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Today:

➤ Systematic approach for understanding which differences are meaningful and which are not.

What is Statistical Significance?

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It helps researchers decide if their findings are reliable and can be generalized to a larger population.

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- 3. Larger samples provide more reliable results
- 4. Significance does not imply causation

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- usually framed in the negative
- determine whether we can reject it based on our data.

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 H_a (Alternative Hypothesis)

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$$t = \frac{\bar{x} - \mu_0}{s_x / \sqrt{n}} = \frac{0.19 - 0.10}{0.394 / \sqrt{100}} = \boxed{2.283}$$

Compare to critical value

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- ▶ Based on this t-statistic, can we reject the null hypothesis?
- Another way of asking: what is the probability that we would observe a sample mean of 0.19 (given N=100) by random chance, if the population mean is 0.10?
- ▶ We call this probability the **p-value**: the likelihood we would observe a value at least as extreme as our sample mean (if the null hypothesis were true), based on chance.

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- ► Type 1 Error: Finding that shaking a hand has an effect on voting (rejecting the null hypothesis) when it in fact does not.
- ► Type 2 Error: Finding that shaking a hand has no effect on voting (retaining the null hypothesis), when in fact it does.

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- ▶ If our p-value is $<= \alpha$, we reject the null hypothesis
- ➤ So in our example, since p = .0224, we reject the hypothesis that the true population mean is 0.1

$$H_0: \mu = \mu_0 \ (= 0.1)$$

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- ▶ Recall that the standard deviation is a measure of the dispersion of **observations** around the **sample mean**.
- ► The standard error of the mean is a measure of the dispersion of **sample means** around the **population mean**.
- Importantly, we can calculate it for a hypothetical sampling distribution, even if we are unable to repeatedly sample from a population.
- ► This is useful, because in many cases we cannot conduct repeated samples, and we still want to know how "likely" our estimate reflects the true population mean.

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- ► For instance: for an average treatment effect, we estimate:
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- ▶ Even if we run an experiment only once, we have two (hypothetical) sampling distributions, one for the treatment and one for the control.

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But do not despair—there is an easy way to do this with the help of R.

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- ▶ In practice, we usually translate standard errors into **confidence intervals** using the normal distribution
- ► Confidence intervals give a range of values that are likely to include the true value of the parameter.

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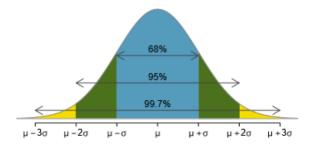
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Example 1

Scenario:

Testing a new drug.

Hypotheses:

 H_0 : The new drug is no more effective than the current drug.

 H_a : The new drug is more effective than the current drug.

Results:

P-value: 0.03. Significance Level (α): 0.05.

Conclusion:

Since 0.03 < 0.05, we reject H_0 and conclude that the new drug is more effective.

Example 2

Scenario:

A political scientist investigates whether exposure to a particular news channel affects support for a new policy.

Hypotheses:

 H_0 : Exposure to the news channel does not affect support for the policy.

 H_a : Exposure to the news channel increases support for the policy.

Results:

Control Group Support: 45%. Treatment Group Support: 48%. P-Value: 0.12. Significance Level (α): 0.05.

Conclusion:

Since the p-value (0.12) is greater than the significance level (0.05), we do not reject the null hypothesis. The result is not statistically significant, indicating that exposure to the news channel does not significantly increase support for the policy.