percent_w_nectar.R

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```r
library(lubridate)
```

```
##
## Attaching package: 'lubridate'
```

```
## The following object is masked from 'package:base':
##
##     date
```

```r
library(lme4)
```

```
## Loading required package: Matrix
```

```r
library(nlme)
```

```
##
## Attaching package: 'nlme'
```

```
## The following object is masked from 'package:lme4':
##
##     lmList
```

```r
library(lsmeans)
```

```
## The 'lsmeans' package is being deprecated.
## Users are encouraged to switch to 'emmeans'.
## See help('transition') for more information, including how
## to convert 'lsmeans' objects and scripts to work with 'emmeans'.
```

```r
library(car)
```

```
## Loading required package: carData
```

```r
setwd("C:/Users/Audrey McCombs/Desktop/MAL")

# Read and minor munging of dataframes

balsam15 <- read.csv("nectar analysis/data files/balsam15.csv", header = T, as.is = T)
balsam16 <- read.csv("nectar analysis/data files/balsam16.csv", header = T, as.is = T)
buckwt15 <- read.csv("nectar analysis/data files/buckwt15.csv", header = T, as.is = T)
buckwt16 <- read.csv("nectar analysis/data files/buckwt16.csv", header = T, as.is = T)

balsam <- rbind(balsam15, balsam16)
buckwt <- rbind(buckwt15, buckwt16)

rm(balsam15)
rm(balsam16)
rm(buckwt15)
rm(buckwt16)

balsam$date <- ymd(balsam$date)
```

```r
balsam$plot <- as.factor(balsam$plot)
balsam$treatment <- as.factor(balsam$treatment)
balsam$plant <- as.factor(balsam$plant)
balsam$year <- as.factor(year((balsam$date)))


buckwt$date <- ymd(buckwt$date)
buckwt$plot <- as.factor(buckwt$plot)
buckwt$treatment <- as.factor(buckwt$treatment)
buckwt$quad <- as.factor(buckwt$quad)
buckwt$year <- as.factor(year((buckwt$date)))

# Calculate percentage of flowers that are/aren't producing nectar

balscontrol <- subset(balsam, treatment == "C")
pz.bac <- sum(balscontrol$volume == "0")/nrow(balscontrol)
pnz.bac <- sum(balscontrol$volume != "0")/nrow(balscontrol)

balsheat <- subset(balsam, treatment == "H")
pz.bah <- sum(balsheat$volume == "0")/nrow(balsheat)
pnz.bah <- sum(balsheat$volume != "0")/nrow(balsheat)

balscontrol15 <- subset(balsam, treatment == "C" & year == "2015")
pz.bac15 <- sum(balscontrol15$volume == "0")/nrow(balscontrol15)
pnz.bac15 <- sum(balscontrol15$volume != "0")/nrow(balscontrol15)

balsheat15 <- subset(balsam, treatment == "H" & year == "2015")
pz.bah15 <- sum(balsheat15$volume == "0")/nrow(balsheat15)
pnz.bah15 <- sum(balsheat15$volume != "0")/nrow(balsheat15)

buckcontrol <- subset(buckwt, treatment == "C")
pz.buc <- sum(buckcontrol$volume == "0")/nrow(buckcontrol)
pnz.buc <- sum(buckcontrol$volume != "0")/nrow(buckcontrol)

buckheat <- subset(buckwt, treatment == "H")
pz.buh <- sum(buckheat$volume == "0")/nrow(buckheat)
pnz.buh <- sum(buckheat$volume != "0")/nrow(buckheat)

rm(balscontrol)
rm(balsheat)
rm(buckcontrol)
rm(buckheat)

