Lecture 10: Bootstrap

STAT 324

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Confidence Interval: The Short Story

Bootstrap

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

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

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

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*. How it works:

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 $\frac{\bar{X} - E(\bar{X})}{\widehat{\text{SD}}(\bar{X})}$ by the distribution of $t_1, t_2, \ldots, t_B$
   - that is, the true distribution of $\frac{\bar{X} - E(\bar{X})}{\widehat{\text{SD}}(\bar{X})}$ is approximately the histogram of the t_j's.

Confidence Intervals using Bootstrap

To find a confidence interval, we need to 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.

Note: in this case, it is most likely that $\hat{t}_{1-\alpha/2} \neq -\hat{t}_{\alpha/2}$!!! There is no guarentee that the distribution is symmetrical, so no reason to think one of the values will be the negative of the other.

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`.

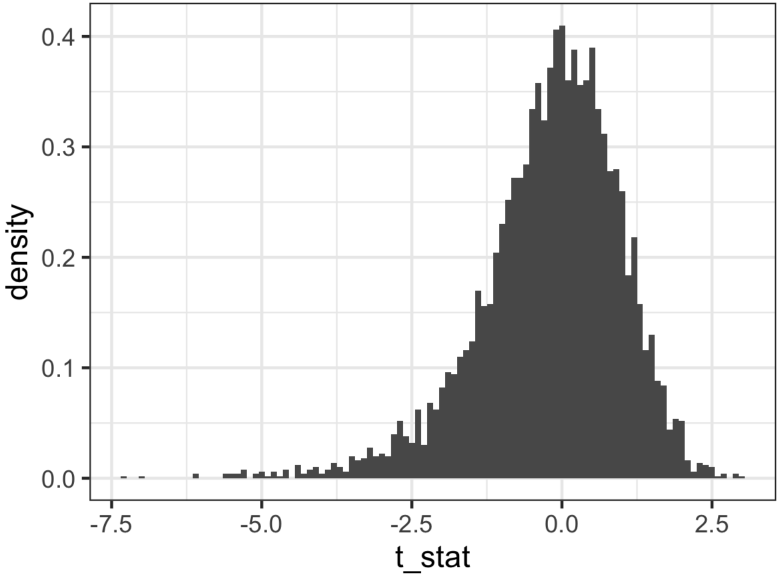
```
orig_sample <- tibble(x = c( 2.80, 16.47, 3.36,  9.31, 5.86,
                            15.25, 27.58, 4.75, 36.20, 1.25,
                            11.45, 10.01, 0.75,  0.59, 1.40,
                            10.54, 20.69, 1.82, 10.16, 2.83))
xbar <- mean(orig_sample$x)
sample_size <- nrow(orig_sample)

bootstrap_samples <- tibble(i = 1:5000) %>%
  mutate(boot_sample = map(i, ~sample_n(orig_sample, size = sample_size, replace = TR
         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

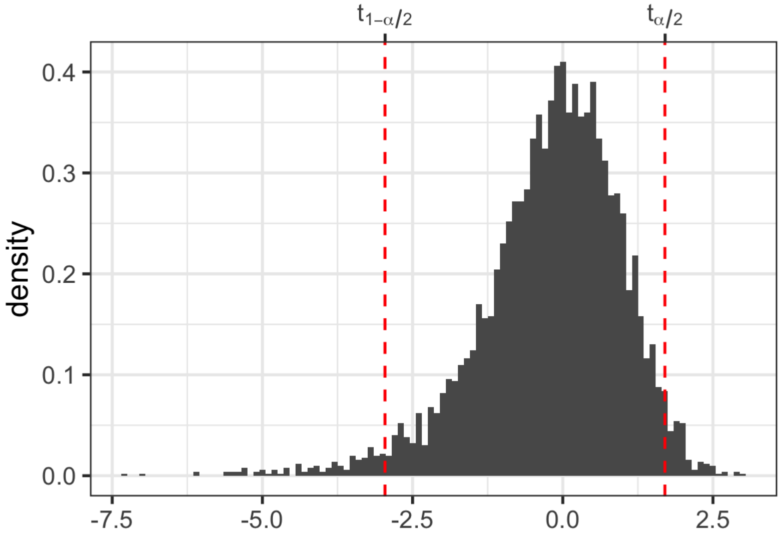
We can then create a histogram of the $\hat{t}_j$'s:

