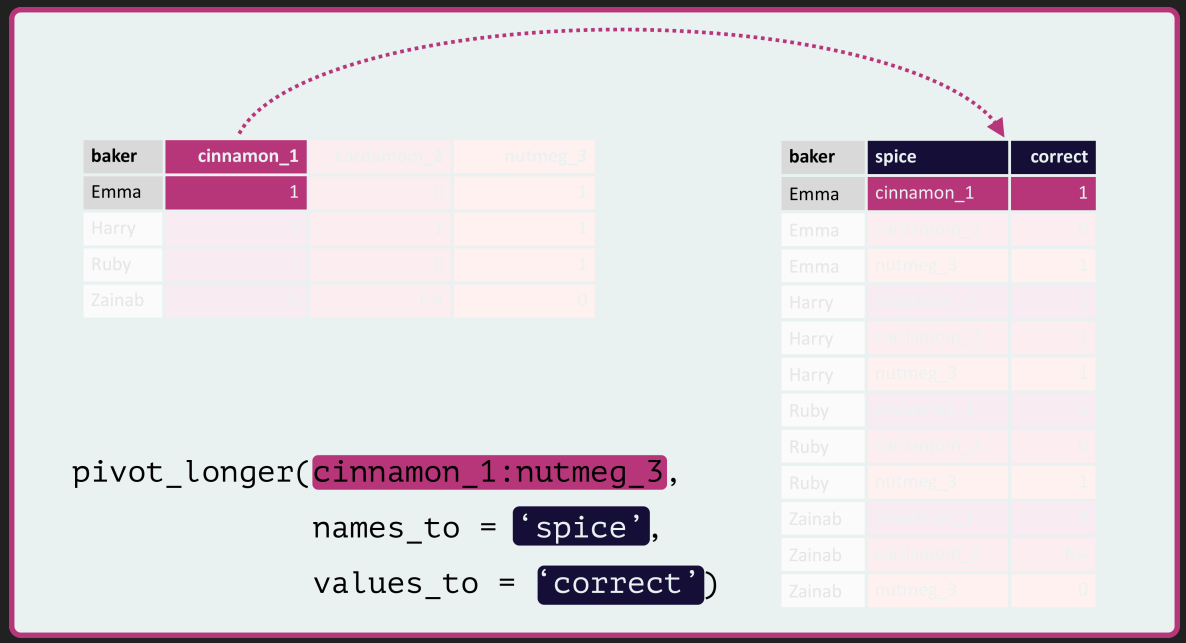
baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry	1	1	1
Ruby	1	0	1
Zainab	0	NA	0

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



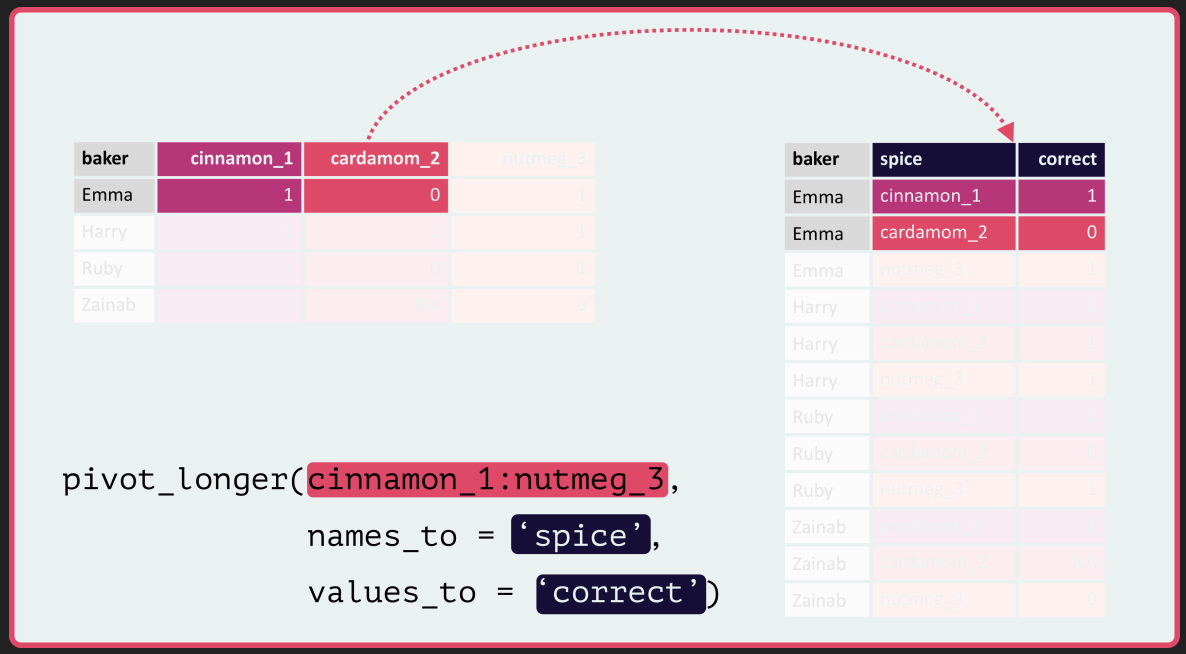
baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry	1	1	1
Ruby	1	0	1
Zainab	0	NA	0