# Create dataframes for regression analysis

balsam$necpres[balsam$volume != "0"] <- "1"
balsam$necpres[balsam$volume == "0"] <- "0"
balsam$necpres <- as.factor(balsam$necpres)
balsam <- balsam[,-c(5:7)]

buckwt$necpres[buckwt$volume != "0"] <- "1"
buckwt$necpres[buckwt$volume == "0"] <- "0"
buckwt$necpres <- as.factor(buckwt$necpres)
```
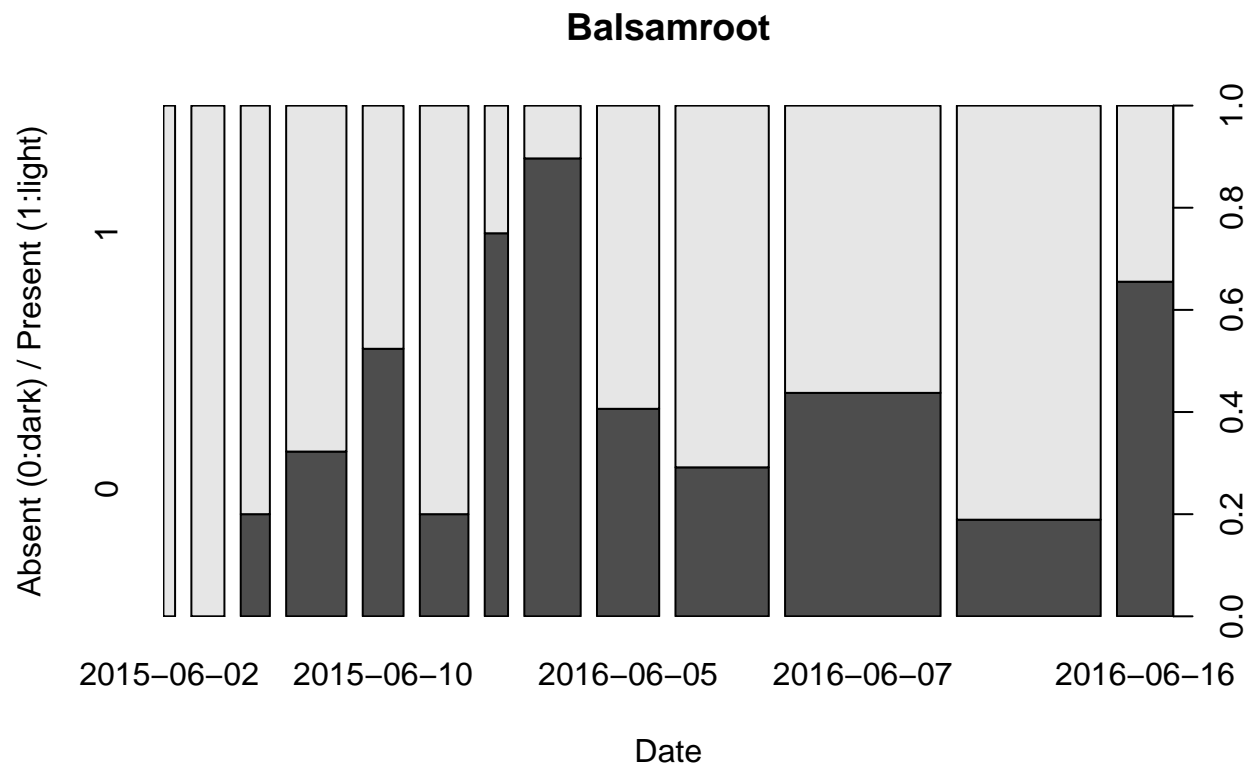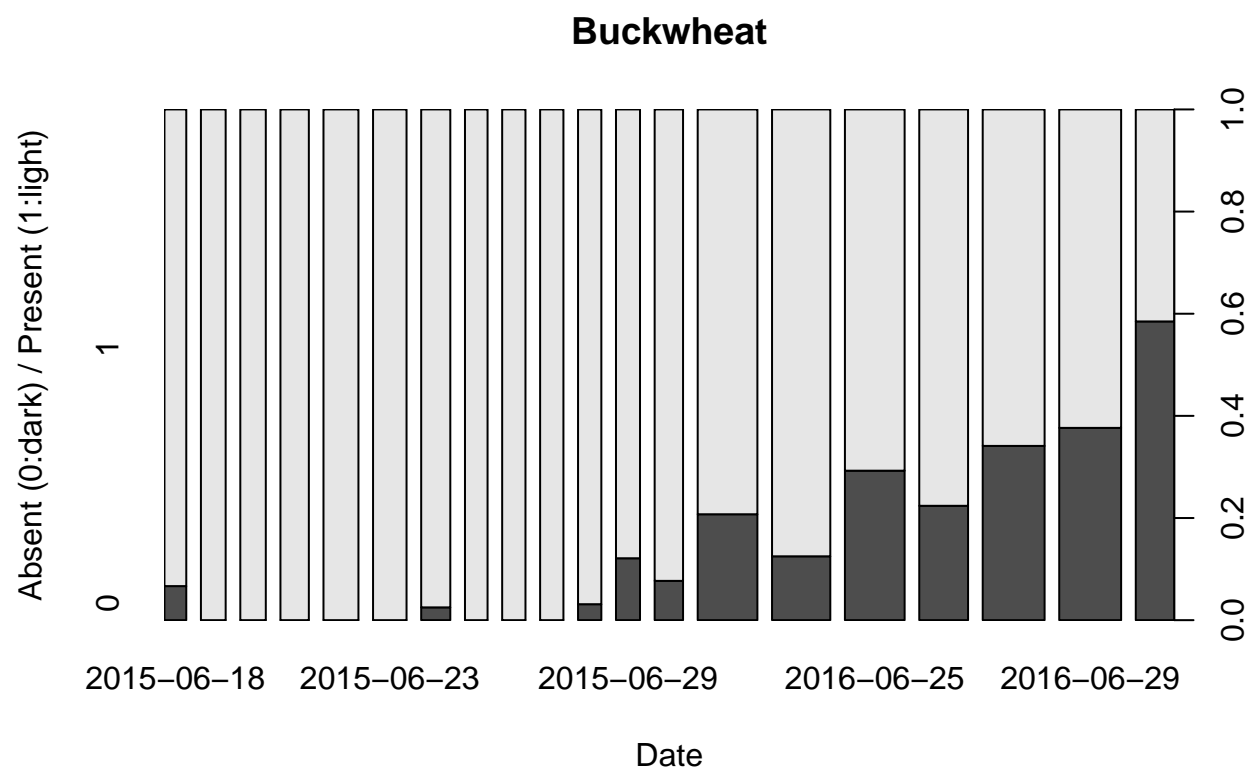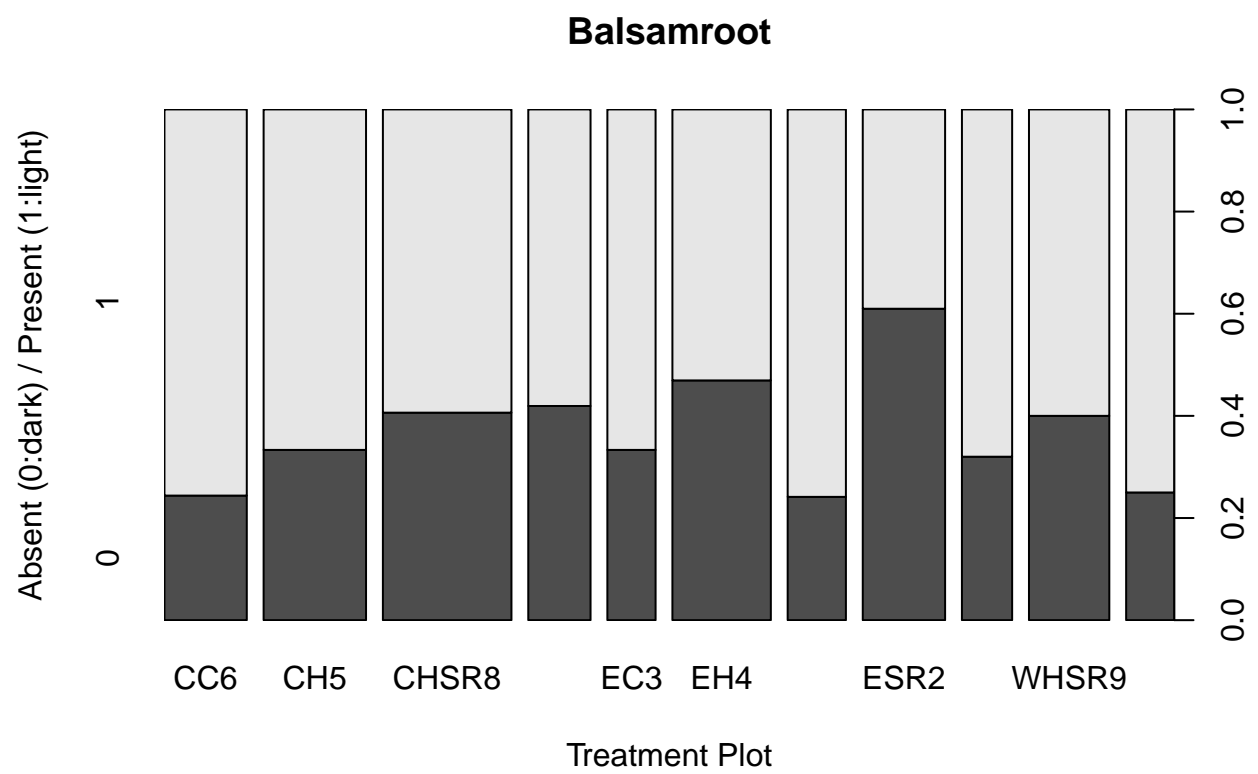
```
buckwt <- buckwt[,-c(5:7)]

