

Confidence Intervals II

Nate Wells

Math 141, 3/11/21

Outline

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- Use bootstrapping as means of creating confidence intervals
- Interpret confidence intervals
- Implement the `infer` package to automate bootstrapped confidence intervals

Section 1

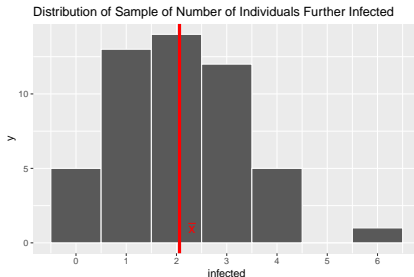
Bootstrapping Confidence Intervals

Reproduction Rate for Covid-19

Researchers are interested in the COVID-19 **reproduction rate** (the average number of individuals each infected person further infects)

- We have a sample of 50 infected individuals and perform contract tracing to determine how many other individuals each infects.

```
## infected n
## 1      0  5
## 2      1 13
## 3      2 14
## 4      3 12
## 5      4  5
## 6      6  1
## mean_infected
## 1          2.06
```



- Goal: Create an interval of plausible values for the reproduction rate.

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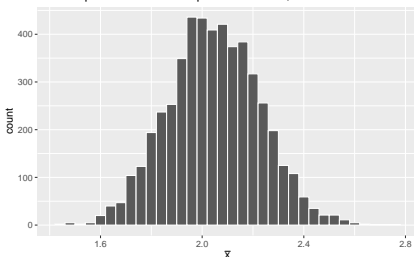
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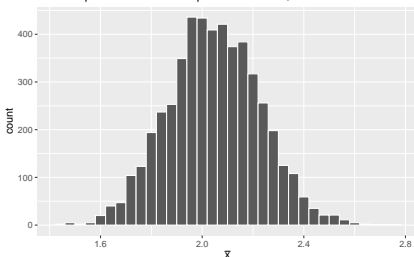
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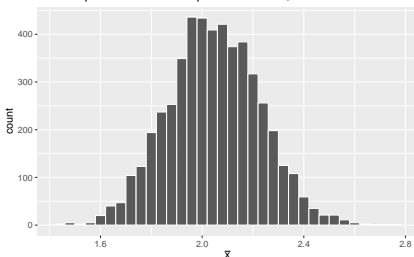
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- 5 The 95% confidence interval is

$$\bar{x} \pm 2 \cdot SE \quad 2.06 \pm 2 \cdot 0.181$$

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General Confidence Intervals

The $C\%$ confidence interval for a parameter is an interval estimate that is computed from sample data by a method that captures the parameter for $C\%$ of all samples.

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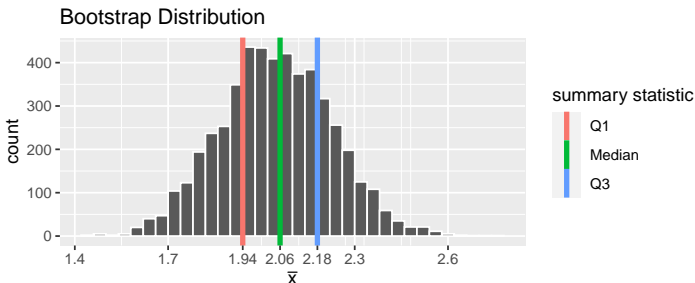
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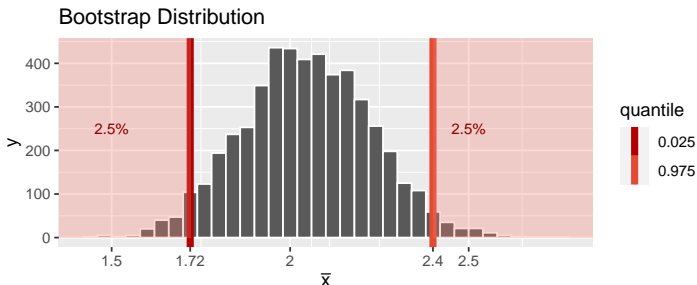
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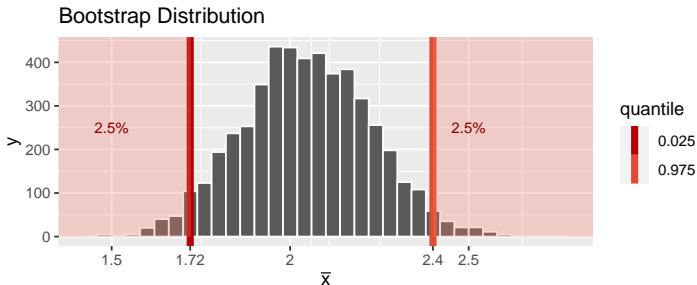
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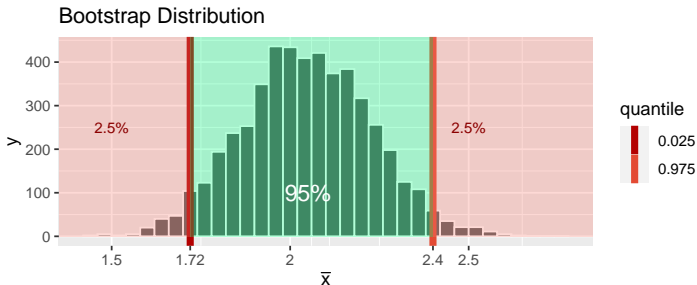
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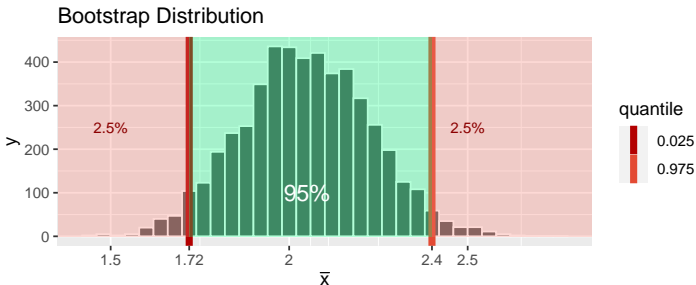
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- But this means that 95% of the data is between the .025 and the .975 quantiles
 - For a sampling distribution that is approximately bell-shaped, the .025 quantile is about $2 \cdot SE$ below the mean, and the .975 quantile is about $2 \cdot SE$ above the mean

The Percentile Method

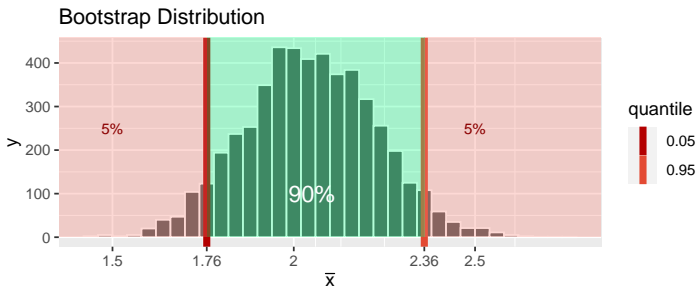
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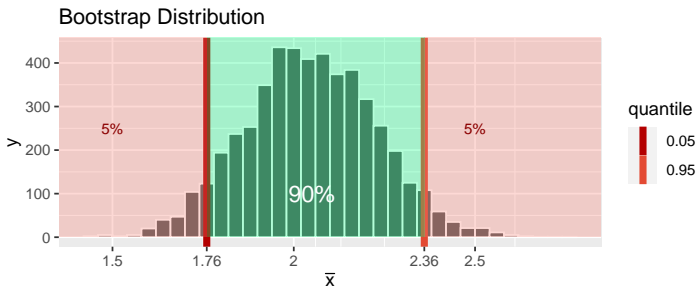
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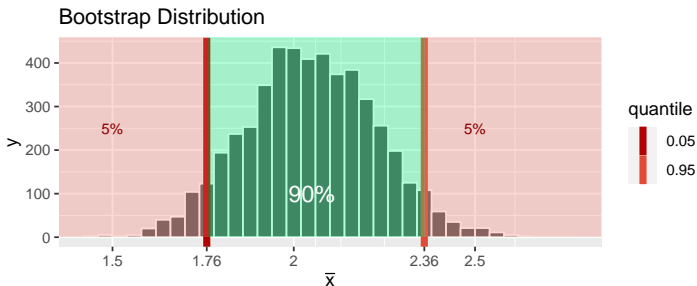
- We can use the quantile function in R to calculate the .05 and .95 quantiles

```
quantile(bootstrap_stats$x_bar, c(.05, .95))
```

```
## 5% 95%
## 1.76 2.36
```

