R ANOVA Tutorial: One-way & Two-way [with Examples]

guru99.com/r-anova-tutorial.html

What is ANOVA?

Analysis of Variance(ANOVA) helps you test differences between two or more group means. ANOVA test is centered around the different sources of variation (variation between and within group) in a typical variable. A primarily ANOVA test provides evidence of the existence of the mean equality between the group. This statistical method is an extension of the t-test. It is used in a situation where the factor variable has more than one group.

In this tutorial, we will learn

- One way ANOVA
- Pairwise comparison
- Two way ANOVA

One-way ANOVA

There are many situations where you need to compare the mean between multiple groups. For instance, the marketing department wants to know if three teams have the same sales performance.

• Team: 3 level factor: A, B, and C

• Sale: A measure of performance

The ANOVA test can tell if the three groups have similar performances.

To clarify if the data comes from the same population, you can perform a **one-way analysis of variance** (one-way ANOVA hereafter). This test, like any other statistical tests, gives evidence whether the H0 hypothesis can be accepted or rejected.

Hypothesis in one-way ANOVA test:

- H0: The means between groups are identical
- H3: At least, the mean of one group is different

In other words, the H0 hypothesis implies that there is not enough evidence to prove the mean of the group (factor) are different from another.

This test is similar to the t-test, although ANOVA test is recommended in situation with more than 2 groups. Except that, the t-test and ANOVA provide similar results.

Assumptions

We assume that each factor is randomly sampled, independent and comes from a normally distributed population with unknown but equal variances.

Interpret ANOVA test

The F-statistic is used to test if the data are from significantly different populations, i.e., different sample means.

To compute the F-statistic, you need to divide the **between-group variability** over the within-group variability.

The **between-group** variability reflects the differences between the groups inside all of the population. Look at the two graphs below to understand the concept of between-group variance.

The left graph shows very little variation between the three group, and it is very likely that the three means tends to the **overall** mean (i.e., mean for the three groups).

The right graph plots three distributions far apart, and none of them overlap. There is a high chance the difference between the total mean and the groups mean will be large.

Low discriminiation between group

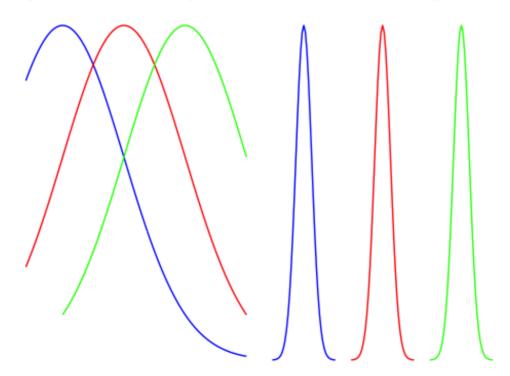
High discrimination between group

The **within group** variability considers the difference between the groups. The variation comes from the individual observations; some points might be totally different than the group means. The within group variability picks up this effect and refer to the sampling error.

To understand visually the concept of within group variability, look at the graph below.

The left part plots the distribution of three different groups. You increased the spread of each sample and it is clear the individual variance is large. The F-test will decrease, meaning you tend to accept the null hypothesis

The right part shows exactly the same samples (identical mean) but with lower variability. It leads to an increase of the F-test and tends in favor of the alternative hypothesis.



You can use both measures to construct the F-statistics. It is very intuitive to understand the F-statistic. If the numerator increases, it means the between-group variability is high, and it is likely the groups in the sample are drawn from completely different distributions.

In other words, a low F-statistic indicates little or no significant difference between the group's average.

Example One way ANOVA Test

You will use the poison dataset to implement the one-way ANOVA test. The dataset contains 48 rows and 3 variables:

- Time: Survival time of the animal
- poison: Type of poison used: factor level: 1,2 and 3
- treat: Type of treatment used: factor level: 1,2 and 3

Before you start to compute the ANOVA test, you need to prepare the data as follow:

- Step 1: Import the data
- Step 2: Remove unnecessary variable
- Step 3: Convert the variable poison as ordered level

```
library(dplyr)
PATH <-
"https://raw.githubusercontent.com/thomaspernet/data_csv_r/master/data/poisons.csv"
#Step 1
df <- read.csv(PATH) % > %
#Step 2
select(-X) % > %
#Step 3
mutate(poison = factor(poison, ordered = TRUE))
glimpse(df)
Output:
## Observations: 48
## Variables: 3
## $ time <dbl> 0.31, 0.45, 0.46, 0.43, 0.36, 0.29, 0.40, 0.23, 0.22, 0...
## $ poison <ord> 1, 1, 1, 1, 2, 2, 2, 2, 3, 3, 3, 1, 1, 1, 1, 1, 2, 2, 2...
## $ treat <fctr> A, B, B, B, B, B, E, ...
```

Our objective is to test the following assumption:

- H0: There is no difference in survival time average between group
- H3: The survival time average is different for at least one group.

In other words, you want to know if there is a statistical difference between the mean of the survival time according to the type of poison given to the Guinea pig.