#Data exploration
with(balsam, plot(as.factor(date), necpres, main = "Balsamroot", xlab = "Date", ylab = "Absent (0:dark)
```

Balsamroot


```
with(buckwt, plot(as.factor(date), necpres, main = "Buckwheat", xlab = "Date", ylab = "Absent (0:dark)
```
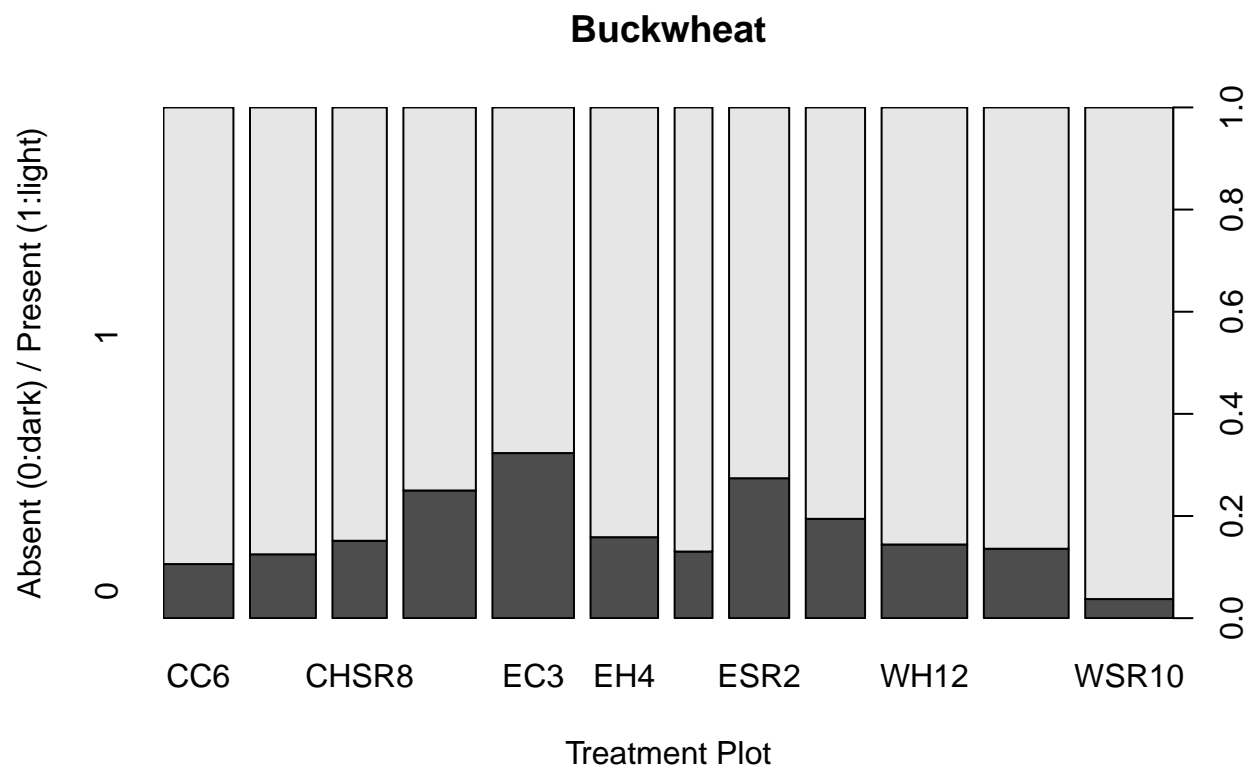
Buckwheat


