Lesson 13: Inference for mean difference from two-sample dependent/paired data (Hypothesis testing 2)

TB sections 5.2

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2025-11-10

Learning Objectives

1. Define paired data and explain how it differs from independent 1-sample data.
2. Construct confidence intervals for the mean difference in paired data and interpret these intervals in the context of the research question.
3. Perform the appropriate hypothesis test for paired data and interpret the results.

Where are we?

Data

- Collecting data
- Categorical vs. Numeric
- Summary statistics
- Data visualization

Probability

- Probability rules
- Independence, conditional
- Random variables and probability distributions
- Linear combinations
- Binomial, Normal, and Poisson

Sampling Variability, and Statistical Inference

- Sampling distributions
- Central Limit Theorem
- Confidence Intervals
- Hypothesis tests

Inference for continuous data/outcomes

- One sample t-test
- 3+ independent samples
- Simple linear regression / correlation
- 2 sample tests: paired and independent
- Power and sample size
- Non-parametric tests

Inference for categorical data/outcomes

- One proportion test
- Fisher's exact test
- Non-parametric tests
- Chi-squared test
- 2 proportion test
- Power and sample size

R

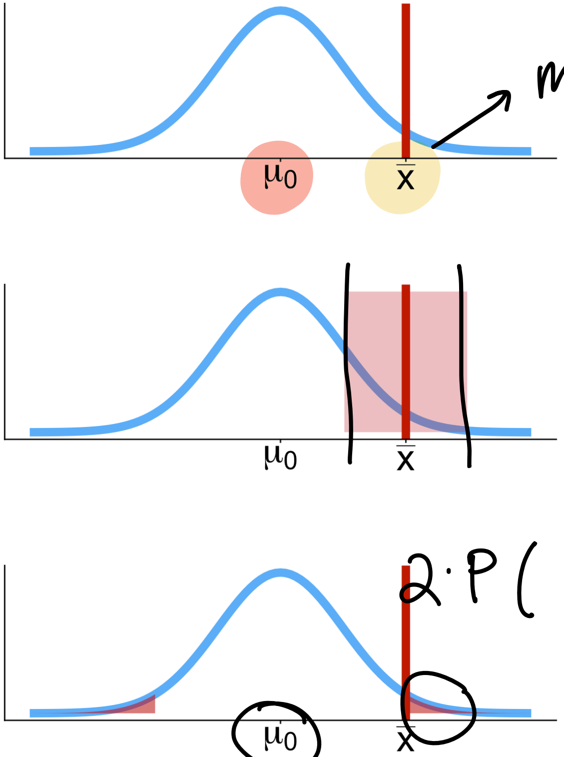
- Basics
- Reproducibility
- Quarto
- Packages
- Data visualization
- Data wrangling
- R Projects
- …

Last 2 times: Inference for a single-sample mean

- Inference for a single-sample mean includes:
  1. Confidence intervals (Lesson 11)
  2. Hypothesis testing (Lesson 12)
     - Find p-value and compare to α

μ_0: what we think pop mean (μ) is

Single-sample mean under the null distribution:



mean from sample

$2 \cdot P(X \geq \bar{x})$

prob that we have $\bar{x}$ or more extreme value

Last time: example of a hypothesis test for a single-sample mean

Example of hypothesis test based on the 1992 JAMA data

Is there evidence to support that the population mean body temperature is different from 98.6°F?

1. **Assumptions:** The individual observations are independent and the number of individuals in our sample is 130. Thus, we can use CLT to approximate the sampling distribution.

2. Set $\alpha = 0.05$

3. **Hypothesis:**

$$\begin{aligned} & H_0 : \mu = 98.6 \\ \text{vs. } & H_A : \mu \neq 98.6 \end{aligned}$$

4-5. Calculate t-statistic and p-value

```r
temps_ttest <- t.test(x = BodyTemps$Temperature, mu = 98.6)
tidy(temps_ttest) %>% gt() %>% tab_options(table.font.size = 36)
```

estimate	statistic	p.value	parameter	conf.low	conf.high	method	alternative
98.24923	-5.454823	2.410632e-07	129	98.122	98.37646	One Sample t-test	two.sided

6. **Conclusion:** We reject the null hypothesis. The average body temperature in the sample was 98.25°F (95% CI 98.12, 98.38°F), which is discernibly different from 98.6°F (p-value < 0.001).

Different types of inference based on different data types

Lesson	Section	Population parameter	Symbol (pop)	Point estimate	Symbol (sample)	SE
~~11~~ 12	5.1	Pop mean	μ	Sample mean	$\overline{x}$	$\frac{s}{\sqrt{n}}$
~~12~~ 13	5.2	Pop mean of paired diff	μ_d or δ	Sample mean of paired diff	$\overline{x}_d$	???
~~13~~ 14	5.3	Diff in pop means	$\mu_1 - \mu_2$	Diff in sample means	$\overline{x}_1 - \overline{x}_2$	
~~15~~ 16	8.1	Pop proportion	p	Sample prop	$\widehat{p}$	
~~15~~ 16	8.2	Diff in pop prop's	$p_1 - p_2$	Diff in sample prop's	$\widehat{p}_1 - \widehat{p}_2$	

Learning Objectives

1. Define paired data and explain how it differs from independent samples in the context of statistical analysis.
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What are paired data?

- **Paired data:** two sets of observations are uniquely paired so that an observation in one set matches an observation in the other

- Examples
    - Enroll pairs of identical twins to study a disease
    - Enroll people and collect data before & after an intervention (longitudinal data)
    - Textbook example: Compare maximal speed of competitive swimmers wearing a wetsuit vs. wearing a regular swimsuit

diff of max speed

- Paired data result in a **natural measure of difference**
    - Example: Enroll parent and child pairs to study cholesterol levels
        - We can look at the difference in cholesterol levels between parent and child

For paired data: Population parameters vs. sample statistics

Population parameter

- Mean difference: δ (“delta”, lowercase)
- Standard deviation: σ_d (“sigma”)
- Variance: σ_d^2

Sample statistic (point estimate)

- Sample mean difference: $\overline{x}_d$
- Sample standard deviation: s_d
- Sample variance: s_d^2

- Using d (for difference) helps us distinguish between a single sample and paired data

Can a vegetarian diet change cholesterol levels?

