One-Way Anova

Ozancan Özdemir

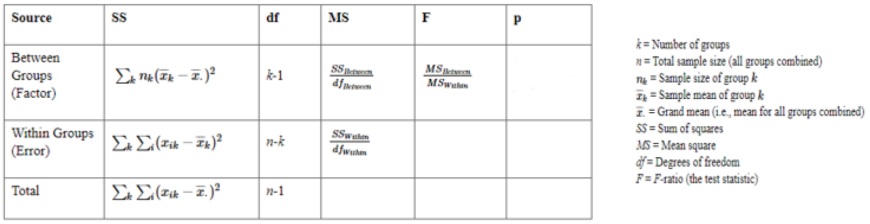
One-Way ANOVA

In a one-way ANOVA, you're interested in comparing the dependent variable means of two or more groups defined by a categorical grouping factor. The null hypothesis is that all the population group means are equal versus the alternative that at least one of the population means. i.e,

Ho: µ1= µ2= µ3=. . . = µk (All the averages are equal) vs H1= At least one of them is different where k represents the number of "independent" samples.

Assumptions

- Sample are independent.
- The response variable is approximately normally distributed.
- The population variances are equal across responses for the group levels (if the largest sample standard deviation divided by the smallest sample standard deviation is not greater than two, then assume that the population variances are equal)



Source	SS	df	MS	F	p
Between Groups (Factor)	$\sum_k n_k(\bar{x}_k - \bar{x}.)^2$	k-1	$\frac{SS_{Between}}{df_{Between}}$	$\frac{MS_{Between}}{MS_{Within}}$	
Within Groups (Error)	$\sum_k \sum_i (x_{ik} - \bar{x}_k)^2$	n-k	$\frac{SS_{Within}}{df_{Within}}$		
Total	$\sum_k \sum_i (x_{ik} - \bar{x}.)^2$	n-1			

k = Number of groups
n = Total sample size (all groups combined)
n_k = Sample size of group k
$\bar{x}_k$ = Sample mean of group k
$\bar{x}.$ = Grand mean (i.e., mean for all groups combined)
SS = Sum of squares
MS = Mean square
df = Degrees of freedom
F = F-ratio (the test statistic)

How to conduct in R?

Our example comes from the cholesterol dataset in the multcomp package, and taken from Westfall, Tobia, Rom, & Hochberg (1999).

```r
#install.packages("multcomp")
library(multcomp)
```

```
## Loading required package: mvtnorm

## Loading required package: survival

## Loading required package: TH.data

## Loading required package: MASS

##
## Attaching package: 'TH.data'

## The following object is masked from 'package:MASS':
##
##     geyser
```

```r
head(cholesterol)
```

```
##     trt response
## 1 1time   3.8612
## 2 1time  10.3868
```

```
## 3 1time   5.9059
## 4 1time   3.0609
## 5 1time   7.7204
## 6 1time   2.7139
```