```
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
```

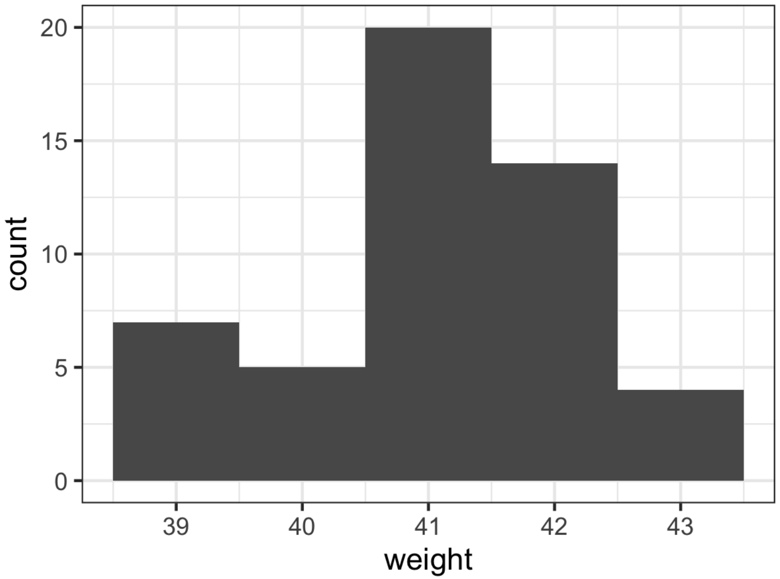
We are interested in the mean birth weight of the chicks. This would not be affected by the diet, so treat as one big sample.

Confidence Intervals: Chick Birth Weights

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

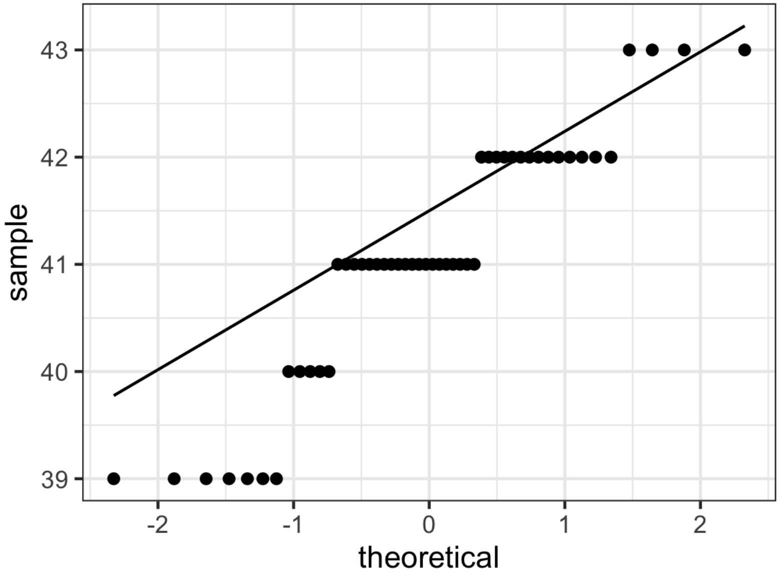
```r
birth_weights <- ChickWeight %>% filter(Time == 0)