- We will illustrate how to perform a hypothesis test and calculate a confidence interval for paired data as we work through this example
- **Scenario**:
  - 43 non-vegetarian people were enrolled in a study and were instructed to adopt a vegetarian diet
  - Cholesterol levels were measured before and after the vegetarian diet

Question: Is there evidence to support that cholesterol levels changed after the vegetarian diet?

- How do we answer this question?
  - First, calculate changes (differences) in cholesterol levels
    - We usually do after - before if the data are longitudinal
  - Then find CI or perform hypothesis test on the difference

EDA: Explore the cholesterol data

- Read in the data with `read.csv()`

```r
chol <- read.csv(here::here("data", "chol213_n40.csv"))
```

- Take a look at the variables with `glimpse()`

```r
glimpse(chol)
```

```
Rows: 43
Columns: 2
$ Before <int> 195, 145, 205, 159, 244, 166, 250, 236, 192, 224, 238, 197, 169…
$ After  <int> 146, 155, 178, 146, 208, 147, 202, 215, 184, 208, 206, 169, 182…
```

→ each row is an individual

↳ chol measures

- Get summary statistics with `get_summary_stats()`

gt(get_summary_stats(chol))

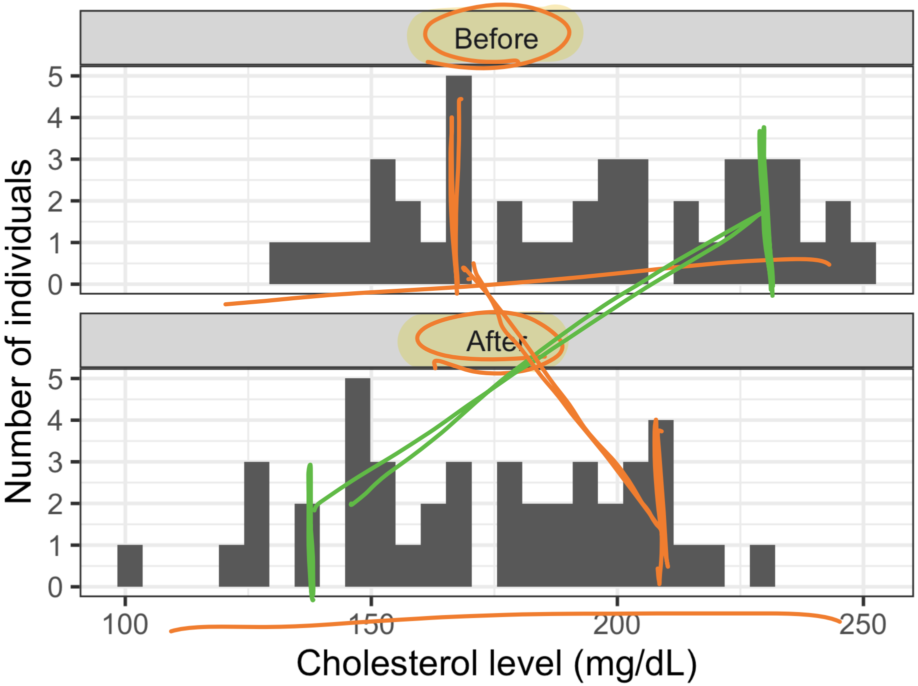
```r
chol %>% get_summary_stats(type = "common") %>%
  gt() %>% tab_options(table.font.size = 40)
```

variable	n	min	max	median	iqr	mean	sd	se	ci
Before	43	132	250	197	56.5	193.977	34.098	5.200	10.494
After	43	101	227	176	50.5	172.209	31.112	4.744	9.575

EDA: Cholesterol levels before and after vegetarian diet

- Behind the scenes: I changed the data from wide to long format to make this plot (to be covered in R08)

```
ggplot(chol_long, aes(x = Cholesterol)) + geom_histogram() +
  facet_wrap(~ Time, ncol = 1) +
  labs(y = "Number of individuals", x = "Cholesterol level (mg/dL)")
```



EDA: Differences in cholesterol levels: After - Before diet

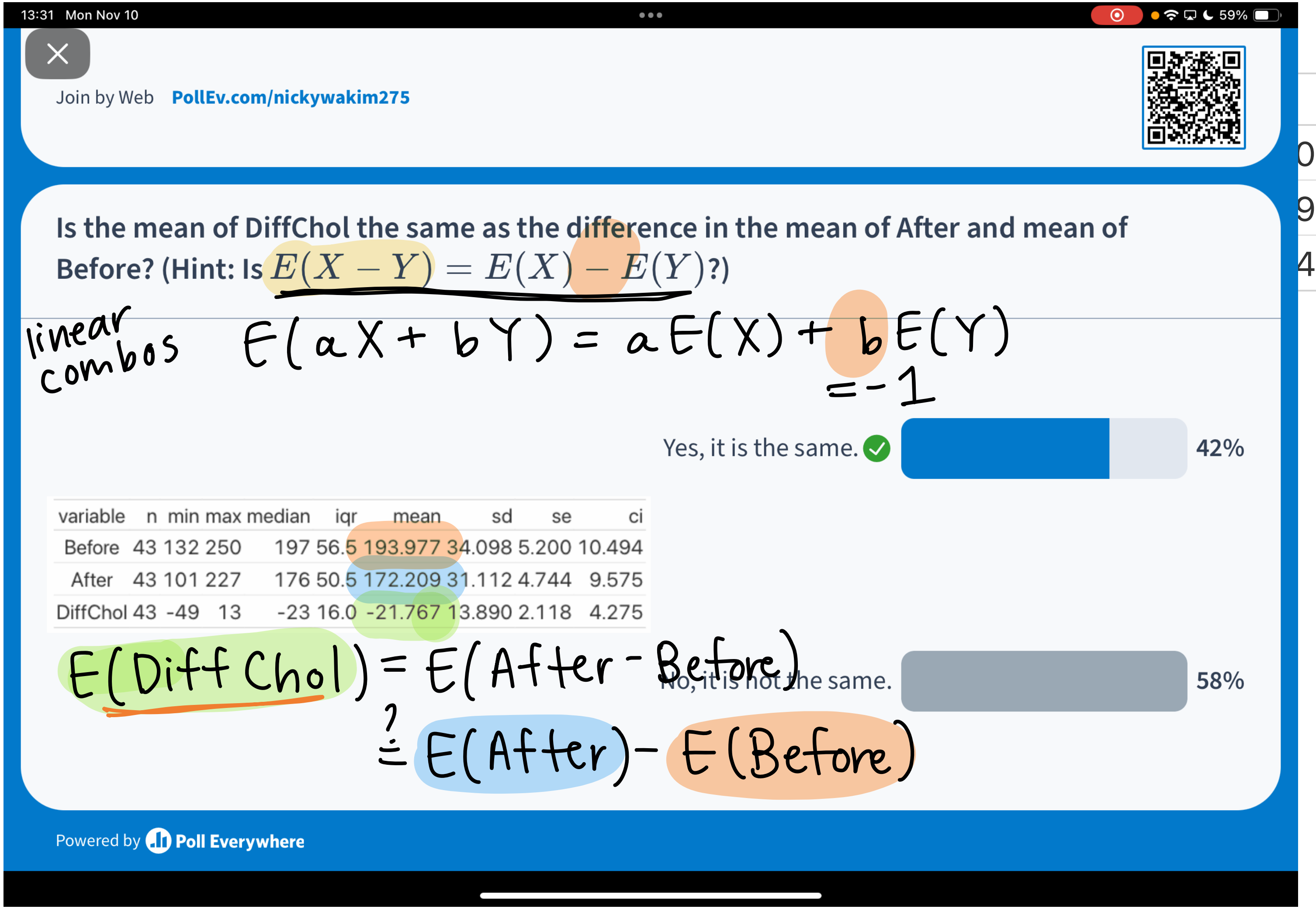
- How do we calculate the difference in cholesterol levels?
- I can create a new variable called “DiffChol” using the `mutate()` function (look more closely at this in R08)

```r
chol <- chol %>%
  mutate(DiffChol = After - Before)
glimpse(chol)
```

```
Rows: 43
Columns: 3
$ Before   <int> 195, 145, 205, 159, 244, 166, 250, 236, 192, 224, 238, 197, 1…
$ After    <int> 146, 155, 178, 146, 208, 147, 202, 215, 184, 208, 206, 169, 1…
$ DiffChol <int> -49, 10, -27, -13, -36, -19, -48, -21, -8, -16, -32, -28, 13,…
```