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

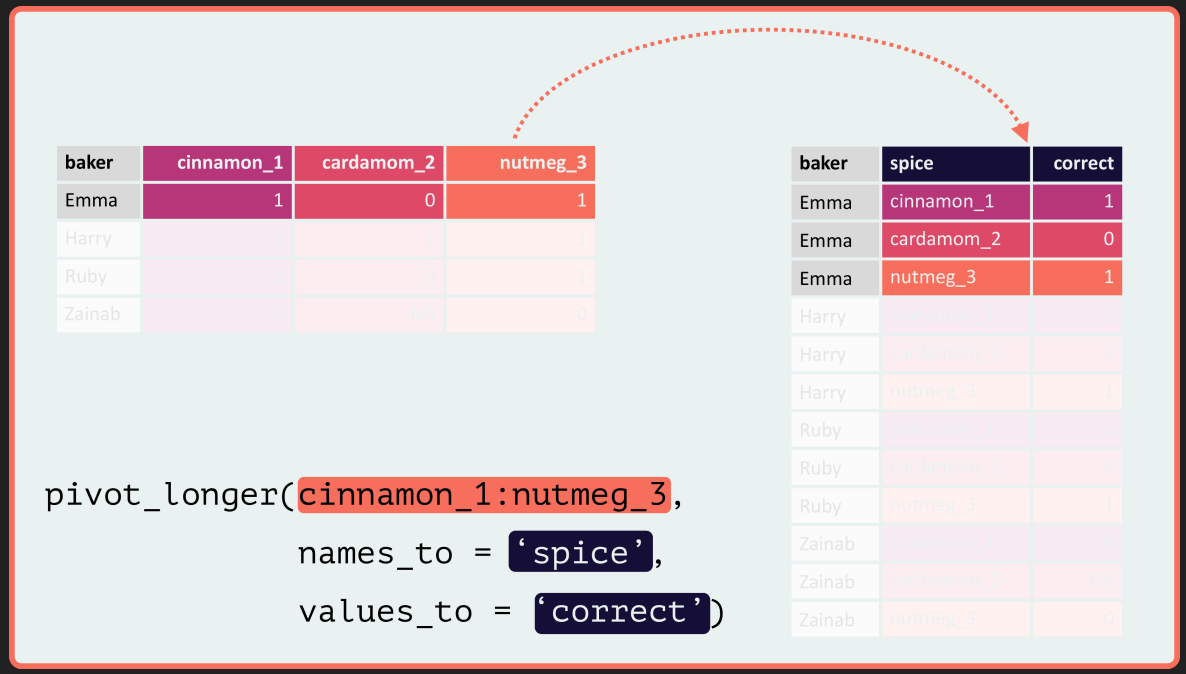


baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry	1	1	1
Ruby	1	0	1
Zainab	0	NA	0

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.



