

Learn How to Conduct a One Sample T-Test in R

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Introduction to the One Sample T-Test

The [one sample t-test](#) is a fundamental tool in [R](#) and is widely utilized across various scientific disciplines. Its primary purpose is to determine whether the average of a single population--known as the true [population mean](#) (μ)--is statistically equal to a specific, hypothesized value (μ_0). This test is particularly useful when the population standard deviation is unknown, which is a common scenario in real-world data analysis.

Before executing the test, it is crucial to understand the underlying assumptions. The one sample t-test assumes that the data is collected from a random sample, the observations are independent, and the data is approximately normally distributed. While the t-test is relatively robust to minor deviations from normality, especially with larger sample sizes, checking these conditions ensures the validity of the statistical inference drawn from the test results. Failing to meet these assumptions might necessitate the use of non-parametric alternatives.

In essence, this test provides a structured way to evaluate a claim about a population average. For instance, if a company claims their product lasts 100 hours, the one sample t-test allows us to sample the product and statistically assess whether the actual mean lifespan aligns with the claimed 100-hour figure. By calculating a test statistic and comparing it against a critical value or calculating a [P-value](#), we can make an objective decision regarding the null hypothesis.

Prerequisites and R Syntax

To perform this statistical test within the R environment, we primarily rely on the built-in function, `t.test()`. This function is highly versatile and handles the necessary calculations for the t-statistic and associated metrics automatically. Understanding the fundamental arguments of this function is essential for correct execution and interpretation of the results.

The core syntax requires two primary inputs: the data vector containing the sample observations and the hypothesized [population mean](#) (μ), which is specified using the `mu` argument. The `mu` parameter represents the value that the population mean is assumed to equal under the [Null Hypothesis](#) (H_0).

The following structure provides the minimal required syntax for executing a basic one sample t-test in [R](#):

```
t.test(data, mu=10)
```

Here, `data` would be replaced by the name of your data vector, and the value `10` would be replaced by the specific mean value you are testing against. Furthermore, the `t.test()` function can be customized using additional parameters, such as `alternative` (to specify a one-tailed test:

"less" or "greater") or `conf.level` (to adjust the confidence level, defaulting to 0.95).

Practical Example: Setting Up the Data

To illustrate the application of the one sample t-test, consider a scenario in botany. Suppose a researcher is investigating a specific species of plant and wants to verify if the mean height of this species is equal to 15 inches, based on historical data. The researcher collects a small, representative sample of 12 plants from the population and meticulously records the height of each plant in inches.

The process begins by structuring this observational data within the [R](#) environment. We must create a vector that holds the collected measurements. This data vector serves as the input for our statistical analysis, representing the observed evidence against which the null hypothesis will be tested.

The following code demonstrates how to create this sample vector and subsequently perform the one sample t-test, comparing the observed sample mean to the hypothesized population mean of 15 inches:

```
#create vector to hold plant heights  
my_data <- c(14, 14, 16, 13, 12, 17, 15, 14, 15, 13, 15, 14)  
  
#perform one sample t-test  
t.test(my_data, mu=15)
```

One Sample t-test

```
data: my_data  
t = -1.6848, df = 11, p-value = 0.1201  
alternative hypothesis: true mean is not equal to 15  
95 percent confidence interval:  
13.46244 15.20423  
sample estimates:  
mean of x  
14.33333
```

Interpreting Key Statistical Metrics

The output generated by the `t.test()` function provides several crucial metrics necessary for drawing a statistical conclusion. Understanding what each value represents and how it is calculated is paramount to accurately interpreting the result of the hypothesis test. We will break

down each component of the output shown above.

The output provides the following key interpretations:

data: This simply confirms the name of the vector used for the t-test calculation. In our example, the data source was `my_data`.

t (T-Statistic): This is the calculated test statistic, which measures the difference between the sample mean and the hypothesized [population mean](#) in units of standard error. A t-statistic close to zero suggests that the sample mean is very similar to the hypothesized mean. The formula used is $t = (\bar{x} - \mu_0) / (s/\sqrt{n})$. In this case, $t = (14.333 - 15) / (1.370689 / \sqrt{12}) = \mathbf{-1.6848}$. The negative sign indicates that the observed sample mean is slightly below the hypothesized value.

df (Degrees of Freedom): This value refers to the number of independent pieces of information available to estimate the population variance. For a one sample t-test, the degrees of freedom are calculated as the sample size minus one ($n - 1$). Since our sample size (n) was 12, the degrees of freedom (df) are $12 - 1 = \mathbf{11}$.

Furthermore, the output details the following inferential statistics:

P-value: This is arguably the most critical component. The P-value represents the probability of observing a sample mean as extreme as, or more extreme than, the one calculated, assuming that the [Null Hypothesis](#) (H_0) is true. A small P-value suggests that the observed data is unlikely under H_0 . Our calculated two-tailed P-value corresponding to $t = -1.6848$ with $df = 11$ is $\mathbf{0.1201}$.

95 percent confidence interval: This interval provides a range of values within which we are 95% confident that the true population mean lies. This interval is calculated based on the sample data and the chosen confidence level (defaulting to 95%). For this example, the interval is calculated to be $\mathbf{\{}}$. Since the hypothesized value (15) falls within this range, it provides complementary evidence that we should not reject the null hypothesis.

Sample Estimates (mean of x): This simply reports the mean of the collected sample data, which is $\mathbf{14.33333}$ inches.

Drawing the Conclusion (Hypothesis Testing)

Hypothesis testing requires a formal statement of the null and alternative hypotheses before drawing a conclusion. For this specific two-tailed one sample t-test, the hypotheses are formally stated as follows:

H_0 (Null Hypothesis): $\mu = 15$ (The true mean height for this species of plant is 15 inches.)

H_a (Alternative Hypothesis): $\mu \neq 15$ (The true mean height for this species of plant is not equal to 15 inches.)

To reach a conclusion, we compare the calculated [P-value](#) to a predetermined significance level (α), typically set at $\alpha = 0.05$. The decision rule is straightforward: if the P-value is less than or equal to α , we reject the null hypothesis (H_0). Conversely, if the P-value is greater than α , we fail to reject the null hypothesis.

In our botanical example, the calculated P-value is $\mathbf{0.1201}$. Since $0.1201 > 0.05$, we statistically fail to reject the [Null Hypothesis](#). This means that based on the evidence collected from our sample of 12 plants, we do not have sufficient statistical evidence, at the 5% significance level, to confidently assert that the true mean height of this species is statistically different from 15 inches. The observed difference between the sample mean (14.33 inches) and the hypothesized population mean (15 inches) can reasonably be attributed to random sampling variation.

Additional Resources for Statistical Analysis in R

Mastering the one sample t-test is often the first step in performing deeper inferential statistical analysis. The principles of hypothesis testing, P-value interpretation, and confidence intervals established here apply broadly to many other statistical tests.

To further enhance your skills in applied statistics using [R](#), consider exploring tutorials and documentation related to other common statistical procedures. These tests build upon the foundational concepts covered in the one sample t-test and are essential for handling more complex data structures and research questions.

The following resources explain how to perform other common statistical tests and procedures using the R programming language: