

This project covers two-sample tests.

1 difference of proportion

We really would like to know when two samples are from populations with the same population proportion.

For example, suppose one week a politician has 620 supporters out of 1200 randomly chosen likely voters, and the next week the number is 580 out of 1200. Is it possible that the population proportions are the same for each sample, or are they different?

Let p_1 be the population proportion for the first week, p_2 that for the second. The null and alternative hypotheses are

$$H_0 : p_1 = p_2, \quad H_A : p_1 \neq p_2.$$

We rewrite these in terms of differences:

$$H_0 : p_1 - p_2 = 0, \quad H_A : p_1 - p_2 \neq 0$$

The null hypotheses for these problems is always the same, the alternative is still one of `less`, `two.sided` or `greater`. In this case, `two.sided`

The p -value is derived from the data and the alternative. The data is 620 and 580, and 1200 and 1200 for the sample sizes. We specify these as a vector of values as follows


```
> prop.test(c(620, 580), c(1200, 1200), alt = "two.sided")
```


```
2-sample test for equality of proportions with continuity correction
```


```
data: c(620, 580) out of c(1200, 1200)
X-squared = 2.535, df = 1, p-value = 0.1113
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.007485  0.074152
sample estimates:
prop 1 prop 2
0.5167 0.4833
```

That is the counts go first, followed by the sample sizes. Values are combined using `c()`.

The p -value of 0.1113 indicates that the assumption of equal population proportions is accepted.

 Question 1: The 2001 poverty was 11.7 percent from a sample of size 50,000. In 2002 the rate went up to 12.1 percent with a sample of 40,000. Do a significance test of difference of proportions with a two-sided alternative. Do you accept or reject at the 0.05 level?

 Question 2: Before a 50 million dollar advertising spree, President Bush had an approval rating of 44% in a survey of 1,200 likely voters. Afterwards, his rating was 47% in a survey of 1,100 likely voters. Is this difference significant at the $\alpha = 0.05$ level?

 Question 3: Last year a random sampling of 900 drivers found 80% in compliance of seat belt laws. This year, a sample of 1000 drivers found 84% in compliance. Has the population proportion increased? Answer using a test of significance at the $\alpha = 0.05$ level.

2 Two sample t -test

The t -statistic can be used to decide if two sample means can be used to test a hypothesis of equality of population means. If the null and alternative are

$$H_0 : \mu_1 = \mu_2, \quad H_A : \mu_1 \neq \mu_2$$

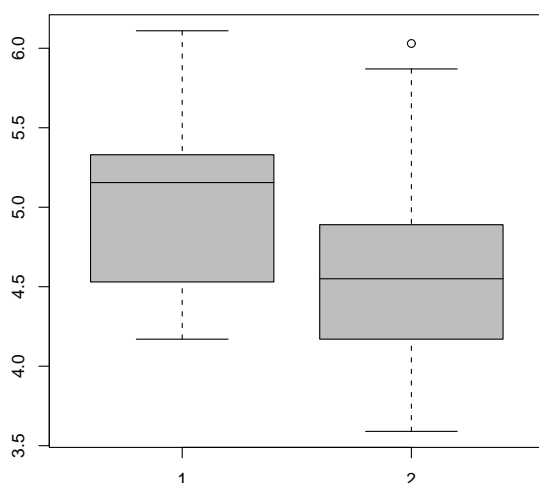
then we can rewrite as differences to get

$$H_0 : \mu_1 - \mu_2 = 0, \quad H_A : \mu_1 - \mu_2 \neq 0.$$

The null is always the same, the alternative one of **less**, **two.sided** or **greater**.

For example, the data set **PlantGrowth** contains measurements on plant growth for three groups: one that is a control group and two that received a treatment. We can compare treatment 1 to the control group as follows

```
> data(PlantGrowth)
> attach(PlantGrowth)
> cgroup = weight[group == "ctrl"]
> tgroup = weight[group == "trt1"]
> boxplot(cgroup, tgroup, col = "gray")
```



(That's a one not an ell for **trt1**.)