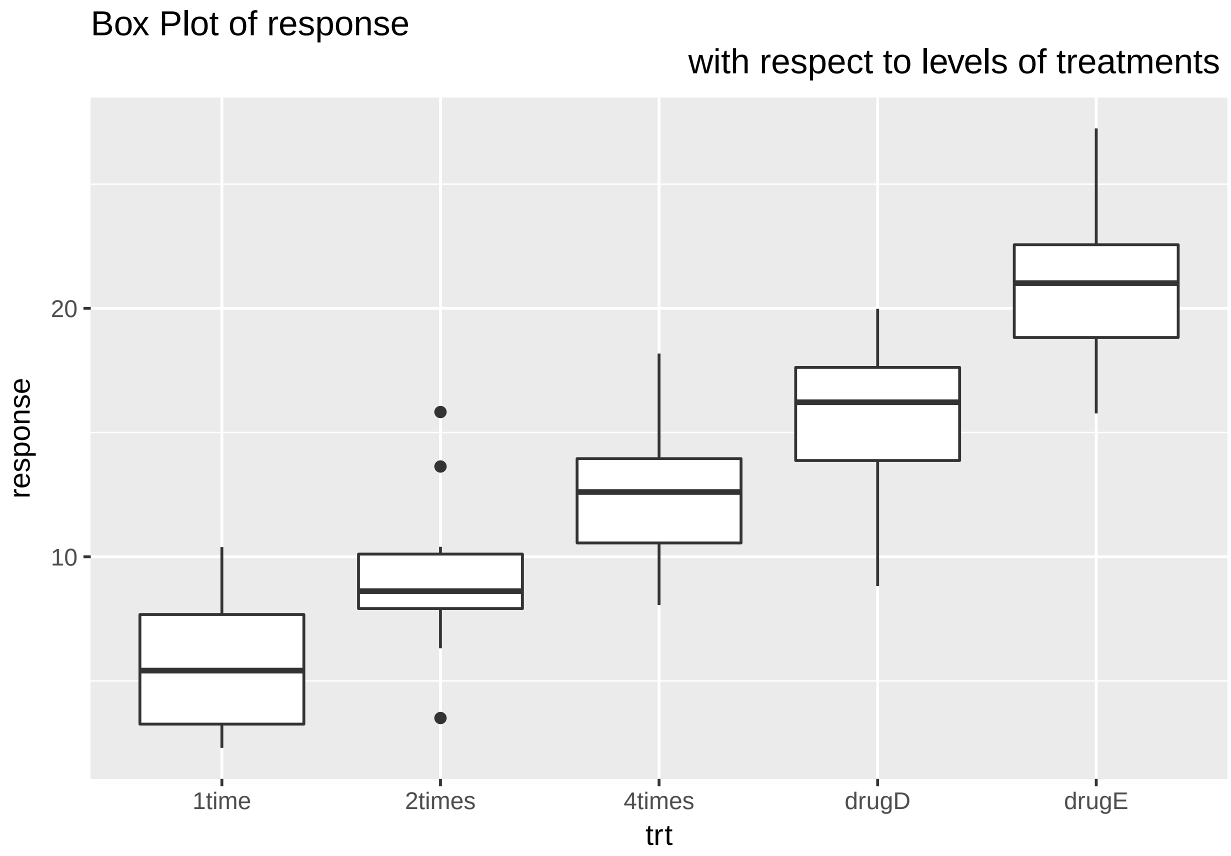
In this data set, fifty patients received one of five cholesterol-reducing drug regiments (trt). Three of the treatment conditions involved the same drug administered as 20 mg once per day (1time), 10mg twice per day (2times), or 5 mg four times per day (4times). The two remaining conditions (drugD and drugE) represented competing drugs. Which drug regimen produced the greatest cholesterol reduction (response)?

Let's first draw the samples with the appropriate plot

```r
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.4.3
```

```r
ggplot(cholesterol,aes(x=trt,y=response))+geom_boxplot()+labs(title="Box Plot of response
                                                            with respect to levels of treatments")
```



It is seen that the average values of samples represented by median are different for each cases. It is an indication of to reject the null hypothesis.

Then, check assumption!

Normality Assumption,

```r
#Check Normality for each sample
shapiro.test(cholesterol$response[cholesterol$trt=="1time"])
```

```
##
```

```
##  Shapiro-Wilk normality test
##
## data:  cholesterol$response[cholesterol$trt == "1time"]
## W = 0.93063, p-value = 0.4541
```

```r
#Since p value is greater than our significance level taken 0.05,
#the response variable follows normal distribution.
```

```r
shapiro.test(cholesterol$response[cholesterol$trt=="2times"])
```

```
##
##  Shapiro-Wilk normality test
##
## data:  cholesterol$response[cholesterol$trt == "2times"]
## W = 0.9432, p-value = 0.5892
```

```r
#Since p value is greater than our significance level taken 0.05,
#the response variable follows normal distribution.
```

```r
shapiro.test(cholesterol$response[cholesterol$trt=="4times"])
```

```
##
##  Shapiro-Wilk normality test
##
## data:  cholesterol$response[cholesterol$trt == "4times"]
## W = 0.95487, p-value = 0.7262
```

```r
#Since p value is greater than our significance level taken 0.05,
#the response variable follows normal distribution.
```

```r
shapiro.test(cholesterol$response[cholesterol$trt=="drugD"])
```

```
##
##  Shapiro-Wilk normality test
##
## data:  cholesterol$response[cholesterol$trt == "drugD"]
## W = 0.93406, p-value = 0.489
```

```r
#Since p value is greater than our significance level taken 0.05,
#the response variable follows normal distribution.
```

```r
shapiro.test(cholesterol$response[cholesterol$trt=="drugE"])
```

```
##
##  Shapiro-Wilk normality test
##
## data:  cholesterol$response[cholesterol$trt == "drugE"]
## W = 0.98085, p-value = 0.9696
```

```r
#Since p value is greater than our significance level taken 0.05,
#the response variable follows normal distribution.
```

