Statistics Kingdom

Home > Mean tests > One-Way ANOVA

ANOVA Calculator

One-Way ANOVA Calculator and Tukey HSD

Significance level (α): 0,05

Outliers: Included

Effect: Medium

Effect type: f

Effect Size: 0.25

Rounding: 4

- (•) Enter raw data directly
- ( ) Enter raw data from excel

Tutorial
ANOVA

Calculators

Kruskal-Wallis test
Two way ANOVA
Levene's test

Enter sample data directly

Groups:	Conventional	Assertiveness-based
Data:	5 8 1 11 2 5 8 1 11 2 5 8 1 11 2 13 10 2 14 7 13 10 2 14 7 13 10 2 14 7 2 5 3 20 1 2 5 3 20 1 2 5 3 20 1 5 5 5 18 5 5 5 5 18 5 5 5 5 18 5 5 1 5 13 5 5 1 5 13 5 5 1 5 13 5	1 1 2 5 4 20 1 1 1 6 5 4 16 3 1 1 6 5 8 16 3 1 1 12 5 8 17 3 1 1 4 1 6 15 7 1 1 8 1 6 15 7 1 1 8 1 6 14 7 1
Skewness:	1.140179	1.396965
Excess kurtosis:	0.126546	0.816107
Normality	0	0
Outliers		17, 17, 17, 17, 17, 17, 17, 17,
Mean	6.10128	5.20604
S	5.52797	5.36877

Calculate | Validate | Insert column | Delete column | Clear | Load last run

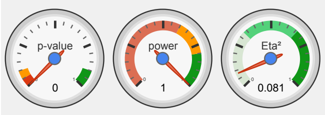
Header: You may change groups' names to the real names.
Data: When entering data, press Enter or , (comma) after each value.
You may paste full column from excel.
The calculator ignores empty cells or non-numeric cells.

Group1 contains 780 values
Group2 contains 1092 values
validation:success

Hover over the cells for more information.

Source	DF	Sum of Square	Mean Square	F Statistic	P-value
Groups (between groups)	1	364.6602	364.6602	12.342	0.0004534
Error (within groups)	1870	55251.6354	29.5463		
Total	1871	55616.2957	29.7254		

R code.



One Way ANOVA test, using F distribution df(1,1870) (right tailed)

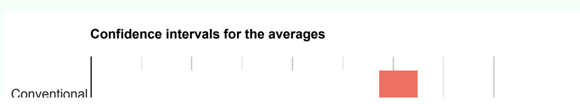
1. H_0 hypothesis
Since p-value<α, H_0 is rejected.
Some of the groups' averages consider to be not equal.
In other words, the difference between the averages of some groups is big enough to be statistically significant.

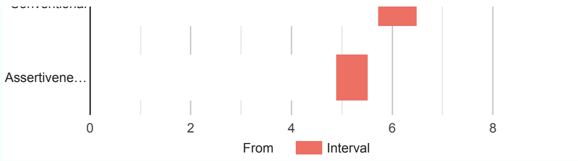
2. P-value
p-value equals **0.000453409**, [p(x ≤ F) = 0.999547]. It means that the chance of type1 error (rejecting a correct H_0) is small: 0.0004534 (0.045%)
The smaller the p-value the stronger it support H_1

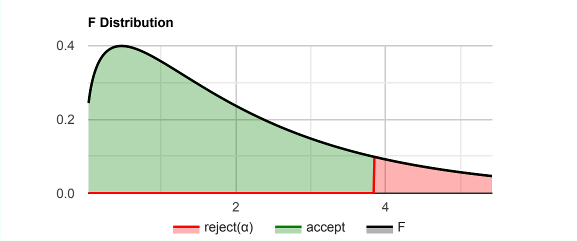
3. The statistics
The test statistic F equals **12.341981**, which is not in the 95% region of acceptance: [-∞ : 3.8464]

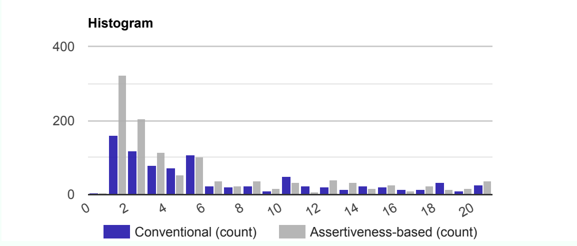
4. Effect size
The observed effect size f is **small** (0.081). That indicates that the magnitude of the difference between the averages is small.
The η^2 equals 0.0066. It means that the **group** explains 0.7% of the variance from the average (similar to R^2 in the linear regression)

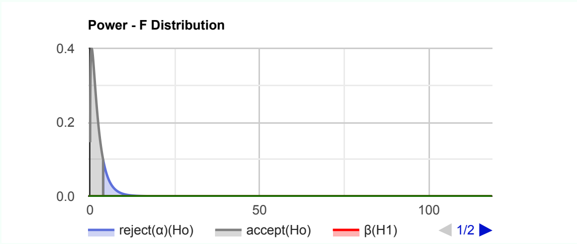
5. Tukey HSD / Tukey Kramer
The means of the following pair are significantly different: **x1-x2**.