The boxplots shows similar shapes, but perhaps the center of the first one (the control group) is larger. We answer this with a two-sided test

```
> t.test(cgroup, tgroup, alt = "two.sided")
```

Welch Two Sample t-test

data: cgroup and tgroup

t = 1.191, df = 16.52, p-value = 0.2504

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-0.2875 1.0295

sample estimates:

mean of x mean of y

5.032 4.661

(We put in both data sets, and the alternative hypothesis.)

The large p -value indicates that we accept the null hypothesis.



Question 4: For the `PlantGrowth` data set, the second treatment group is found with these commands

```
> tgroup2 = weight[group == "trt2"]
```

Make a boxplot of the data, then do a test of significance of

$$H_0 : \mu_1 - \mu_2 = 0, \quad H_A : \mu_1 - \mu_2 \neq 0.$$

Do you accept or reject at the 0.05 level?



Question 5: Car researchers check the braking distance of two cars. They have the following data

car 1: 125 128 134 130 125

car 2: 130 140 128 133 138

Do a test of significance to see if the two have a common population mean. Use a two sided alternative, and a significance level of 0.05.



Question 6: Medical researchers are investigating the effects of two dosages of some drug. If the smaller dosage is just as effective as the larger, then the smaller would be recommended as it is cheaper, and likely to have fewer side effects. More effective means that the population mean is larger. Perform a significance test to see if the difference is statistically significant at the 0.05 level.

The data they have is:

smaller dose: 5.1 10.8 8.7 9.8 9.9 10.0 7.0 7.1

larger dose : 9.0 12.1 10.0 11.3 12.6 9.6 9.3 10.4

2.1 Equal variances?

When the variance is equal, the `t.test` function can be given the argument `var.equal=TRUE`. The degrees of freedom used to find the p -value are bigger in this case. For example, the boxplot shows that spread on the control and first treatment group is the same. We could redo that problem with

```
> t.test(cgroup, tgroup, alt = "two.sided", var.equal = TRUE)
```

Two Sample t-test

data: cgroup and tgroup

t = 1.191, df = 18, p-value = 0.249

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-0.2833 1.0253

sample estimates:

mean of x mean of y

5.032 4.661

Notice the p -value is a bit smaller.



Question 7: Repeat the previous three exercises using `var.equal=TRUE` if appropriate.

3 Paired t -test

When the data is paired off in a way that the two samples are not independent, but rather are expected to depend on the individual or experimental unit, then a paired t -test may be appropriate.

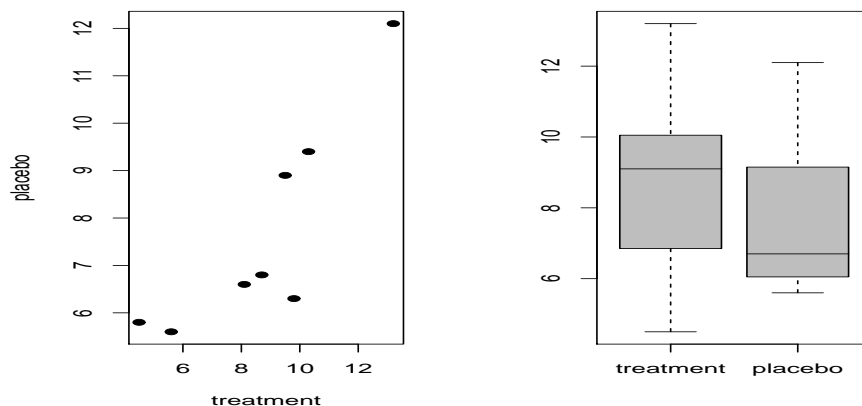
For example, in twin studies, pairs of identical twins are used in the study. One twin is given the treatment, the other a placebo. Differences are attributed to the treatment and not to genetic differences, as these are hopefully controlled by using identical twins.

A study on a hair-loss prevention uses eight pairs of identical twins. After a seven-week treatment, results are measured with a numeric scale for which higher numbers are better. The data they have is

```
treatment: 9.5 8.7 9.8 8.1 4.5 10.3 13.2 5.6
placebo  : 8.9 6.8 6.3 6.6 5.8 9.4 12.1 5.6
```

These are paired data, notice a scatterplot of the two shows a connection. As well we make boxplots.