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- Suppose we want to construct a 90% confidence interval for the reproduction rate
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- Our 90% confidence interval is therefore 1.76 to 2.36

```
quantile(bootstrap_stats$x_bar, c(.05, .95))
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- Increase sample size.
 - The standard deviation of the sampling distribution decreases as sample size increases. More sample means are closer to the true parameter
- Decrease confidence level.
 - The margin of error is determined by the percentiles. A 95% confidence interval is formed by the 2.5th and 97.5th percentiles in the bootstrap distribution.
 - Decreasing confidence level brings the percentiles closer to the 50th percentile, decreasing the width of the interval.

Section 2

Confidence Interval Misunderstandings

Common Confidence Interval Misunderstandings

Suppose we wish to estimate the number of hours a Reed student sleeps on a typical night. We obtain the following 95% confidence interval: (7.86, 8.34)

Common Confidence Interval Misunderstandings

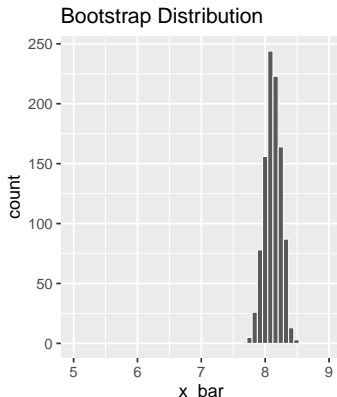
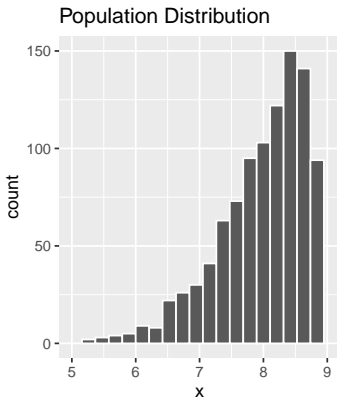
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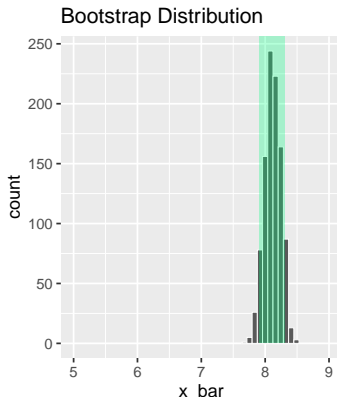