$$\begin{aligned} \text{DiffChol} &= \text{After} - \text{Before} \\ &= 146 - 195 = -49 \end{aligned}$$

Poll Everywhere Question 1



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Is the mean of DiffChol the same as the difference in the mean of After and mean of Before? (Hint: Is $E(X-Y) = E(X) - E(Y)$?)

linear combos $E(aX + bY) = aE(X) + \underset{=-1}{b}E(Y)$

Yes, it is the same. ✓ 42%

variable	n	min	max	median	iqr	mean	sd	se	ci
Before	43	132	250	197	56.5	193.977	34.098	5.200	10.494
After	43	101	227	176	50.5	172.209	31.112	4.744	9.575
DiffChol	43	-49	13	-23	16.0	-21.767	13.890	2.118	4.275

No, it is not the same. 58%

$E(\text{Diff Chol}) = E(\text{After} - \text{Before})$

$\overset{?}{=} E(\text{After}) - E(\text{Before})$

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ci
0.494
9.575
4.275

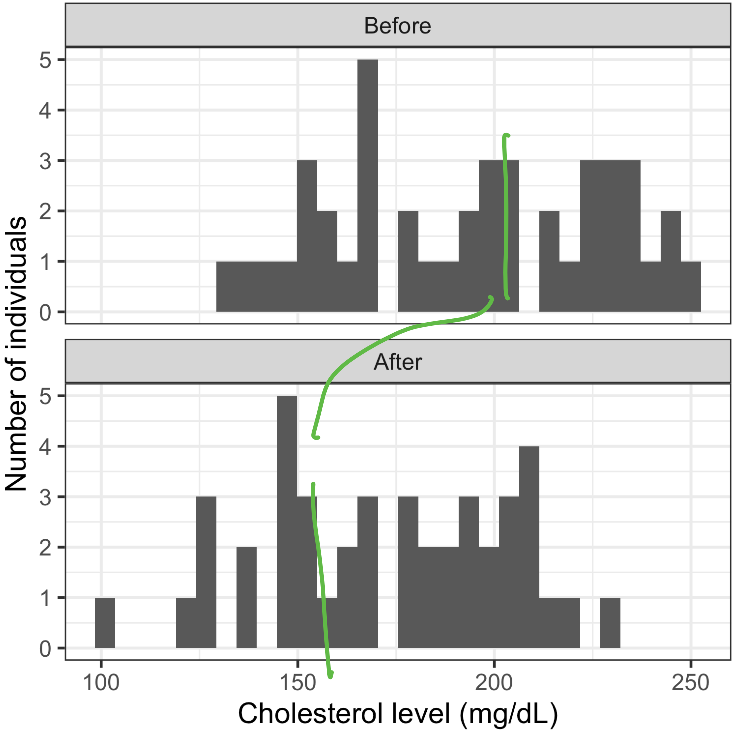
$E(\text{After}) - E(\text{Before})$

$= 172.209 - 193.977$

$= -21.768$

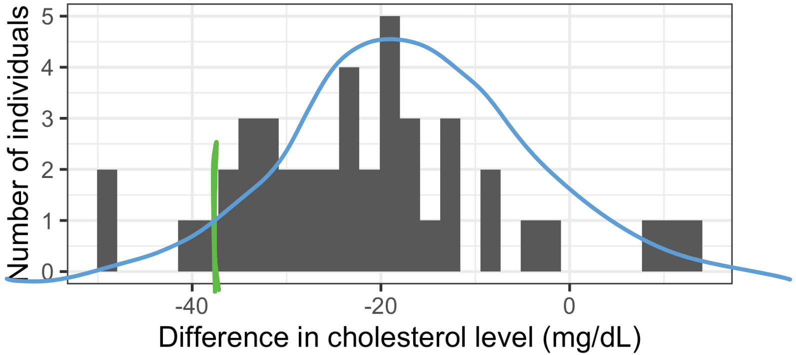
EDA: Differences in cholesterol levels: After - Before diet

- Code for below plot



Difference:

```
ggplot(chol, aes(x=DiffChol)) +
  geom_histogram() +
  labs(y = "Number of individuals",
       x = "Difference in cholestero
```



δ (pop diff) is also normally distributed (by central limit theorem)

Same distribution: single-sample mean & paired mean difference (1/2)

