Contrasts

Hugo Toledo-Alvarado

Read Dataframe

```
filedir<-"https://raw.githubusercontent.com/Hugo-Toledo/Applied-Statistics-R-UNIPD/master/data/lambs.csv"
es1<-read.table(file = filedir,stringsAsFactors = TRUE,header = TRUE, sep = ",")

head(es1) #See the Data
```

```
##        treatment   breed  matr birth_weight age_beginning sex weight_jul_.08
## 1 fieno + conc. brogna 26157         2.50           112   F           19.0
## 2 fieno + conc. brogna 26158         2.80           107   M           23.2
## 3 fieno + conc. brogna 26159         2.30           106   F           14.4
## 4 fieno + conc. brogna 26163         3.55            93   M           16.8
## 5 fieno + conc.   foza 26167         3.30            76   M           20.8
## 6 fieno + conc.   foza 26170         4.20            73   F           14.8
##   weight_agoust_08 weight_agoust_31 weight_sept_29 weight_october_28
## 1             20.0               22           25.0              25.0
## 2             25.5               27           32.0              32.5
## 3             15.0               17           19.0              18.5
## 4             17.5               19           22.5              23.0
## 5             20.5               24           26.5              27.5
## 6             17.0               19           21.5              22.0
##   slaughtering_weight
## 1                25.2
## 2                32.6
## 3                18.4
## 4                23.2
## 5                27.2
## 6                21.6
```

```
table(es1$sex,es1$breed, by=es1$treatment) #Frequency table for factors
```

```
## , , by = fieno + conc.
##
##
##     alpagota brogna foza
##   F        2      2    2
##   M        2      2    2
##
## , , by = fieno + conc. + CLA
##
##
##     alpagota brogna foza
##   F        2      2    2
##   M        2      2    2
##
## , , by = pascolo
##
##
##     alpagota brogna foza
##   F        2      2    2
##   M        2      2    2
```

ANOVA test

```
# Fit the linear model
tm<-lm(slaughtering_weight ~ sex + breed + treatment, data=es1)
summary(tm) # Linear Model Summary
```

```
##
## Call:
## lm(formula = slaughtering_weight ~ sex + breed + treatment, data = es1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.5917  -3.5806  -0.2958   3.7687  12.4444
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   24.700      2.388  10.345 2.06e-11 ***
## sexM                           5.706      1.949   2.927  0.00647 **
## breedbrogna                   -3.208      2.388  -1.344  0.18910
## breedfoza                      3.050      2.388   1.277  0.21124
## treatmentfieno + conc. + CLA   1.100      2.388   0.461  0.64832
## treatmentpascolo               6.492      2.388   2.719  0.01078 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.848 on 30 degrees of freedom
## Multiple R-squared:  0.4435, Adjusted R-squared:  0.3507
## F-statistic: 4.782 on 5 and 30 DF,  p-value: 0.002482
```

```
fm<-aov(slaughtering_weight ~ sex + breed + treatment, data=es1) # Fit the ANOVA
summary(fm) # ANOVA table
```

```
##            Df Sum Sq Mean Sq F value  Pr(>F)
## sex         1  293.0   293.0   8.566 0.00647 **
## breed       2  235.1   117.5   3.436 0.04533 *
## treatment   2  289.7   144.8   4.235 0.02399 *
## Residuals  30 1026.1    34.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

LSM

```r
# LSM
library(lsmeans)
```

```
## Loading required package: estimability
```

```r
lsmeans(tm,"sex")          #LSM for sex
```

```
##  sex   lsmean       SE df lower.CL upper.CL
##  F   27.17778 1.378471 30 24.36256 29.99299
##  M   32.88333 1.378471 30 30.06812 35.69855
##
## Results are averaged over the levels of: breed, treatment
## Confidence level used: 0.95
```

```r
lsmeans(tm,"breed")        #LSM for breed
```

```
##  breed       lsmean       SE df lower.CL upper.CL
##  alpagota 30.08333 1.688275 30 26.63542 33.53125
##  brogna   26.87500 1.688275 30 23.42708 30.32292
##  foza     33.13333 1.688275 30 29.68542 36.58125
##
## Results are averaged over the levels of: sex, treatment
## Confidence level used: 0.95
```

```r
lsmeans(tm,"treatment")    #LSM for treatment
```

```
##  treatment              lsmean       SE df lower.CL upper.CL
##  fieno + conc.        27.50000 1.688275 30 24.05208 30.94792
##  fieno + conc. + CLA  28.60000 1.688275 30 25.15208 32.04792
##  pascolo              33.99167 1.688275 30 30.54375 37.43958
##
## Results are averaged over the levels of: sex, breed
## Confidence level used: 0.95
```