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()
```

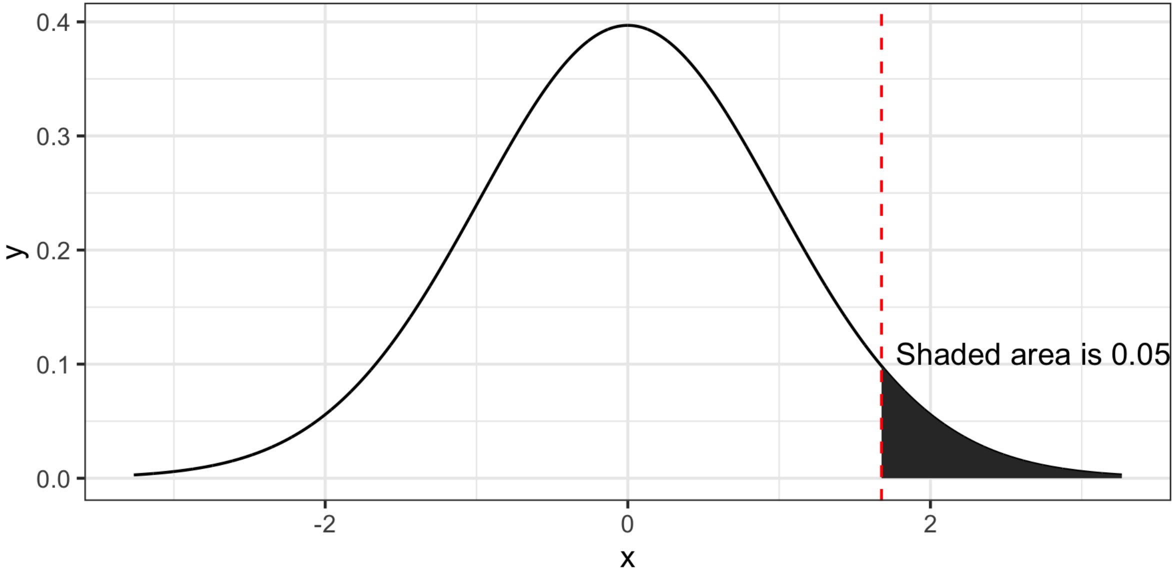


Definitely not normal.

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:

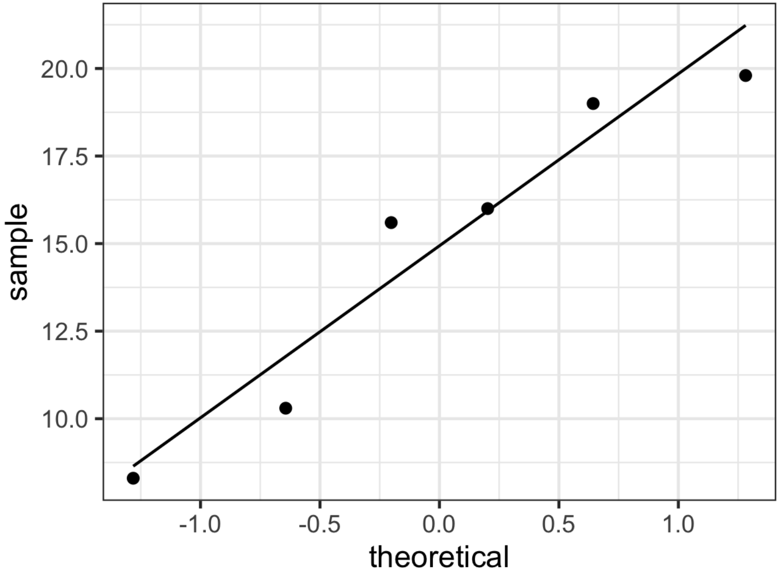
```
BOD
```