Homogenity of Variance,

In this assumption, our null hypothesis is that all samples have equal variances and alternative hypothesis suggests that at least one of them has different variance. Our aim is to be failed to reject the null hypothesis.

```r
bartlett.test(response~trt,data=cholesterol) #Since p value is greater than 0.05, it can be said that
```

```
##
```

```
##  Bartlett test of homogeneity of variances
##
## data:  response by trt
## Bartlett's K-squared = 0.57975, df = 4, p-value = 0.9653
```

```
#there is no evidence to conclude that the samples have different variance values.
```

After checking assumptions, the One-Way Anova is conducted as follows,

```
fit<-aov(response~trt,data=cholesterol) #fitting anova model
summary(fit)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## trt          4 1351.4   337.8   32.43 9.82e-13 ***
## Residuals   45  468.8    10.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Studying the output of the ANOVA table above we see that the F-statistic is 32.43 with a p-value equal to 9.82e-13 . We clearly reject the null hypothesis of equal means for all five drug groups.

The ANOVA F-test answers the question whether there are significant differences in the K population means. However, it does not provide us with any information about how they differ. Therefore, when you reject H0 in ANOVA, additional analyses are required to determine what is driving the difference in means. There are several tests in the literature such as LSD test, Tukey Test, pairwise t-test..

```
TukeyHSD(fit)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = response ~ trt, data = cholesterol)
##
## $trt
##                    diff        lwr       upr     p adj
## 2times-1time    3.44300 -0.6582817  7.544282 0.1380949
## 4times-1time    6.59281  2.4915283 10.694092 0.0003542
## drugD-1time     9.57920  5.4779183 13.680482 0.0000003
## drugE-1time    15.16555 11.0642683 19.266832 0.0000000
## 4times-2times   3.14981 -0.9514717  7.251092 0.2050382
## drugD-2times    6.13620  2.0349183 10.237482 0.0009611
## drugE-2times   11.72255  7.6212683 15.823832 0.0000000
## drugD-4times    2.98639 -1.1148917  7.087672 0.2512446
## drugE-4times    8.57274  4.4714583 12.674022 0.0000037
## drugE-drugD     5.58635  1.4850683  9.687632 0.0030633
```

In this test, each output is obtained from indivual tests. For example, the first test is about the difference between drugs 1time and drugs 2times. The null hypothesis suggests that there is no difference between these samples while the alternative hypothesis suggests that there is a difference between them. To make a decision, the p value is observed and since p value is greater than our significance value, it can be said that there is no significant difference between these two samples. The other tests are interpreted in the same way.

In addition to Tukey Test, pairwise t test is also helpful for this purpose. The syntax of this test is as follows,

```
pairwise.t.test(reponse, factor, p.adjust = method, alternative = c("two.sided", "less", "greater"))
```

```
pairwise.t.test(cholesterol$response, cholesterol$trt, p.adjust = "bonferroni")
```

```
##
```

```
##  Pairwise comparisons using t tests with pooled SD
##
## data:  cholesterol$response and cholesterol$trt
##
##        1time   2times  4times  drugD
## 2times 0.21333 -       -       -
## 4times 0.00038 0.34352 -       -
## drugD  3.5e-07 0.00106 0.44316 -
## drugE  1.1e-12 2.3e-09 3.8e-06 0.00348
##
## P value adjustment method: bonferroni
```

```
#We prefer bonferroni method, because it gives the narrowest confidence interval.
```

Each enrty in this matrix shows the p-value of the tests where the null hypothesis that there is no difference between samples. It is seen that the results are matched with one coming from Tukey HSD test.