IE6200: Engineernig Probability and Statistics

LAB 07: Hypothesis Testing

Prof. Mohammad Dehghani

Contents

1 Sampling

Sampling is the selection of a subset of individuals from a statistical population to estimate characteristics of the whole population. Two advantages of sampling are lower cost and faster data collection than measuring the entire population. Some of the ways to sample are:

1. **Simple Random Sample:** In this type of selection, every member and set of members has an equal chance of being included in the sample. This method is a good way because random samples are usually fair representative since they don't favor certain members.
2. **Stratified random sample:** In this type of selection, the population is first split into groups. The overall sample consists of some members from every group. The members from each group are chosen randomly. This method is a good way of sampling because it guarantees that members from each group will be represented in the sample.
3. **Cluster random sample:** In this type of selection, the population is first split into groups. The overall sample consists of every member from some of the groups. The groups are selected at random. This method gets every member from some of the groups, so it's good when each group reflects the population as a whole.
4. **Systematic random sample:** In this type of selection, members of the population are put in some order. A starting point is selected at random, and every n^{th} member is selected to be in the sample.

2   Confidence Interval

A *Confidence Interval* (CI) is a type of interval estimate, computed from the statistics of the observed data, that might contain the true value of an unknown population parameter. The interval has an associated confidence level that quantifies the level of confidence that the parameter lies in the interval. Confidence intervals consist of a range of potential values of the unknown population parameter. However, the interval computed from a particular sample does not necessarily include the true value of the parameter. Factors affecting the width of the confidence interval include the size of the sample, the confidence level, and the variability in the sample. A larger sample will tend to produce a better estimate of the population parameter, when all other factors are equal. A higher confidence level will tend to produce a broader confidence interval. A confidence interval can be expressed using three pieces of information:

1. **Confidence level:** A confidence level refers to the percentage of all possible samples that can be expected to include the true population parameter. For example, 95% confidence level implies that 95% of the confidence intervals would include the true population parameter.
2. **Statistic:** A statistic is a characteristic of a sample. Generally, a statistic is used to estimate the value of a population parameter.
3. **Margin of error:** The margin of error expresses the maximum expected difference between the true population parameter and a sample estimate of that parameter.

Using the above information, the range of the confidence interval is defined by the sample statistic $\pm$ margin of error. And the uncertainty associated with the confidence interval is specified by the confidence level.

3   Test of Hypothesis

Hypothesis testing is a statistical method that is used in making statistical decisions using experimental data. Hypothesis Testing is basically an assumption that we make about the population parameter.

Statistical Hypotheses

The best way to determine whether a statistical hypothesis is true would be to examine the entire population. Since that is often impractical, a random sample from the population is examined. If sample data are not consistent with the statistical hypothesis, the hypothesis is rejected. There are two types of statistical hypotheses.

1. **Null hypothesis:** The null hypothesis, denoted by H_0, is usually the hypothesis that sample observations result purely from chance. For example, null hypothesis is denoted by; $H_0 : \mu_1 = \mu_2$, which shows that there is no difference between the two population means.
2. **Alternative hypothesis:** The alternative hypothesis, denoted by H_1 or H_a, is the hypothesis that sample observations are influenced by some non-random cause. For example, alternative hypothesis is denoted by; H_1 or $H_a : \mu_1 \neq \mu_2$, which shows that the two population means are different.

Hypothesis Tests

Statisticians follow a formal process to determine whether to reject a null hypothesis, based on sample data. This process, called hypothesis testing, consists of four steps.

1. **State the hypotheses:** This involves stating the null and alternative hypotheses. The hypotheses are stated in such a way that they are mutually exclusive. That is, if one is true, the other must be false.
2. **Formulate an analysis plan:** The analysis plan describes how to use sample data to evaluate the null hypothesis. The evaluation often focuses around a single test statistic.
3. **Analyze sample data:** Find the value of the test statistic (mean score, proportion, t statistic, z-score, etc.) described in the analysis plan.
4. **Interpret results:** Apply the decision rule described in the analysis plan. If the value of the test statistic is unlikely, based on the null hypothesis, reject the null hypothesis.

