Analysis of Factorial Experiment in R

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Loading packages

```
library(agricolae)
library(ExpDes)
library(multcomp)
library(tidyverse)
library(emmeans)
```

Two-factor Factorial in CRD

Loading and managing the data

```
options(digits=6)
crd_data <- read.csv("twofactorial_crd.csv")
head(crd_data)
```

```
##   Pesticide Variety Yield
## 1        P1      V1    49
## 2        P1      V1    39
## 3        P1      V2    55
## 4        P1      V2    41
## 5        P1      V3    66
## 6        P1      V3    68
```

```
crd_data %>%
  group_by(Pesticide) %>%
  summarize(M=mean(Yield))
```

```
## # A tibble: 4 x 2
##   Pesticide     M
##   <chr>     <dbl>
## 1 P1           53
## 2 P2         67.8
## 3 P3         51.2
## 4 P4         73.8
```

```
crd_data %>%
  group_by(Variety) %>%
  summarize(M=mean(Yield))
```

```
## # A tibble: 3 x 2
##   Variety     M
##   <chr>   <dbl>
## 1 V1       46.9
## 2 V2       59.2
## 3 V3       78.2
```

ANOVA using aov()

```
out1 <- aov(Yield ~ Pesticide + Variety + Pesticide:Variety,
            data = crd_data)
```

```
summary(out1)
```

```
##                   Df Sum Sq Mean Sq F value  Pr(>F)
## Pesticide          3   2227     742    17.6 0.00011 ***
## Variety            2   3996    1998    47.2   2e-06 ***
## Pesticide:Variety  6    457      76     1.8 0.18168
## Residuals         12    508      42
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(out1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Yield ~ Pesticide + Variety + Pesticide:Variety, data = crd_data)
##
## $Pesticide
##            diff       lwr       upr      p adj
## P2-P1  14.83333   3.68622  25.98045 0.009001
## P3-P1  -1.83333 -12.98045   9.31378 0.960234
## P4-P1  20.83333   9.68622  31.98045 0.000629
## P3-P2 -16.66667 -27.81378  -5.51955 0.003883
## P4-P2   6.00000  -5.14712  17.14712 0.415509
## P4-P3  22.66667  11.51955  33.81378 0.000297
##
## $Variety
##          diff      lwr      upr      p adj
## V2-V1  12.375  3.70017  21.0498 0.006539
## V3-V1  31.375 22.70017  40.0498 0.000001
## V3-V2  19.000 10.32517  27.6748 0.000216
##
## $`Pesticide:Variety`
##                  diff       lwr       upr    p adj
```

```
## P2:V1-P1:V1    8.5 -17.318729 34.31873 0.962324
## P3:V1-P1:V1   -3.5 -29.318729 22.31873 0.999979
## P4:V1-P1:V1    6.5 -19.318729 32.31873 0.994460
## P1:V2-P1:V1    4.0 -21.818729 29.81873 0.999924
## P2:V2-P1:V1   18.5  -7.318729 44.31873 0.269500
## P3:V2-P1:V1    3.5 -22.318729 29.31873 0.999979
## P4:V2-P1:V1   35.0   9.181271 60.81873 0.005485
## P1:V3-P1:V1   23.0  -2.818729 48.81873 0.098292
## P2:V3-P1:V1   44.5  18.681271 70.31873 0.000660
## P3:V3-P1:V1   21.5  -4.318729 47.31873 0.139425
## P4:V3-P1:V1   48.0  22.181271 73.81873 0.000320
## P3:V1-P2:V1  -12.0 -37.818729 13.81873 0.769940
## P4:V1-P2:V1   -2.0 -27.818729 23.81873 1.000000
## P1:V2-P2:V1   -4.5 -30.318729 21.31873 0.999768
## P2:V2-P2:V1   10.0 -15.818729 35.81873 0.902399
## P3:V2-P2:V1   -5.0 -30.818729 20.81873 0.999394
## P4:V2-P2:V1   26.5   0.681271 52.31873 0.042379
## P1:V3-P2:V1   14.5 -11.318729 40.31873 0.559505
## P2:V3-P2:V1   36.0  10.181271 61.81873 0.004344
## P3:V3-P2:V1   13.0 -12.818729 38.81873 0.688133
## P4:V3-P2:V1   39.5  13.681271 65.31873 0.001956
## P4:V1-P3:V1   10.0 -15.818729 35.81873 0.902399
## P1:V2-P3:V1    7.5 -18.318729 33.31873 0.983812
## P2:V2-P3:V1   22.0  -3.818729 47.81873 0.124226
## P3:V2-P3:V1    7.0 -18.818729 32.81873 0.990217
## P4:V2-P3:V1   38.5  12.681271 64.31873 0.002450
## P1:V3-P3:V1   26.5   0.681271 52.31873 0.042379
## P2:V3-P3:V1   48.0  22.181271 73.81873 0.000320
## P3:V3-P3:V1   25.0  -0.818729 50.81873 0.060949
## P4:V3-P3:V1   51.5  25.681271 77.31873 0.000160
## P1:V2-P4:V1   -2.5 -28.318729 23.31873 0.999999
## P2:V2-P4:V1   12.0 -13.818729 37.81873 0.769940
## P3:V2-P4:V1   -3.0 -28.818729 22.81873 0.999996
## P4:V2-P4:V1   28.5   2.681271 54.31873 0.026050
## P1:V3-P4:V1   16.5  -9.318729 42.31873 0.399164
## P2:V3-P4:V1   38.0  12.181271 63.81873 0.002744
## P3:V3-P4:V1   15.0 -10.818729 40.81873 0.517354
## P4:V3-P4:V1   41.5  15.681271 67.31873 0.001257
## P2:V2-P1:V2   14.5 -11.318729 40.31873 0.559505
## P3:V2-P1:V2   -0.5 -26.318729 25.31873 1.000000
## P4:V2-P1:V2   31.0   5.181271 56.81873 0.014211
## P1:V3-P1:V2   19.0  -6.818729 44.81873 0.242656
## P2:V3-P1:V2   40.5  14.681271 66.31873 0.001566
## P3:V3-P1:V2   17.5  -8.318729 43.31873 0.329912
## P4:V3-P1:V2   44.0  18.181271 69.81873 0.000733
## P3:V2-P2:V2  -15.0 -40.818729 10.81873 0.517354
## P4:V2-P2:V2   16.5  -9.318729 42.31873 0.399164
## P1:V3-P2:V2    4.5 -21.318729 30.31873 0.999768
## P2:V3-P2:V2   26.0   0.181271 51.81873 0.047850
## P3:V3-P2:V2    3.0 -22.818729 28.81873 0.999996
## P4:V3-P2:V2   29.5   3.681271 55.31873 0.020430
## P4:V2-P3:V2   31.5   5.681271 57.31873 0.012598
## P1:V3-P3:V2   19.5  -6.318729 45.31873 0.217998
## P2:V3-P3:V2   41.0  15.181271 66.81873 0.001402
```

```
## P3:V3-P3:V2  18.0  -7.818729 43.81873 0.298580
## P4:V3-P3:V2  44.5  18.681271 70.31873 0.000660
## P1:V3-P4:V2 -12.0 -37.818729 13.81873 0.769940
## P2:V3-P4:V2   9.5 -16.318729 35.31873 0.926373
## P3:V3-P4:V2 -13.5 -39.318729 12.31873 0.645435
## P4:V3-P4:V2  13.0 -12.818729 38.81873 0.688133
## P2:V3-P1:V3  21.5  -4.318729 47.31873 0.139425
## P3:V3-P1:V3  -1.5 -27.318729 24.31873 1.000000
## P4:V3-P1:V3  25.0  -0.818729 50.81873 0.060949
## P3:V3-P2:V3 -23.0 -48.818729  2.81873 0.098292
## P4:V3-P2:V3   3.5 -22.318729 29.31873 0.999979
## P4:V3-P3:V3  26.5   0.681271 52.31873 0.042379
```

