

BuckGraphs.R

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```
library(ggplot2)
library(dplyr)

##
## Attaching package: 'dplyr'

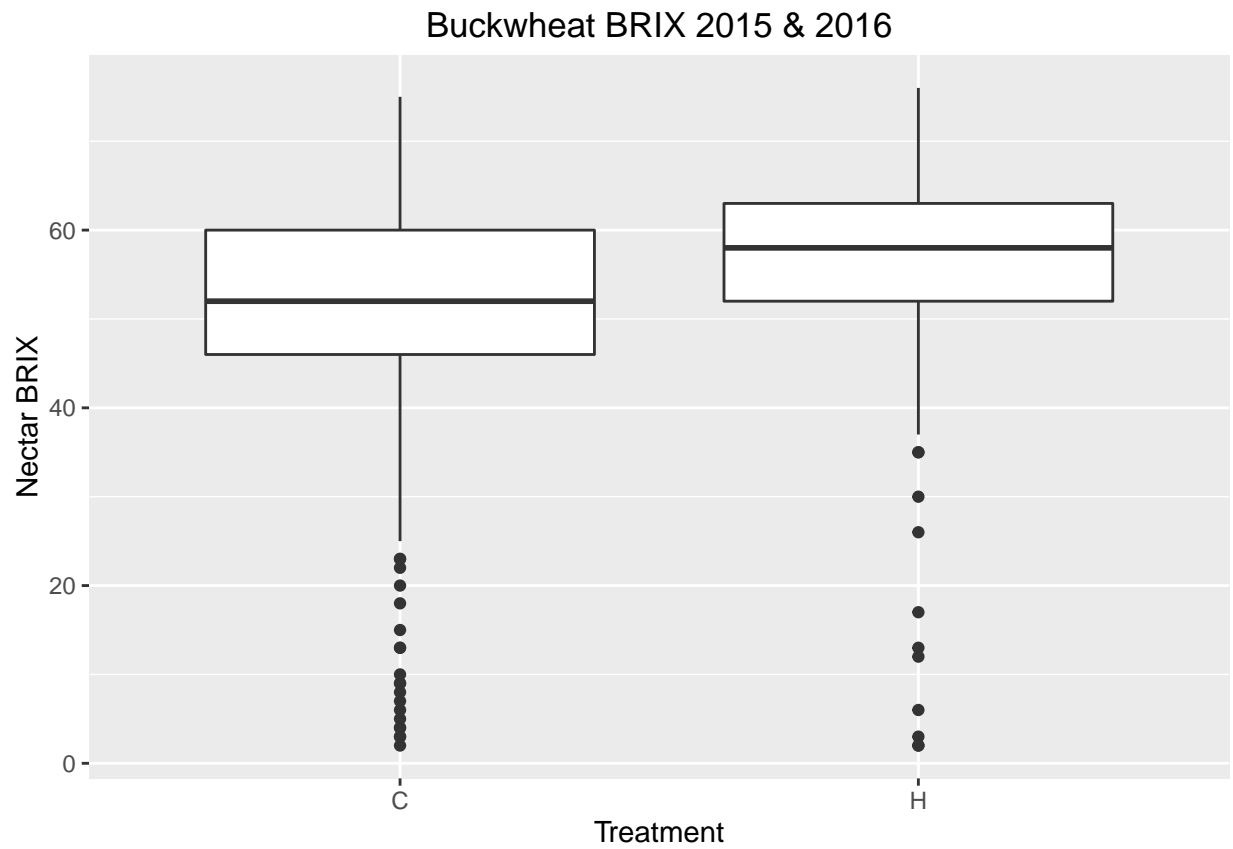
## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