Decision Errors

Two types of errors can result from a hypothesis test:

1. **Type I error:** A Type I error occurs when the researcher rejects a null hypothesis when it is true. The probability of committing a Type I error is called the significance level. This probability is also called alpha, and is often denoted by α.
2. **Type II error:** A Type II error occurs when the researcher fails to reject a null hypothesis that is false. The probability of committing a Type II error is called Beta, and is often denoted by β. The probability of not committing a Type II error is called the Power of the test.

Decision Rules

The analysis plan includes decision rules for rejecting the null hypothesis. In practice, statisticians describe these decision rules in two ways - with reference to a P-value or with reference to a region of acceptance. Both the approaches are equivalent. Some statistics may use the P-value approach; others may use the region of acceptance approach.

1. **P-value:** The strength of evidence in support of a null hypothesis is measured by the P-value. Suppose the test statistic is equal to S. The P-value is the probability of observing a test statistic as extreme as S, assuming the null hypothesis is true. If the P-value is less than the significance level, we reject the null hypothesis.

2. **Region of acceptance:** The region of acceptance is a range of values. If the test statistic falls within the region of acceptance, the null hypothesis is not rejected. The region of acceptance is defined so that the chance of making a Type I error is equal to the significance level. The set of values outside the region of acceptance is called the region of rejection. If the test statistic falls within the region of rejection, the null hypothesis is rejected. In such cases, the hypothesis is said to be rejected at the α level of significance.

One-Tailed and Two-Tailed Tests

A test of a statistical hypothesis, where the region of rejection is on only one side of the sampling distribution, is called a one-tailed test. For example, suppose the null hypothesis states that the mean is less than or equal to 10. The alternative hypothesis would be that the mean is greater than 10. The region of rejection would consist of a range of numbers located on the right side of sampling distribution; that is, a set of numbers greater than 10.

A test of a statistical hypothesis, where the region of rejection is on both sides of the sampling distribution, is called a two-tailed test. For example, suppose the null hypothesis states that the mean is equal to 10. The alternative hypothesis would be that the mean is less than 10 or greater than 10. The region of rejection would consist of a range of numbers located on both sides of sampling distribution; that is, the region of rejection would consist partly of numbers that were less than 10 and partly of numbers that were greater than 10.

3.1   One Sample Z-test

A *one-sample z-test* is used to test whether a population parameter is significantly different from some hypothesized value. The one-sample z-test can be used when the population is normally distributed, and the population variance is known. This test can be used by following below mentioned steps:

1. **Define hypotheses:** The table below shows three sets of null and alternative hypotheses. Each makes a statement about how the true population mean μ is related to some hypothesized value μ_0.

Table 1: One-sample Z test

Null Hypothesis	Alternative Hypothesis	Type
$\mu = \mu_0$	$\mu \neq \mu_0$	Two-Tailed
$\mu \geq \mu_0$	$\mu < \mu_0$	Left-Tailed
$\mu \leq \mu_0$	$\mu > \mu_0$	Right-Tailed

2. **Specify significance level:** Often, researchers choose significance levels equal to 0.01, 0.05, or 0.10; but any value between 0 and 1 can be used.

3. **Compute test statistic:** The test statistic is a z-score (z) defined by the following equation.

$$Z_{calc} = \frac{(\overline{x} - \mu_0)}{\frac{\sigma}{\sqrt{n}}} \tag{1}$$

where

x is the observed sample mean,

μ_0 is the hypothesized population mean (from the null hypothesis),

σ is the standard deviation of the population.

4. **Compute P-value:** The P-value is the probability of observing a sample statistic as extreme as the test statistic. Since the test statistic is a z-score, use the Normal Distribution Calculator to assess the probability associated with the z-score.

5. **Evaluate null hypothesis:** The evaluation involves comparing the P-value to the significance level, and rejecting the null hypothesis when the P-value is less than the significance level.

3.2   One Sample t-test

A *one-sample t-test* is used to test whether a population mean is significantly different from some hypothesized value. The one-sample t-test can be used when the population variances are unknown, and with large or small samples.

This test can be used by following below mentioned steps:

1. **Define hypotheses:** The table below shows three sets of null and alternative hypotheses. Each makes a statement about how the true population mean μ is related to some hypothesized value μ_0.

<div align="center">

Table 2: One-sample t-test

Null Hypothesis	Alternative Hypothesis	Type
$\mu = \mu_0$	$\mu \neq \mu_0$	Two-Tailed
$\mu \geq \mu_0$	$\mu < \mu_0$	Left-Tailed
$\mu \leq \mu_0$	$\mu > \mu_0$	Right-Tailed

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2. **Specify significance level:** Often, researchers choose significance levels equal to 0.01, 0.05, or 0.10; but any value between 0 and 1 can be used.