This pattern continues until a whole row is used up.

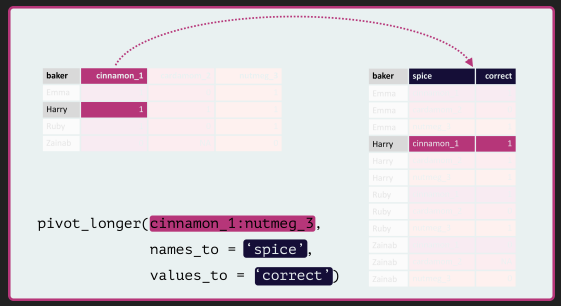


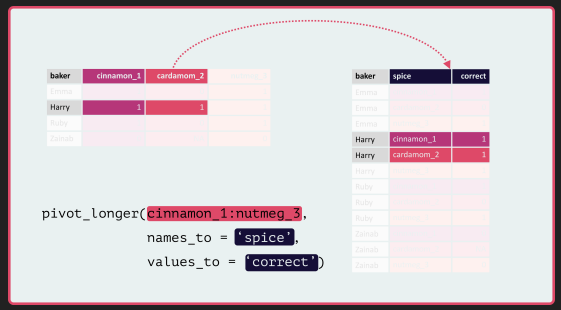
baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry			
Ruby			
Zainab		NA	

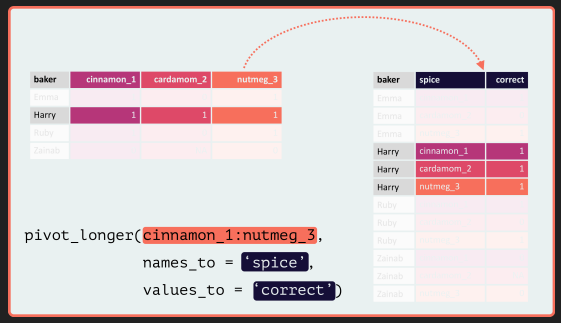
baker	spice	correct
Emma	cinnamon_1	1
Emma	cardamom_2	0
Emma	nutmeg_3	1
Harry		
Harry		
Harry		
Ruby		
Ruby		
Ruby		
Zainab		
Zainab		NA
Zainab		

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

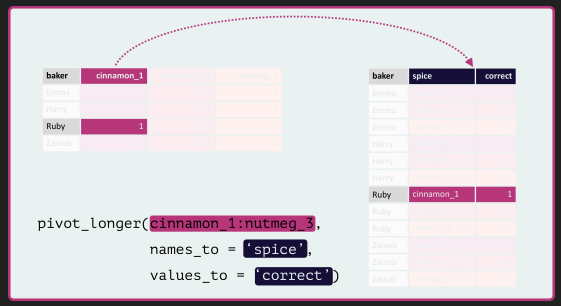
Then it repeats for the next row of values...

