# 2015 Scott Valley Alfalfa Summary

Andrew Brown
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#### AOV - Cutting 1

```
## $C
##
   Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.92934, p-value = 0.5101
##
## $H
##
##
    Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.80763, p-value = 0.03453
##
##
## $L
##
   Shapiro-Wilk normality test
##
##
## data: X[[i]]
## W = 0.96315, p-value = 0.8395
##
##
## $M
##
##
    Shapiro-Wilk normality test
## data: X[[i]]
## W = 0.91039, p-value = 0.3568
##
##
    Shapiro-Wilk normality test
##
## data: sqrt(sv_bio1$bio)
## W = 0.94488, p-value = 0.1031
##
##
    Bartlett test of homogeneity of variances
##
## data: sv_bio1$bio by sv_bio1$treat
## Bartlett's K-squared = 5.4911, df = 3, p-value = 0.1392
                 Df Sum Sq Mean Sq F value Pr(>F)
##
```

```
## sv_bio1$treat 3
                    25.1 8.378
                                    0.709 0.555
## Residuals
                28 330.8 11.816
     Tukey multiple comparisons of means
##
      95% family-wise confidence level
##
## Fit: aov(formula = sqrt(sv_bio1$bio) ~ sv_bio1$treat)
## $`sv_bio1$treat`
            diff
                       lwr
                                upr
                                         p adj
## H-C 1.9989272 -2.693642 6.691496 0.6544697
## L-C 0.6907587 -4.001810 5.383328 0.9776019
## M-C -0.3035842 -4.996153 4.388985 0.9979942
## L-H -1.3081684 -6.000737 3.384400 0.8711174
## M-H -2.3025114 -6.995080 2.390057 0.5463149
## M-L -0.9943430 -5.686912 3.698226 0.9376925
```

#### AOV - Cutting 2

```
## $C
##
    Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.92461, p-value = 0.4684
##
##
## $H
##
   Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.80055, p-value = 0.02902
##
## $L
##
   Shapiro-Wilk normality test
##
##
## data: X[[i]]
## W = 0.85647, p-value = 0.1107
##
##
## $M
##
  Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.97433, p-value = 0.9296
##
## Bartlett test of homogeneity of variances
```

```
##
## data: sv_bio2$bio by sv_bio2$treat
## Bartlett's K-squared = 6.0633, df = 3, p-value = 0.1086
                 Df Sum Sq Mean Sq F value Pr(>F)
##
## sv_bio2$treat 3 145544
                             48515
                                      6.92 0.00125 **
## Residuals
                 28 196299
                              7011
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
     Tukey multiple comparisons of means
##
       95% family-wise confidence level
##
##
## Fit: aov(formula = sv_bio2$bio ~ sv_bio2$treat)
##
## $`sv_bio2$treat`
            diff
                        lwr
                                   upr
## H-C -165.7025 -280.00662 -51.398381 0.0025061
## L-C -23.3300 -137.63412 90.974119 0.9437772
## M-C -115.9575 -230.26162 -1.653381 0.0458218
## L-H 142.3725
                   28.06838 256.676619 0.0103597
        49.7450 -64.55912 164.049119 0.6391258
## M-H
## M-L -92.6275 -206.93162 21.676619 0.1445129
melt1=melt(sv_bio1, id.vars=c("treat"))
melt2=melt(sv bio2, id.vars=c("treat"))
means1.sem <- ddply(melt1, c("treat", "variable"), summarise, mean=mean(value),</pre>
                    sdv=sd(value), sem=sd(value)/sqrt(length(value)))
means2.sem <- ddply(melt2, c("treat", "variable"), summarise, mean=mean(value),</pre>
                    sdv=sd(value), sem=sd(value)/sqrt(length(value)))
means1.sem <- transform(means1.sem, lower=mean-sem, upper=mean+sem,
                        tacre=mean*0.00404685642,coefvar=sdv/mean*100)
means2.sem <- transform(means2.sem, lower=mean-sem, upper=mean+sem,
                        tacre=mean*0.00404685642, coefvar=sdv/mean*100)
```

## Stats - Cutting 1

```
## treat mean sdv sem lower upper tacre coefvar

## 1 C 280.8275 121.85229 43.08129 237.7462 323.9088 1.136469 43.39044

## 2 H 349.0675 170.25747 60.19510 288.8724 409.2626 1.412626 48.77494

## 3 L 294.6800 92.61241 32.74343 261.9366 327.4234 1.192528 31.42813

## 4 M 259.4575 70.79111 25.02844 234.4291 284.4859 1.049987 27.28428
```

### Stats - Cutting 2