```
with(balsam, plot(plot, necpres, main = "Balsamroot", xlab = "Treatment Plot", ylab = "Absent (0:dark) ,
```

Balsamroot


```
with(buckwt, plot(plot, necpres, main = "Buckwheat", xlab = "Treatment Plot", ylab = "Absent (0:dark) /
```

Buckwheat


```r
#Remove 2015 buckwheat from analysis (because all 1's)
buckwt <- subset(buckwt, year != "2015", select = date:necpres)


# Models
  #balsamroot
modbals <- glmer(necpres ~ treatment * year + (1|plot/plant) + (1| year:date), data = balsam, family = b
summary(modbals)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: necpres ~ treatment * year + (1 | plot/plant) + (1 | year:date)
##    Data: balsam
##
##      AIC      BIC   logLik deviance df.resid
##    513.6    541.8   -249.8    499.6      412
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2901 -0.8135  0.4517  0.6754  2.2653
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  plant:plot (Intercept) 0.1692   0.4113
##  year:date  (Intercept) 2.0089   1.4173
##  plot       (Intercept) 0.0000   0.0000
```

```
## Number of obs: 419, groups:  plant:plot, 56; year:date, 13; plot, 11
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)         0.2996     0.6254   0.479   0.6319
## treatmentH          0.8095     0.4564   1.774   0.0761 .
## year2016            0.1278     0.9153   0.140   0.8890
## treatmentH:year2016 -0.7051    0.5305  -1.329   0.1838
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) trtmnH yr2016
## treatmentH -0.405
## year2016   -0.675  0.264
## trtmnH:2016 0.334 -0.810 -0.326
```

```
#interaction?
Anova(modbals, type = 3)
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: necpres
##               Chisq Df Pr(>Chisq)
## (Intercept)  0.2295  1    0.63191
## treatment    3.1464  1    0.07609 .
## year         0.0195  1    0.88898
## treatment:year 1.7670 1   0.18376
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
balsam$count <- as.numeric(balsam$necpres) - 1
cellMean <- with(balsam, tapply(count, list(treatment, year), sum))
cellMean
```

```
##   2015 2016
## C   31   85
## H   61   83
```

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

```
##          year
## treatment 2015 2016
##         C   56  130
##         H  100  133
```

```
necpres.grid <- ref.grid(modbals)
int.necpres <- pairs(necpres.grid, by = "year")
int.necprestable <- update(int.necpres, by = NULL)
int.necprestable
```

```
##  contrast year    estimate        SE df z.ratio p.value
##  C - H    2015 -0.8095371 0.4563806 NA  -1.774  0.0761
##  C - H    2016 -0.1044233 0.3118917 NA  -0.335  0.7378
##
## Results are given on the log odds ratio (not the response) scale.
```