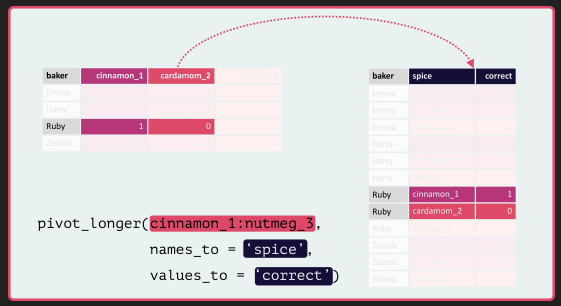


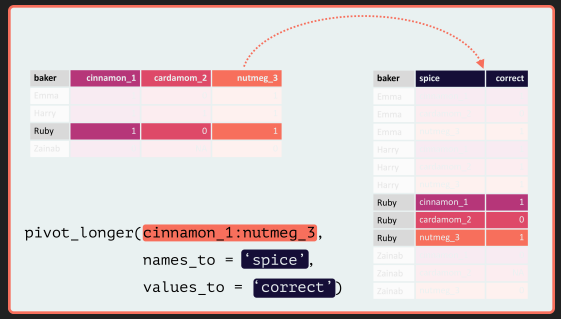




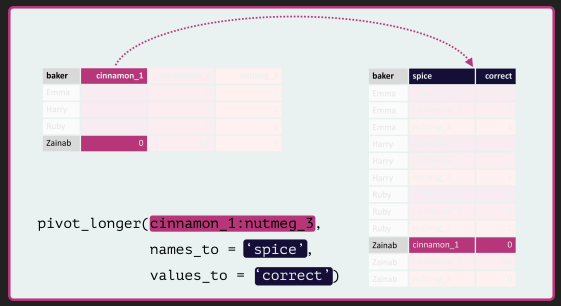
...and so forth...

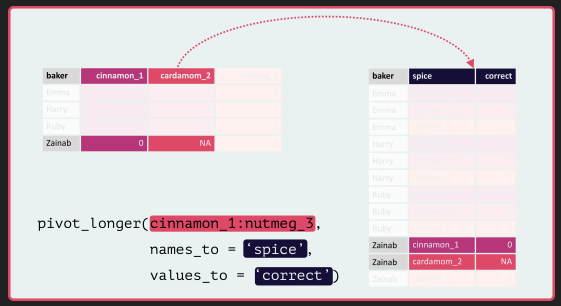

baker cinnamon_1
Ruby 1
baker spice correct
Ruby cinnamon_1 1
pivot_longer(cinnamon_1:nutmeg_3,
names_to = 'spice',
values_to = 'correct')

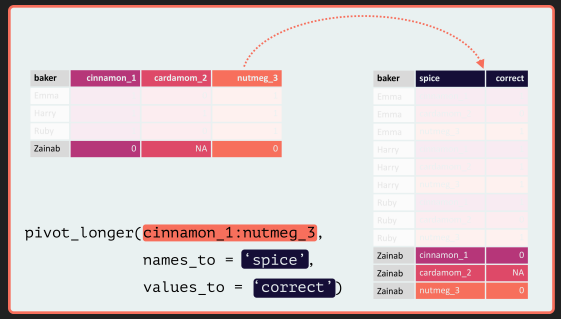

baker cinnamon_1 cardamom_2
Ruby 1 0
baker spice correct
Ruby cinnamon_1 1
Ruby cardamom_2 0
pivot_longer(cinnamon_1:nutmeg_3,
names_to = 'spice',
values_to = 'correct')


baker cinnamon_1 cardamom_2 nutmeg_3
Ruby 1 0 1
baker spice correct
Ruby cinnamon_1 1
Ruby cardamom_2 0
Ruby nutmeg_3 1
pivot_longer(cinnamon_1:nutmeg_3,
names_to = 'spice',
values_to = 'correct')

