Lecture 10: Bootstrap

STAT 324

Ralph Trane
University of Wisconsin–Madison

Spring 2020

WISCONSIN
UNIVERSITY OF WISCONSIN–MADISON

Confidence Interval: The Short Story

Bootstrap

To find confidence interval, we use the distribution of $\frac{\bar{X}-E(\bar{X})}{\text{SD}(\bar{X})}$.

If $\bar{X} \sim N$, and $\text{SD}(\bar{X})$ is known, then $\frac{\bar{X}-E(\bar{X})}{\text{SD}(\bar{X})} \sim N$.

If $\bar{X} \sim N$, and $\text{SD}(\bar{X})$ is unknown, then $\frac{\bar{X}-E(\bar{X})}{\widehat{\text{SD}}(\bar{X})} \sim t_{n-1}$.

So, when is $\bar{X} \sim N$?

1. If the data are normal, i.e. $X_1, \ldots, X_n \sim N$.
    - check using histogram and/or QQ-plot
2. If $n \geq 30$, then CLT tells us $\bar{X} \sim N$ (in most real life scenarios...)

Bootstrap

What if the data are not normal, and $n < 30$?!?!?!?!

Bootstrap

What is the "gold standard" for finding the distribution of anything?

Sample from the population many, many times, and create a histogram.

That's all fun and games in theory, but in practice we cannot really do that.

Remember, all of statistics is build on one fundamental assumption: the sample looks like the population.

So what if we just... resample from the sample...?

Bootstrap

This approach is called *bootstraping*. How it works:

1. Grab your bootstraps
2. Pull yourself up!

Bootstrap

This approach is called *bootstraping*:

1. Given a sample, calculate $\bar{x}$.
2. Generate a new sample of size n from the original sample by sampling with replacement (!)
   - we call the first new sample $x_{11}, x_{12}, \ldots, x_{1n}$, the second new sample $x_{11}, x_{12}, \ldots, x_{1n}$, ..., the B'th new sample $x_{B1}, x_{B2}, \ldots, x_{Bn}$
   - these new samples are called *bootstrap samples*
3. For each bootstrap sample, calculate $t_j = \frac{\bar{x}_{\cdot j} - \bar{x}}{s_j/\sqrt{n}}$.
   - here, $\bar{x}_{\cdot j}$ is the average of the j'th bootstrap sample, while $\bar{x}$ is the average of the original sample.
4. Estimate the distribution of $\frac{\bar{X} - E(\bar{X})}{\widehat{\mathrm{SD}}(\bar{X})}$ by the distribution of $t_1, t_2, \ldots, t_B$
   - that is, the true distribution of $\frac{\bar{X} - E(\bar{X})}{\widehat{\mathrm{SD}}(\bar{X})}$ is approximately the histogram of the t_j's.

Confidence Intervals using Bootstrap

To find a confidence interval, we need find x_1, x_2 such that

$$P\left(x_1 \leq \frac{\bar{X} - E(\bar{X})}{\widehat{\mathrm{SD}}(\bar{X})} \leq x_2\right) = 1 - \alpha.$$

We can use the bootstrap samples to estimate the distribution of $\frac{\bar{X} - E(\bar{X})}{\widehat{\mathrm{SD}}(\bar{X})}$, and find the cut-offs such that there's $\alpha/2$ to the left of x_1 and $\alpha/2$ to the right of x_2.

We will call $x_1 = \hat{t}_{1-\alpha/2}$, and $x_2 = \hat{t}_{\alpha/2}$ -- the $1-\alpha/2$ and $\alpha/2$ critical values of the distribution of the $\hat{t}_j$'s.

Confidence Intervals using Bootstrap

This code takes an origina sample (`orig_sample`), creates 5000 bootstrap samples, and calculates $\hat{t}_1, \ldots, \hat{t}_{5000}$.

All of this will be in the data set `bootstrap_samples`.

