Latin Square Design

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**Aim**

**Engines**

H0: There is no significant difference in the performance of the five engines.

HI: There is a significant difference in the performance of the five engines.

**Mechanics**

H0: The persons who tuned up the engines have no significant effect on engine performance.

H1: The persons who tuned up the engines have a significant effect on engine performance.

**Procedure**

**Alpha level** = 0.01

**library**(lsmeans)

## Warning: package 'lsmeans' was built under R version 3.5.3

## Loading required package: emmeans

## Warning: package 'emmeans' was built under R version 3.5.3

## The 'lsmeans' package is now basically a front end for 'emmeans'.  
## Users are encouraged to switch the rest of the way.  
## See help('transition') for more information, including how to  
## convert old 'lsmeans' objects and scripts to work with 'emmeans'.

rname <- **c**(**rep**("E1",5),**rep**("E2",5),**rep**("E3",5),**rep**("E4",5),**rep**("E5",5))  
cname <- **c**(**rep**("M1",1),**rep**("M2",1),**rep**("M3",1),**rep**("M4",1),**rep**("M5",1))  
seed <- **c**("A","B","C","D","E","B","C","D","E","A","C","D","E","A","B","D","E","A","B","C","E","A","B","C","D")  
freq <- **c**(31,24,20,20,18,21,27,23,25,31,21,27,25,29,21,21,25,33,25,22,21,37,24,24,20)  
mydata <- **data.frame**(rname,cname,seed,freq)  
mydata

## rname cname seed freq  
## 1 E1 M1 A 31  
## 2 E1 M2 B 24  
## 3 E1 M3 C 20  
## 4 E1 M4 D 20  
## 5 E1 M5 E 18  
## 6 E2 M1 B 21  
## 7 E2 M2 C 27  
## 8 E2 M3 D 23  
## 9 E2 M4 E 25  
## 10 E2 M5 A 31  
## 11 E3 M1 C 21  
## 12 E3 M2 D 27  
## 13 E3 M3 E 25  
## 14 E3 M4 A 29  
## 15 E3 M5 B 21  
## 16 E4 M1 D 21  
## 17 E4 M2 E 25  
## 18 E4 M3 A 33  
## 19 E4 M4 B 25  
## 20 E4 M5 C 22  
## 21 E5 M1 E 21  
## 22 E5 M2 A 37  
## 23 E5 M3 B 24  
## 24 E5 M4 C 24  
## 25 E5 M5 D 20

**matrix**(mydata**$**seed,5,5)

## [,1] [,2] [,3] [,4] [,5]  
## [1,] "A" "B" "C" "D" "E"   
## [2,] "B" "C" "D" "E" "A"   
## [3,] "C" "D" "E" "A" "B"   
## [4,] "D" "E" "A" "B" "C"   
## [5,] "E" "A" "B" "C" "D"

**matrix**(mydata**$**freq,5,5)

## [,1] [,2] [,3] [,4] [,5]  
## [1,] 31 21 21 21 21  
## [2,] 24 27 27 25 37  
## [3,] 20 23 25 33 24  
## [4,] 20 25 29 25 24  
## [5,] 18 31 21 22 20

myfit = **lm**(freq**~**rname**+**cname**+**seed,mydata)  
myfit

##   
## Call:  
## lm(formula = freq ~ rname + cname + seed, data = mydata)  
##   
## Coefficients:  
## (Intercept) rnameE2 rnameE3 rnameE4 rnameE5   
## 28.6 2.8 2.0 2.6 2.6   
## cnameM2 cnameM3 cnameM4 cnameM5 seedB   
## 5.0 2.0 1.6 -0.6 -9.2   
## seedC seedD seedE   
## -9.4 -10.0 -9.4

**str**(mydata)

## 'data.frame': 25 obs. of 4 variables:  
## $ rname: Factor w/ 5 levels "E1","E2","E3",..: 1 1 1 1 1 2 2 2 2 2 ...  
## $ cname: Factor w/ 5 levels "M1","M2","M3",..: 1 2 3 4 5 1 2 3 4 5 ...  
## $ seed : Factor w/ 5 levels "A","B","C","D",..: 1 2 3 4 5 2 3 4 5 1 ...  
## $ freq : num 31 24 20 20 18 21 27 23 25 31 ...

a = **anova**(myfit)  
a

## Analysis of Variance Table  
##   
## Response: freq  
## Df Sum Sq Mean Sq F value Pr(>F)   
## rname 4 26.8 6.7 2.3103 0.11737   
## cname 4 95.6 23.9 8.2414 0.00195 \*\*   
## seed 4 362.8 90.7 31.2759 2.911e-06 \*\*\*  
## Residuals 12 34.8 2.9   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusion**

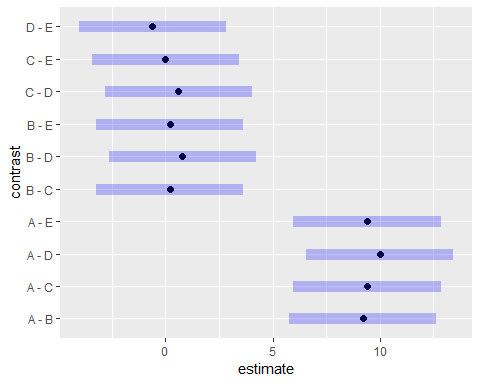
1. The p-value for mechanics is greater than 0.01. Hence, we accept the null hypothesis. Hence, we can conclude that there is no signifcant difference in the for the perfomance.
2. From the above, we reject the null hypothesis at 1% level of significance that there is a significant difference in the performance in the five engines. Hence, we proceed with the post hoc test.

**Post-hoc Test**

x = **lsmeans**(myfit,"seed")  
**pairs**(x)

## contrast estimate SE df t.ratio p.value  
## A - B 9.2 1.08 12 8.542 <.0001   
## A - C 9.4 1.08 12 8.728 <.0001   
## A - D 10.0 1.08 12 9.285 <.0001   
## A - E 9.4 1.08 12 8.728 <.0001   
## B - C 0.2 1.08 12 0.186 0.9997   
## B - D 0.8 1.08 12 0.743 0.9420   
## B - E 0.2 1.08 12 0.186 0.9997   
## C - D 0.6 1.08 12 0.557 0.9789   
## C - E 0.0 1.08 12 0.000 1.0000   
## D - E -0.6 1.08 12 -0.557 0.9789   
##   
## Results are averaged over the levels of: rname, cname   
## P value adjustment: tukey method for comparing a family of 5 estimates

**plot**(**pairs**(x))



**Post-hoc Conclusion**

From the graph, we can conclude that the treatements A-E, A-D, A-C and A-B are significantly different while treatments D-E, C-E, C-D, B-E, B-D and B-C are not significantly different.

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