

What is the process for conducting a left-tailed hypothesis test on a population mean in statistics?

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A left-tailed hypothesis test on a population mean is a statistical procedure used to determine whether the mean value of a population is significantly less than a specified value. The process begins by formulating a null hypothesis, which states that there is no significant difference between the population mean and the specified value. Next, a random sample is taken from the population and the sample mean is calculated. This is then compared to the specified value using a one-sample t-test. If the calculated t-statistic falls within the critical region, the null hypothesis is rejected and it can be concluded that the population mean is significantly less than the specified value. However, if the t-statistic falls outside the critical region, the null hypothesis is not rejected and there is insufficient evidence to conclude that the population mean is significantly less than the specified value. Overall, the process for conducting a left-tailed hypothesis test on a population mean involves formulating a null hypothesis, collecting and analyzing data, and making a decision based on the results of the statistical test.

Statistics - Hypothesis Testing a Mean (Left Tailed)

A population mean is an average of value a population.

Hypothesis tests are used to check a claim about the size of that population mean.

Hypothesis Testing a Mean

The following steps are used for a hypothesis test:

Check the conditions
Define the claims
Decide the significance level
Calculate the test statistic
Conclusion

For example:

Population: Nobel Prize winners
Category: Age when they received the prize.

And we want to check the claim:

"The average age of Nobel Prize winners when they received the prize is **less** than 60"

By taking a sample of 30 randomly selected Nobel Prize winners we could find that:

The mean age in the sample (\bar{x}) is 62.1

The standard deviation of age in the sample (s) is 13.46

From this sample data we check the claim with the steps below.

1. Checking the Conditions

The conditions for calculating a confidence interval for a proportion are:

The sample is randomly selected And either:

The population data is normally distributed Sample size is large enough

A moderately large sample size, like 30, is typically large enough.

In the example, the sample size was 30 and it was randomly selected, so the conditions are fulfilled.

Note: Checking if the data is normally distributed can be done with specialized statistical tests.

2. Defining the Claims

We need to define a **null hypothesis** ((H_{0})) and an **alternative hypothesis** ((H_{1})) based on the claim we are checking.

The claim was:

"The average age of Nobel Prize winners when they received the prize is **less** than 60"

In this case, the **parameter** is the mean age of Nobel Prize winners when they received the prize ((μ)).

The null and alternative hypothesis are then:

Null hypothesis: The average age was 60.

Alternative hypothesis: The average age was **less** than 60.

Which can be expressed with symbols as:

$(H_{0}): (\mu = 60)$

$(H_{1}): (\mu < 60)$

This is a '**left** tailed' test, because the alternative hypothesis claims that the proportion is **less** than in the null hypothesis.

If the data supports the alternative hypothesis, we **reject** the null hypothesis and **accept** the alternative hypothesis.

3. Deciding the Significance Level

The significance level (α) is the **uncertainty** we accept when rejecting the null hypothesis in a hypothesis test.

The significance level is a percentage probability of accidentally making the wrong conclusion.

Typical significance levels are:

($\alpha = 0.1$) (10%) ($\alpha = 0.05$) (5%) ($\alpha = 0.01$) (1%)

A lower significance level means that the evidence in the data needs to be stronger to reject the null hypothesis.

There is no "correct" significance level - it only states the uncertainty of the conclusion.

Note: A 5% significance level means that when we reject a null hypothesis:

We expect to reject a **true** null hypothesis 5 out of 100 times.

4. Calculating the Test Statistic

The test statistic is used to decide the outcome of the hypothesis test.

The test statistic is a standardized value calculated from the sample.

The formula for the test statistic (TS) of a population mean is:

$$\frac{\bar{x} - \mu}{s \cdot \sqrt{n}}$$

$(\bar{x} - \mu)$ is the **difference** between the **sample** mean ((\bar{x})) and the claimed **population** mean ((μ)).

(s) is the sample standard deviation.

(n) is the sample size.

In our example:

The claimed (H_0) population mean ((μ)) was (60)

The sample mean ((\bar{x})) was (62.1)

The sample standard deviation ((s)) was (13.46)

The sample size ((n)) was (30)

So the test statistic (TS) is then:

$$\left(\frac{62.1-60}{13.46}\right) \cdot \sqrt{30} = \frac{2.1}{13.46} \cdot \sqrt{30} \approx 0.156 \cdot 5.477 = \underline{0.855}$$

You can also calculate the test statistic using programming language functions:

Example

With Python use the scipy and math libraries to calculate the test statistic.

```
import scipy.stats as stats
```

```
import math
```

```
# Specify the sample mean (x_bar), the sample standard deviation (s), the mean claimed in the null-hypothesis (mu_null), and the sample size (n)
```

```
x_bar = 62.1
```

```
s = 13.46
```

```
mu_null = 60
```

```
n = 30
```

```
# Calculate and print the test statistic
```

```
print((x_bar - mu_null)/(s/math.sqrt(n)))
```

Example

With R use built-in math and statistics functions to calculate the test statistic.

```
# Specify the sample mean (x_bar), the sample standard deviation (s), the mean claimed in the null-hypothesis (mu_null), and the sample size (n)
```

```
x_bar <- 62.1
```

```
s <- 13.46
```

```
mu_null <- 60
```

```
n <- 30
```

```
# Output the test statistic
```

```
(x_bar - mu_null)/(s/sqrt(n))
```

5. Concluding

There are two main approaches for making the conclusion of a hypothesis test:

The **critical value** approach compares the test statistic with the critical value of the significance level. The **P-value** approach compares the P-value of the test statistic and with the significance level.

Note: The two approaches are only different in how they present the conclusion.

The Critical Value Approach

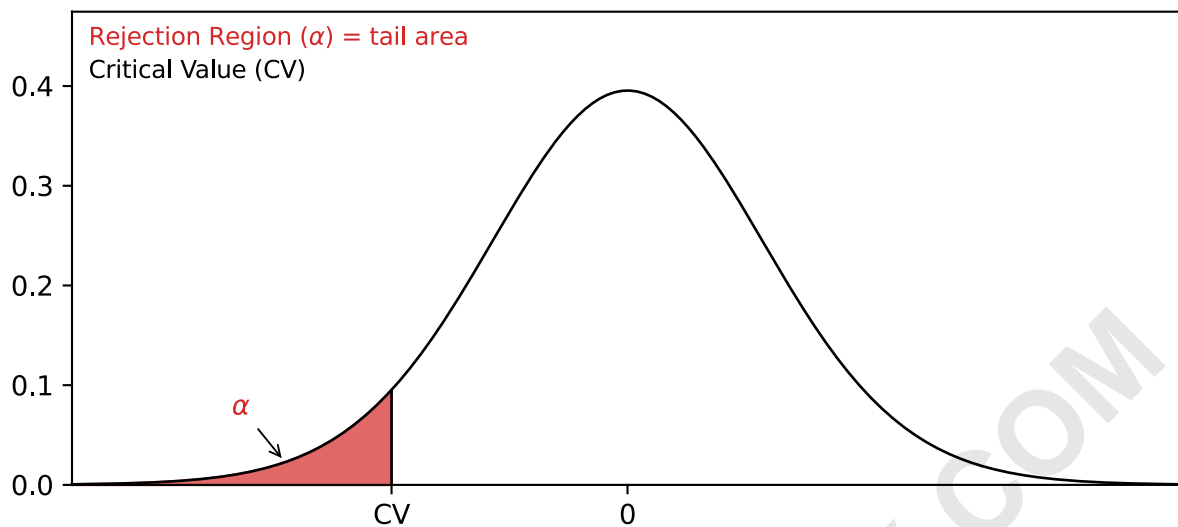
For the critical value approach we need to find the **critical value** (CV) of the significance level ((alpha)).