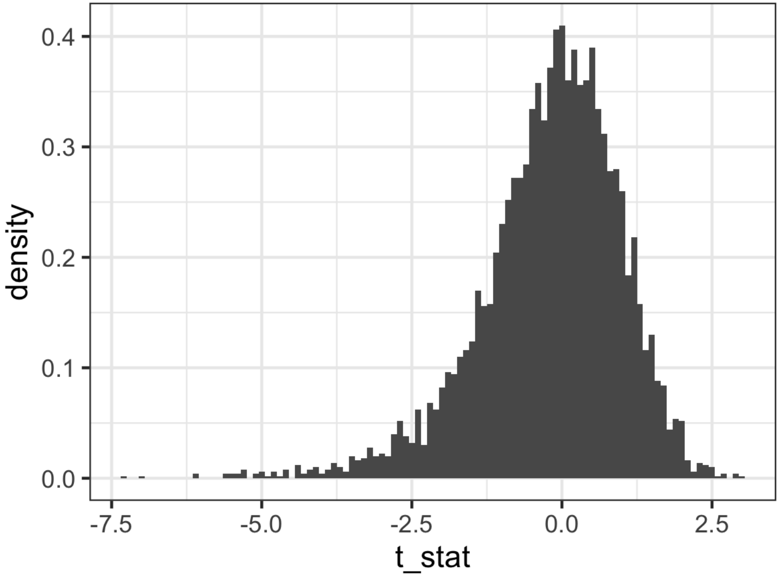
```
orig_sample <- tibble(x = c( 2.80, 16.47, 3.36,  9.31, 5.86,
                            15.25, 27.58, 4.75, 36.20, 1.25,
                            11.45, 10.01, 0.75,  0.59, 1.40,
                            10.54, 20.69, 1.82, 10.16, 2.83))
xbar <- mean(orig_sample$x)
sample_size <- nrow(orig_sample)

bootstrap_samples <- tibble(i = 1:5000) %>%
  mutate(boot_sample = map(i, ~sample_n(orig_sample, size = sample_s
         boot_mean = map_dbl(boot_sample, mean),
         boot_sd = map_dbl(boot_sample, sd),
         t_stat = (boot_mean - xbar)/(boot_sd/sqrt(sample_size)))
```

Confidence Intervals using Bootstrap

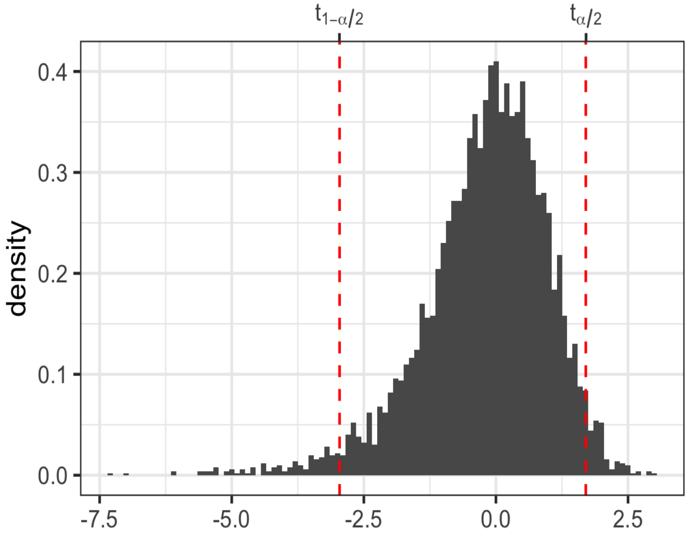
We can then create a histogram of the $\hat{t}_j$'s:

```
ggplot(bootstrap_samples,
       aes(x = t_stat)) +
  geom_histogram(binwidth = 0.1,
                 aes(y = ..density..))
```



Confidence Intervals using Bootstrap

$\hat{t}_{1-\alpha/2}$ and $\hat{t}_{\alpha/2}$ are by definition the numbers that cut-off $1-\alpha/2$ and $\alpha/2$ of the area to the right, respectively.



