Split-Plot

```
rm(list = ls())       # Clean the workspace
library(lsmeans)      # Call the library
# Read Data
mydata<-read.table(file = "C:/Users/toledo/Dropbox/UNIPD/Biostatistics Curse  R Spring 2018/curso STAT PhD 201
                   sep = "\t",header = TRUE,stringsAsFactors = TRUE)
mydata$Room<-as.factor(mydata$Room)    # Set the variable as factor
str(mydata)                            # See the structure of my data
```

```
## 'data.frame':    48 obs. of  4 variables:
##  $ Room   : Factor w/ 4 levels "1","2","3","4": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Energy : Factor w/ 3 levels "A1","A2","A3": 1 1 1 1 2 2 2 2 3 3 ...
##  $ Protein: Factor w/ 4 levels "B1","B2","B3",..: 1 2 3 4 1 2 3 4 1 2 ...
##  $ ADG    : num  17.2 23.1 18.3 20.1 22.9 ...
```

```
contrasts(mydata$Energy)<-contr.SAS    # Set the contrast as SAS
contrasts(mydata$Protein)<-contr.SAS   # Set the contrast as SAS
contrasts(mydata$Room)<-contr.SAS      # Set the contrast as SAS
table(mydata$Energy,mydata$Protein,mydata$Room) # Frequencies for factors
```

```
## , ,  = 1
##
##
##      B1 B2 B3 B4
##   A1  1  1  1  1
##   A2  1  1  1  1
##   A3  1  1  1  1
##
## , ,  = 2
##
##
##      B1 B2 B3 B4
##   A1  1  1  1  1
##   A2  1  1  1  1
##   A3  1  1  1  1
##
## , ,  = 3
##
##
##      B1 B2 B3 B4
##   A1  1  1  1  1
##   A2  1  1  1  1
##   A3  1  1  1  1
##
## , ,  = 4
##
##
##      B1 B2 B3 B4
##   A1  1  1  1  1
##   A2  1  1  1  1
##   A3  1  1  1  1
```

```
mymodel<-lm(ADG ~ Room + Energy + Room:Energy + Protein + Energy:Protein,
            data = mydata )    # fit the model with interactions
summary(mymodel)               # See the results
```

```
##
## Call:
## lm(formula = ADG ~ Room + Energy + Room:Energy + Protein + Energy:Protein,
```

```
##     data = mydata)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.2906 -0.9873 -0.3387  0.8969  4.0569
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      18.70812    1.43611  13.027 3.71e-13 ***
## Room1             3.66750    1.53527   2.389  0.02415 *
## Room2             1.21250    1.53527   0.790  0.43655
## Room3             2.49750    1.53527   1.627  0.11541
## Energy1           0.08312    2.03097   0.041  0.96765
## Energy2           0.51687    2.03097   0.254  0.80104
## Protein1         -2.30000    1.53527  -1.498  0.14571
## Protein2         -1.67750    1.53527  -1.093  0.28420
## Protein3          0.06500    1.53527   0.042  0.96654
## Room1:Energy1    -4.96000    2.17120  -2.284  0.03043 *
## Room2:Energy1    -4.64500    2.17120  -2.139  0.04160 *
## Room3:Energy1    -2.62750    2.17120  -1.210  0.23671
## Room1:Energy2     0.04250    2.17120   0.020  0.98453
## Room2:Energy2     0.55750    2.17120   0.257  0.79930
## Room3:Energy2    -0.68750    2.17120  -0.317  0.75395
## Energy1:Protein1  4.25500    2.17120   1.960  0.06042 .
## Energy2:Protein1  1.66500    2.17120   0.767  0.44982
## Energy1:Protein2  7.85250    2.17120   3.617  0.00121 **
## Energy2:Protein2  5.09500    2.17120   2.347  0.02653 *
## Energy1:Protein3  0.50000    2.17120   0.230  0.81960
## Energy2:Protein3  3.49250    2.17120   1.609  0.11935
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.171 on 27 degrees of freedom
## Multiple R-squared:  0.7343, Adjusted R-squared:  0.5375
## F-statistic: 3.731 on 20 and 27 DF,  p-value: 0.0008578
```

```
anova(mymodel)                # ANOVA table SS type III
```

```
## Analysis of Variance Table
##
## Response: ADG
##                Df  Sum Sq Mean Sq F value    Pr(>F)
## Room            3  40.813  13.604  2.8859 0.0539912 .
## Energy          2  94.320  47.160 10.0040 0.0005612 ***
## Protein         3  66.954  22.318  4.7343 0.0088343 **
## Room:Energy     6  47.247   7.875  1.6704 0.1667282
## Energy:Protein  6 102.414  17.069  3.6208 0.0091544 **
## Residuals      27 127.281   4.714
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#ref.grid(mymodel)
lsmeans(mymodel,"Protein")    # LSM for factor
```

```
##  Protein   lsmean        SE df lower.CL upper.CL
##  B1      19.39917 0.6267713 27 18.11314 20.68520
##  B2      22.36417 0.6267713 27 21.07814 23.65020
##  B3      21.12167 0.6267713 27 19.83564 22.40770
##  B4      19.72583 0.6267713 27 18.43980 21.01186
##
## Results are averaged over the levels of: Room, Energy
```

```
## Confidence level used: 0.95
```

```
lsmeans(mymodel,"Energy")     # LSM for factor
```

```
##  Energy   lsmean        SE df lower.CL upper.CL
##  A1     19.75125 0.5427998 27 18.63752 20.86498
##  A2     22.63250 0.5427998 27 21.51877 23.74623
##  A3     19.57437 0.5427998 27 18.46064 20.68811
##
## Results are averaged over the levels of: Room, Protein
## Confidence level used: 0.95
```

```
lsmeans(mymodel,~Energy:Protein) # LSM for factor with interaction
```

```
##  Energy Protein  lsmean     SE df lower.CL upper.CL
##  A1     B1      19.5325 1.0856 27 17.30503 21.75997
##  A2     B1      20.4125 1.0856 27 18.18503 22.63997
##  A3     B1      18.2525 1.0856 27 16.02503 20.47997
##  A1     B2      23.7525 1.0856 27 21.52503 25.97997
##  A2     B2      24.4650 1.0856 27 22.23753 26.69247
##  A3     B2      18.8750 1.0856 27 16.64753 21.10247
##  A1     B3      18.1425 1.0856 27 15.91503 20.36997
##  A2     B3      24.6050 1.0856 27 22.37753 26.83247
##  A3     B3      20.6175 1.0856 27 18.39003 22.84497
##  A1     B4      17.5775 1.0856 27 15.35003 19.80497
##  A2     B4      21.0475 1.0856 27 18.82003 23.27497
##  A3     B4      20.5525 1.0856 27 18.32503 22.77997
##
## Results are averaged over the levels of: Room
## Confidence level used: 0.95
```

```
# Fit the model with the interaction as an error term
mymodel.1<-aov(ADG ~ Room + Energy + Error(Room:Energy) + Protein + Energy:Protein,
               data = mydata)
summary(mymodel.1) # See the results
```

```
##
## Error: Room:Energy
##           Df Sum Sq Mean Sq F value Pr(>F)
## Room       3  40.81   13.60   1.728 0.2602
## Energy     2  94.32   47.16   5.989 0.0372 *
## Residuals  6  47.25    7.87
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Error: Within
##                Df Sum Sq Mean Sq F value  Pr(>F)
## Protein         3  66.95  22.318   4.734 0.00883 **
## Energy:Protein  6 102.41  17.069   3.621 0.00915 **
## Residuals      27 127.28   4.714
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```