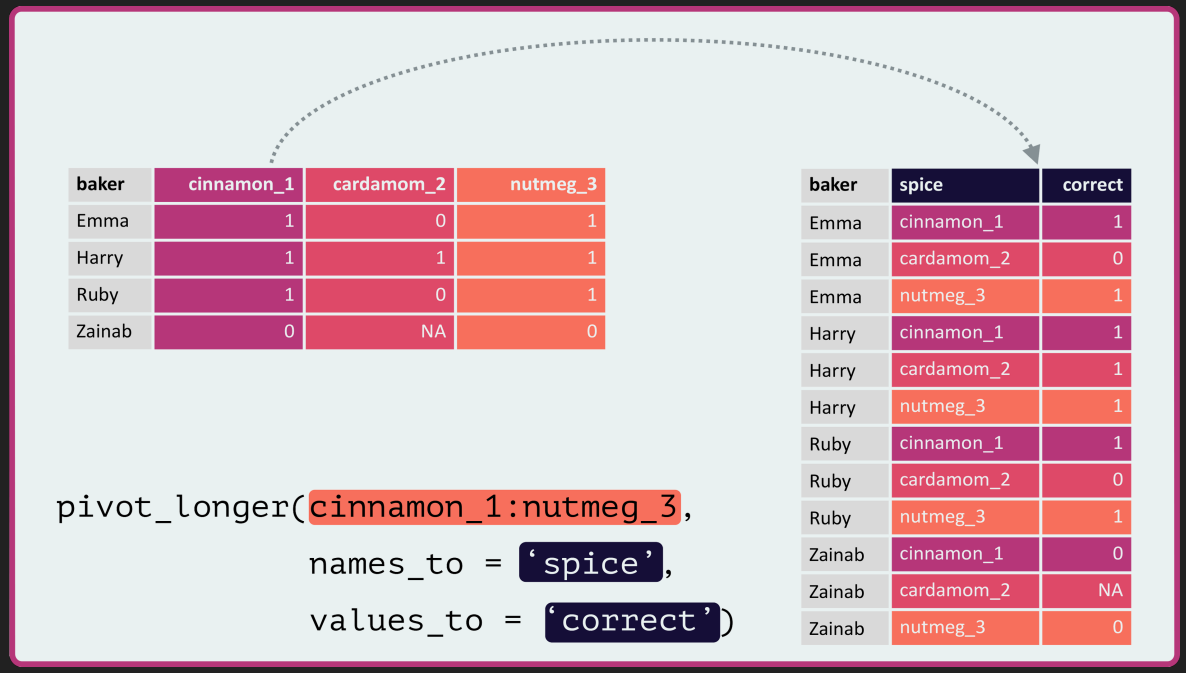
...until we run out of rows...







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

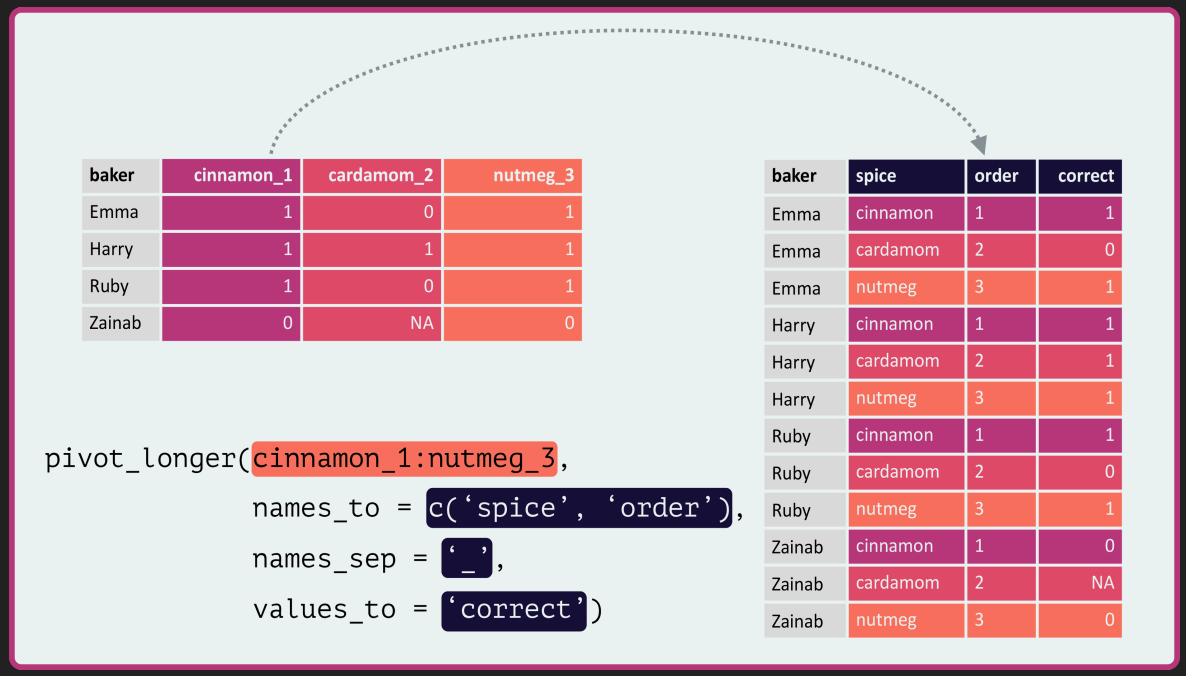


baker	cinnamon_1	cardamom_2	nutmeg_3
Emma	1	0	1
Harry	1	1	1
Ruby	1	0	1
Zainab	0	NA	0