ANOVA using fact2.crd() in ExpDes package

```r
with(crd_data, fat2.crd(factor1 = Pesticide,
                        factor2 = Variety,
                        resp = Yield,
                        fac.names = c("Pesticide", "Variety"),
                        quali = c(TRUE, TRUE),
                        mcomp = "tukey"))
```

```
## ------------------------------------------------------------------------------
## Legend:
## FACTOR 1:  Pesticide
## FACTOR 2:  Variety
## ------------------------------------------------------------------------------
##
##
## Analysis of Variance Table
## ------------------------------------------------------------------------------
##                    DF   SS MS    Fc   Pr>Fc
## Pesticide           3 2227  4 17.56 0.00011
## Variety             2 3996  2 47.24 0.00000
## Pesticide*Variety   6  457  5  1.80 0.18168
## Residuals          12  508  3
## Total              23 7188  1
## ------------------------------------------------------------------------------
## CV = 10.58 %
##
## ------------------------------------------------------------------------------
## Shapiro-Wilk normality test
## p-value:  0.0654941
## According to Shapiro-Wilk normality test at 5% of significance, residuals can be considered normal.
## ------------------------------------------------------------------------------
##
## No significant interaction: analyzing the simple effect
## ------------------------------------------------------------------------------
## Pesticide
## Tukey's test
## ------------------------------------------------------------------------------
## Groups Treatments Means
```

```
## a      P4       73.8333
## a      P2       67.8333
##  b     P1       53
##  b     P3       51.1667
## ---------------------------------------------------------------------
##
## Variety
## Tukey's test
## ---------------------------------------------------------------------
## Groups Treatments Means
## a      V3       78.25
##  b     V2       59.25
##    c   V1       46.875
## ---------------------------------------------------------------------
```

Two-factorial in RCBD

```r
rcbd_data <- read.csv("two_factorial_rcbd.csv")
head(rcbd_data)
```

```
##     Day  A     B    TS A1 B1
## 1 day1 c1 Mylar  9.2  1  1
## 2 day1 c2 Mylar  8.7  2  1
## 3 day1 c3 Mylar  9.1  3  1
## 4 day1 c4 Mylar 12.4  4  1
## 5 day1 c5 Mylar 10.5  5  1
## 6 day2 c1 Mylar  8.2  1  1
```

ANOVA using aov()

```r
out2 <- aov(TS ~ Day + A + B + A:B,
            data = rcbd_data)

summary(out2)
```

```
##             Df Sum Sq Mean Sq F value  Pr(>F)
## Day          2   18.6    9.29   11.85 0.00019 ***
## A            4    6.3    1.58    2.02 0.11925
## B            2   10.1    5.07    6.47 0.00490 **
## A:B          8   33.1    4.14    5.28 0.00043 ***
## Residuals   28   22.0    0.78
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Post hoc analysis on the treatment combinations

## Table of means

```
rcbd_data %>%
  group_by(A, B) %>%
  summarize(meanTS = round(mean(TS),2))
```

```
## # A tibble: 15 x 3
## # Groups:   A [5]
##    A     B     meanTS
##    <chr> <chr>  <dbl>
##  1 c1    Mylar   8.6
##  2 c1    Nylon   7.6
##  3 c1    Peth    8.6
##  4 c2    Mylar   8.57
##  5 c2    Nylon   7.73
##  6 c2    Peth   11.5
##  7 c3    Mylar   8.87
##  8 c3    Nylon   9.73
##  9 c3    Peth    9.2
## 10 c4    Mylar  10.8
## 11 c4    Nylon   7.87
## 12 c4    Peth    8.77
## 13 c5    Mylar   9.97
## 14 c5    Nylon   8.73
## 15 c5    Peth    8.57
```

Interaction Plot

```
emmeans::emmip(out2, B ~ A,
               xlab = "Additives",
               ylab = "Mean Tensile Strength",
               tlab = "Polymers")
```