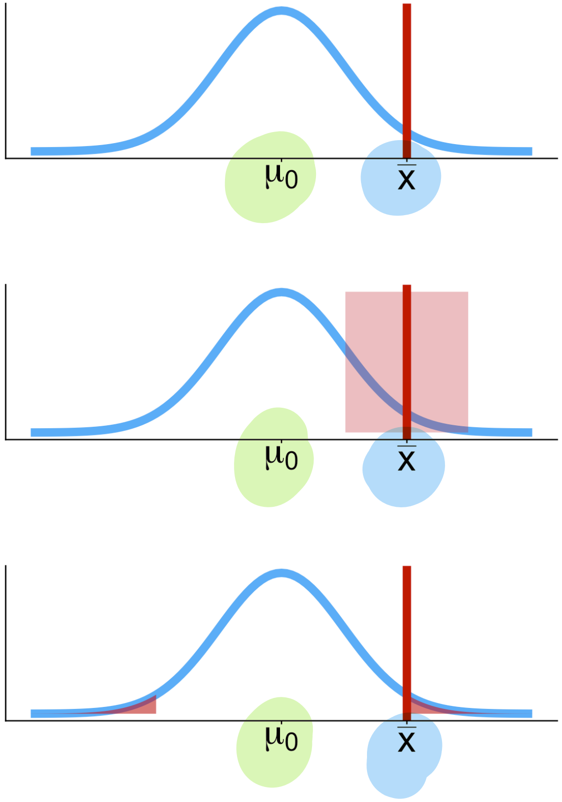
- Even though we are looking at a difference, we have a single sample mean to represent the difference
  - Before, we had single sample mean $\overline{x}$
  - Now we have a sample mean difference $\overline{x}_d$

- Distribution for the mean difference for paired data is the same as the distribution for a single mean
  - Use the t-distribution to build our inference

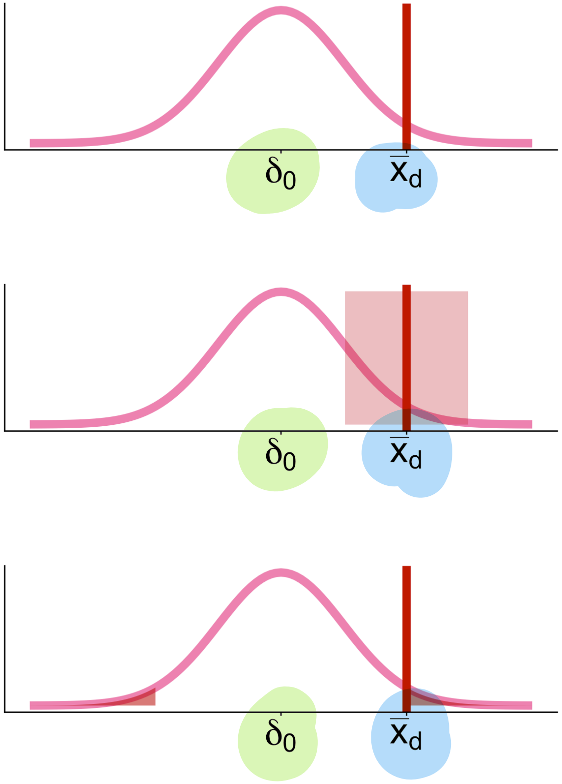
- We can use the same procedure for confidence intervals and hypothesis testing as we did for the single-sample mean

Same distribution: single-sample mean & paired mean difference (2/2)

Single-sample mean:



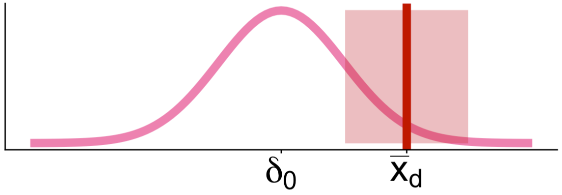
Paired mean difference:



Approaches to answer a research question

- **Research question is a generic form for paired data:** Is there evidence to support that the population mean difference is different than δ_0?

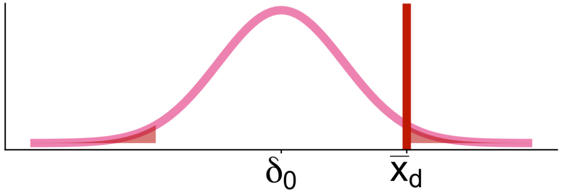
Calculate **CI for the mean difference** δ:



$$\overline{x}_d \pm t^* \cdot \frac{s_d}{\sqrt{n}}$$

- with t^* = t-score that aligns with specific confidence interval

Run a **hypothesis test:**



Hypotheses

$$H_0: \delta = \delta_0$$
$$H_A: \delta \neq \delta_0$$

$(or \ <, >)$

Test statistic

$$t_{\overline{x}_d} = \frac{\overline{x}_d - \delta_0}{\frac{s_d}{\sqrt{n}}}$$

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95% CI for the mean difference in cholesterol levels

```r
chol %>%
  select(DiffChol) %>%
  get_summary_stats(type = "common") %>%
  gt() %>% tab_options(table.font.size = 40)
```

picking variable DiffChol

taking summary stats

cleaning up presentation

variable	n	min	max	median	iqr	mean	sd	se	ci
DiffChol	43	-49	13	-23	16	-21.767	13.89	2.118	4.275

95% CI for population mean difference δ:

$$\bar{x}_d \pm t^* \cdot \frac{s_d}{\sqrt{n}}$$

$$-21.767 \pm 2.018 \cdot \frac{13.89}{\sqrt{43}}$$

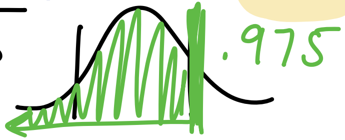
$$-21.767 \pm 2.018 \cdot 2.118$$

$$-21.767 \pm 4.275$$

$$(-26.042, -17.493)$$

df = n - 1 = 43 - 1

Used t^* = `qt(0.975, df=42)` = 2.018



Conclusion:

We are 95% confident that the (population) mean difference in cholesterol levels after a vegetarian diet is between -26.042 mg/dL and -17.493 mg/dL.