```r
# Contrasts
#tm$contrasts$sex
#tm$contrasts$breed
#tm$contrasts$treatment
contrasts(es1$sex)         #Grid for contrasts
```

```
##   M
## F 0
## M 1
```

```r
contrasts(es1$breed)       #Grid for contrasts
```

```
##          brogna foza
## alpagota      0    0
## brogna        1    0
## foza          0    1
```

```r
contrasts(es1$treatment)   #Grid for contrasts
```

```
##                     fieno + conc. + CLA pascolo
## fieno + conc.                         0       0
## fieno + conc. + CLA                   1       0
## pascolo                               0       1
```

```r
fm<-aov(slaughtering_weight ~ sex + breed + treatment + age_beginning, data=es1) # Fit the ANOVA
summary(fm) #ANOVA table
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## sex          1  293.0   293.0  13.664 0.000906 ***
```

3

```
## breed           2  235.1   117.5   5.481 0.009568 **
## treatment       2  289.7   144.8   6.755 0.003904 **
## age_beginning   1  404.3   404.3  18.856 0.000157 ***
## Residuals      29  621.8    21.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
tm<-lm(slaughtering_weight ~ sex + breed + treatment + age_beginning, data=es1) # Fit the linear model
summary(tm) # Linear Model Summary
```

```
##
## Call:
## lm(formula = slaughtering_weight ~ sex + breed + treatment +
##     age_beginning, data = es1)
##
## Residuals:
##       Min       1Q    Median       3Q      Max
## -11.3549  -2.4533  -0.3365   2.7244   9.4278
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 0.66837    5.84818   0.114 0.909799
## sexM                        3.76233    1.60706   2.341 0.026309 *
## breedbrogna                 2.62136    2.31860   1.131 0.267497
## breedfoza                  10.87573    2.61178   4.164 0.000256 ***
## treatmentfieno + conc. + CLA 1.71782   1.89573   0.906 0.372323
## treatmentpascolo            6.26988    1.89107   3.316 0.002466 **
## age_beginning               0.19010    0.04378   4.342 0.000157 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.63 on 29 degrees of freedom
## Multiple R-squared:  0.6628, Adjusted R-squared:  0.593
## F-statistic: 9.499 on 6 and 29 DF,  p-value: 8.57e-06
```

```
#contrasts(es1$sex)<-c(1,0)
contrasts(es1$sex)<-contr.SAS          #Change contrast grid
#contrasts(es1$breed)<-cbind(c(1,0,0), c(0,1,0))
contrasts(es1$breed)<-contr.SAS        #Change contrast grid
#contrasts(es1$treatment)<-cbind(c(1,0,0), c(0,1,0))
contrasts(es1$treatment)<-contr.SAS    ##Change contrast grid

fm1<-aov(slaughtering_weight ~ sex + breed + treatment + age_beginning, data=es1) # Fit the ANOVA
summary(fm1) #Anova table
```

```
##                Df Sum Sq Mean Sq F value   Pr(>F)
## sex             1  293.0   293.0  13.664 0.000906 ***
## breed           2  235.1   117.5   5.481 0.009568 **
## treatment       2  289.7   144.8   6.755 0.003904 **
## age_beginning   1  404.3   404.3  18.856 0.000157 ***
## Residuals      29  621.8    21.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
tm1<-lm(slaughtering_weight ~ sex + breed + treatment + age_beginning, data=es1) # Fit the linear model
summary(tm1) # Linear Model Summary
```

```
##
## Call:
## lm(formula = slaughtering_weight ~ sex + breed + treatment +
##     age_beginning, data = es1)
##
```

```
## Residuals:
##      Min      1Q  Median      3Q     Max
## -11.3549 -2.4533 -0.3365  2.7244  9.4278
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   21.57630    4.63376   4.656 6.59e-05 ***
## sex1          -3.76233    1.60706  -2.341 0.026309 *
## breed1       -10.87573    2.61178  -4.164 0.000256 ***
## breed2        -8.25437    1.94547  -4.243 0.000206 ***
## treatment1    -6.26988    1.89107  -3.316 0.002466 **
## treatment2    -4.55206    1.90025  -2.396 0.023275 *
## age_beginning  0.19010    0.04378   4.342 0.000157 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.63 on 29 degrees of freedom
## Multiple R-squared:  0.6628, Adjusted R-squared:  0.593
## F-statistic: 9.499 on 6 and 29 DF,  p-value: 8.57e-06
```