For a population mean test, the critical value (CV) is a **T-value** from a student's t-distribution.

This critical T-value (CV) defines the **rejection region** for the test.

The rejection region is an area of probability in the tails of the standard normal distribution.

Because the claim is that the population mean is **less** than 60, the rejection region is in the left tail:



The size of the rejection region is decided by the significance level ((alpha)).

The student's t-distribution is adjusted for the uncertainty from smaller samples.

This adjustment is called degrees of freedom (df), which is the sample size ((n) - 1)

In this case the degrees of freedom (df) is: (30 - 1 = 29)

Choosing a significance level ((alpha)) of 0.05, or 5%, we can find the critical T-value from a T-table, or with a programming language function:

Example

With Python use the Scipy Stats library `t.ppf()` function find the T-Value for an (alpha) = 0.05 at 29 degrees of freedom (df).

```
import scipy.stats as stats
```

```
print(stats.t.ppf(0.05, 29))
```

Example

With R use the built-in `qt()` function to find the t-value for an (alpha) = 0.05 at 29 degrees of freedom (df).

```
qt(0.05, 29)
```

Using either method we can find that the critical T-Value is (approx -1.699)

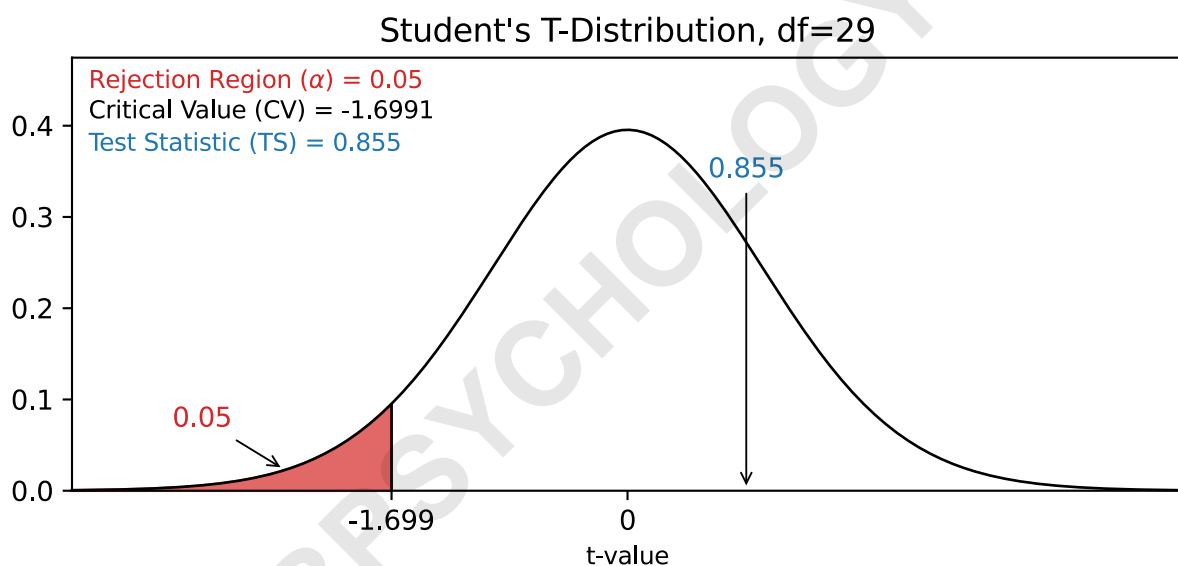
For a **left** tailed test we need to check if the test statistic (TS) is **smaller** than the critical value (CV).

If the test statistic is smaller the critical value, the test statistic is in the **rejection region**.

When the test statistic is in the rejection region, we **reject** the null hypothesis ((H_0)).

Here, the test statistic (TS) was (approx 0.855) and the critical value was (approx -1.699)

Here is an illustration of this test in a graph:



Since the test statistic was **bigger** than the critical value we **keep** the null hypothesis.