95% CI for the mean difference in cholesterol levels (using R)

- We can use R to get those same values

$H_0: \underline{\delta} = 0$

```
t.test(x = chol$DiffChol, mu = 0)
```

go into column w/ name DiffChol

```
	One Sample t-test

data:  chol$DiffChol
t = -10.276, df = 42, p-value = 4.946e-13
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -26.04229 -17.49259
sample estimates:
mean of x
-21.76744
```

- ▶ We can tidy the output

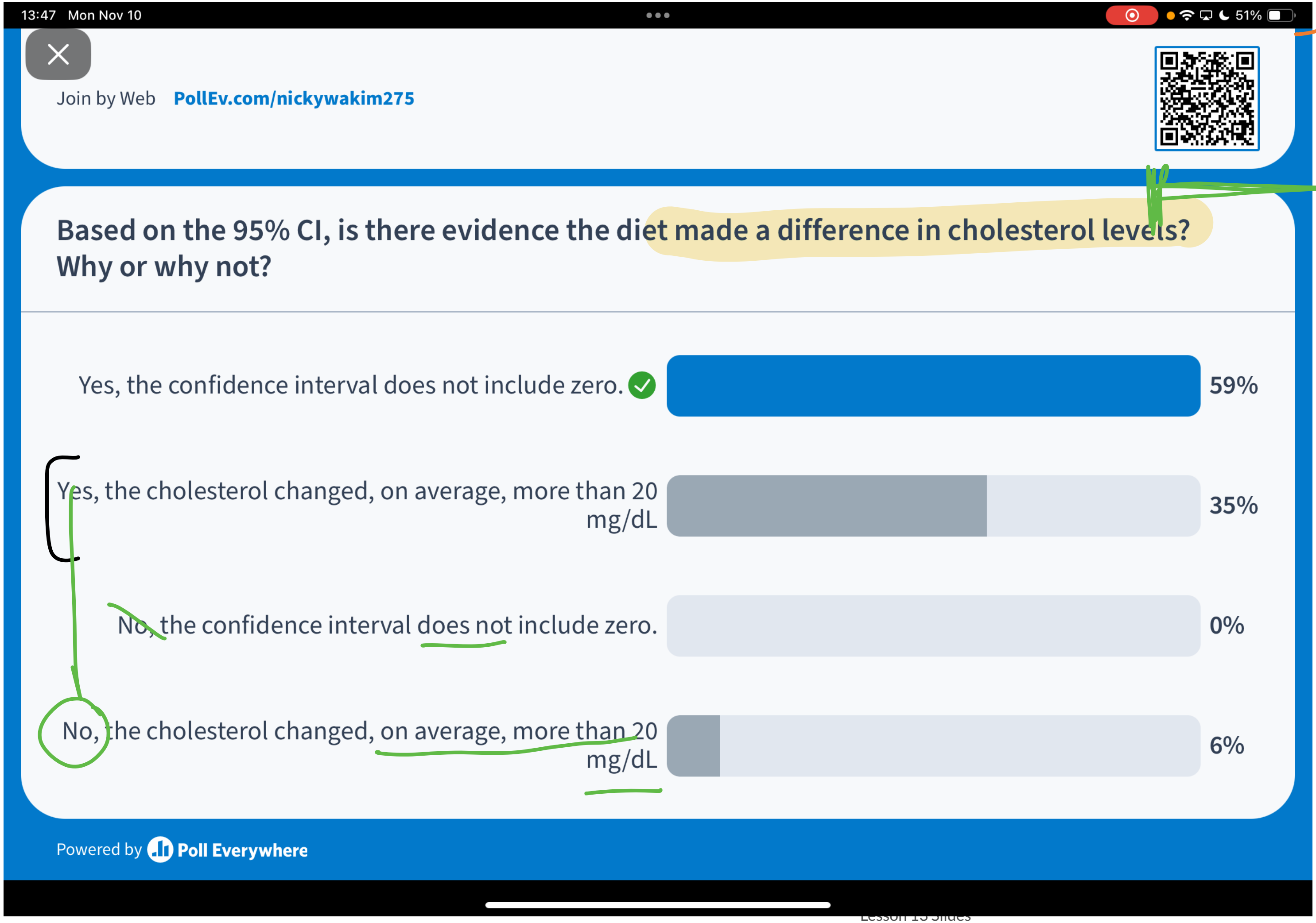
estimate	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-21.76744	-10.27603	4.945625e-13	42	-26.04229	-17.49259	One Sample t-test	two.sided

Conclusion:

We are 95% confident that the (population) mean difference in cholesterol levels after a vegetarian diet is

between -26.042 mg/dL & -17.493 mg/dL

Poll Everywhere Question 2



13:47 Mon Nov 10

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Based on the 95% CI, is there evidence the diet made a difference in cholesterol levels? Why or why not?

Yes, the confidence interval does not include zero. ✓	59%
Yes, the cholesterol changed, on average, more than 20 mg/dL	35%
No, the confidence interval does not include zero.	0%
No, the cholesterol changed, on average, more than 20 mg/dL	6%

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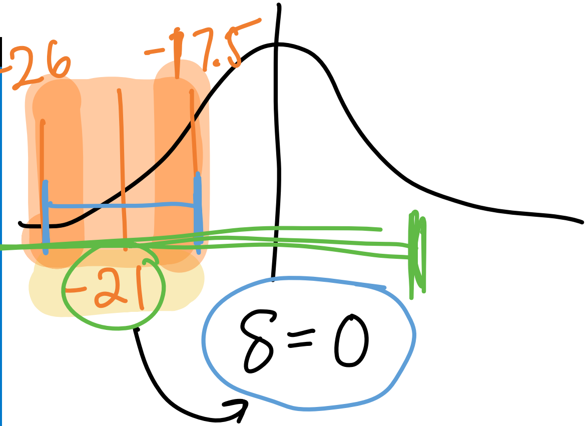

CI does not cover 0

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Reference: Steps in a Hypothesis Test

1. Check the **assumptions**
2. Set the **level of significance** α
3. Specify the **null** (H_0) and **alternative** (H_A) **hypotheses**
    1. In symbols
    2. In words
    3. Alternative: one- or two-sided?
4. Calculate the **test statistic**.
5. Calculate the **p-value** based on the observed test statistic and its sampling distribution
6. Write a **conclusion** to the hypothesis test
    1. Do we reject or fail to reject H_0?
    2. Write a conclusion in the context of the problem

before we look @ data

Step 1: Check the assumptions

- The assumptions to run a hypothesis test on a sample are:
  - **Independent pairs**: Each pair is independent from all other pairs,
  - **Approximately normal sample or big n**: the distribution of the sample should be approximately normal, *or* the sample size should be at least 30