3. **Find degrees of freedom:** The degrees of freedom (DF) is:

$$\boxed{DF = n - 1} \tag{2}$$

   where n is the number of observations in the sample.

4. **Compute test statistic:** The test statistic is a t-score (t) defined by the following equation.

$$\boxed{t_{calc} = \frac{(\overline{x} - \mu_0)}{\frac{s}{\sqrt{n}}}} \tag{3}$$

   where

   x is the observed sample mean,

   μ_0 is the hypothesized population mean (from the null hypothesis),

   s is the standard deviation of the sample.

5. **Compute P-value:** The P-value is the probability of observing a sample statistic as extreme as the test statistic. Since the test statistic is a t statistic, use the t Distribution Calculator to assess the probability associated with the t statistic, having the degrees of freedom computed above.

6. **Evaluate null hypothesis:** The evaluation involves comparing the P-value to the significance level, and rejecting the null hypothesis when the P-value is less than the significance level.

3.3   Two Sample Z-test

A *two-sample Z-test* is used to test the difference (d_0) between two population means. A common application is to determine whether the means are equal. The two-sample Z-test can be used when the population variances is known, and with large or small samples. This test can be used by following below mentioned steps:

1. **Define hypotheses:** The table below shows three sets of null and alternative hypotheses. Each makes a statement about the difference d between the mean of one population μ_1 and the mean of another population μ_2.

Table 3: Two-sample Z test

Null Hypothesis	Alternative Hypothesis	Type
$\mu_1 - \mu_2 = d$	$\mu_1 - \mu_2 \neq d$	Two-Tailed
$\mu_1 - \mu_2 \geq d$	$\mu_1 - \mu_2 < d$	Left-Tailed
$\mu_1 - \mu_2 \leq d$	$\mu_1 - \mu_2 > d$	Right-Tailed

2. **Specify significance level:** Often, researchers choose significance levels equal to 0.01, 0.05, or 0.10; but any value between 0 and 1 can be used.

3. **Compute test statistic:** The test statistic is a Z-score (Z) defined by the following equation.

$$Z_{calc} = \frac{(\overline{x}_1 - \overline{x}_2 - d)}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}} \tag{4}$$

where

$\overline{x}_1$ is the mean of sample 1,

$\overline{x}_2$ is the mean of sample 2,

d is the hypothesized difference between population means,

σ_1 is the standard deviation of population 1,

σ_2 is the standard deviation of population 2,

n_1 is the size of sample 1,

n_2 is the size of sample 2.

4. **Compute P-value:** The P-value is the probability of observing a sample statistic as extreme as the test statistic. Since the test statistic is a z-score, use the Normal Distribution Calculator to assess the probability associated with the z-score.

5. **Evaluate null hypothesis:** The evaluation involves comparing the P-value to the significance level, and rejecting the null hypothesis when the P-value is less than the significance level.

3.4 Two Sample t-test

A *two-sample t-test* is used to test the difference (d_0) between two population means. A common application is to determine whether the means are equal. The two-sample t-test can be used when the population variances is unknown and assumped equal or unequal, and with large or small samples. This test can be used by following below mentioned steps:

1. **Define hypotheses:** The table below shows three sets of null and alternative hypotheses. Each makes a statement about the difference d between the mean of one population μ_1 and the mean of another population μ_2.

Table 4: Two-sample t-test

Null Hypothesis	Alternative Hypothesis	Type
$\mu_1 - \mu_2 = d$	$\mu_1 - \mu_2 \neq d$	Two-Tailed
$\mu_1 - \mu_2 \geq d$	$\mu_1 - \mu_2 < d$	Left-Tailed
$\mu_1 - \mu_2 \leq d$	$\mu_1 - \mu_2 > d$	Right-Tailed

2. **Specify significance level:** Often, researchers choose significance levels equal to 0.01, 0.05, or 0.10; but any value between 0 and 1 can be used.