```
## Warning: 'aes_()' was deprecated in ggplot2 3.0.0.
## i Please use tidy evaluation idioms with 'aes()'
## i The deprecated feature was likely used in the emmeans package.
##   Please report the issue at <https://github.com/rvlenth/emmeans/issues>.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```
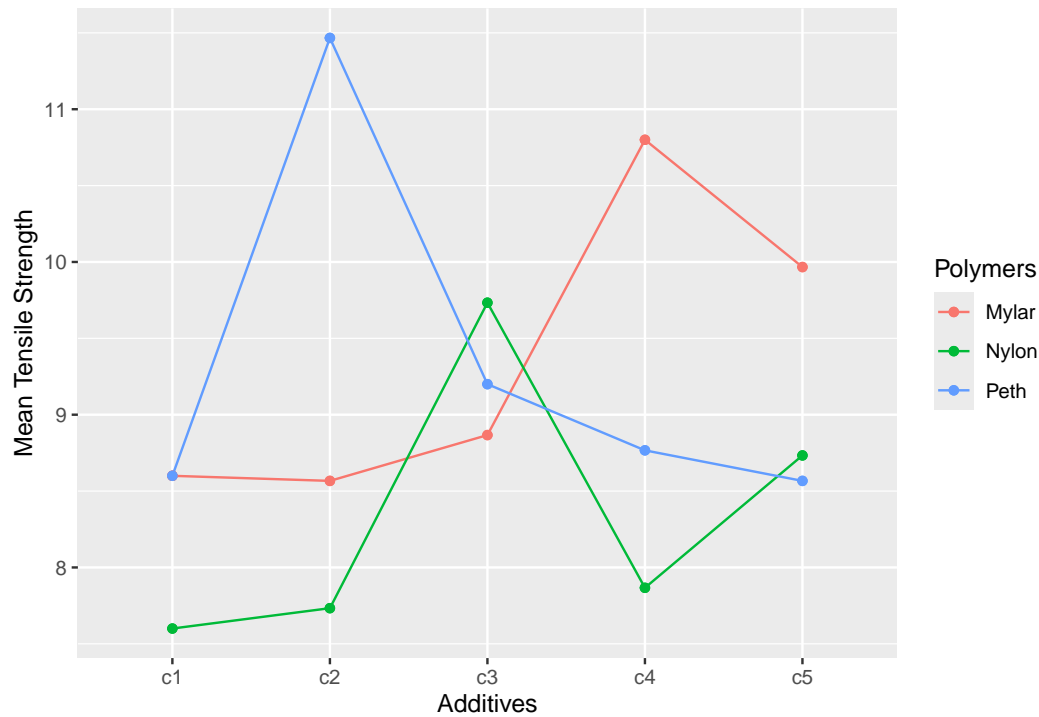
Post hoc analysis of significant interaction

We can use the *emmeans()* function in the **emmeans** package to perform post hoc analysis when interaction effect is signficant. A sample code chunck is given below.

```
emmeans(out2, list(pairwise ~ B | A),
        adjust = "tukey",
        lmer.df = "satterthwaite")
```

```
## $'emmeans of B | A'
## A = c1:
##  B      emmean    SE df lower.CL upper.CL
##  Mylar   8.60 0.511 28     7.55     9.65
##  Nylon   7.60 0.511 28     6.55     8.65
##  Peth    8.60 0.511 28     7.55     9.65
##
## A = c2:
##  B      emmean    SE df lower.CL upper.CL
##  Mylar   8.57 0.511 28     7.52     9.61
##  Nylon   7.73 0.511 28     6.69     8.78
##  Peth   11.47 0.511 28    10.42    12.51
##
## A = c3:
##  B      emmean    SE df lower.CL upper.CL
##  Mylar   8.87 0.511 28     7.82     9.91
##  Nylon   9.73 0.511 28     8.69    10.78
##  Peth    9.20 0.511 28     8.15    10.25
##
## A = c4:
```

```
##  B      emmean    SE df lower.CL upper.CL
##  Mylar  10.80 0.511 28     9.75    11.85
##  Nylon   7.87 0.511 28     6.82     8.91
##  Peth    8.77 0.511 28     7.72     9.81
##
## A = c5:
##  B      emmean    SE df lower.CL upper.CL
##  Mylar   9.97 0.511 28     8.92    11.01
##  Nylon   8.73 0.511 28     7.69     9.78
##  Peth    8.57 0.511 28     7.52     9.61
##
## Results are averaged over the levels of: Day
## Confidence level used: 0.95
##
## $`pairwise differences of B | A`
## A = c1:
##  2             estimate    SE df t.ratio p.value
##  Mylar - Nylon    1.000 0.723 28   1.383  0.3630
##  Mylar - Peth     0.000 0.723 28   0.000  1.0000
##  Nylon - Peth    -1.000 0.723 28  -1.383  0.3630
##
## A = c2:
##  2             estimate    SE df t.ratio p.value
##  Mylar - Nylon    0.833 0.723 28   1.153  0.4906
##  Mylar - Peth    -2.900 0.723 28  -4.011  0.0012
##  Nylon - Peth    -3.733 0.723 28  -5.164  0.0001
##
## A = c3:
##  2             estimate    SE df t.ratio p.value
##  Mylar - Nylon   -0.867 0.723 28  -1.199  0.4637
##  Mylar - Peth    -0.333 0.723 28  -0.461  0.8899
##  Nylon - Peth     0.533 0.723 28   0.738  0.7434
##
## A = c4:
##  2             estimate    SE df t.ratio p.value
##  Mylar - Nylon    2.933 0.723 28   4.058  0.0010
##  Mylar - Peth     2.033 0.723 28   2.813  0.0234
##  Nylon - Peth    -0.900 0.723 28  -1.245  0.4374
##
## A = c5:
##  2             estimate    SE df t.ratio p.value
##  Mylar - Nylon    1.233 0.723 28   1.706  0.2207
##  Mylar - Peth     1.400 0.723 28   1.937  0.1472
##  Nylon - Peth     0.167 0.723 28   0.231  0.9712
##
## Results are averaged over the levels of: Day
## P value adjustment: tukey method for comparing a family of 3 estimates
```