You will proceed as follow:

- Step 1: Check the format of the variable poison
- Step 2: Print the summary statistic: count, mean and standard deviation
- Step 3: Plot a box plot
- Step 4: Compute the one-way ANOVA test
- Step 5: Run a pairwise t-test

Step 1) You can check the level of the poison with the following code. You should see three character values because you convert them in factor with the mutate verb.

```
levels(df$poison)
```

Output:

```
## [1] "1" "2" "3"
```

Step 2) You compute the mean and standard deviation.

```
df % > %
  group_by(poison) % > %
  summarise(
  count_poison = n(),
  mean_time = mean(time, na.rm = TRUE),
  sd_time = sd(time, na.rm = TRUE)
)
```

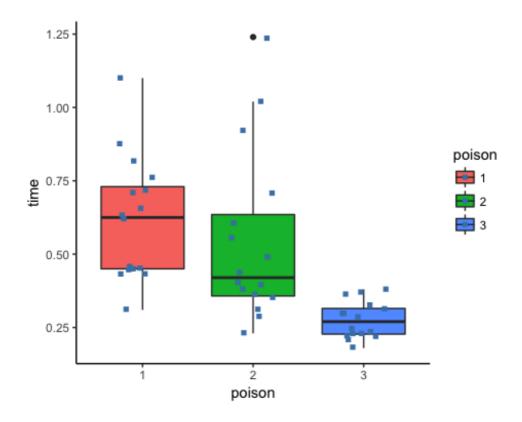
Output:

```
##
# A tibble: 3 x 4
     poison count_poison mean_time
                                      sd_time
##
                  <int>
                             <dbl>
                                        <dbl>
## 1
          1
                      16 0.617500 0.20942779
## 2
          2
                      16 0.544375 0.28936641
## 3
          3
                      16 0.276250 0.06227627
```

Step 3) In step three, you can graphically check if there is a difference between the distribution. Note that you include the jittered dot.

```
ggplot(df, aes(x = poison, y = time, fill = poison)) +
   geom_boxplot() +
   geom_jitter(shape = 15,
        color = "steelblue",
        position = position_jitter(0.21)) +
   theme_classic()
```

Output:



Step 4) You can run the one-way ANOVA test with the command aov. The basic syntax for an ANOVA test is:

```
aov(formula, data)
Arguments:
   formula: The equation you want to estimate
   data: The dataset used
```

The syntax of the formula is:

```
y \sim X1+ X2+...+Xn # X1 + X2 +... refers to the independent variables y \sim . # use all the remaining variables as independent variables
```

You can answer our question: Is there any difference in the survival time between the Guinea pig, knowing the type of poison given.

Note that, it is advised to store the model and use the function summary() to get a better print of the results.

```
anova_one_way <- aov(time~poison, data = df)
summary(anova_one_way)</pre>
```

Code Explanation

- aov(time ~ poison, data = df): Run the ANOVA test with the following formula
- summary(anova_one_way): Print the summary of the test

Output:

```
## Df Sum Sq Mean Sq F value Pr(>F)
## poison    2 1.033 0.5165 11.79 7.66e-05 ***
## Residuals    45 1.972 0.0438
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value is lower than the usual threshold of 0.05. You are confident to say there is a statistical difference between the groups, indicated by the "*".

Pairwise comparison

The one-way ANOVA test does not inform which group has a different mean. Instead, you can perform a Tukey test with the function TukeyHSD().

```
TukeyHSD(anova_one_way)
```

Output:

```
Tukey multiple comparisons of means
                                               Upper bound of the difference
    95% family-wise confidence level
                                                    in mean between group
Fit: aov(formula = time ~ poison, data = df)
                                                               Adjusted p-value when there
                                                                   are multiple groups
$poison
          diff
                                    upr
                       lwr
2-1 -0.073125 -0.2525046 0.10625464 0.5881654
3-1 -0.341250 -0.5206296 -0.16187036 0.0000971
                                                        Lower bound of the difference in
3-2 -0.268125 -0.4475046 -0.08874536 0.0020924 ==
                                                            mean between group
```

Two-way ANOVA

A two-way ANOVA test adds another group variable to the formula. It is identical to the one-way ANOVA test, though the formula changes slightly:

y=x1+x2

with is a quantitative variable and and are categorical variables.

Hypothesis in two-way ANOVA test:

- H0: The means are equal for both variables (i.e., factor variable)
- H3: The means are different for both variables

You add treat variable to our model. This variable indicates the treatment given to the Guinea pig. You are interested to see if there is a statistical dependence between the poison and treatment given to the Guinea pig.

We adjust our code by adding treat with the other independent variable.

```
anova_two_way <- aov(time~poison + treat, data = df)
summary(anova_two_way)</pre>
```

Output:

```
## poison 2 1.0330 0.5165 20.64 5.7e-07 ***

## treat 3 0.9212 0.3071 12.27 6.7e-06 ***

## Residuals 42 1.0509 0.0250
```

You can conclude that both poison and treat are statistically different from 0. You can reject the NULL hypothesis and confirm that changing the treatment or the poison impact the time of survival.

Summary

We can summarize the test in the table below:

Test	code	hypothesis	p- value
One way ANOVA	aov(y ~ X, data = df)	H3: Average is different for at least one group	0.05
Pairwise	TukeyHSD(ANOVA summary)		0.05
Two way ANOVA	aov(y ~ X1 + X2, data = df)	H3: Average is different for both group	0.05