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

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

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

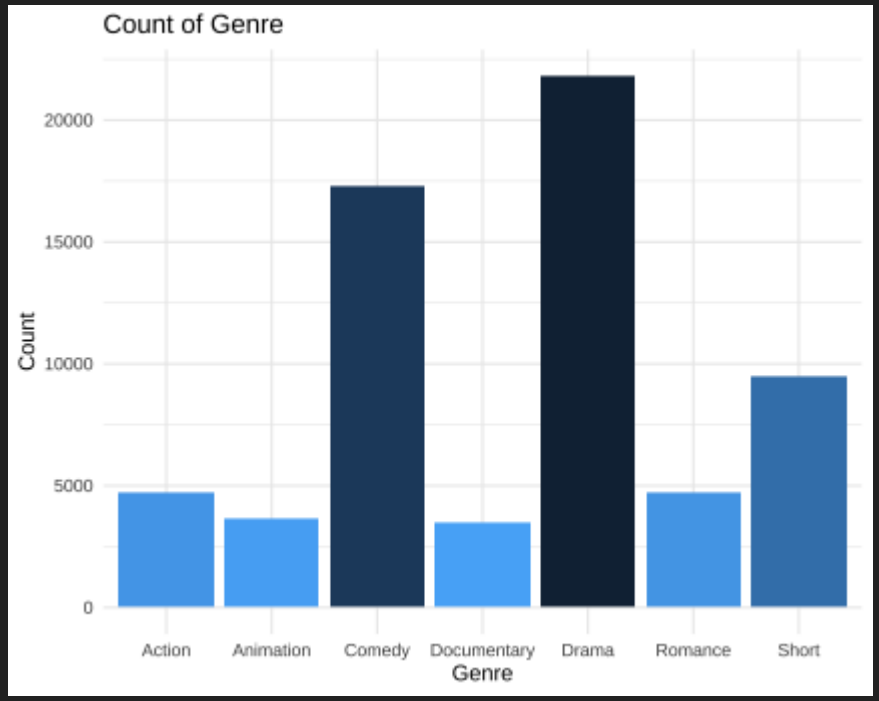
Now that we know how to pivot, we can just `group_by` genre type and then `tally`

```
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()
```