```
##   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()
```



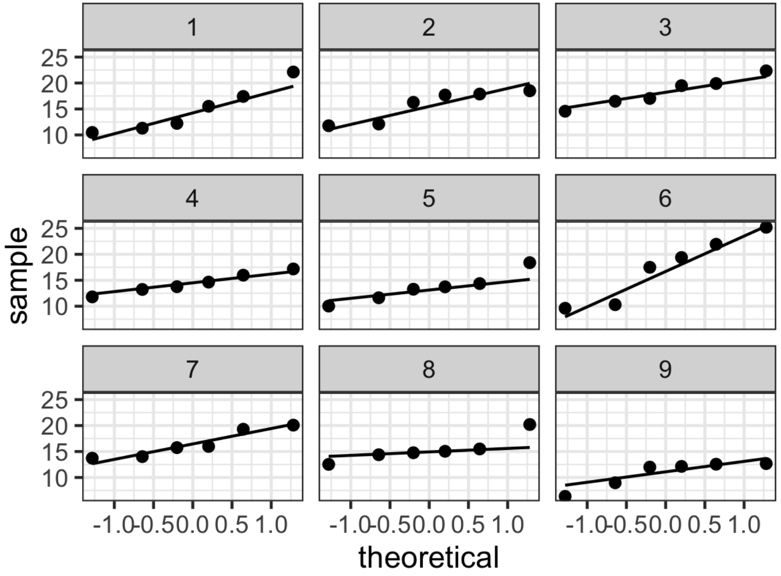
Confidence Intervals: Biochemical Oxyden Demand

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.

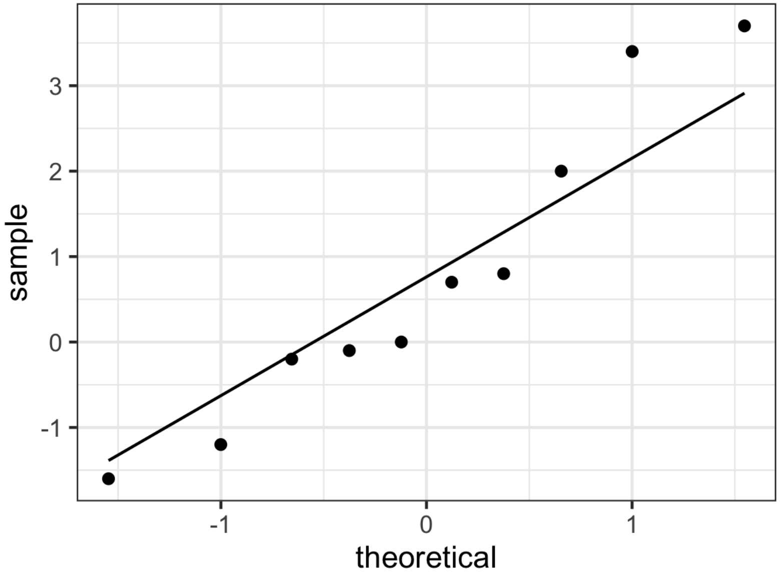
```
sleep1 <- sleep %>% filter(group == 1)
sleep1
```