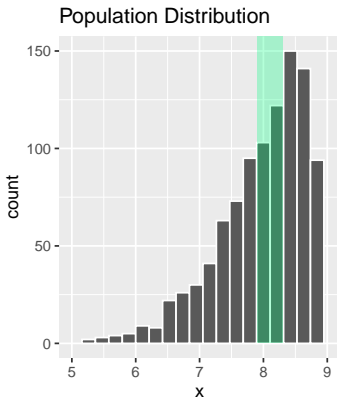
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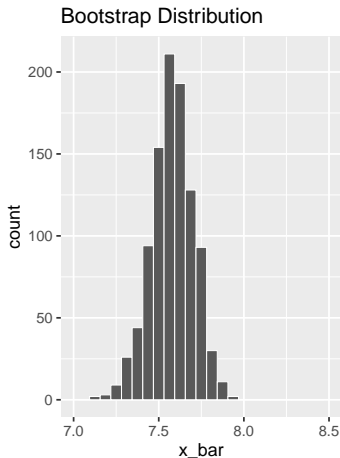
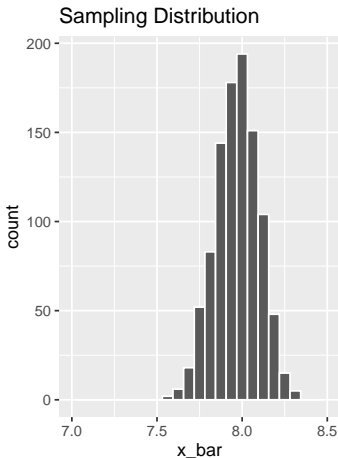


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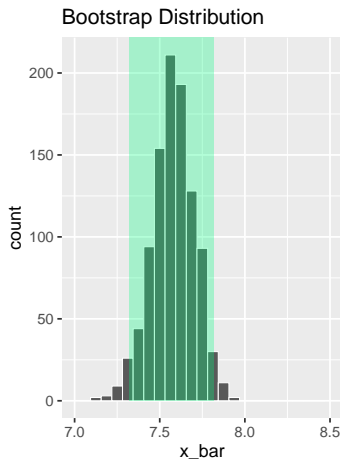
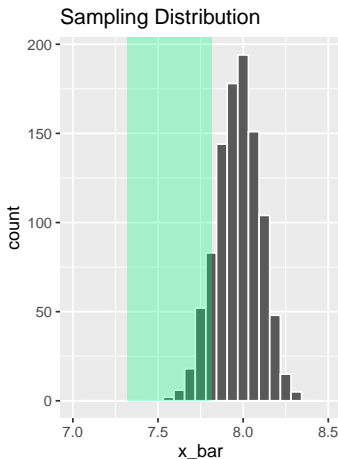
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 - At this point, the interval either does or does not contain the fixed (but unknown) parameter
 - One sample happened to have a sample mean of 4.9, producing a confidence interval of (4.6, 5.2).
 - Based on what you know about sleep patterns, do you think there is a 95% chance this interval contains the true parameter?
 - What is a plausible alternative explanation for this interval?

Section 3

The *infer* package

The `infer` Package

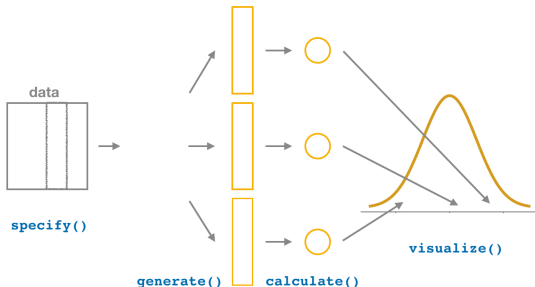
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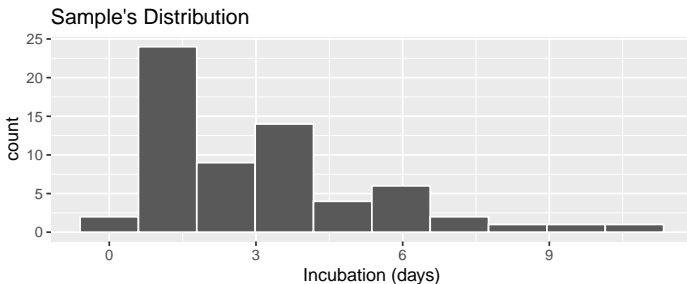
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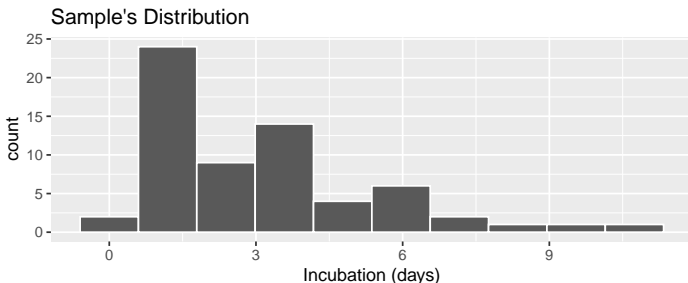
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- What is the population of interest? What is the parameter?
- What is the sample? What is the statistic?

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- To investigate the infection rate

