ANOVA

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**Aim**

An initial varietal trial was conducted to study the performance of 6 new strains of mustard with 3 replications. The seed yield in kg/ha was recorded. The details of the experiment are given. Analyze with one way anova to check the significant difference between strains.

**Procedure**

H0: There is no significant difference between the strains.

H1: There is a significant difference between the strains.

datafile<-read.table(file="clipboard",header=TRUE)  
datafile

## strain treatment  
## 1 RK-04-3 539.69  
## 2 RK-04-3 412.35  
## 3 RK-04-3 319.73  
## 4 RK-04-4 261.85  
## 5 RK-04-4 65.05  
## 6 RK-04-4 111.36  
## 7 RGN-124 389.19  
## 8 RGN-124 516.54  
## 9 RGN-124 203.97  
## 10 HYT-27 192.39  
## 11 HYT-27 215.55  
## 12 HYT-27 157.66  
## 13 PBR-275 250.27  
## 14 PBR-275 203.97  
## 15 PBR-275 366.04  
## 16 HUJM-03-03 296.58  
## 17 HUJM-03-03 273.43  
## 18 HUJM-03-03 308.16

model<-aov(treatment~strain,data=datafile)  
summary(model)

## Df Sum Sq Mean Sq F value Pr(>F)   
## strain 5 165793 33159 3.577 0.0327 \*  
## Residuals 12 111235 9270   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

library(agricolae)

## Warning: package 'agricolae' was built under R version 3.4.4

out<-LSD.test(model,"strain",p.adj="bonferroni",alpha=0.01)  
out

## $statistics  
## MSerror Df Mean CV t.value MSD  
## 9269.611 12 282.4322 34.08918 4.549577 357.6483  
##   
## $parameters  
## test p.ajusted name.t ntr alpha  
## Fisher-LSD bonferroni strain 6 0.01  
##   
## $means  
## treatment std r LCL UCL Min Max Q25  
## HUJM-03-03 292.7233 17.68329 3 122.93186 462.5148 273.43 308.16 285.005  
## HYT-27 188.5333 29.13706 3 18.74186 358.3248 157.66 215.55 175.025  
## PBR-275 273.4267 83.47961 3 103.63519 443.2181 203.97 366.04 227.120  
## RGN-124 369.9000 157.17531 3 200.10853 539.6915 203.97 516.54 296.580  
## RK-04-3 423.9233 110.43576 3 254.13186 593.7148 319.73 539.69 366.040  
## RK-04-4 146.0867 102.89323 3 -23.70481 315.8781 65.05 261.85 88.205  
## Q50 Q75  
## HUJM-03-03 296.58 302.370  
## HYT-27 192.39 203.970  
## PBR-275 250.27 308.155  
## RGN-124 389.19 452.865  
## RK-04-3 412.35 476.020  
## RK-04-4 111.36 186.605  
##   
## $comparison  
## NULL  
##   
## $groups  
## treatment groups  
## RK-04-3 423.9233 a  
## RGN-124 369.9000 a  
## HUJM-03-03 292.7233 a  
## PBR-275 273.4267 a  
## HYT-27 188.5333 a  
## RK-04-4 146.0867 a  
##   
## attr(,"class")  
## [1] "group"

**Conclusion**

Since the value of F-calculated is more than probability value at 0.01 alpha level, null hypothesis is rejected. Therefore, there is a significant difference between the strains.

**Aim**

A feeding trial with 3 feeds namely (i) Pasture(control), (ii) Pasture and Concentrates and (iii) Pasture, Concentrates and Minerals was conducted at the Yellachihalli Sheep Farm, Mysore, to study their effect on wool yield of Sheep with totally controlled condition. For this purpose, twenty-two ewe lambs were allotted at random to each of the three treatments and the weight records of the total wool yield (in gms) of first two clipping were obtained. Compare 3 different feeding trails.

**Procedure**

H0: There is no significant difference between the feeding trails.

H1: There is a significant difference between the feeding trails.

datafile<-read.table(file="clipboard",header=TRUE)  
datafile

## group trails  
## 1 feed1 850.50  
## 2 feed1 453.60  
## 3 feed1 878.85  
## 4 feed1 623.70  
## 5 feed1 510.30  
## 6 feed1 765.45  
## 7 feed1 680.40  
## 8 feed1 595.35  
## 9 feed1 538.65  
## 10 feed1 850.50  
## 11 feed1 850.50  
## 12 feed1 793.80  
## 13 feed1 1020.60  
## 14 feed1 708.75  
## 15 feed1 652.05  
## 16 feed1 623.70  
## 17 feed1 396.90  
## 18 feed1 822.15  
## 19 feed2 510.30  
## 20 feed2 963.90  
## 21 feed2 652.05  
## 22 feed2 1020.60  
## 23 feed2 878.85  
## 24 feed2 567.00  
## 25 feed2 680.40  
## 26 feed2 538.65  
## 27 feed2 567.00  
## 28 feed2 510.30  
## 29 feed2 425.25  
## 30 feed2 567.00  
## 31 feed2 623.70  
## 32 feed2 538.65  
## 33 feed2 737.10  
## 34 feed2 453.60  
## 35 feed2 481.95  
## 36 feed2 368.55  
## 37 feed2 567.00  
## 38 feed2 595.35  
## 39 feed2 567.00  
## 40 feed2 595.35  
## 41 feed3 992.25  
## 42 feed3 850.50  
## 43 feed3 1474.20  
## 44 feed3 510.30  
## 45 feed3 850.50  
## 46 feed3 793.80  
## 47 feed3 453.60  
## 48 feed3 935.55  
## 49 feed3 1190.70  
## 50 feed3 481.95  
## 51 feed3 623.70  
## 52 feed3 878.85  
## 53 feed3 1077.30  
## 54 feed3 850.50  
## 55 feed3 680.40

model<-aov(trails~group,data=datafile)  
summary(model)

## Df Sum Sq Mean Sq F value Pr(>F)   
## group 2 486056 243028 5.992 0.00455 \*\*  
## Residuals 52 2109004 40558   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

library(agricolae)

## Warning: package 'agricolae' was built under R version 3.4.4

out<-LSD.test(model,"group",p.adj="bonferroni",alpha=0.01)  
out

## $statistics  
## MSerror Df Mean CV  
## 40557.76 52 703.08 28.64391  
##   
## $parameters  
## test p.ajusted name.t ntr alpha  
## Fisher-LSD bonferroni group 3 0.01  
##   
## $means  
## trails std r LCL UCL Min Max Q25 Q50  
## feed1 700.875 166.3923 18 573.9583 827.7917 396.90 1020.6 602.4375 694.575  
## feed2 609.525 163.6203 22 494.7245 724.3255 368.55 1020.6 517.3875 567.000  
## feed3 842.940 277.2481 15 703.9097 981.9703 453.60 1474.2 652.0500 850.500  
## Q75  
## feed1 843.4125  
## feed2 644.9625  
## feed3 963.9000  
##   
## $comparison  
## NULL  
##   
## $groups  
## trails groups  
## feed3 842.940 a  
## feed1 700.875 ab  
## feed2 609.525 b  
##   
## attr(,"class")  
## [1] "group”

**Conclusion**

Since the value of F-calculated is more than probability value at 0.01 alpha level, null hypothesis is rejected. Therefore, there is a significant difference between the feeding trails.