In this case, the numbers are:

```
bootstrap_samples %>%
  summarize(t_left = quantile(t_stat, 0.025),
            t_right = quantile(t_stat, 0.975))
```

```
## # A tibble: 1 x 2
##   t_left t_right
##    <dbl>   <dbl>
## 1  -2.96    1.70
```

Confidence Intervals using Bootstrap

So,

$$1-\alpha = P\left(\hat{t}_{1-\alpha/2} \le \frac{\bar{X}-E(\bar{X})}{\widehat{\mathrm{SD}}(\bar{X})} \le \hat{t}_{\alpha/2}\right)$$

$$= P\left(\hat{t}_{1-\alpha/2}\widehat{\mathrm{SD}}(\bar{X}) \le \bar{X}-\mu \le \hat{t}_{\alpha/2}\widehat{\mathrm{SD}}(\bar{X})\right)$$

$$= P\left(-\bar{X}+\hat{t}_{1-\alpha/2}\widehat{\mathrm{SD}}(\bar{X}) \le -\mu \le -\bar{X}+\hat{t}_{\alpha/2}\widehat{\mathrm{SD}}(\bar{X})\right)$$

$$= P\left(\bar{X}-\hat{t}_{1-\alpha/2}\widehat{\mathrm{SD}}(\bar{X}) \ge \mu \ge \bar{X}-\hat{t}_{\alpha/2}\widehat{\mathrm{SD}}(\bar{X})\right)$$

$$= P\left(\bar{X}-\hat{t}_{\alpha/2}\widehat{\mathrm{SD}}(\bar{X}) \le \mu \le \bar{X}-\hat{t}_{1-\alpha/2}\widehat{\mathrm{SD}}(\bar{X})\right)$$

Confidence Intervals using Bootstrap

A $(1-\alpha)\cdot 100\%$ Confidence Interval for the true mean μ is
$[\bar{X} - \hat{t}_{\alpha/2}\widehat{\mathrm{SD}}(\bar{X}), \bar{X} - \hat{t}_{1-\alpha/2}\widehat{\mathrm{SD}}(\bar{X})]$.

We are $(1-\alpha)\cdot 100\%$ confident that the true value is in this interval.

Confidence Intervals: Chick Birth Weights

The `ChickWeight` data have data regarding the effect of diet on early growth of chicks.

```
ChickWeight
```

```
## # A tibble: 578 x 4
##    weight  Time Chick Diet
##     <dbl> <dbl> <ord> <fct>
##  1     42     0 1     1
##  2     51     2 1     1
##  3     59     4 1     1
##  4     64     6 1     1
##  5     76     8 1     1
##  6     93    10 1     1
##  7    106    12 1     1
##  8    125    14 1     1
##  9    149    16 1     1
## 10    171    18 1     1
## # … with 568 more rows
```

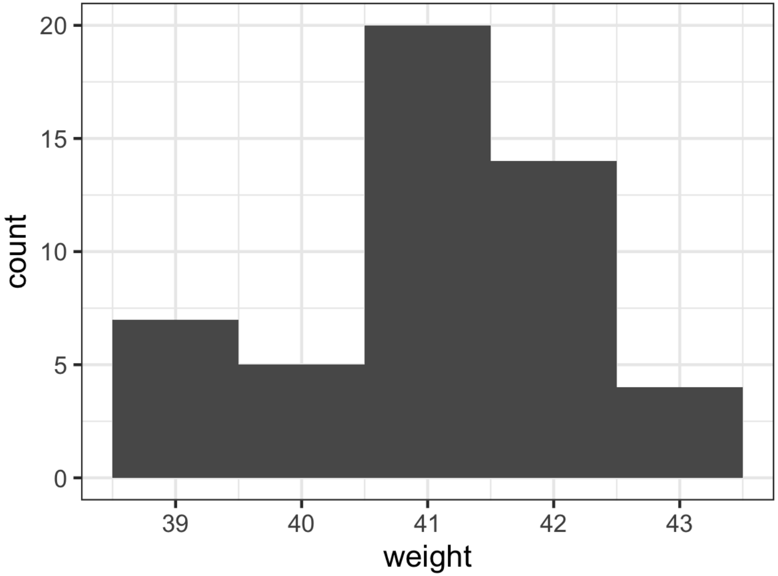
We are interested in the mean birth weight of the chicks. This would not be affected by the diet, so treat as one big sample.