```
covid %>%  
  specify(response = Incubation)
```

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- The resulting data frame has a number of rows equal `reps × sample_size`

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```
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  specify(response = Incubation) %>%
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- After applying `calculate` the resulting data frame consists of one bootstrap statistic for each replicate (saved to the variable `stat`)

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- By using `specify` and `calculate` (and omitting `generate`) we can do just that, paralleling similar calculation for the bootstrap statistics

```
covid_stat<- covid %>%
  specify(response = Incubation) %>%
  calculate(stat = "mean")
covid_stat
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```
## # A tibble: 1 x 1
##   stat
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- Note: we saved the value of this calculation as `covid_stat` so we could use it later

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```
covid_boot<- covid %>%
  specify(response = Incubation) %>%
  generate( reps = 2000, type = "bootstrap") %>%
  calculate(stat = "mean")

head(covid_boot)
```

```
## # A tibble: 6 x 2
##   replicate stat
##   <int> <dbl>
## 1         1  2.65
## 2         2  3.15
## 3         3  2.67
## 4         4  3.39
## 5         5  3.27
## 6         6  3.35
```

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- In order to perform any statistical inference, we need to ensure appropriate shape conditions on bootstrap distribution are met
- Use the `visualize` verb to quickly generate a reasonably nice-looking histogram of the bootstrap distribution.

visualize Bootstrap Distribution

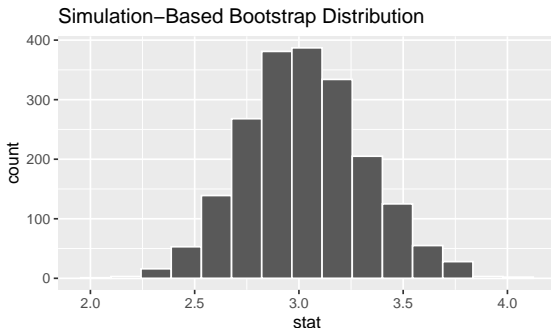
- In order to perform any statistical inference, we need to ensure appropriate shape conditions on bootstrap distribution are met
- Use the `visualize` verb to quickly generate a reasonably nice-looking histogram of the bootstrap distribution.

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covid_boot %>% visualize()
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```
percentile_ci <- covid_boot %>%
  get_ci(level = .95, type = "percentile")
percentile_ci
```

```
## # A tibble: 1 x 2
##   lower_ci upper_ci
##   <dbl>    <dbl>
## 1     2.49     3.63
```

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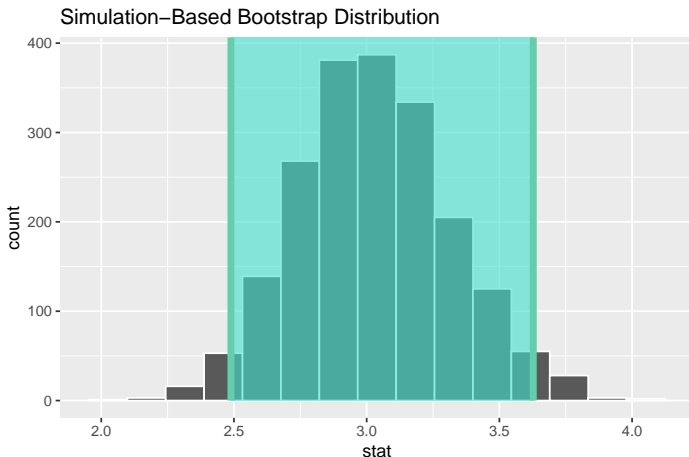
```
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```

- When using the percentile type, the first value printed is the lower and the second is the upper bound.

Shade Confidence Intervals

- Once you've used `get_ci` to obtain endpoints of the confidence interval, you can shade the sampling distribution with the confidence interval region.

```
covid_boot %>% visualize()+shade_ci(endpoints = percentile_ci)
```



Standard Error Method

- The confidence interval using the standard error method will be of the form

$$\text{statistic} \pm 2 \cdot SE$$

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```
se_ci<-covid_boot %>%
  get_ci(level = .95, type = "se", point_estimate = covid_stat)
se_ci
```

```
## # A tibble: 1 x 2
##   lower_ci upper_ci
##   <dbl>     <dbl>
## 1     2.46     3.60
```

