ModBalsMassBoth.R

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```
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)
rm(balssug15)
rm(balssug16)

balssugboth$lnmass <- log(balssugboth$mass)
balssugboth$year <- as.factor(year(balssugboth$date))

cellN <- with(balssugboth, table(treatment, year))
cellN
```

```
##          year
## treatment 2015 2016
##         C   30   80
##         H   56   71
```

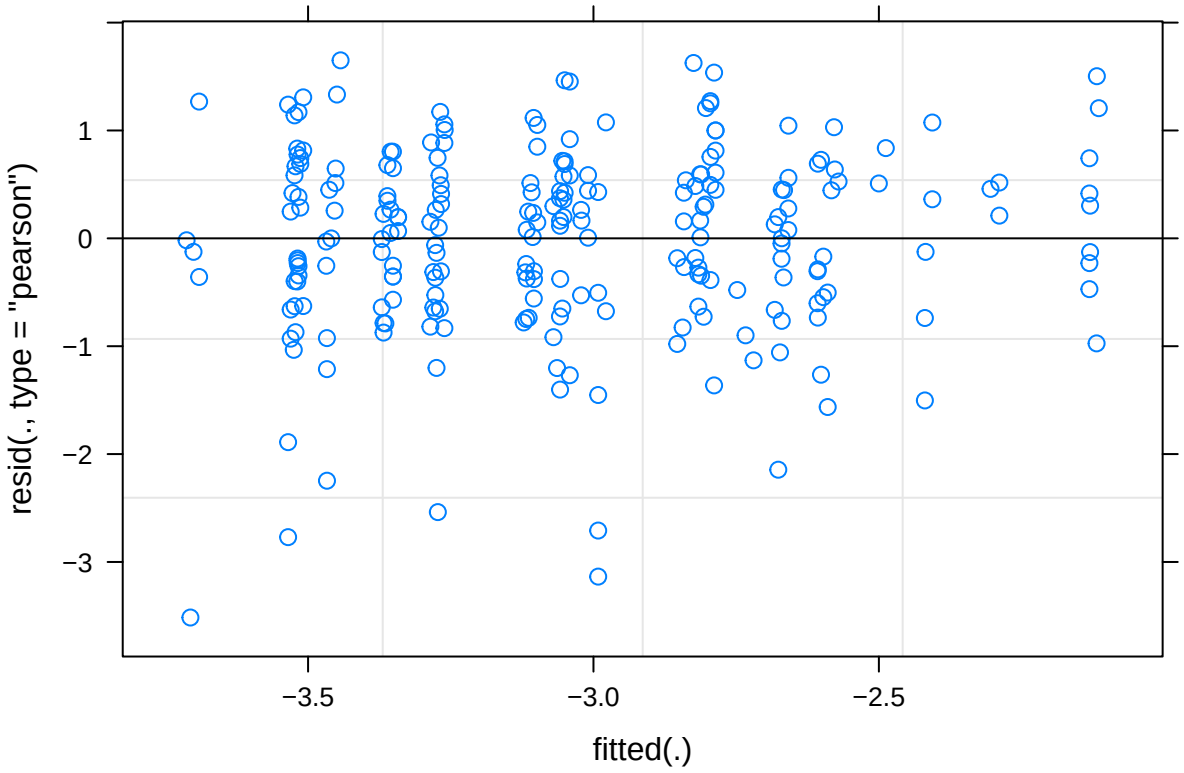
```
cellMean <- with(balssugboth, tapply(mass, list(treatment, year), mean))
cellMean
```

```
##         2015       2016
## C 0.09528345 0.04865045
## H 0.10940649 0.05275608
```

```
modlnmass <- lmer(lnmass ~ treatment * year + (1|plot/plant) + (1|year:date), data = balssugboth)
summary(modlnmass)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: lnmass ~ treatment * year + (1 | plot/plant) + (1 | year:date)
##    Data: balssugboth
##
## REML criterion at convergence: 624.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.0354 -0.5796  0.1490  0.6692  1.8944
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  plant:plot (Intercept) 0.003164 0.05625
##  year:date  (Intercept) 0.095434 0.30892
##  plot       (Intercept) 0.000000 0.00000
##  Residual               0.758768 0.87107
## Number of obs: 237, groups:  plant:plot, 51; year:date, 13; plot, 11
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)         -2.74194    0.20430 -13.421
## treatmentH           0.17486    0.20151   0.868
## year2016            -0.63844    0.27238  -2.344
## treatmentH:year2016  0.07156    0.24954   0.287
##
## Correlation of Fixed Effects:
##             (Intr) trtmnH yr2016
## treatmentH  -0.647
## year2016    -0.749  0.484
## trtmnH:2016  0.521 -0.804 -0.561
```

```
plot(modlnmass)
```




```
#inflmass <- influence(modlnmass, obs = T)
#plot(inflmass, which = "cook", main = "Balsam mass")

lnmass.grid <- ref.grid(modlnmass)
```

```
## Loading required namespace: lmerTest
```

```
summary(lnmass.grid)
```

```
##  treatment year prediction        SE    df
##  C         2015  -2.741939 0.2043046 22.98
##  H         2015  -2.567078 0.1705370 14.07
##  C         2016  -3.380380 0.1805473  8.58
##  H         2016  -3.133959 0.1771096  8.95
##
## Degrees-of-freedom method: satterthwaite
```

```
mass.treat <- lsmeans(lnmass.grid, "treatment")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
pairs(mass.treat)
```

```
##  contrast   estimate        SE    df t.ratio p.value
##  C - H    -0.2106416 0.1254874 33.84  -1.679  0.1024
##
## Results are averaged over the levels of: year
```

```r
mass.year <- lsmeans(lnmass.grid, "year")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```r
pairs(mass.year)
```

```
##  contrast     estimate        SE   df t.ratio p.value
##  2015 - 2016 0.6026613 0.2272135 8.02   2.652  0.0291
##
## Results are averaged over the levels of: treatment
```

```r
int.mass <- pairs(lnmass.grid, by = "year")
int.masstable <- update(int.mass, by = NULL)
int.masstable
```

```
##  contrast year   estimate        SE    df t.ratio p.value
##  C - H    2015 -0.1748617 0.2015071 51.27  -0.868  0.3896
##  C - H    2016 -0.2464214 0.1484042 69.24  -1.660  0.1013
```

```r
test(pairs(int.masstable), joint = T)
```

```
##  df1    df2     F p.value
##    1 106.62 0.082  0.7748
```

```r
Anova(modlnmass, type = 3)
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: lnmass
##                   Chisq Df Pr(>Chisq)
## (Intercept)    180.1190  1    < 2e-16 ***
## treatment        0.7530  1    0.38552
## year             5.4940  1    0.01908 *
## treatment:year   0.0822  1    0.77429
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```