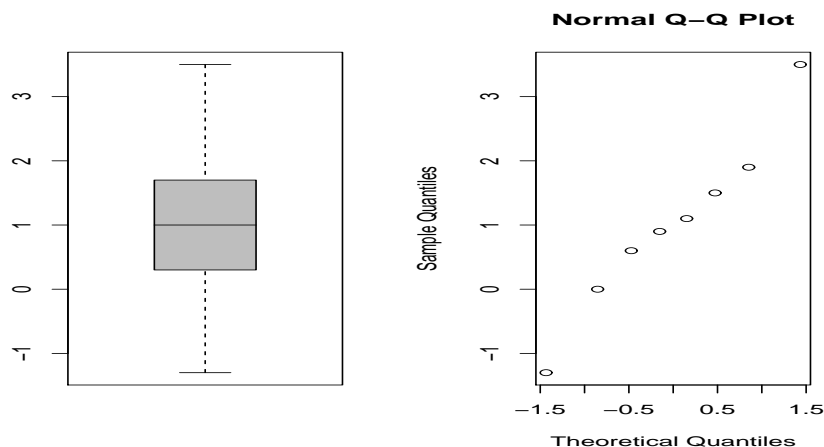
```
> treatment = c(9.5, 8.7, 9.8, 8.1, 4.5, 10.3, 13.2, 5.6)
> placebo = c(8.9, 6.8, 6.3, 6.6, 5.8, 9.4, 12.1, 5.6)
> par(mfrow = c(1, 2))
> plot(placebo ~ treatment, pch = 16)
> boxplot(data.frame(treatment, placebo), col = "gray")
```



The figure shows the data to be correlated. This means the t -statistic we used previously will not work, as there was an assumption of independent samples when the standard deviation is computed.

No worries, what we see is that the differences should be random. That is, the difference between treatment and placebo for each twin. We plot this to see

```
> par(mfrow = c(1, 2))
> boxplot(treatment - placebo, col = "gray")
> qqnorm(treatment - placebo)
```



So a t -test of the differences is of interest:

```
> t.test(treatment - placebo, mu = 0, alt = "two.sided")
```

One Sample t -test

```
data: treatment - placebo
t = 2.067, df = 7, p-value = 0.0776
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.1478  2.1978
sample estimates:
mean of x
 1.025
```

(Compare this to the t -test if we don't realize the data is not independent

```
> t.test(treatment, placebo, alt = "two.sided")
```

Welch Two Sample t -test

```
data: treatment and placebo
t = 0.8179, df = 13.52, p-value = 0.4276
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.672  3.722
sample estimates:
mean of x mean of y
 8.713    7.688
```

The `t.test()` function will do paired tests with the argument `paired=TRUE`. For example, compare

```
> t.test(treatment, placebo, alt = "two.sided", paired = TRUE)
```

Paired t -test

```
data: treatment and placebo
t = 2.067, df = 7, p-value = 0.0776
```

```
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.1478  2.1978
sample estimates:
mean of the differences
      1.025
```



Question 8: Burt's twin data set contains the following

| | | | | | | | | | | |
|---------|----|----|----|-----|-----|-----|-----|----|----|----|
| twin 1: | 82 | 80 | 88 | 108 | 116 | 117 | 132 | 71 | 75 | 93 |
| twin 2: | 82 | 90 | 91 | 115 | 115 | 129 | 131 | 78 | 79 | 82 |

The numbers are IQ scores for identical twins that were separated at birth. It was used to support the theory that IQ scores are based on genetics and not the environment.

Perform a test of significance to see if the two samples have the same population mean. (Are the two samples independent? Correlated? Why?)



Question 9: The data set `shoes` in the MASS library is loaded by

```
> data(shoes, package = "MASS")
> attach(shoes)
```

The variables A and B contain shoe wear measurements for two types of shoes. Ten children wore one of each type of shoe, and the measurements are paired off to show this. Do a test of significance to see if the mean amount of wear is the same? (Is the data independent? Correlated? Why?)