

MATH 1342

Section 8.1

Inference for the Mean of a Population

In chapter 7, we discussed one type of inference about a population – the confidence interval. In this chapter we will begin discussion the **significance test**.

H_0 : is the **null hypothesis**. The **null hypothesis** states that there is no effect or change in the population. It is the statement being tested in a test of significance.

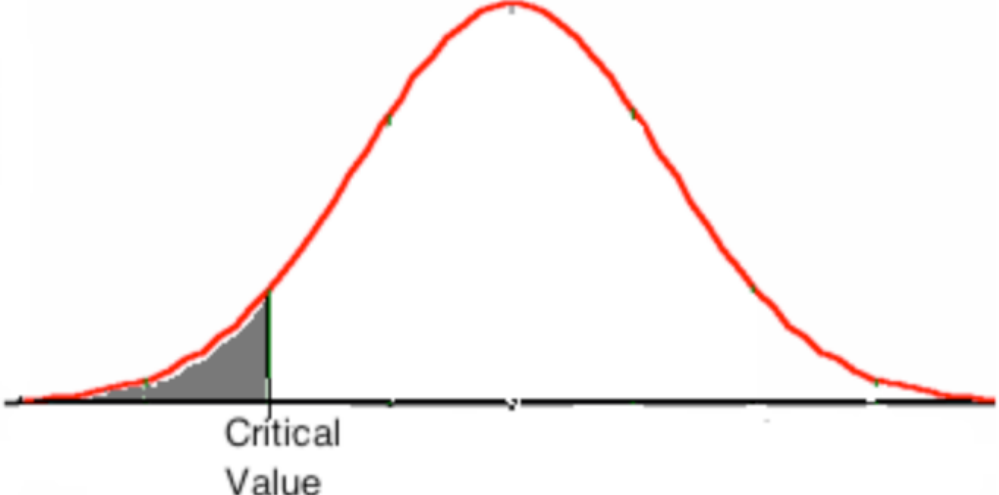
H_a : is the **alternate hypothesis**. The **alternative hypothesis** describes the effect we suspect is true, in other words, it is the alternative to the “no effect” of the null hypothesis.

Since there are only two hypotheses, there are only two possible decisions: *reject the null hypothesis in favor of the alternative* or *don't reject the null hypothesis*. We will never say that we accept the null hypothesis.

For inference about a population mean:

$H_0 : \mu = \mu_0$ where μ_0 represents the given population mean.

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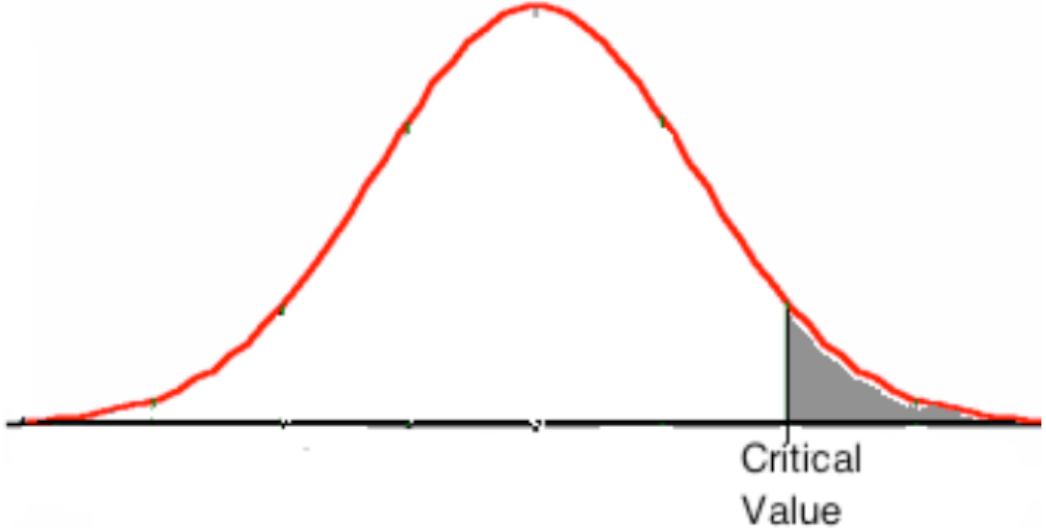
Alternate Hypothesis	Rejection Region
$H_a : \mu < \mu_0$	 <p>The figure shows a normal distribution curve drawn in red. The horizontal axis is black. A vertical green line is drawn from the x-axis to the curve, labeled 'Critical Value' below the axis. The area under the curve to the left of this line is shaded in gray, representing the rejection region for the hypothesis test.</p>

If you are given a Significance Level, α , this can be used to determine the critical value and the rejection region. The total area of the rejection region will have the value of α .