3. **Find degrees of freedom:** The degrees of freedom (DF) is:

a) When population variance is unknown and equal variance is assumed:

$$DF = n_1 + n_2 - 2 \tag{5}$$

b) When population variance is unknown and unequal variance is assumed:

$$DF = \frac{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)^2}{\frac{\left(\frac{s_1^2}{n_1}\right)^2}{n_1 - 1} + \frac{\left(\frac{s_2^2}{n_2}\right)^2}{n_2 - 1}} \tag{6}$$

4. **Compute test statistic:** The test statistic is a t-score (t) defined by the following equation.

$$t_{calc} = \frac{(\overline{x}_1 - \overline{x}_2 - d)}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} \tag{7}$$

where

$\overline{x}_1$ is the mean of sample 1,

$\overline{x}_2$ is the mean of sample 2,

d is the hypothesized difference between population means,

s_1 is the standard deviation of sample 1,

s_2 is the standard deviation of sample 2,

n_1 is the size of sample 1,

n_2 is the size of sample 2.

5. **Compute P-value:** The P-value is the probability of observing a sample statistic as extreme as the test statistic. Since the test statistic is a t statistic, use the t Distribution Calculator to assess the probability associated with the t statistic, having the degrees of freedom computed above.

6. **Evaluate null hypothesis:** The evaluation involves comparing the P-value to the significance level, and rejecting the null hypothesis when the P-value is less than the significance level.

3.5   Chi-Squared Test

A *chi-squared test* is used to test whether a population variance is significantly different from some hypothesized value. The chi-square test can be used when the population variances is known. This test can be used by following below mentioned steps:

1. **Define hypotheses:** The table below shows three sets of null and alternative hypotheses. Each makes a statement about how the true population variance σ^2 is related to some hypothesized value σ_o.

<p align="center">Table 5: Chi-Squared Test</p>

Null Hypothesis	Alternative Hypothesis	Type
$\sigma^2 = \sigma_o^2$	$\sigma^2 \neq \sigma_o^2$	Two-Tailed
$\sigma^2 \geq \sigma_o^2$	$\sigma^2 < \sigma_o^2$	Left-Tailed
$\sigma^2 \leq \sigma_o^2$	$\sigma^2 > \sigma_o^2$	Right-Tailed

2. **Specify significance level:** Often, researchers choose significance levels equal to 0.01, 0.05, or 0.10; but any value between 0 and 1 can be used.

3. **Find degrees of freedom:** The degrees of freedom (DF) is:

$$DF = n - 1 \tag{8}$$

4. **Compute test statistic:** The test statistic is a t-score (t) defined by the following equation.

$$\chi_{calc}^2 = \frac{(n-1)S^2}{\sigma_o^2} \tag{9}$$

   where x is the observed sample mean, M is the hypothesized population mean (from the null hypothesis), and s is the standard deviation of the sample.

5. **Compute P-value:** The P-value is the probability of observing a sample statistic as extreme as the test statistic. Since the test statistic is a t statistic, use the t Distribution Calculator to assess the probability associated with the t statistic, having the degrees of freedom computed above.

6. **Evaluate null hypothesis:** The evaluation involves comparing the P-value to the significance level, and rejecting the null hypothesis when the P-value is less than the significance level.

4   Case Study: Hypothesis Testing

4.1   Dataset

The following is a Census Income dataset extracted from the 1994 Census database and includes information about various features of the population. It is comprised of 32,561 records and 14 attributes. (Source: https://archive.ics.uci.edu/ml/datasets/Adult)

4.2   Attributes

- **Age:** The age of a person in years
- **Workclass:** Description about whether a person is privately employed, associated with some government agency or something else
- **Education:** Highest education level of a person
- **Education Years:** Number of years a person obtained formal education
- **Marital Status:** Whether a person is married, divorced, never married, etc
- **Occupation:** Description about occupation of person, example - tech support, craft repair, etc
- **Relationship:** Primarily relationship description of a person like husband, wife, etc
- **Race:** Description of the race of a person
- **Sex:** Describes the gender of a person
- **Capital Gain:** Amount of capital gained, if any
- **Capital Loss:** Amount of capital lost, if any
- **Hours Per Week:** Number of hours worked by a person per week
- **Native Country:** The country from where a person belongs
- **Income:** Whether income of a person is <=50K or >=50K

❶ The variables will be assumed to follow normal distribution for analysis purposes.

4.3   Required Packages

For this session, we will make use of tidyverse and the in built stats package.

```
library(tidyverse)
```

❶ You might need to install these packages if they are not installed already.