We can manually assign the letter designations, based on the above results.

But we can use the *cld()* function in the **multcomp** package to make letter assignments automatic. This is illustrated in the code chunk below.

```
emm <- emmeans(out2, list(pairwise ~ B | A),
        adjust = "tukey",
        lmer.df = "satterthwaite")
cld(emm,
    alpha=0.05,
    Letters=letters,
    adjust="tukey",
    reversed = T)
```

```
## A = c1:
##  B      emmean    SE df lower.CL upper.CL .group
##  Mylar   8.60 0.511 28     7.30     9.90  a
##  Peth    8.60 0.511 28     7.30     9.90  a
##  Nylon   7.60 0.511 28     6.30     8.90  a
##
## A = c2:
##  B      emmean    SE df lower.CL upper.CL .group
##  Peth   11.47 0.511 28    10.17    12.76  a
##  Mylar   8.57 0.511 28     7.27     9.86   b
##  Nylon   7.73 0.511 28     6.44     9.03   b
##
## A = c3:
##  B      emmean    SE df lower.CL upper.CL .group
##  Nylon   9.73 0.511 28     8.44    11.03  a
##  Peth    9.20 0.511 28     7.90    10.50  a
##  Mylar   8.87 0.511 28     7.57    10.16  a
##
## A = c4:
##  B      emmean    SE df lower.CL upper.CL .group
##  Mylar  10.80 0.511 28     9.50    12.10  a
##  Peth    8.77 0.511 28     7.47    10.06   b
##  Nylon   7.87 0.511 28     6.57     9.16   b
##
## A = c5:
##  B      emmean    SE df lower.CL upper.CL .group
##  Mylar   9.97 0.511 28     8.67    11.26  a
##  Nylon   8.73 0.511 28     7.44    10.03  a
##  Peth    8.57 0.511 28     7.27     9.86  a
##
## Results are averaged over the levels of: Day
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 3 estimates
## P value adjustment: tukey method for comparing a family of 3 estimates
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

ANOVA using fat2.rbd() in the ExpDes package

```r
with(rcbd_data, fat2.rbd(factor1 = A,
                         factor2 = B,
                         block = Day,
                         resp = TS,
                         quali = c(TRUE, TRUE),
                         fac.names = c("Additives", "Polymers"),
                         mcomp = "tukey"))
```

```
## ------------------------------------------------------------------------
## Legend:
## FACTOR 1:  Additives
## FACTOR 2:  Polymers
## ------------------------------------------------------------------------
##
##
## Analysis of Variance Table
## ------------------------------------------------------------------------
##                    DF    SS MS     Fc    Pr>Fc
## Block               2 18.58  6 11.848 0.00019
## Additives           4  6.33  3  2.017 0.11925
## Polymers            2 10.15  5  6.471 0.00490
## Additives*Polymers  8 33.10  4  5.278 0.00043
## Residuals          28 21.95  2
## Total              44 90.10  1
## ------------------------------------------------------------------------
## CV = 9.83 %
##
## ------------------------------------------------------------------------
## Shapiro-Wilk normality test
## p-value:  0.0984005
## According to Shapiro-Wilk normality test at 5% of significance, residuals can be considered normal.
## ------------------------------------------------------------------------
##
##
##
## Significant interaction: analyzing the interaction
## ------------------------------------------------------------------------
##
## Analyzing  Additives  inside of each level of  Polymers
## ------------------------------------------------------------------------
## ------------------------------------------------------------------------
## Analysis of Variance Table
## ------------------------------------------------------------------------
##                          DF       SS      MS      Fc Pr.Fc
## Block                     2 18.57644 9.28822 11.8482  2e-04
## Polymers                  2 10.14578 5.07289   6.471 0.0049
## Additives:Polymers Mylar  4 11.67600   2.919  3.7235 0.0149
## Additives:Polymers Nylon  4  9.70667 2.42667  3.0955 0.0314
## Additives:Polymers Peth   4 18.04400   4.511  5.7543 0.0016
## Residuals                28 21.95022 0.78394
## Total                    44 90.09911
## ------------------------------------------------------------------------
##
```