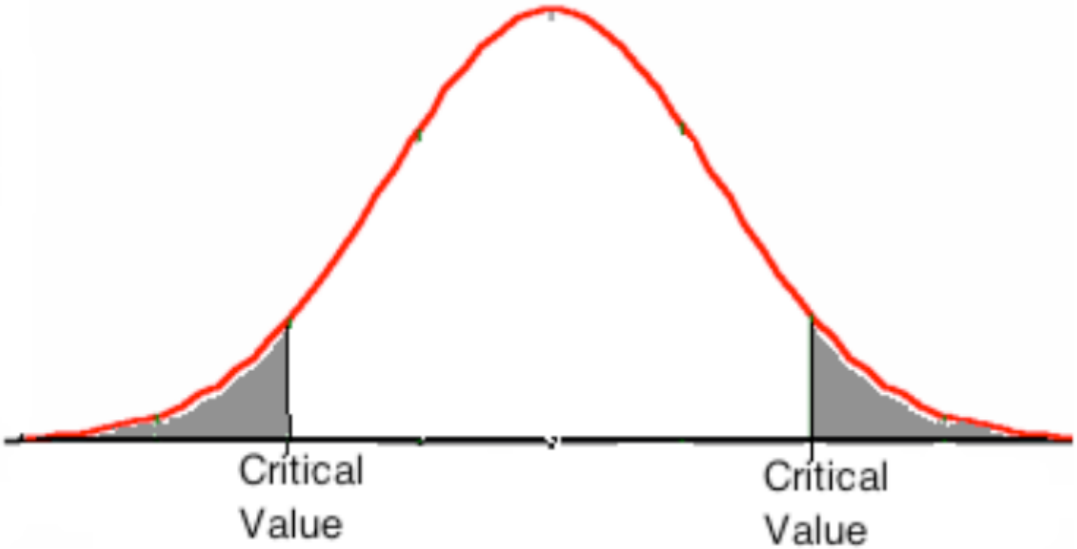
The rejection region is the set of values of the test statistic that will lead to a rejection of the null hypothesis.

The critical value is the boundary of the rejection region.

For inference about a population mean:

Alternate Hypothesis	Rejection Region
$H_a : \mu > \mu_0$	 <p>The diagram shows a normal distribution curve drawn in red. The horizontal axis is marked with a vertical line labeled "Critical Value". The area under the curve to the right of this line is shaded in gray, representing the rejection region for the hypothesis test.</p>

For inference about a population mean:

Alternate Hypothesis	Rejection Region
$H_a : \mu \neq \mu_0$	 <p>A normal distribution curve is shown with a red outline. The horizontal axis is marked with two vertical lines, each labeled "Critical Value". The areas under the curve to the left of the first critical value and to the right of the second critical value are shaded in gray, representing the rejection regions for a two-tailed test.</p>

The probability, computed assuming that the null hypothesis is true, that the test statistic would take a value as extreme or more extreme than that actually observed is called the ***p*-value** of the test. A result with a small *p*-value is called **statistically significant**. This means that chance alone would rarely produce so extreme a result. We say that a value is **statistically significant** when the *p*-value is as small as, or smaller than, the given significance level, α . If we are not given α , we can interpret the results like this:

- If the *p*-value is less than 1%, we say that there is overwhelming evidence to infer that the alternative hypothesis is true. (We also say that the test is highly significant)
- If the *p*-value is between 1% and 5%, we say that there is strong evidence to infer that the alternative hypothesis is true. (We also say that the test is significant)
- If the *p*-value is between 5% and 10%, we say that there is weak evidence to infer that the alternative hypothesis is true. (We also say that the test not statistically significant)
- If the *p*-value is exceeds 10%, we say that there is no evidence to infer that the alternative hypothesis is true.