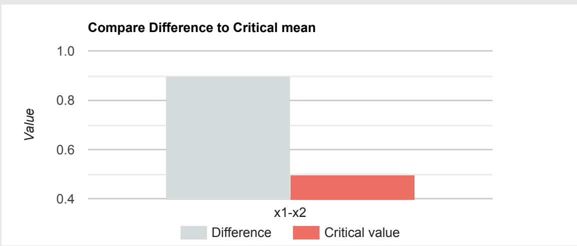
Validation

- **Test power**
  The test priori power is strong: 1
- **Equality of variances**
  The tool used the Levene's test to assess the equality of variances.
  The population's variances consider to be **equal**. (p-value = 0.0956).
  Levene's test power consider to be strong (1).
  The groups' size consider similar. (The ratio between the bigger group and the smaller group is: 1.4)
  The ANOVA test consider to be robust to the homogeneity of variances assumtion when the groups' sizes are similar.
- **Normality assumption**
  The assumption was checked based on the Shapiro-Wilk Test. (α=0.05)
  It is assumed that all the groups distribute normally or have a big sample size, at least 30.

Tukey HSD / Tukey Kramer

Pair	Difference	SE	Q	Lower CI	Upper CI	Critical Mean	p-value
x1-x2	0.8952	0.1802	4.9683	0.3955	1.395	0.4998	0.0004534

Group	x2
x1	0.9



ANOVA

What is the ANOVA?

The ANOVA test checks if the difference between the averages of two or more groups is significant, using sample data.
ANOVA is usually used when there are at least three groups since for two groups, the *two-tailed* pooled variance t-test and the *right-tailed* ANOVA test have the same result.
The basic ANOVA test contains only one categorical value, one-way ANOVA. For example, if you compare the performence of three schools, the categorical variable is school, and the possible values of the categorical variable are School-A, School-B, School-C. There are more complex ANOVA tests that contain two categorical variables (Two-way ANOVA calculator), or more. When performing a one-way ANOVA test, we try to determine if the difference between the averages reflects a real difference between the groups, or is due to the random noise inside each group.
The F statistic represents the ratio of the variance between the groups and the variance inside the groups. Unlike many other statistic tests, the smaller the F statistic the more likely the averages are equal.

Example: Compare four fertilizers used in four fields
H_0: The average weight of crops per square meter is equal in all fields.
H_1: At least one field yields a different average per square meter.

Right-tailed, for ANOVA test you can use only the right tail. Why?

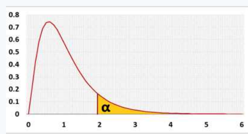
Hypotheses

H_0: $\mu_1 = ... = \mu_k$
H_1: not($\mu_1 = ... = \mu_k$)

ANOVA formula

$$F = \frac{MSG}{MSE}$$

F distribution



Assumptions

- Independent samples
- Normal distribution of the analyzed population
- Equal standard deviation, $\sigma_1=\sigma_2=...=\sigma_k$
  The assumption is more important when the groups' sizes not similar

Required Sample Data

- Sample data from all compared groups

Parameters

- **k** - Number of groups.
- **n_i** - Sample side of group i
- **n** - Overall sample side, includes all the groups (Σn_i, i=1 to k)
- **$\bar{x}_i$** - Average of group i.
- **$\bar{x}$** - Overall average ($\Sigma x_{i,j}$ / n, i=1 to k, j=1 to n_i)
- **S_i** - Standard deviation of group i

Results calculations

Source	Degrees of Freedom	Sum of Squares	Mean Square	F statistic	p-value
Groups (between groups)	k - 1	$SSG=\sum_{i=1}^{k} n_i\,(\bar{x}_i-\bar{x})^2$	MSG = SSG / (k - 1)	F = MSG / MSE	P(x > F)
Error (within groups)	n - k	$SSE=\sum_{i=1}^{k}(n_i-1)\,S_i^2$	MSE = SSE / (n - k)		
Total	n - 1	SS(total) = SSG + SSE	Sample Variance = SS(total) / (n - 1)		

R Code

The following R code should produce the same results

```
value0 <-
c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2
value1 <-
c(3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,4,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5
value2 <-
c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,11,11,11,11,11,11,11,11,11,11,11,11,11,11,11,11,11,11,11,11,11,11,12,12,12,12,12,12,12,12,12,12,12,12,12,12,12,12,13,13,13,13,13,13,13,13,13,13,13,13,13,14,14,14,14,14,14,14,14,14,14,14,14,14,14,14,14,14,15,
value3 <-
c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,
value4 <-
c(2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3
value5 <-
c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,6,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,
value6 <-
c(17,17,17,17,17,17,17,17,17,17,17,17,17,17,17,17,18,18,18,18,18,18,18,18,18,18,19,19,19,19,19,19,19,19,19,19,19,19,19,19,19,19,19,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20,20)
value <- c(value0,value1,value2,value3,value4,value5,value6)
group1 <- c(rep("Conventional", 780), rep("Assertiveness-based", 1092))
my.dataframe<-data.frame(value, group1)
res.aov <- aov(value ~ group1, data = my.dataframe)
summary(res.aov)
TukeyHSD(res.aov)
```