4.4   Importing the dataset

```
census <- read.csv('census.csv', header = TRUE, sep = ',')

str(census)
```

```
'data.frame':   32561 obs. of  14 variables:
 $ age            : int  39 50 38 53 28 37 49 52 31 42 ...
 $ workclass      : Factor w/ 9 levels " ?"," Federal-gov",..: 8 7 5 5 5 5 5 7 5 5 ...
 $ education      : Factor w/ 16 levels " 10th"," 11th",..: 10 10 12 2 10 13 7 12 13 10 ...
 $ education_years: int  13 13 9 7 13 14 5 9 14 13 ...
```

```
$ marital_status : Factor w/ 7 levels " Divorced"," Married-AF-spouse",..: 5 3 1 3 3 3 4 3 5 3 ...
$ occupation     : Factor w/ 15 levels " ?"," Adm-clerical",..: 2 5 7 7 11 5 9 5 11 5 ...
$ relationship   : Factor w/ 6 levels " Husband"," Not-in-family",..: 2 1 2 1 6 6 2 1 2 1 ...
$ race           : Factor w/ 5 levels " Amer-Indian-Eskimo",..: 5 5 5 3 3 5 3 5 5 5 ...
$ sex            : Factor w/ 2 levels " Female"," Male": 2 2 2 2 1 1 1 2 1 2 ...
$ capital_gain   : int  2174 0 0 0 0 0 0 0 14084 5178 ...
$ capital_loss   : int  0 0 0 0 0 0 0 0 0 0 ...
$ hours_per_week : int  40 13 40 40 40 40 16 45 50 40 ...
$ native_country : Factor w/ 42 levels " ?"," Cambodia",..: 40 40 40 40 6 40 24 40 40 40 ...
$ income         : Factor w/ 2 levels " <=50K"," >50K": 1 1 1 1 1 1 1 2 2 2 ...
```

For the purposes of analysis, it is assumed that the dataset available is representative of the entire population, and from that sampling will be done for conducting various statistical tests.

4.5   Sampling

Before conducting the hypothesis testing, we need some samples to run our tests on assuming our data is represents the entire popultion. We will create a random sample of 1,000 records using the sample_n() function from the dplyr package which allows us to select random rows from a data frame, as well as another more samples by subsetting the population that hold a Masters degree using the filter() function.

```
censusSample <- sample_n(census, 1000)
```

```
censusMasters <- census %>%
  dplyr::filter(education == ' Masters' )
```

4.6   One Sample Z-test

The first statistical test that we will perform is a *one sample z-test*. Assuming our entire dataset is the population, we want to test if the mean age of our sample data is equivalent to the population mean age.

The sample mean age (μ) is

```
mean(censusSample$age)
```

```
[1] 38.841
```

And the population mean age (μ_0) is

```
mean(census$age)
```

```
[1] 38.58165
```

Thus, our null and alternate hypothesis are:

$X \equiv$ R.V. of age of a person

- H_0: $\mu = 38.58$

- H_a: $\mu \neq 38.58$

R does not have a pre-defined function to perform z-test, as such, we will create our own function that takes sample and population data as inputs in vector form, and return the corresponding z-value. Based on the z-value obtained, and the critical value chosen, we can then make a decision regarding the sample and population means.

```r
z.test <- function(sample, pop){
  sample_mean = mean(sample)
  pop_mean = mean(pop)
  n = length(sample)
  var = var(pop)
  z = (sample_mean - pop_mean) / (sqrt(var/(n)))
  return(z)
}
```

❶ To learn more about creating functions, read chapter 19 from the following link, https://r4ds.had.co.nz/index.html

If we consider a significane level of $\alpha = 0.05$, we will fail to reject the null hypothesis if the *z-value* lies in the range $[-1.96, 1.96]$ (from z-tables).

```r
z.test(censusSample$age, census$age)
```

```
[1] 0.6012617
```

Since the *z-value* lies within the range $[-1.96, 1.96]$, we thus fail to reject null hypothesis and conclude there is no significant difference between sample mean age and population mean age.

4.7   One Sample t-test

The next test that we will perform is the *one sample t-test*, which is used to test the hypothesis about the mean, but when variance is not known about the population but is known to be normally distributed. We will perform the test to see if the mean age of people holding a Masters degree is equivalent to the mean population age.

