LSD\_Lab\_7

Jeevan

03/09/2019

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

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))