To summarize:	if α is given:	$p < \alpha$ means to RH_0 $p > \alpha$ means to FRH_0
	if α is not given:	$p < 10\%$ means Rh_0 (with varying certainty) $p > 10\%$ means FRH_0

Steps to follow:

When performing a significance test, we follow these steps:

1. Check assumptions.
2. State the null and alternate hypotheses.
3. Graph the rejection region, labeling the critical values.
4. Calculate the test statistic.
5. Find the p -value. If this answer is less than the significance level, α , we can reject the null hypothesis in favor of the alternate.
6. Give your conclusion using the context of the problem. When stating the conclusion you can give results with a confidence of $(1 - \alpha)(100)\%$.

Z Test (to calculate the test statistic):

z – test

Assumptions:

1. An SRS of size n from the population.
2. Known population standard deviation, σ .
3. Either a normal population or a large sample ($n \geq 30$).

To compute the z – test statistic, we use the formula:
$$z = \frac{\bar{x} - \mu_0}{\sigma / \sqrt{n}}.$$

T Test (to calculate the test statistic):

t – test

Assumptions:

1. An SRS of size n from the population.
2. Unknown population standard deviation.
3. Either a normal population or large sample ($n \geq 30$).

To compute the *t* – test statistic, we use the formula: $t = \frac{\bar{x} - \mu_0}{s / \sqrt{n}}$, where s is the sample standard deviation. The *t* – test will use $n - 1$ degrees of freedom.

Example:

Example 1: A laboratory is asked to evaluate the claim that the amount of the active ingredient in a bug spray is 18.2 grams for a 70-gram bottle with a standard deviation of 1.38 grams. The mean amount of the active ingredient in 40 randomly selected 70-gram bottles of the bug spray is $\bar{x} = 16.828$ grams. Do these analyses indicate that the amount of the active ingredient is different than the original claim at an $\alpha = 0.05$ significance level?

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$$H_0: \mu = 18.2$$

$$H_a: \mu \neq 18.2$$

Population:

$$\mu = 18.2$$

$$\sigma = 1.38$$

$$\bar{x} = 16.828$$

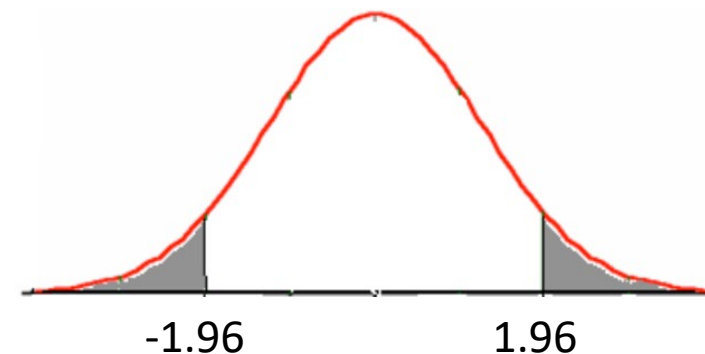
$$\alpha = 0.05$$

Since the population standard deviation is given, use a z-test.

Rejection Region is 2-sides, so the area of one tail is $0.05/2 = 0.025$.

$$qnorm(1-0.025) = 1.96$$

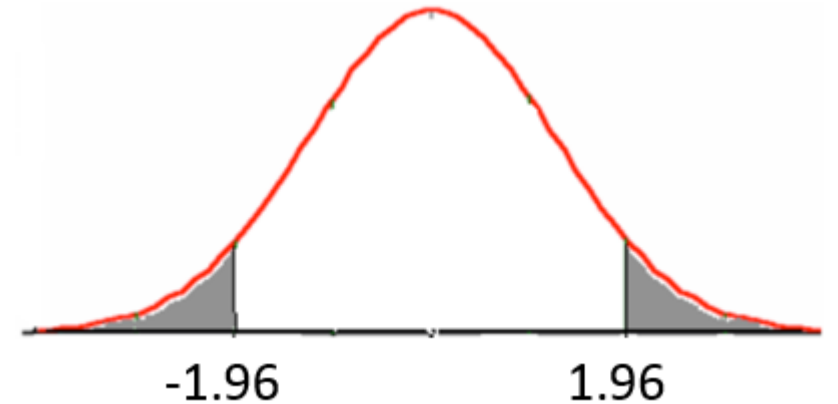
$$qnorm(0.025) = 1.96$$



Example (Continued):

$$z = \frac{\bar{x} - \mu_0}{\sigma/\sqrt{n}} = \frac{16.828 - 18.2}{1.38/\sqrt{40}} = -6.288$$

$z = -6.288$ falls within our rejection region
($-6.288 < -1.96$)



P-Value: $P(Z < -6.288) + P(Z > 6.288) = 2P(Z < -6.288) \approx 0$

(Since $p < \alpha$, we can conclude that we can reject the null hypothesis.)