```
##
##
##   Additives   inside of the level  Mylar   of   Polymers
## -----------------------------------------------------------------------
## Tukey's test
## -----------------------------------------------------------------------
## Groups Treatments Means
## a       c4       10.8
## ab      c5       9.96667
## ab      c3       8.86667
##  b      c1       8.6
##  b      c2       8.56667
## -----------------------------------------------------------------------
##
##
##   Additives   inside of the level  Nylon   of   Polymers
## -----------------------------------------------------------------------
## Tukey's test
## -----------------------------------------------------------------------
## Groups Treatments Means
## a       c3       9.73333
## ab      c5       8.73333
## ab      c4       7.86667
## ab      c2       7.73333
##  b      c1       7.6
## -----------------------------------------------------------------------
##
##
##   Additives   inside of the level  Peth   of   Polymers
## -----------------------------------------------------------------------
## Tukey's test
## -----------------------------------------------------------------------
## Groups Treatments Means
## a       c2       11.4667
##  b      c3       9.2
##  b      c4       8.76667
##  b      c1       8.6
##  b      c5       8.56667
## -----------------------------------------------------------------------
##
##
##
## Analyzing  Polymers  inside of each level of   Additives
## -----------------------------------------------------------------------
## -----------------------------------------------------------------------
## Analysis of Variance Table
## -----------------------------------------------------------------------
##                         DF       SS       MS       Fc  Pr.Fc
## Block                    2 18.57644  9.28822 11.8482   2e-04
## Additives                4  6.32578  1.58144  2.0173 0.1192
## Polymers:Additives c1    2  2.00000        1  1.2756  0.295
## Polymers:Additives c2    2 23.04222 11.52111 14.6965      0
## Polymers:Additives c3    2  1.14667  0.57333  0.7314 0.4902
## Polymers:Additives c4    2 13.54889  6.77444  8.6416 0.0012
```

```
## Polymers:Additives c5  2  3.50889  1.75444    2.238 0.1254
## Residuals             28 21.95022  0.78394
## Total                 44 90.09911
## -----------------------------------------------------------------------------
##
##
##
## Polymers  inside of the level  c1  of  Additives
##
## According to the F test, the means of this factor are statistical equal.
## -----------------------------------------------------------------------------
##     Levels      Means
## 1    Mylar       8.6
## 2    Nylon       7.6
## 3     Peth       8.6
## -----------------------------------------------------------------------------
##
##
## Polymers  inside of the level  c2  of  Additives
## -----------------------------------------------------------------------------
## Tukey's test
## -----------------------------------------------------------------------------
## Groups Treatments Means
## a      Peth   11.4667
## b     Mylar   8.56667
## b     Nylon   7.73333
## -----------------------------------------------------------------------------
##
##
## Polymers  inside of the level  c3  of  Additives
##
## According to the F test, the means of this factor are statistical equal.
## -----------------------------------------------------------------------------
##     Levels      Means
## 1    Mylar   8.86667
## 2    Nylon   9.73333
## 3     Peth   9.20000
## -----------------------------------------------------------------------------
##
##
## Polymers  inside of the level  c4  of  Additives
## -----------------------------------------------------------------------------
## Tukey's test
## -----------------------------------------------------------------------------
## Groups Treatments Means
## a     Mylar   10.8
## b      Peth   8.76667
## b     Nylon   7.86667
## -----------------------------------------------------------------------------
##
##
## Polymers  inside of the level  c5  of  Additives
##
## According to the F test, the means of this factor are statistical equal.
```

```
## ----------------------------------------------------------------------
##      Levels     Means
## 1    Mylar    9.96667
## 2    Nylon    8.73333
## 3     Peth    8.56667
## ----------------------------------------------------------------------
```