Confidence Intervals: Chick Birth Weights

Want to find a confidence interval for μ = true mean birth weight.

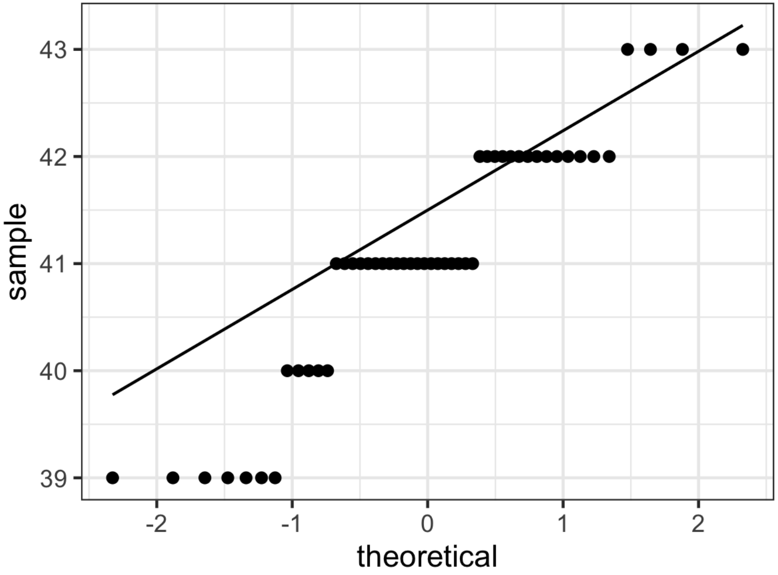
```
birth_weights <- ChickWeight %>% filter(Time == 0)

ggplot(birth_weights,
       aes(x = weight)) +
  geom_histogram(binwidth = 1)
```



Confidence Intervals: Chick Birth Weights

```
ggplot(birth_weights,
       aes(sample = weight)) +
  geom_qq() +
  geom_qq_line()
```

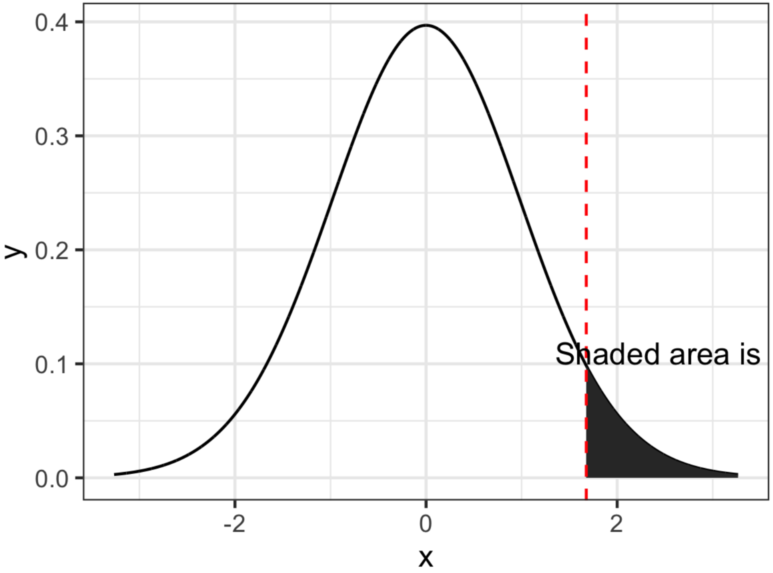


Definitely not normal.