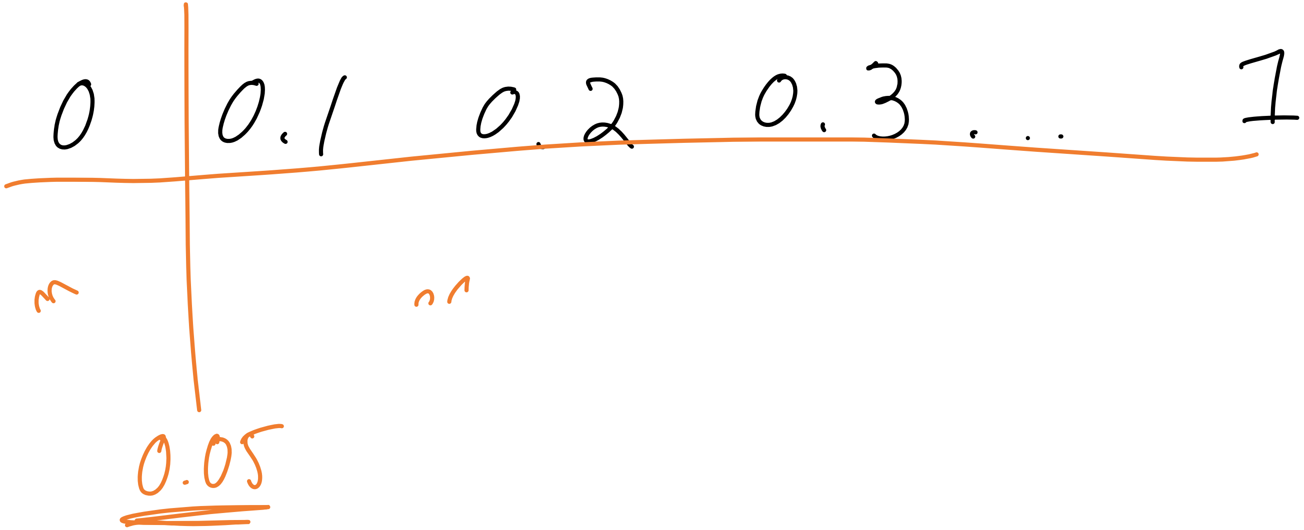
- These are the criteria for the Central Limit Theorem in Lesson ~~09~~ 10: Variability in estimates

- In our example, we would check the assumptions with a statement:
  - The pairs of observations are independent from each other and the number of pairs in our sample is 43. Thus, we can use CLT to approximate the sampling distribution.

Step 2: Set the level of significance α

- **Before doing a hypothesis test**, we set a cut-off for how small the p-value should be in order to reject H_0.
- Typically choose $\alpha = 0.05$

- See Lesson ~~11~~ 12: Hypothesis Testing 1: Single-sample mean



Step 3: Null & Alternative Hypotheses (1/2)

In statistics, a **hypothesis** is a statement about the value of an **unknown population parameter**.

A **hypothesis test** consists of a test between two competing hypotheses:

1. a **null** hypothesis H_0 (pronounced "H-naught") vs.
2. an **alternative** hypothesis H_A (also denoted H_1)

Example of hypotheses in words:

$$\begin{aligned} H_0 &: \text{The population mean difference in cholesterol levels after a vegetarian diet is zero} \\ \text{vs. } H_A &: \text{The population mean difference in cholesterol levels after a vegetarian diet is} \\ &\quad \text{different than zero} \end{aligned}$$

1. H_0 is a claim that there is "no effect" or "no difference of interest."
2. H_A is the claim a researcher wants to establish or find evidence to support. It is viewed as a "challenger" hypothesis to the null hypothesis H_0

Step 3: Null & Alternative Hypotheses (2/2)

Notation for hypotheses (for paired data)

$$H_0 : \delta = \delta_0$$
$$\text{vs. } H_A : \delta \neq, <, \text{or}, > \delta_0$$

Hypotheses test for example

$$H_0 : \delta = 0$$
$$\text{vs. } H_A : \delta \neq 0$$

We call δ_0 the *null value* (hypothesized population mean difference from H_0)

$H_A : \delta \neq \delta_0$

- not choosing a priori whether we believe the population mean difference is greater or less than the null value δ_0

$H_A : \delta < \delta_0$

- believe the population mean difference is **less** than the null value δ_0

$H_A : \delta > \delta_0$

- believe the population mean difference is **greater** than the null value δ_0

- $H_A : \delta \neq \delta_0$ is the most common option, since it's the most conservative

Step 4: Test statistic (where we do not know population sd)

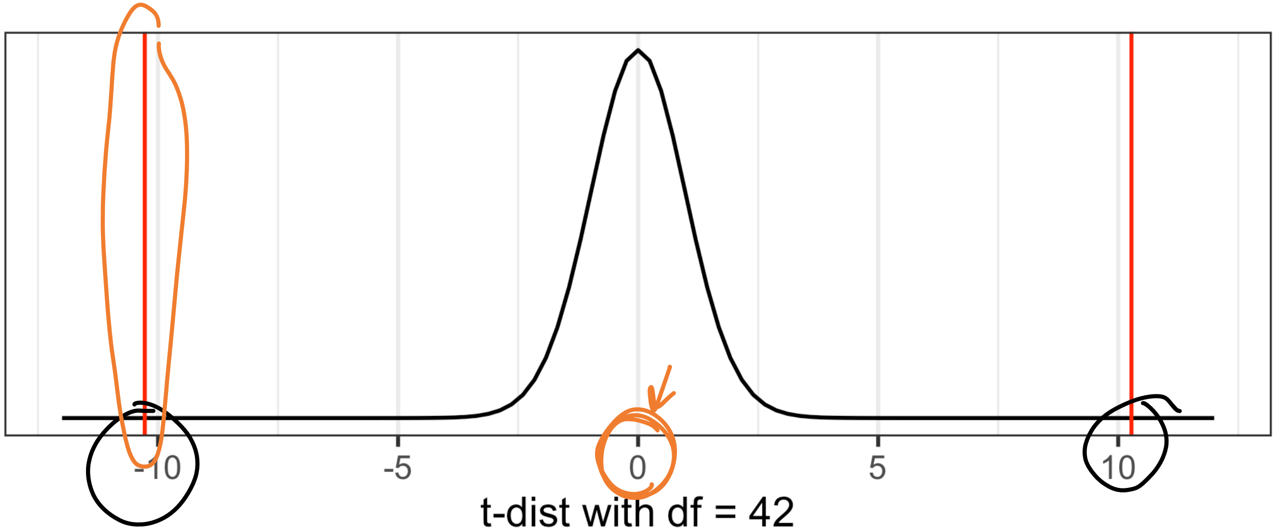
based on sample sd

From our example: Recall that $\overline{x}_d = -21.767$, $s_d = 13.89$, and $n = 43$