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```
se_ci <- covid_boot %>%  
  get_ci(level = .95, type = "se", point_estimate = covid_stat)  
se_ci
```

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

- Note: for the se method, we also need to specify our point estimate (which is why we saved it as a variable before)

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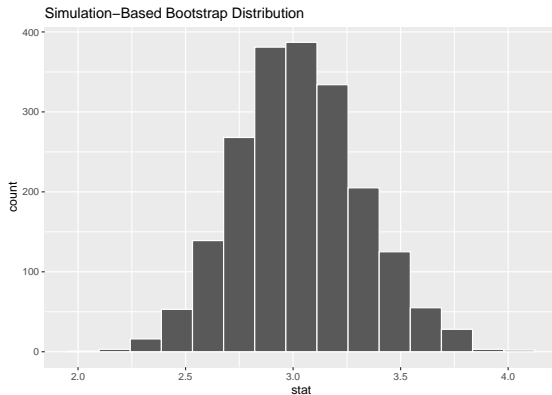
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- Why?

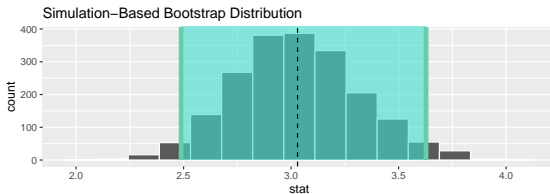
visualize Confidence Intervals

```
covid_boot %>% visualize()
```

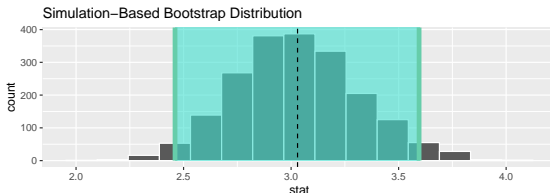


visualize Confidence Intervals

```
covid_boot %>% visualize() +  
  shade_confidence_interval(endpoints = percentile_ci)+  
  geom_vline(xintercept = 3.03, linetype = "dashed")
```

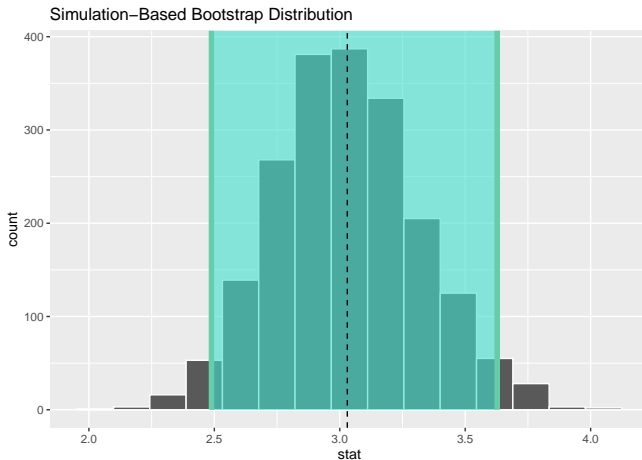


```
covid_boot %>% visualize() +  
  shade_confidence_interval(endpoints = se_ci)+  
  geom_vline(xintercept = 3.03, linetype = "dashed")
```



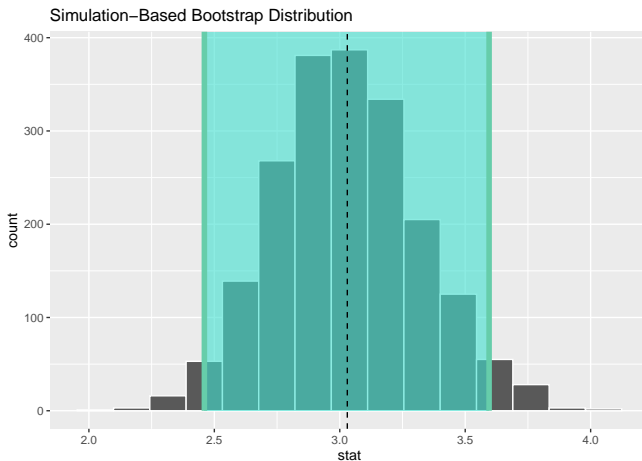
visualize Confidence Intervals

Percentile Method



visualize Confidence Intervals

SE Method



visualize Confidence Intervals

SE Method (with Percentile in blue)

