ModBalsMassBoth.R

Audrey McCombs Thu Nov 24 20:42:22 2016

```
library(ggplot2)
library(lme4)
## Loading required package: Matrix
library(nlme)
##
## Attaching package: 'nlme'
## The following object is masked from 'package:lme4':
##
##
       lmList
library(lsmeans)
## Warning: package 'lsmeans' was built under R version 3.2.5
## Loading required package: estimability
## Warning: package 'estimability' was built under R version 3.2.5
library(lubridate)
## Warning: package 'lubridate' was built under R version 3.2.5
## Attaching package: 'lubridate'
## The following object is masked from 'package:base':
##
##
       date
library(multcompView)
## Warning: package 'multcompView' was built under R version 3.2.5
library(car)
```

Warning: package 'car' was built under R version 3.2.5

```
setwd("D:/Iowa State University/Debinski Lab/Nectar data/MAL")
balssug15 <- read.csv("nectar analysis/data files/balssugar15.csv", header = T)
balssug16 <- read.csv("nectar analysis/data files/balssugar16.csv", header = T)
balssugboth <- rbind(balssug15,balssug16)</pre>
balssugboth$year <- as.factor(year(balssugboth$date))</pre>
cellN <- with(balssugboth, table(treatment, year))</pre>
cellN
##
            year
## treatment 2015 2016
           С
               28
           Η
               54
                    71
##
cellMean <- with(balssugboth, tapply(mass, list(treatment, year), mean))</pre>
cellMean
##
           2015
                      2016
## C 0.09401065 0.04865045
## H 0.10265737 0.05275608
modmass <- lmer(mass ~ treatment * year + (1|plant), data = balssugboth)</pre>
mass.grid <- ref.grid(modmass)</pre>
## Loading required namespace: lmerTest
summary(mass.grid)
  treatment year prediction
              2015 0.09880479 0.012612065 97.80
## C
## H
              2015 0.10414677 0.009310685 70.59
## C
              2016 0.04724487 0.007822351 51.79
              2016 0.05333785 0.007972659 69.02
## H
##
## Degrees-of-freedom method: satterthwaite
lsmeans(mass.grid, "treatment")
## NOTE: Results may be misleading due to involvement in interactions
  treatment
                                   SE
                                         df
                                              lower.CL
                                                          upper.CL
              0.07302483 0.007779929 52.65 0.05741782 0.08863184
## C
              0.07874231 0.006742734 34.80 0.06505100 0.09243362
##
##
## Results are averaged over the levels of: year
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
```

```
lsmeans(mass.grid, "year")
## NOTE: Results may be misleading due to involvement in interactions
## year
             lsmean
                             SE
                                   df
                                        lower.CL
                                                   upper.CL
## 2015 0.10147578 0.007838256 86.96 0.08589628 0.11705527
## 2016 0.05029136 0.005584632 59.75 0.03911947 0.06146325
## Results are averaged over the levels of: treatment
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
mass.treat <- lsmeans(mass.grid, "treatment")</pre>
## NOTE: Results may be misleading due to involvement in interactions
pairs(mass.treat)
                                        df t.ratio p.value
## contrast
                 estimate
                                  SE
           -0.005717474 0.01029523 43.72 -0.555 0.5815
## C - H
## Results are averaged over the levels of: year
pairs.treat <- pairs(mass.treat)</pre>
test(pairs.treat, joint = T)
## df1
          df2
                  F p.value
##
      1 43.72 0.308 0.5815
mass.year <- lsmeans(mass.grid, "year")</pre>
## NOTE: Results may be misleading due to involvement in interactions
pairs(mass.year)
## contrast
                  estimate
                                    SE
                                           df t.ratio p.value
## 2015 - 2016 0.05118442 0.008902864 175.34 5.749 <.0001
## Results are averaged over the levels of: treatment
pairs.year <- pairs(mass.year)</pre>
test(pairs.year, joint = T)
## df1
           df2
                    F p.value
     1 175.34 33.053 <.0001
```

```
int.mass <- pairs(mass.grid, by = "year")</pre>
int.mass
## year = 2015:
## contrast
               estimate SE df t.ratio p.value
## C - H -0.005341975 0.01567651 86.96 -0.341 0.7341
## year = 2016:
## contrast
                estimate SE
                                     df t.ratio p.value
## C - H -0.006092973 0.01116926 59.75 -0.546 0.5874
int.masstable <- update(int.mass, by = NULL)</pre>
int.masstable
## contrast year estimate
                                          df t.ratio p.value
                                SE
## C - H 2015 -0.005341975 0.01567651 86.96 -0.341 0.7341
## C - H 2016 -0.006092973 0.01116926 59.75 -0.546 0.5874
test(pairs(int.masstable), joint = T)
## df1 df2 F p.value
## 1 175.34 0.002 0.9664
Anova(modmass, type = 3)
## Analysis of Deviance Table (Type III Wald chisquare tests)
## Response: mass
                 Chisq Df Pr(>Chisq)
## (Intercept) 61.3739 1 4.72e-15 ***
## treatment 0.1161 1 0.7332820
## year 13.3995 1 0.0002517 ***
## treatment:year 0.0018 1 0.9663573
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```