This means that the sample data does not support the alternative hypothesis.

And we can summarize the conclusion stating:

The sample data does **not** support the claim that "The average age of Nobel Prize winners when they received the prize is less than 60" at a **5% significance level**.

The P-Value Approach

For the P-value approach we need to find the **P-value** of the test statistic (TS).

If the P-value is **smaller** than the significance level (α), we **reject** the null hypothesis (H_0).

The test statistic was found to be (approx 0.855)

For a population proportion test, the test statistic is a T-Value from a student's t-distribution.

Because this is a **left** tailed test, we need to find the P-value of a t-value **smaller** than 0.855.

The student's t-distribution is adjusted according to degrees of freedom (df), which is the sample size ($(30) - 1 = \underline{29}$)

We can find the P-value using a T-table, or with a programming language function:

Example

With Python use the Scipy Stats library `t.cdf()` function find the P-value of a T-value smaller than 0.855 at 29 degrees of freedom (df):

```
import scipy.stats as stats
```

```
print(stats.t.cdf(0.855, 29))
```

Example

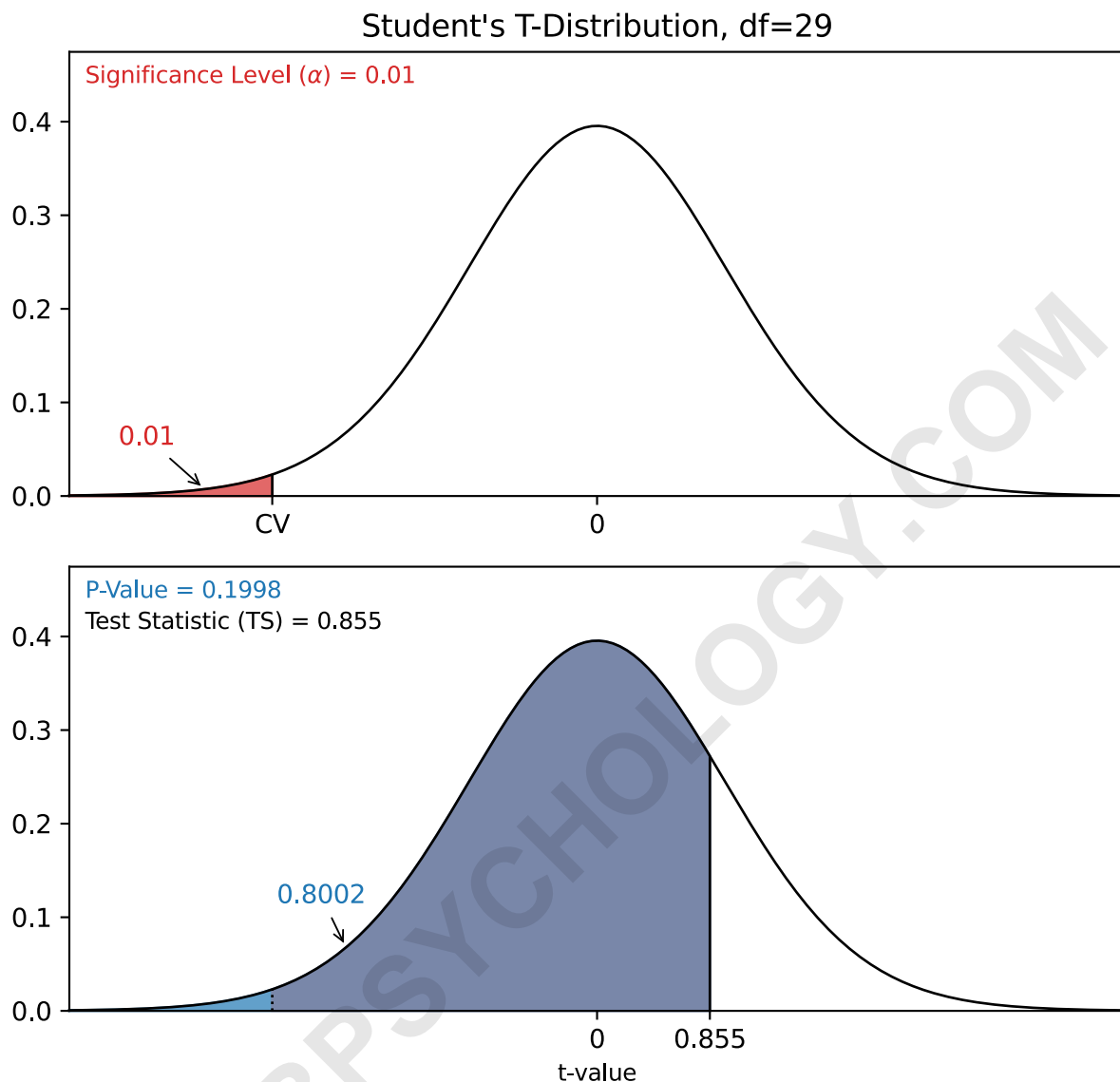
With R use the built-in `pt()` function find the P-value of a T-Value smaller than 0.855 at 29 degrees of freedom (df):

```
pt(0.855, 29)
```