```
summary(necpres.grid)
```

```
##  treatment year prediction        SE df
##  C          2015  0.2995892 0.6253857 NA
##  H          2015  1.1091263 0.6069270 NA
##  C          2016  0.4273521 0.6751771 NA
##  H          2016  0.5317754 0.6693038 NA
##
## Results are given on the logit (not the response) scale.
```

```
lsmeans(necpres.grid, "treatment")
```

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

##  treatment    lsmean        SE df  asymp.LCL asymp.UCL
##  C          0.3634706 0.4626671 NA -0.5433403  1.270281
##  H          0.8204508 0.4556146 NA -0.0725374  1.713439
##
## Results are averaged over the levels of: year
## Results are given on the logit (not the response) scale.
## Confidence level used: 0.95
```

```
lsmeans(necpres.grid, "year")
```

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

##  year    lsmean        SE df  asymp.LCL asymp.UCL
##  2015 0.7043577 0.5724186 NA -0.4175620  1.826278
##  2016 0.4795637 0.6539088 NA -0.8020741  1.761201
##
## Results are averaged over the levels of: treatment
## Results are given on the logit (not the response) scale.
## Confidence level used: 0.95
```

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

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

```
pairs(necpres.treat)
```

```
##  contrast   estimate        SE df z.ratio p.value
##  C - H    -0.4569802 0.2871149 NA  -1.592  0.1115
##
## Results are averaged over the levels of: year
## Results are given on the log odds ratio (not the response) scale.
```

```
necpres.year <- lsmeans(necpres.grid, "year")
```

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

```
pairs(necpres.year)
```

```
##  contrast     estimate        SE df z.ratio p.value
##  2015 - 2016 0.224794 0.8658311 NA    0.26  0.7952
##
## Results are averaged over the levels of: treatment
## Results are given on the log odds ratio (not the response) scale.
```

```r
#buckwheat (only 2016)
modbuck <- glmer(necpres ~ treatment + (1|plot) + (1|date), data = buckwt, family = binomial)
summary(modbuck)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: necpres ~ treatment + (1 | plot) + (1 | date)
##    Data: buckwt
##
##      AIC      BIC   logLik deviance df.resid
##    607.3    624.4   -299.6    599.3      530
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2254 -0.8488  0.4219  0.6269  1.5189
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  plot   (Intercept) 0.4367   0.6609
##  date   (Intercept) 0.4618   0.6796
## Number of obs: 534, groups:  plot, 12; date, 7
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.7905     0.4002   1.975   0.0483 *
## treatmentH    0.3609     0.4374   0.825   0.4093
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr)
## treatmentH -0.535
```

```r
Anova(modbuck)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: necpres
##            Chisq Df Pr(>Chisq)
## treatment 0.6807  1     0.4093
```

```r
buckwt$count <- as.numeric(buckwt$necpres) - 1
cellMean <- with(buckwt, tapply(count, list(treatment, year), sum))
cellMean
```

```
##   2015 2016
## C   NA  190
## H   NA  186
```

```r
cellN <- with(buckwt, table(treatment, year))
cellN
```

```
##          year
## treatment 2015 2016
##         C    0  286
```

```
##          H    0  248
```

```
necpres.grid.buck <- ref.grid(modbuck)
summary(necpres.grid.buck)
```

```
## treatment prediction        SE df
## C            0.7904996 0.4002213 NA
## H            1.1514068 0.4053525 NA
##
## Results are given on the logit (not the response) scale.
```

```
lsmeans(necpres.grid.buck, "treatment")
```

```
## treatment    lsmean        SE df   asymp.LCL asymp.UCL
## C           0.7904996 0.4002213 NA 0.006080314  1.574919
## H           1.1514068 0.4053525 NA 0.356930410  1.945883
##
## Results are given on the logit (not the response) scale.
## Confidence level used: 0.95
```

```
necpres.treat <- lsmeans(necpres.grid.buck, "treatment")
pairs(necpres.treat)
```

```
## contrast    estimate        SE df z.ratio p.value
## C - H     -0.3609072 0.4374291 NA  -0.825  0.4093
##
## Results are given on the log odds ratio (not the response) scale.
```