Confidence Intervals: Chick Birth Weights

BUT… $n = 50$! So, by CLT $\bar{X} \sim N$. Therefore, can construct a CI. Since we do not know true σ, find a 90% CI as $\bar{x} \pm t_{n-1,0.05}\frac{s}{\sqrt{n}}$.

What is $t_{n-1,0.05}$? The value on x-axis such that we cut-off 0.05 to the right.



Confidence Intervals: Chick Birth Weights

In R: remember that `quanile` finds the cut-off that cuts off to the left. To cut off 0.05 to the right, we cut off 0.95 to the left:

```
T_49 <- StudentsT(df = 49) # n-1

(t_crit <- quantile(T_49, 0.95))
```

```
## [1] 1.676551
```

So, 90% CI is

```
birth_weights %>%
  summarize(mean = mean(weight),
            sd = sd(weight),
            LL = mean - t_crit * sd/sqrt(50),
            UL = mean + t_crit * sd/sqrt(50))
```

```
## # A tibble: 1 x 4
##    mean    sd    LL    UL
##   <dbl> <dbl> <dbl> <dbl>
## 1  41.1  1.13  40.8  41.3
```

Confidence Intervals: Biochemical Oxyden Demand

Measuring water quality over time. Done by measuring biochemical oxygen demand.

Data:

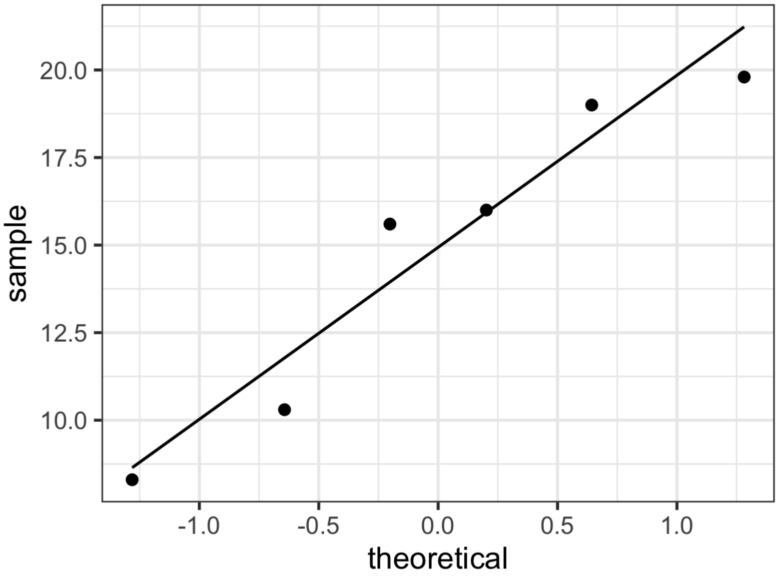
```
BOD
```

```
##   Time demand
## 1    1    8.3
## 2    2   10.3
## 3    3   19.0
## 4    4   16.0
## 5    5   15.6
## 6    7   19.8
```

n small, so cannot use CLT to conclude that $\bar{X} \sim N$. However, if the data is normal, we can still get to that same conclusion!

Confidence Intervals: Biochemical Oxyden Demand

```
ggplot(BOD, aes(sample = demand)) +
  geom_qq() +
  geom_qq_line()
```



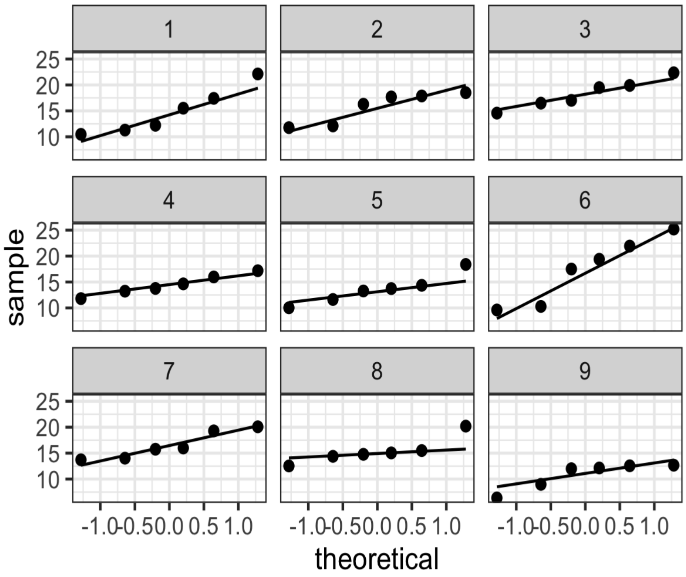
Confidence Intervals: Biochemical Oxyden Demand