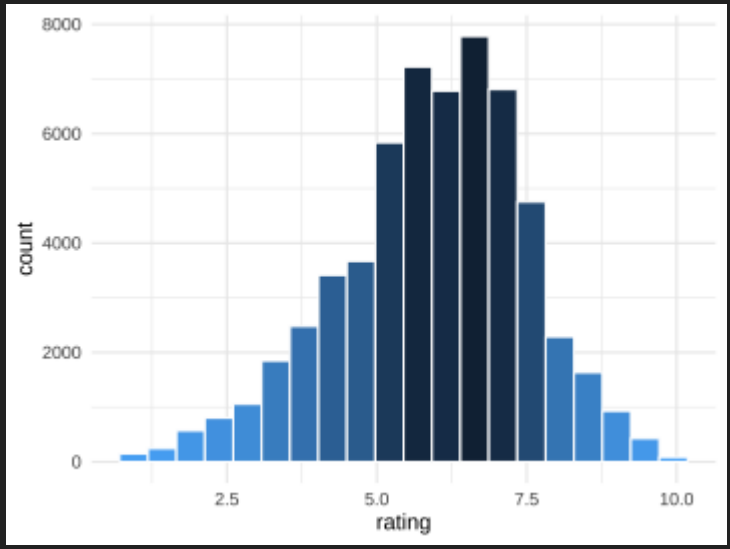


Back to the movies

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(movies_sample, aes(x = rating, fill = -..count..)) +
       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 to 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 values is only a single estimation. What you did earlier was top 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
```

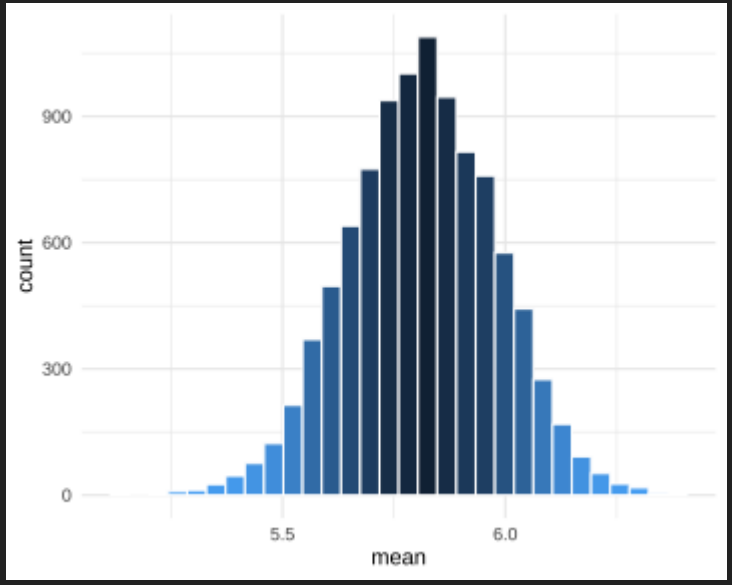
But a sample of 10 is so lame. Let's think big and try 10000!

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

Estimating the population

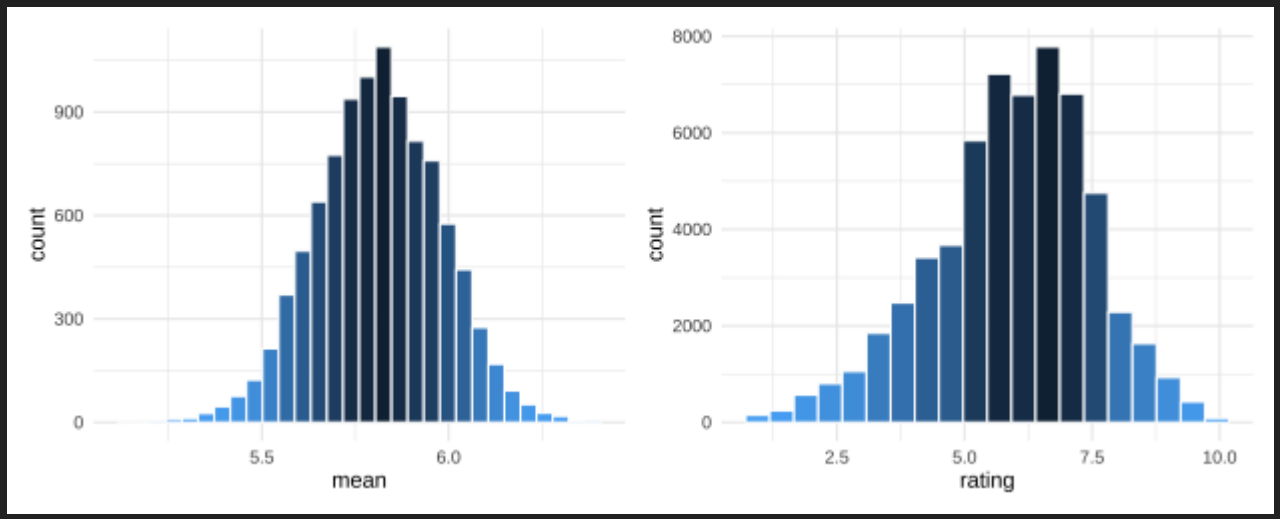
```
samp <- ggplot(data = not_lame ,
       mapping = aes(x = mean,
                     fill = -..count..)) +
  geom_histogram(bins = 30,
                 color = "white",
                 show.legend = FALSE) +
  theme_minimal()

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!