```
##    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()
```



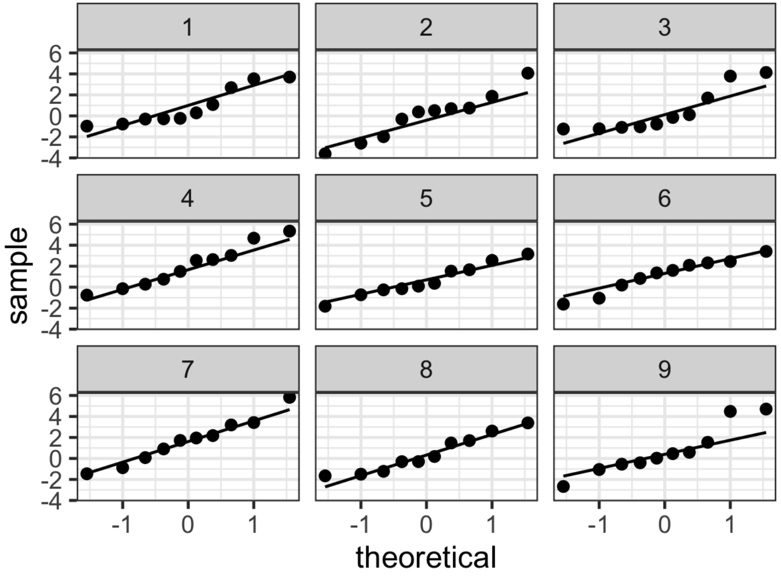
Confidence Intervals: Effect of Drug on Sleep

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:

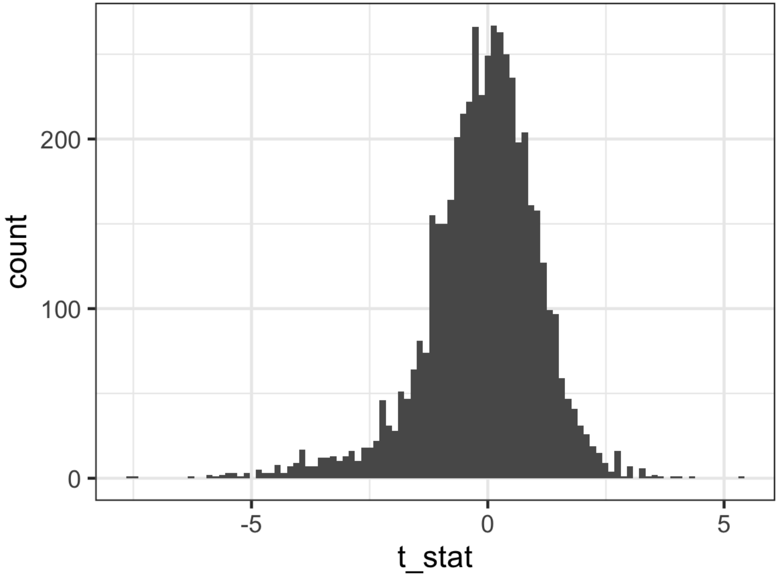
```r
xbar <- mean(sleep1$extra)

bootstrap_samples <- tibble(i = 1:5000) %>%
  mutate(boot_samples = map(i, ~sample_n(sleep1, size = 10, replace = TRUE)$extra),
         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:

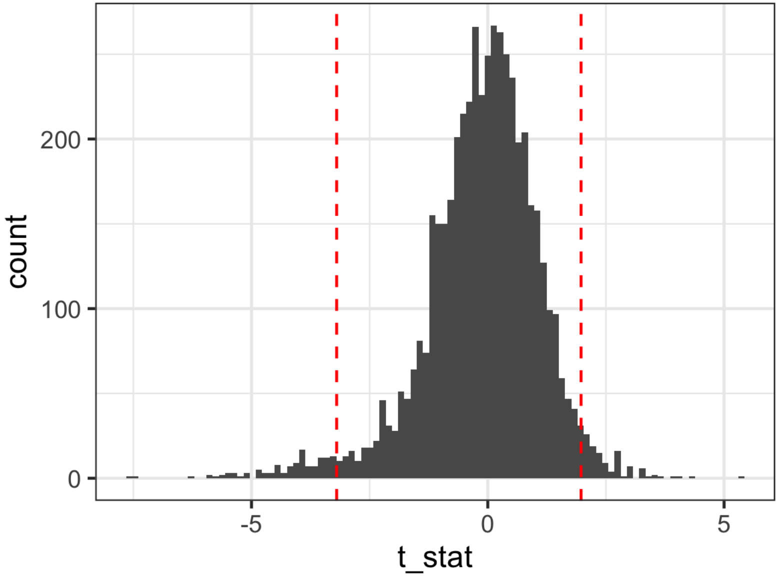
```
ggplot(data = bootstrap_samples,
       aes(x = t_stat)) +
  geom_histogram(bins = 100)
```



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

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