The test statistic is:

$$t_{\overline{x}_d} = \frac{\overline{x}_d - \delta_0}{\underbrace{\frac{s_d}{\sqrt{n}}}_{SE}} = \frac{-21.767 - 0}{\frac{13.89}{\sqrt{43}}} = -10.276$$

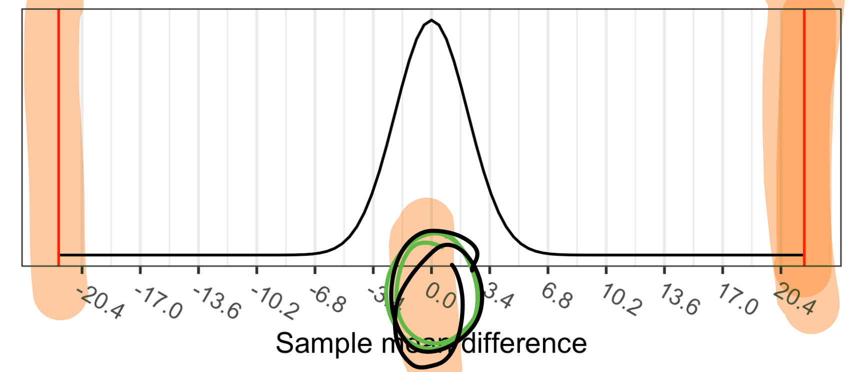
- Statistical theory tells us that $t_{\overline{x}}$ follows a **Student's t-distribution** with $df = n - 1 = 42$

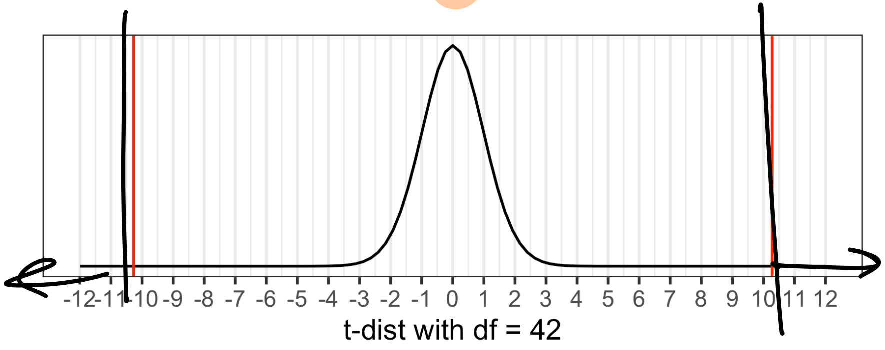


Step 5: p-value

The **p-value** is the **probability** of obtaining a test statistic *just as extreme or more extreme* than the observed test statistic assuming the null hypothesis H_0 is true.

Sampling distribution of mean difference





Calculate the p-value using the **Student's t-distribution** with $df = n - 1 = 43 - 1 = 42$:

$$\text{p-value} = P(T \leq -10.276) + P(T \geq 10.276)$$
$$= 4.946032 \times 10^{-13} < 0.001$$

```
2*pt(-10.276, df = 43-1,
     lower.tail = TRUE)
```

```
[1] 4.946032e-13
```

low p-val: not likely that our observed test stat came from distribution w/ mean of δ_0 (prescribed pop mean difference)

Step 4-5: test statistic and p-value together using `t.test()`

- I will have reference slides at the end of this lesson to show other options

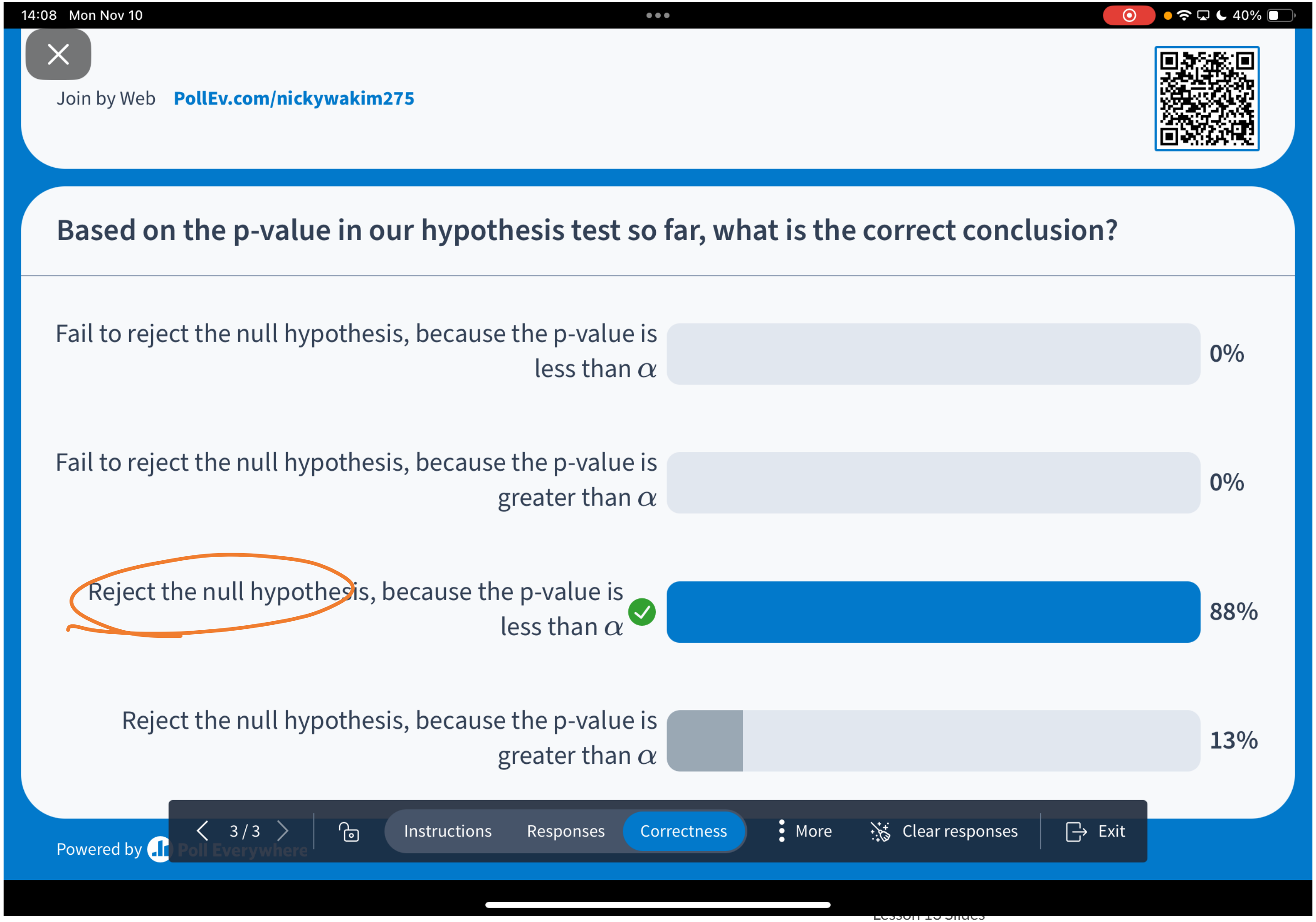
```
t.test(x = chol$DiffChol, mu = 0)
```

```

	One Sample t-test

data:  chol$DiffChol
t = -10.276, df = 42, p-value = 4.946e-13
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -26.04229 -17.49259
sample estimates:
mean of x 
-21.76744 
```