Is it straight enough? Not sure. Compare to other samples of same size that are *actually* from a normal with same mean and SD as our sample. Then ask: does our sample seem that much different?

```
X <- Normal(mu = mean(BOD$demand), sigma = sd(BOD$demand))

normal_samples <- tibble(i = 1:9) %>%
  mutate(data = map(i, ~random(X, n = nrow(BOD)))) %>%
  unnest_longer(data)
```

```
ggplot(normal_samples,
       aes(sample = data)) +
  geom_qq() +
  geom_qq_line() +
  facet_wrap(~i)
```



Confidence Intervals: Biochemical Oxyden Demand

I would probably say no.

So, we assume $X_1, \dots, X_6 \sim N$. We do not know σ, so find 99% CI as $\bar{x} \pm t_{n-1,0.005} \frac{s}{\sqrt{n}}$.

```
T_5 <- StudentsT(df = 5) # n-1

(t_crit <- quantile(T_5, 0.995))
```

```
## [1] 4.032143
```

So, 99% CI is

```
BOD %>%
  summarize(mean = mean(demand),
            sd = sd(demand),
            LL = mean - t_crit * sd/sqrt(50),
            UL = mean + t_crit * sd/sqrt(50))
```

```
##       mean       sd       LL       UL
## 1 14.83333 4.630623 12.19281 17.47386
```

Confidence Intervals: Effect of Drug on Sleep

Scientists are interested in the effect of soporific drugs on amount of sleep. Data actually has data for 10 patients in 2 groups, but we will only consider one of the groups.

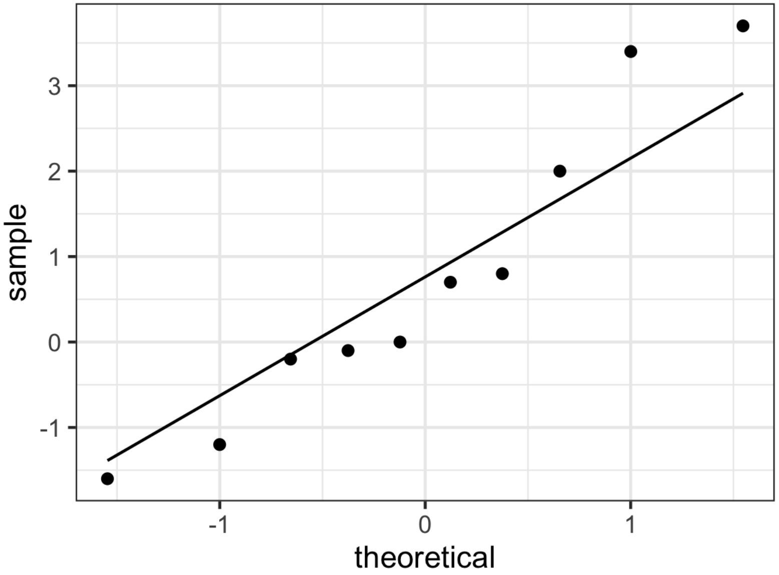
```
sleep1 <- sleep %>% filter(group == 1)
sleep1
```

```
##    extra group ID
## 1    0.7     1  1
## 2   -1.6     1  2
## 3   -0.2     1  3
## 4   -1.2     1  4
## 5   -0.1     1  5
## 6    3.4     1  6
## 7    3.7     1  7
## 8    0.8     1  8
## 9    0.0     1  9
## 10   2.0     1 10
```

Small n, so no CLT. Is it normal?

