Activity 6A: Cholesterol II

Confidence Intervals for Two Independent Means

Learning outcomes

Part 1: Confidence Interval for Two Independent Means

- Use bootstrapping to find a confidence interval for a difference in means.
- Interpret a confidence interval for a difference in means.
- Use a confidence interval to determine the conclusion of a hypothesis test.

Review from last week

Researchers investigated whether eating corn flakes compared to oat bran had an effect on serum cholesterol levels. Twenty-eight (28) individuals were randomly assigned a diet that included either corn flakes (14 individuals) or oat bran (14 individuals). After two weeks, cholesterol levels (mmol/L) of the participant were recorded.

Last week we used cards to simulate what differences in mean cholesterol levels we might have seen if the null hypothesis was true. However, today we're not interested in deciding if we believe the means of these two groups are similar or different.

Today, we are interested in estimating what range of values the **true** difference in means might take on.

Reminder - Data set

Diet	Cholesterol
CORNFLK	4.61
OATBRAN	3.84
CORNFLK	6.42

Diet	Cholesterol
OATBRAN	5.57
CORNFLK	5.4
OATBRAN	5.85

Reminder - Output from `t_test()`

statistic	t_df	p_value	alternative	estimate	lower_ci	upper_ci
0.9469	25.81	0.3525	two.sided	0.3629	-0.4251	1.151

1. Based on the p-value you obtained from *Activity 5: Cholesterol I*, do you believe 0 is a plausible value for $\mu_{\text{CORNFLK}} - \mu_{\text{OATBRAN}}$?

Yes, with our p-value of 0.352, we failed to reject the null hypothesis with an α cutoff of 0.05 (aka $0.352 > 0.05 \implies$ fail to reject) and thus **did not** have evidence to conclude the difference in population mean cholesterol levels between corn flakes and oat bran is different from 0. Therefore, 0 is a plausible value for $\mu_{\text{CORNFLK}} - \mu_{\text{OATBRAN}}$.

Confidence interval

A **confidence interval** represents a range of plausible values for a population parameter. In this case, our population parameter is $\mu_{\text{CORNFLK}} - \mu_{\text{OATBRAN}}$, or the true difference in mean cholesterol levels between corn flake and oat bran diets.

The best way to estimate what range of values a parameter might have is to go out and collect more samples. However, that is often not feasible. So, instead we mimic this process by *resampling with replacement* from our original sample. This process is called **bootstrapping**.

Bootstrapping cholesterol & diets

When bootstrapping with two groups, we're assuming that the sample within each group is *representative* of other possible values in the population. Here, we are assuming that the participants included in our sample are representative of the cholesterol of all other individuals.

Because we **are not** assuming the null is true (that there is no difference in the means of these two groups), we **do not** combine the groups together. Rather, we keep the groups separate and sample from each group separately.

2. Let's walk through how we would carry out this process:

Step 1: Get 28 cards.

Step 2: Write the diet and cholesterol for each individual on the cards.

Step 3: Resample 28 cards with replacement from the original sample.

Step 4: Calculate the summary statistic of interest from the new resample.

3. What statistic do we have after step 4?

We need the observed difference in mean cholesterol levels between corn flakes and oat bran for our new resample ($\bar{x}_{\text{CORNFLK}} - \bar{x}_{\text{OATBRAN}}$).

4. Once we create a bootstrap distribution of 1000 simulations, at what value do you expect the distribution to be centered? Explain your reasoning.

We expect the bootstrap sampling distribution to be centered at our original observed sample statistic ($\bar{x}_{\text{CORNFLK}} - \bar{x}_{\text{OATBRAN}}$) of 0.363, because this is our point estimate / best guess for our population parameter.

Creating a bootstrap distribution in R

We will use the **infer** package (again) to make our bootstrap distribution. The process we used for this situation will look very similar to before, since all we are changing is the statistic we calculate!

5. Fill in the blanks for the code below.

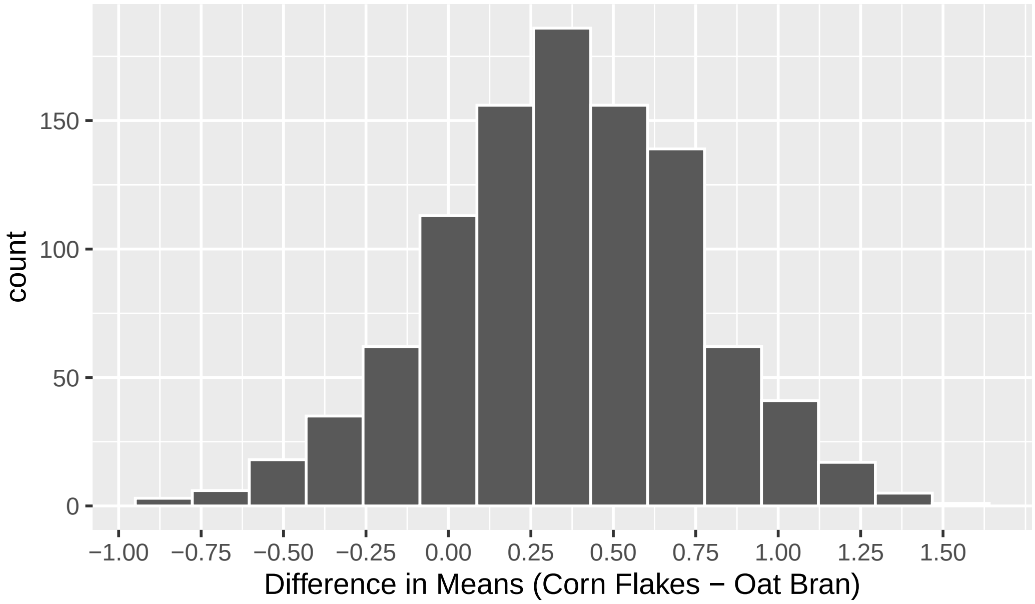
```
cholesterol_data_long %>%

  specify(response = Cholesterol, explanatory = Diet) %>%

  generate(reps = 1000, type = "bootstrap") %>%

  calculate(stat = "diff in means",
            order = c("CORNFLK", "OATBRAN")
            )
```