The sample mean age (μ) is

```r
mean(censusMasters$age)
```

```
[1] 44.04991
```

And the population mean age (μ_0) is

```r
mean(census$age)
```

```
[1] 38.58165
```

Thus, our null and alternate hyposthesis are:

$X \equiv$ R.V. of age of a person

- H_0: $\mu = 38.58$

- H_a: $\mu \neq 38.58$

To conduct the test, we can use the t.test() function, and for one sample, the inputs needed are the vectors for ages of Masters degree holders and the mean population age. The outputs returned are the t-value, **p-value**, alternative hypothesis statement, 95% confidence inteval value (unless otherwise specified) and the mean of input vector

```
t.test(censusMasters$age, mu = mean(census$age))
```

```
    One Sample t-test

data:  censusMasters$age
t = 20.506, df = 1722, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 38.58165
95 percent confidence interval:
 43.52689 44.57293
sample estimates:
mean of x
 44.04991
```

As the $p-value \leq 0.05$, we reject the null hypothesis and conclude that there is a significant difference between the sample mean age of Masters degree holdersand population mean age.

4.8   Two Sample Z-test

To test if the means of two different set of samples taken from two different populations is the same of not, we can perform a *two sample z-test*. First, we will create a function that calculates the *z-value* for two different set of samples. The inputs for this function will be the two sample vectors (of age in this case), and the variances of each of the vectors calculated using the var() function.

```
z_test2 = function(a, b, var_a, var_b){
  n.a = length(a)
  n.b = length(b)
  z = (mean(a) - mean(b)) / (sqrt((var_a)/n.a + (var_b)/n.b))
  return(z)
}
```

To create two different populations, we will divide the dataset into two and take a sample from each.

```
cen_1 <- census[1:16000,] #select all columns and rows from 1 to 16000
cen_2 <- census[16001:32561,] #select all columns and rows from 16001 to 32561
cen_1_sample <- sample_n(cen_1, 1000) #sample 1000 rows from the first population
cen_2_sample <- sample_n(cen_2, 1000) #sample 1000 rows from the second population
```

$X_1 \equiv$ R.V. of age of a person from first sample

$X_2 \equiv$ R.V. of age of a person from second sample

The mean age of sample 1 is therefore (μ_1)

```
mean(cen_1_sample$age)
```

[1] 38.793

The mean age of sample 2 is therefore (μ_2)

```
mean(cen_2_sample$age)
```

[1] 39.043

Thus, our null and alternate hyposthesis are:

- H_0: $\mu_1 - \mu_2 = 0$
- H_0: $\mu_1 - \mu_2 \neq 0$

```
z_test2(cen_1_sample$age, cen_2_sample$age, var(cen_1_sample$age), var(cen_2_sample$age))
```

[1] -0.4031903

Thus, for a significane level of $\alpha = 0.05$, we fail to reject the null hypothesis since the *z-value* lies within the range $[-1.96, 1.96]$ and conclude that there is no significant difference between the mean age of two samples.

4.9   Two Sample t-test

We can conduct a *two sample t-test* to test the significance between means of two samples means if populations are independent and the variances are unknown. To do so, we can again use the t.test() function and supply the two samples whose means are to be tested as vectors. The outputs are again the same as a *one sample t-test*.

$X_1 \equiv$ R.V. of age of a person from first sample

$X_2 \equiv$ R.V. of age of a person from second sample

The mean age of sample 1 is therefore (μ_1)

```
mean(cen_1_sample$age)
```

[1] 38.793

The mean age of sample 2 is therefore (μ_2)

```
mean(cen_2_sample$age)
```

[1] 39.043

Thus, our null and alternate hyposthesis are:

- H_0: $\mu_1 - \mu_2 = 0$
- H_0: $\mu_1 - \mu_2 \neq 0$

```
t.test(cen_1_sample$age, cen_2_sample$age)
```

```
	Welch Two Sample t-test

data:  cen_1_sample$age and cen_2_sample$age
t = -0.40319, df = 1997.2, p-value = 0.6869
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.4660217  0.9660217
sample estimates:
mean of x mean of y
   38.793    39.043
```

Since $p-value \geq 0.05$, we fail to reject the null hypothesis and conclude that there is no significant difference between the mean age of two samples, reaching the same conclusion as the *two sample z-test*.