Confidence Intervals: Effect of Drug on Sleep

```
ggplot(sleep1,
       aes(sample = extra)) +
  geom_qq() +
  geom_qq_line()
```



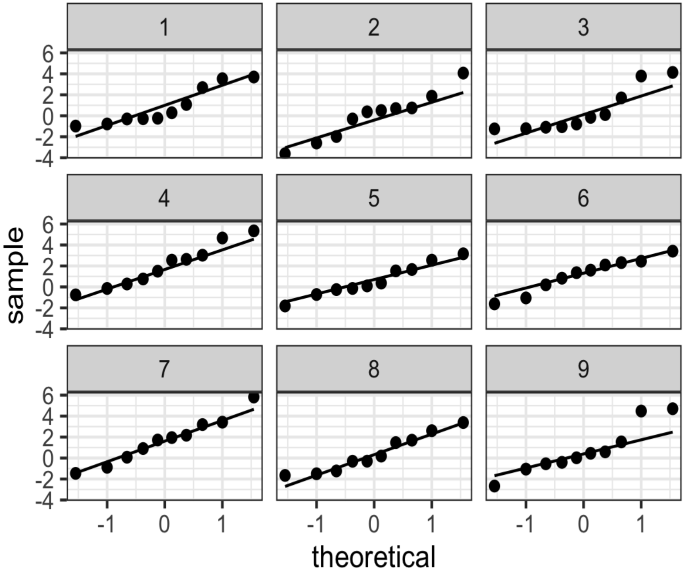
Confidence Intervals: Effect of Drug on Sleep

Is it straight enough? Not sure. Compare to other samples of same size that are *actually* from a normal with same mean and SD as our sample. Then ask: does our sample seem that much different?

```
X <- Normal(mu = mean(sleep1$extra), sigma = sd(sleep1$extra))

normal_samples <- tibble(i = 1:9) %>%
  mutate(data = map(i, ~random(X, n = nrow(sleep1)))) %>%
  unnest_longer(data)
```

```
ggplot(normal_samples,
       aes(sample = data)) +
  geom_qq() +
  geom_qq_line() +
  facet_wrap(~i)
```



Confidence Intervals: Effect of Drug on Sleep

Not sure. After consulting with the scientists in charge of the study, it is decided that we do **NOT** want to assume normality.

So, non-normal data, and n too small for CLT. So, we opt for a bootstrap approach:

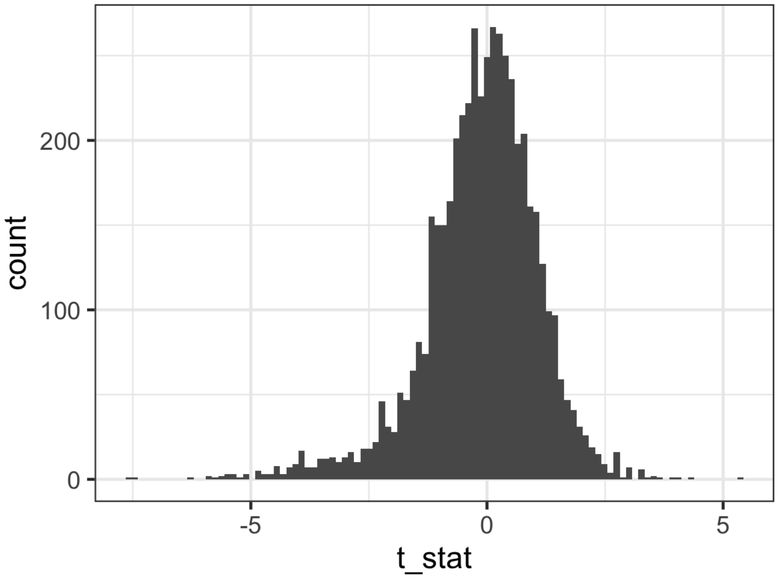
```
xbar <- mean(sleep1$extra)

bootstrap_samples <- tibble(i = 1:5000) %>%
  mutate(boot_samples = map(i, ~sample_n(sleep1, size = 10, replace =
         boot_mean = map_dbl(boot_samples, mean),
         boot_sd = map_dbl(boot_samples, sd),
         t_stat = (boot_mean - xbar)/(boot_sd/sqrt(10)))
```

Confidence Intervals: Effect of Drug on Sleep

Distribution from bootstrap:

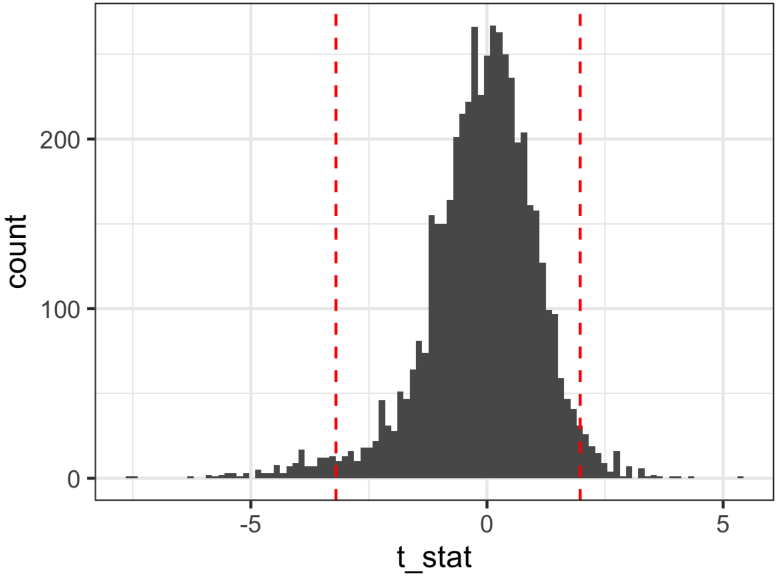
```
ggplot(data = bootstrap_samples,
       aes(x = t_stat)) +
  geom_histogram(bins = 100)
```



Confidence Intervals: Effect of Drug on Sleep

Want to create a 95% CI for the true mean. Find $\hat{t}_{0.025}$ and $\hat{t}_{0.975}$:

```
ggplot(data = bootstrap_samples,
       aes(x = t_stat)) +
  geom_histogram(bins = 100) +
  geom_vline(xintercept = quantile(bootstrap_samples$t_stat,
                                   p = c(0.025, 0.975)),
             color = "red", linetype = "dashed")
```



Confidence Intervals: Effect of Drug on Sleep

We find these, estimated mean ($\bar{x}$), and standard deviation (s) in R

```
bootstrap_samples %>%
  summarize(t_left = quantile(t_stat, 0.025),
            t_right = quantile(t_stat, 0.975))
```

```
## # A tibble: 1 x 2
##   t_left t_right
##    <dbl>   <dbl>
## 1  -3.20    1.97
```

```
sleep1 %>%
  summarize(mean = mean(extra),
            sd = sd(extra),
            n = n())
```

```
##   mean      sd  n
## 1 0.75 1.78901 10
```

Confidence Intervals: Effect of Drug on Sleep

So, we find the lower limit of 95% CI as

$$\begin{aligned}\bar{x} - \hat{t}_{0.975}\frac{s}{\sqrt{n}} &= 0.75 - 1.973\frac{1.789}{\sqrt{10}} \\ &= -0.37\end{aligned}$$

and the upper limit as

So, we find the lower limit of 95% CI as

$$\begin{aligned}\bar{x} - \hat{t}_{0.025}\frac{s}{\sqrt{n}} &= 0.75 - (-3.198)\frac{1.789}{\sqrt{10}} \\ &= 2.56\end{aligned}$$