Two-way Anova for RCBD Design

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Question

In order to select tree species for fuel, fodder and timber an experiment was conducted at Kanpur in a randomized complete block design with ten different trees and four replications. The plant height was recorded in cms. Analyse the data and draw your conclusions.

Test used

Two-way Anova.

Aim

Blocks

H0: There is no significant difference between the means of the different blocks.

HI: There is a significant difference between atleast one pair of means of the different blocks.

Factor 2

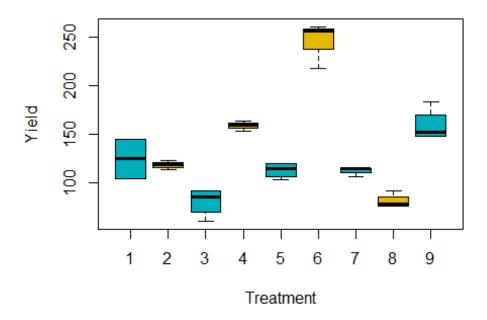
H0: There is no significant difference between the means of the different treatments.

H1: There is a significant difference between atleast one pair of means of the different treatments.

Alpha level = 0.05

Procedure

```
data <- read.table(file = "clipboard", header = TRUE)</pre>
str(data)
## 'data.frame':
                   36 obs. of 3 variables:
## $ treatment: int 1 2 3 4 5 6 7 8 9 1 ...
## $ block
            : int 1111111112...
## $ yield
              : num 144.4 113.5 60.9 163.4 110.1 ...
Treatment and blocks are categorical variables. Therefore, they are being con
verted into factors in R.
attach(data)
treatment <- as.factor(data$treatment)</pre>
block <- as.factor(data$block)</pre>
str(data)
## 'data.frame':
                   36 obs. of 3 variables:
## $ treatment: int 1 2 3 4 5 6 7 8 9 1 ...
## $ block
            : int 111111112...
## $ yield
              : num 144.4 113.5 60.9 163.4 110.1 ...
boxplot(data$yield ~ data$treatment, xlab = "Treatment", ylab = "Yield",
       col = c("#00AFBB", "#E7B800"))
```



```
m1 <- aov(data$yield ~ data$treatment + data$block)</pre>
summary(m1)
##
                  Df Sum Sq Mean Sq F value Pr(>F)
## data$treatment
                  1
                       2094
                             2094.0
                                      0.803 0.0377
## data$block
                   1
                        232
                              232.2
                                      0.089 0.767
## Residuals
                  33
                      86110 2609.4
Probability value for treatment is less than 0.05. Hence, the treatments are
significantly different. We proceed with post-hoc test.
lm1 <- lm(yield~treatment+block)</pre>
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 'Ismeans' objects and scripts to work with 'emmeans'.
lsm1 <- lsmeans(lm1, "treatment")</pre>
pairs(lsm1)
   contrast estimate
                        SE df t.ratio p.value
                6.317 9.61 24
## 1 - 2
                                0.658 0.9989
##
  1 - 3
               43.710 9.61 24
                                4.549 0.0035
  1 - 4
              -33.830 9.61 24 -3.521 0.0383
## 1 - 5
               11.585 9.61 24 1.206 0.9474
```

```
1 - 6
             -122.825 9.61 24 -12.783 <.0001
##
    1 - 7
               12.225 9.61 24
                                 1.272 0.9299
    1 - 8
##
               43.472 9.61 24
                                 4.525 0.0037
##
    1 - 9
              -34.182 9.61 24
                                -3.558 0.0353
    2 - 3
##
               37.392 9.61 24
                                 3.892 0.0166
##
    2 - 4
              -40.148 9.61 24
                                -4.179 0.0085
##
    2 -
        5
                 5.268 9.61 24
                                 0.548 0.9997
    2 -
##
        6
             -129.143 9.61 24 -13.441 <.0001
##
    2 - 7
                5.907 9.61 24
                                 0.615 0.9993
##
    2 - 8
                37.155 9.61 24
                                 3.867 0.0175
    2 - 9
##
              -40.500 9.61 24
                                -4.215 0.0078
    3 - 4
##
              -77.540 9.61 24
                                -8.070 <.0001
##
    3 -
        5
              -32.125 9.61 24
                                -3.344 0.0563
##
    3 - 6
             -166.535 9.61 24 -17.333 <.0001
                                -3.277 0.0649
##
    3 - 7
              -31.485 9.61 24
##
    3 - 8
                -0.237 9.61 24
                                -0.025 1.0000
    3 - 9
##
              -77.892 9.61 24
                                -8.107 <.0001
##
    4 -
        5
               45.415 9.61 24
                                 4.727 0.0023
##
    4 - 6
              -88.995 9.61 24
                                -9.263 <.0001
                                 4.793 0.0019
##
    4 - 7
               46.055 9.61 24
##
    4 - 8
               77.302 9.61 24
                                 8.046 < .0001
    4 - 9
                -0.352 9.61 24
##
                                -0.037 1.0000
##
    5 - 6
             -134.410 9.61 24 -13.989 <.0001
    5
##
      - 7
                0.640 9.61 24
                                 0.067 1.0000
##
    5 - 8
               31.887 9.61 24
                                 3.319 0.0594
    5 - 9
##
              -45.767 9.61 24
                                -4.763 0.0021
##
    6 - 7
              135.050 9.61 24
                                14.056 < .0001
##
    6 - 8
              166.298 9.61 24
                                17.308 < .0001
    6 - 9
##
               88.642 9.61 24
                                 9.226 < .0001
##
    7 - 8
               31.247 9.61 24
                                 3.252 0.0683
##
    7 - 9
              -46.407 9.61 24
                                -4.830 0.0018
##
    8 - 9
              -77.655 9.61 24
                                -8.082 <.0001
##
## Results are averaged over the levels of: block
## P value adjustment: Tukey method for comparing a family of 9 estimates
```

Conclusion

- 1. The calculated probability value for the blocks is greater than 0.05. Hence, it can be concluded that the means of the blocks are not significantly different.
- 2. The calculated probability value for the treatment is less than 0.05. Therefore, the null hypothesis is rejected. Hence, we can conclude that there is a significant difference between atleast one pair of means of the treatments. The results of the post hoc test indicates that treatment 6(L Loucoc Tree) has the highest yield and can be chosen for the experiment.