- We can "tidy" the results

```
t.test(x = chol$DiffChol, mu = 0) %>% tidy() %>% gt() %>%
  tab_options(table.font.size = 40) # use a different size in your HW
```

Poll Everywhere Question 3



Based on the p-value in our hypothesis test so far, what is the correct conclusion?

Fail to reject the null hypothesis, because the p-value is less than α	0%
Fail to reject the null hypothesis, because the p-value is greater than α	0%
[✓ Reject the null hypothesis, because the p-value is less than α] ✓	88%
Reject the null hypothesis, because the p-value is greater than α	13%

p-val:

4.946×10^{-13}

< 0.001

$\alpha = 0.05$

$\text{p-val} < 0.001$

$< \alpha = 0.05$

if $\text{p-val} \geq \alpha$

fail to reject

Step 6: Conclusion to hypothesis test

$$H_0 : \delta = \delta_0$$
$$\text{vs. } H_A : \delta \neq \delta_0$$

- Need to compare p-value to our selected $\alpha = 0.05$
- Do we reject or fail to reject H_0?

If p-value $< \alpha$, reject the null hypothesis

- There is sufficient evidence that the (population) mean difference is discernibly different from δ_0 (p-value = ___)
- The mean difference (insert measure) in the sample was $\overline{x}_d$ (95% CI ___,___), which is discernibly different from δ_0 (p-value = ____).

If p-value $\geq \alpha$, fail to reject the null hypothesis

- There is insufficient evidence that the (population) mean difference of (insert measure) is discernibly different from δ_0 (p-value = ___)
- The mean difference (insert measure) in the sample was $\overline{x}_d$ (95% CI ___,___), which is not discernibly different from δ_0 (p-value = ____).

Step 6: Conclusion to hypothesis test

$$H_0 : \delta = 0$$
$$\text{vs. } H_A : \delta \neq 0$$

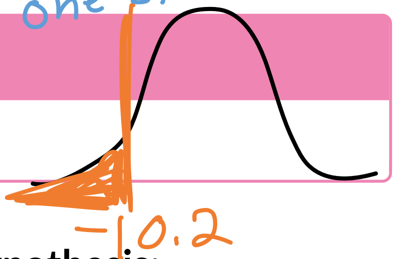
- Recall the p-value = $4.9456253 \times 10^{-13}$
- Use α = 0.05.
- Do we reject or fail to reject H_0?

Conclusion statement:

- Stats class conclusion (and good enough for our class!)
  - There is sufficient evidence that the (population) mean difference in cholesterol levels after a vegetarian diet is different from 0 mg/dL (p-value < 0.001).
- More realistic manuscript conclusion:
  - After a vegetarian diet, cholesterol levels decreased by on average 21.77 mg/dL (95% CI: 17.49, 26.04), which is discernably different than 0 (p-value < 0.001).

What if we wanted to test whether the diet *decreased* cholesterol levels?

one sided:



Example of hypothesis test

Is there evidence to support that cholesterol levels decreased after the vegetarian diet?

1. **Assumptions:** The pairs of observations are independent from each other and the number of pairs in our sample is 43. Thus, we can use CLT to approximate the sampling distribution.

2. Set $\alpha = 0.05$

3. **Hypothesis:**

$$H_0 : \delta = 0$$
$$\text{vs. } H_A : \delta < 0$$

p-val :

$P(T \leq -10.276)$

4-5.

```
chol_ttest <- t.test(x = chol$DiffChol, mu = 0, alternative = "less")
tidy(chol_ttest) %>% gt() %>% tab_options(table.font.size = 36)
```

estimate	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-21.76744	-10.27603	2.472813e-13	42	-Inf	-18.20461	One Sample t-test	less

6. **Conclusion:** We reject the null hypothesis. There is sufficient evidence that cholesterol levels decreased with the vegetarian diet (p-value < 0.001).

Reference: Ways to run a paired t-test in R

R option 1: Run a 1-sample `t.test` using the paired differences

$H_A : \delta \neq 0$

```r
t.test(x = chol$DiffChol, mu = 0)
```

```

	One Sample t-test

data:  chol$DiffChol
t = -10.276, df = 42, p-value = 4.946e-13
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -26.04229 -17.49259
sample estimates:
mean of x 
-21.76744 
```

Run the code without `mu = 0`. Do the results change? Why or why not?

R option 2: Run a 2-sample `t.test` with `paired = TRUE` option

$H_A : \delta \neq 0$

- For a 2-sample t-test we specify both `x=` and `y=`
- Note: `mu = 0` is the default value and doesn't need to be specified

```r
t.test(x = chol$Before, y = chol$After, mu = 0, paired = TRUE)
```

```

	Paired t-test

data:  chol$Before and chol$After
t = 10.276, df = 42, p-value = 4.946e-13
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 17.49259 26.04229
sample estimates:
mean difference 
       21.76744 
```

What is different in the output compared to option 1?