6. What is the difference between this code and the code to generate a null distribution (what we did in *Activity 5: Cholesterol I*)?

When creating our null distribution in Activity 5, we set our ‘type = ”permute”‘ instead of ‘type = ”bootstrap”‘.

Obtaining a confidence interval

A bootstrap distribution from 1000 reps is plotted below.



7. Where is this distribution centered? Why does this make sense? How does it compare to our Null Distribution from the previous activity?

The distribution is centered at about 0.363; this makes sense because it is our observed summary statistic from our original sample. Our null distribution was centered at 0 because were were simulating the sampling distribution **if** the null was true.

8. What are the two ways we could use this distribution to obtain a confidence interval?

We can use this distribution to (1) find the values associated with quantiles that correspond to our confidence level; aka ”percentile method” or (2) use the bootstrap sampling distribution to estimate our standard error for the difference in means; aka the ”standard error method”.

Percentile method

I’ve provided a table of different percentiles to help you create your confidence interval.

Quantile	Value
0.5%	-0.703

Quantile	Value
1%	-0.572
2.5%	-0.446
5%	-0.298
10%	-0.138
90%	0.824
95%	0.992
97.5%	1.097
99%	1.215
99.5%	1.307

9. Suppose we are interested in constructing a 95% confidence interval. Using the table above, report the end points of this confidence interval.

To construct a 95% confidence interval, we select our 2.5th and 97.5th quantile values so there is 2.5% in both tails and 95% in the middle of our distribution: (-0.446, 1.097).

10. Interpret the confidence interval in the context of this investigation.

We are 95% confident the true difference in mean cholesterol level between corn flakes and oat bran is between -0.446 mmol/L and 1.097 mmol/L ($\mu_{cornflakes} - \mu_{oatbran}$).

SE method

A percentile confidence interval uses **only** the bootstrap distribution. The SE method on the other hand uses information from both the bootstrap distribution and the t-distribution.

Because this method uses a t-distribution it should only be used **if the bootstrap distribution is bell-shaped and symmetric**.

11. Do you believe this condition is violated?

Our bootstrap distribution is bell-shaped/symmetric, therefore we can use the t-distribution.

Alright, let's see how this confidence interval works. Our formula looks like this:

$$(\bar{x}_{\text{CORNFLK}} - \bar{x}_{\text{OATBRAN}}) \pm t^*_{df} \times SE_{boot}$$

There are three pieces to the interval:

- the observed statistic $(\bar{x}_{\text{CORNFLK}} - \bar{x}_{\text{OATBRAN}})$
- the t-distribution multiplier (t^*_{df})

- the standard error from the bootstrap distribution (SE_{boot})

12. What is the observed statistic (aka point estimate) for this investigation?

$\bar{x}_{\text{CORNFLK}} - \bar{x}_{\text{OATBRAN}} = 0.3628571$

13. Using the table below, what is the standard deviation for the bootstrap distribution (aka the estimated standard error for the difference in mean cholesterol levels)?

```
favstats(~stat, data = bootstrap_dist)
```

```
       min       Q1    median       Q3      max      mean        sd    n
-0.8588718 0.103817 0.3650861 0.618274 1.557857 0.3538702 0.3847116 1000
missing
      0
```

$SE_{\text{boot}} = 0.385$

14. Using the table below, circle the correct multiplier we should use to make our interval.

R code	Value
qt(0.90, df = 12)	1.3562173
qt(0.90, df = 13)	1.3501713
qt(0.90, df = 26)	1.3149719
qt(0.95, df = 12)	1.7822876
qt(0.95, df = 13)	1.7709334
qt(0.95, df = 26)	1.7056179
qt(0.975, df = 12)	2.1788128
qt(0.975, df = 13)	2.1603687
qt(0.975, df = 26)	2.0555294
qt(0.995, df = 12)	3.0545396
qt(0.995, df = 13)	3.0122758
qt(0.995, df = 26)	2.7787145

We are looking for a 95% confidence interval; thus we need the 97.5th quantile from the t-distribution with 13 degrees of freedom (smallest of $n_{CORNFLK} - 1$ and $n_{OATBRAN} - 1$: $t^*_{13} = 2.16$.