```r
car::Anova(tm1, type = "III") #Anova table with SS III
```

```
## Anova Table (Type III tests)
##
## Response: slaughtering_weight
##               Sum Sq Df F value     Pr(>F)
## (Intercept)   464.88  1 21.6814 6.587e-05 ***
## sex           117.52  1  5.4809 0.0263086 *
## breed         500.38  2 11.6685 0.0001914 ***
## treatment     251.26  2  5.8593 0.0072910 **
## age_beginning 404.30  1 18.8561 0.0001568 ***
## Residuals     621.80 29
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
lsmeans(tm1,"sex")          #LSM for sex
```

```
## sex   lsmean       SE df lower.CL upper.CL
## F   28.14939 1.114114 29 25.87077 30.42801
## M   31.91172 1.114114 29 29.63310 34.19034
##
## Results are averaged over the levels of: breed, treatment
## Confidence level used: 0.95
```

```r
lsmeans(tm1,"breed")        #LSM for breed
```

```
## breed       lsmean       SE df lower.CL upper.CL
## alpagota 25.53153 1.698696 29 22.05730 29.00575
## brogna   28.15289 1.368714 29 25.35355 30.95222
## foza     36.40725 1.534671 29 33.26850 39.54601
##
## Results are averaged over the levels of: sex, treatment
## Confidence level used: 0.95
```

```r
lsmeans(tm1,"treatment")   #LSM for treatment
```

```
## treatment            lsmean       SE df lower.CL upper.CL
## fieno + conc.       27.36799 1.337049 29 24.63341 30.10256
## fieno + conc. + CLA 29.08581 1.341377 29 26.34238 31.82923
## pascolo             33.63787 1.339184 29 30.89893 36.37681
##
## Results are averaged over the levels of: sex, breed
## Confidence level used: 0.95
```

Orthogonal Contrasts

```r
#c1<-c(-1,-1,2)
#c2<-c(1,-1, 0)
#mat1<-cbind(c1,c2)
mat1<-matrix(c(-1,-1,2,
               1,-1,0),ncol=2)  # Create the contrast for treatment
mat2<-matrix(c(1,-1,0),ncol = 1) # Create the contrast for breed

#contrasts(es1$treatment)<-mat1
#contrasts(es1$breed)<-mat2
model1<-aov(slaughtering_weight ~ sex + breed + treatment + age_beginning,
            contrasts = list(treatment=mat1, breed=mat2), data=es1) # Fit the linear model
#ANOVA table with the effects splited for each contrast
summary.aov(model1,split=list(treatment=list("Secco vs Pascolo"=1,"CLA vs noCLA"=2),
                        breed=list("Brogna vs Alpagata"=1)))
```

```
##                             Df Sum Sq Mean Sq F value  Pr(>F)
## sex                          1  293.0  292.98   7.867 0.00875 **
## breed                        1   61.8   61.76   1.658 0.20767
##    breed: Brogna vs Alpagata 1   61.8   61.76   1.658 0.20767
## treatment                    2  289.7  144.84   3.889 0.03149 *
##    treatment: Secco vs Pascolo 1  282.4  282.43   7.583 0.00991 **
##    treatment: CLA vs noCLA   1    7.3    7.26   0.195 0.66200
## age_beginning                1   82.1   82.11   2.205 0.14801
## Residuals                   30 1117.3   37.24
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Polynomial Contrasts#
mat3<-matrix(c(-1,0,1,
               1,-2,1),ncol=2)   #Create the contrast for treatment Linear and Quadratic
#contrasts(es1$treatment)<-mat3
#contrasts(es1$breed)<-contr.SAS
model2<-aov(slaughtering_weight ~ sex + breed + treatment + age_beginning,
            contrasts=list(treatment=mat3),data=es1) # Fit the linear model
#ANOVA table with the effects splited for the contrast
summary.aov(model2,split=list(treatment=list("Linear"=1,"Quadratic"=2)))
```

```
##                          Df Sum Sq Mean Sq F value   Pr(>F)
## sex                       1  293.0   293.0  13.664 0.000906 ***
## breed                     2  235.1   117.5   5.481 0.009568 **
## treatment                 2  289.7   144.8   6.755 0.003904 **
##    treatment: Linear      1  252.9   252.9  11.793 0.001812 **
##    treatment: Quadratic   1   36.8    36.8   1.718 0.200233
## age_beginning             1  404.3   404.3  18.856 0.000157 ***
## Residuals                29  621.8    21.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#attributes(model2$qr$qr) # See the model grid


#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
# NOTE: Another way to obtain the constrast
#library(multcomp)
#contr<-rbind("Linear"=c(-1,0,1),
#             "Quadratic"=c(1,-2,1))
#model3<-glht(fm1,linfct=mcp(treatment=contr))
#summary(model4)
#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
#######################################
```