Using either method we can find that the P-value is (approx 0.800)

This tells us that the significance level (α) would need to be smaller 0.80, or 80%, to **reject** the null hypothesis.

Here is an illustration of this test in a graph:



This P-value is far **bigger** than any of the common significance levels (10%, 5%, 1%).

So the null hypothesis is **kept** at all of these significance levels.

And we can summarize the conclusion stating:

The sample data does **not** support the claim that "The average age of Nobel Prize winners when they received the prize is less than 60" at a **10%, 5%, or 1% significance level**.

Calculating a P-Value for a Hypothesis Test with Programming

Many programming languages can calculate the P-value to decide outcome of a hypothesis test.

Using software and programming to calculate statistics is more common for bigger sets of data, as calculating manually becomes difficult.

The P-value calculated here will tell us the **lowest possible significance level** where the null-hypothesis can be rejected.

Example

With Python use the scipy and math libraries to calculate the P-value for a left tailed hypothesis test for a mean.

Here, the sample size is 30, the sample mean is 62.1, the sample standard deviation is 13.46, and the test is for a mean smaller 60.

```
import scipy.stats as stats
```

```
import math
```

```
# Specify the sample mean (x_bar), the sample standard deviation (s), the mean claimed in the null-hypothesis (mu_null), and the sample size (n)
```

```
x_bar = 62.1
```

```
s = 13.46
```

```
mu_null = 60
```

```
n = 30
```

```
# Calculate the test statistic
```

```
test_stat = (x_bar - mu_null)/(s/math.sqrt(n))
```

```
# Output the p-value of the test statistic (left tailed test)
```

```
print(stats.t.cdf(test_stat, n-1))
```

Example

With R use built-in math and statistics functions find the P-value for a left tailed hypothesis test for a mean.

Here, the sample size is 30, the sample mean is 62.1, the sample standard deviation is 13.46, and the test is for a mean smaller 60.

Specify the sample mean (\bar{x}), the sample standard deviation (s), the mean claimed in the null-hypothesis (μ_{null}), and the sample size (n)

```
x_bar <- 62.1
```

```
s <- 13.46
```

```
mu_null <- 60
```

```
n <- 30
```

```
# Calculate the test statistic
```

```
test_stat = (x_bar - mu_null)/(s/sqrt(n))
```

```
# P-value the p-value of the test statistic (left tailed test)
```

```
pt(test_stat, n-1)
```

Left-Tailed and Two-Tailed Tests

This was an example of a **left** tailed test, where the alternative hypothesis claimed that parameter is **smaller** than the null hypothesis claim.

You can check out an equivalent step-by-step guide for other types here:

[Right-Tailed Test](#) [Two-Tailed Test](#)

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