15. Using your answers to questions 12, 13, and 14, create a 95% confidence interval for the difference in mean cholesterol levels between the corn flake and oat bran diet.

$(\bar{x}_{\text{CORNFLK}} - \bar{x}_{\text{OATBRAN}}) \pm t^*_{df} \times SE_{boot}$ = 0.363 ± 2.16 × 0.385 = (-0.492, 1.218)

16. What value do check to see if this interval contains? Does our interval contain this value?

We look to see if our null value of 0 (aka no difference in means) falls within our confidence interval. Our interval contains 0, therefore we fail to reject the null hypothesis of $\mu_{cornflakes} - \mu_{oatbran} = 0$.

Using the t-distribution to create a confidence interval

So far we've found a confidence interval using the percentile and SE methods. Both of these used some aspect of the bootstrap distribution. One final option is to use the t-distribution only to create our confidence interval.

17. What distribution does a bootstrap distribution approximate?

The bootstrap distribution approximates the tue sampling distribution from our population. That is, it approximates the distribution of statistics that could have happened if we would have collected many many samples from the population.

18. If we wanted to use a t-distribution to approximate this distribution, what conditions do we need to check?

We need to check independence of observations and normality of our response variable in order to us a t-distribution to approximate this distribution.

When we use theory-based methods to obtain our confidence interval, we use formulas to approximate the true standard error of the sampling distribution. So, where we used the standard deviation of the bootstrap distribution, now we will use a mathematical formula.

The formula for calculating the standard error of $\bar{x}_{\text{CORNFLK}} - \bar{x}_{\text{OATBRAN}}$ is:

$$SE = \sqrt{\frac{s^2_{\text{CORNFLK}}}{n_{\text{CORNFLK}}} + \frac{s^2_{\text{OATBRAN}}}{n_{\text{OATBRAN}}}}$$

```
favstats(Cholesterol ~ Diet, data = cholesterol_data_long)
```

```
     Diet  min     Q1 median     Q3  max     mean        sd  n missing
1 CORNFLK 2.25 3.9125   4.44 4.9100 6.42 4.443571 0.9688344 14       0
2 OATBRAN 1.84 3.6900   3.84 4.7025 5.85 4.080714 1.0569802 14       0
```

19. Using the formula and the summary statistics above, calculate the estimated standard error of the sampling distribution. *Hint:* s is the standard deviation!

$$SE = \sqrt{\frac{s^2_{\text{CORNFLK}}}{n_{\text{OATBRAN}}} + \frac{s^2_{\text{CORNFLK}}}{n_{\text{OATBRAN}}}} = \sqrt{\frac{0.969^2}{14} + \frac{1.057^2}{14}} = \sqrt{0.067 + 0.0798} = 0.383$$

Now that we have the standard error, we can put all of the pieces of the confidence interval together! The "formula" for a t-based confidence interval is:

$$\overline{x}_{\text{CORNFLK}} - \overline{x}_{\text{OATBRAN}} \pm t^*_{df} \times SE$$

20. Using the multiplier you found in #14, calculate a 95% confidence interval for $\mu_{\text{CORNFLK}} - \mu_{\text{OATBRAN}}$.

$$(\bar{x}_{\text{CORNFLK}} - \bar{x}_{\text{OATBRAN}}) \pm t^*_{df} \times SE_{boot} = 0.363 \pm 2.16 \times 0.383 = (-0.464, 1.190)$$

21. Alright, you've made **three** confidence intervals. How are they similar or different?

The percentile interval was (-0.446, 1.097). The SE interval was (-0.492, 1.218). The t-distribution intervale was (-0.464, 1.190). Overall, these confidence intervals are quite similar. The SE interval is the widest and the percentile interval is the narrowest.

Take-home messages

- To create one simulated sample on the bootstrap distribution for a difference in sample means, label $n_1 + n_2$ cards with the original response values. Keep groups separate and randomly draw with replacement n_1 times from group 1 and n_2 times from group 2. Calculate and plot the resampled difference in means.
- When using a bootstrap distribution to obtain a confidence interval, there are two methods you can use: the percentile method and the SE method.
- The SE method for creating confidence intervals requires the bootstrap distribution be bell-shaped and symmetric.

- The percentile method makes no assumptions about the shape of the bootstrap distribution.
- You can choose between simulation-based methods (e.g., bootstrapping) and theory-based methods (e.g., t-distribution) to create a confidence interval.
- Simulation-based conditions only require that the observations are independent.
- Theory-based methods require that the observations are independent **and** that the distribution of each group is nearly normal.
- If the conditions for theory-based methods **are not** violated, then both methods (theory & simulation) will yield similar results.
- If the conditions for theory-based methods **are** violated, then the methods **will not** yield similar results.
- If the conditions for theory-based methods **are** violated, using a t-distribution to find a p-value will **underestimate** the true p-value. A t-distribution will also result in a confidence interval that is **too narrow**!