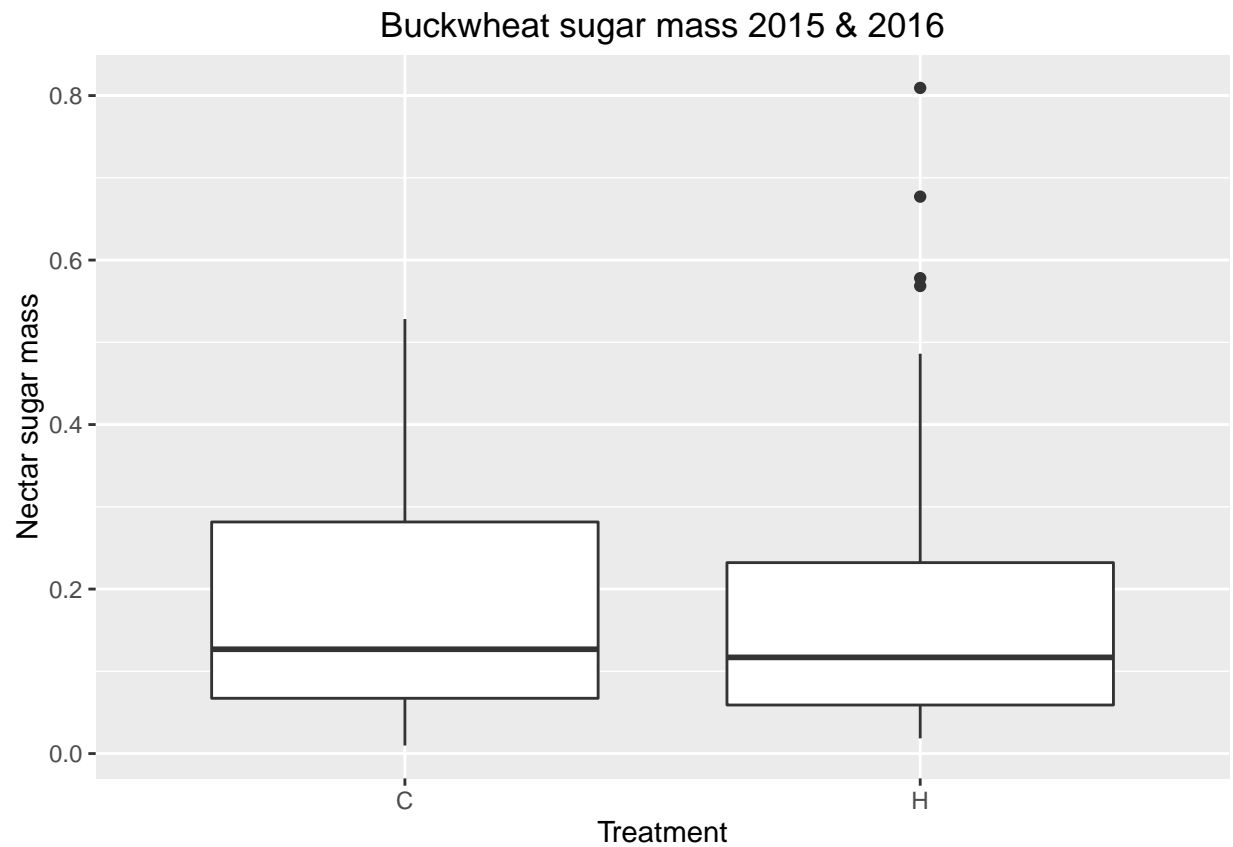
setwd("D:/Iowa State University/Debinski Lab/Nectar data/MAL")

bucksug15 <- read.csv("nectar analysis/data files/bucksugar15.csv", header = T)
bucksug16 <- read.csv("nectar analysis/data files/bucksugar16.csv", header = T)
bucksugboth <- rbind(bucksug15,bucksug16)

ggplot(bucksugboth, aes(x=treatment, y=BRIX)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar BRIX") + ggtitle("Buckwheat BRIX 2015 & 2016")
```



```
ggplot(bucksugboth, aes(x=treatment, y=mass)) + geom_boxplot() +  
  xlab("Treatment") +  
  ylab("Nectar sugar mass") + ggtitle("Buckwheat sugar mass 2015 & 2016")
```



```
buckvol15 <- read.csv("nectar analysis/data files/buckvol15.csv", header = T)
buckvol16 <- read.csv("nectar analysis/data files/buckvol16.csv", header = T)
buckvolboth <- rbind(buckvol15,buckvol16)

ggplot(buckvolboth, aes(x=treatment, y=volume)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar Volume (microliters)") + ggtitle("Buckwheat Volume 2015 & 2016")
```