Conclusion: Based on 95% certainty, we can reject the null hypothesis, in favor of saying that the amount of active ingredient is not 18.2 grams per can.

Mr. Murphy is an avid golfer. Suppose he has been using the same golf clubs for quite some time. Based on this experience, he knows that his average distance when hitting a ball with his current driver (the longest-hitting club) under ideal conditions is 200 yards with a standard deviation of 9. After some preliminary swings with a new driver, he obtained the following sample of driving distances:

205	198	220	210	194	201	213	191	211	203
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He feels that the new club does a better job. Do you agree?

What is the sample mean?

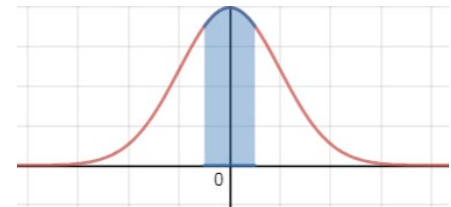
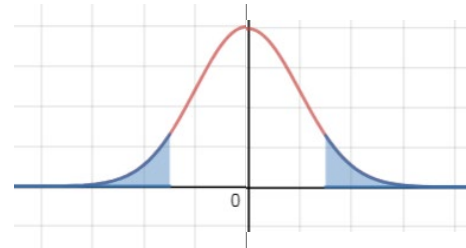
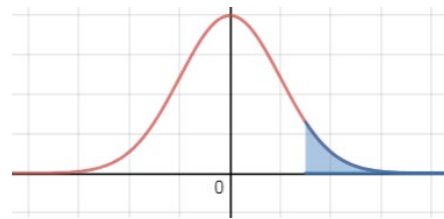
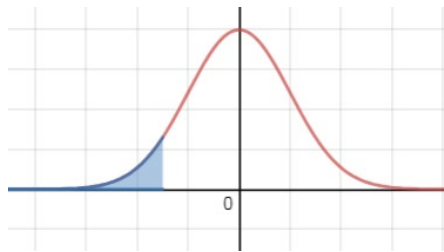
What is the population mean?

Which test statistic can be used?

What is our null hypothesis?

What is our alternate hypothesis?

Which of the following is a correct representation of our rejection region?



What is the value of the test statistic?

What is the p-value?

Do we reject the null hypothesis in favor of the alternate hypothesis?

Examples:

An association of college bookstores reported that the average amount of money spent by students on textbooks for the Fall 2010 semester was \$325.16. A random sample of 75 students at the local campus of the state university indicated an average bill for textbooks for the semester in question to be \$312.34 with a standard deviation of \$76.42. Do these data provide significant evidence that the actual average bill is different from the \$325.16 reported? Test at the 1% significance level.

Matches Pairs T-Test

Matched pairs is a special test when we are comparing corresponding values in data. This test is used only when our data samples are DEPENDENT upon one another (like before and after results).

Matched pairs t – test assumptions:

1. Each sample is an SRS of size n from the same population.
2. The test is conducted on paired data (the samples are NOT independent).
3. Unknown population standard deviation.
4. Either a normal population or large samples ($n \geq 30$).

Example:

A new law has been passed giving city police greater powers in apprehending suspected criminals. For six neighborhoods, the numbers of reported crimes one year before and one year after the new law are shown. Does this indicate that the number of reported crimes have dropped?

Neighborhood	1	2	3	4	5	6
Before	18	35	44	28	22	37
After	21	23	30	19	24	29

A study is conducted to determine the effectiveness of a weight-loss gym routine. A simple random sample of 10 people were selected and their weight before and after 6 weeks of this program were measured. [Calculate after – before.] Test at a 5% significance level.

Person	1	2	3	4	5	6	7	8	9	10
Before	250	285	300	166	243	190	204	260	285	240
After	230	245	265	150	250	185	200	210	240	200

What is the null hypothesis?

What is the alternate hypothesis?

What is the sample mean?

What is the sample standard deviation?

Which test should be used here?

Draw the correct rejection region.

What is/are the critical value(s)?

What is the value of the test statistic?

Does this value fall with our rejection region?

What is the p-value?

Is the gym routine effective (within our significance level)?