BalsamGraphs.R

Audrey McCombs

Fri Dec 16 19:08:20 2016

```r
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
```

```r
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)

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

Balsamroot BRIX 2015 & 2016
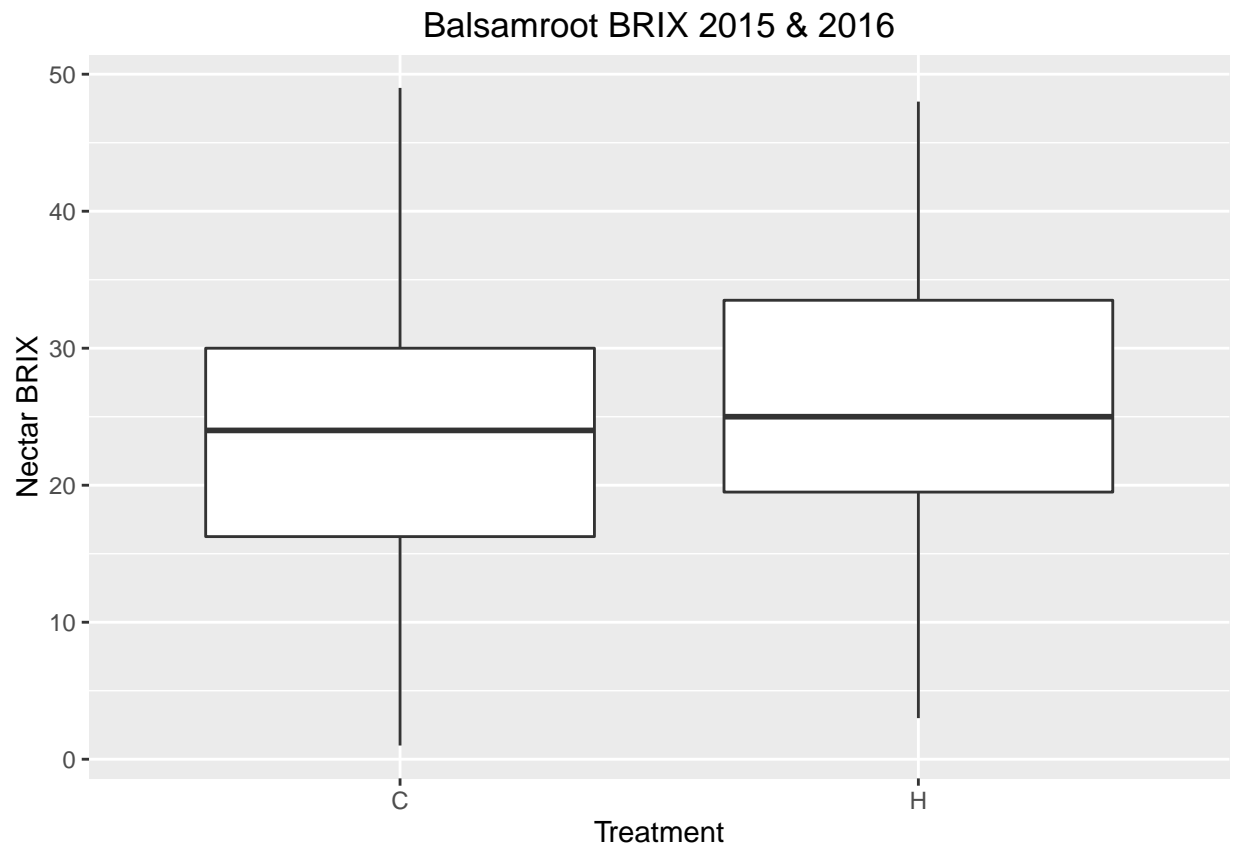

```
ggplot(balssugboth, aes(x=treatment, y=mass)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar sugar mass") + ggtitle("Balsamroot sugar mass 2015 & 2016")
```

Balsamroot sugar mass 2015 & 2016
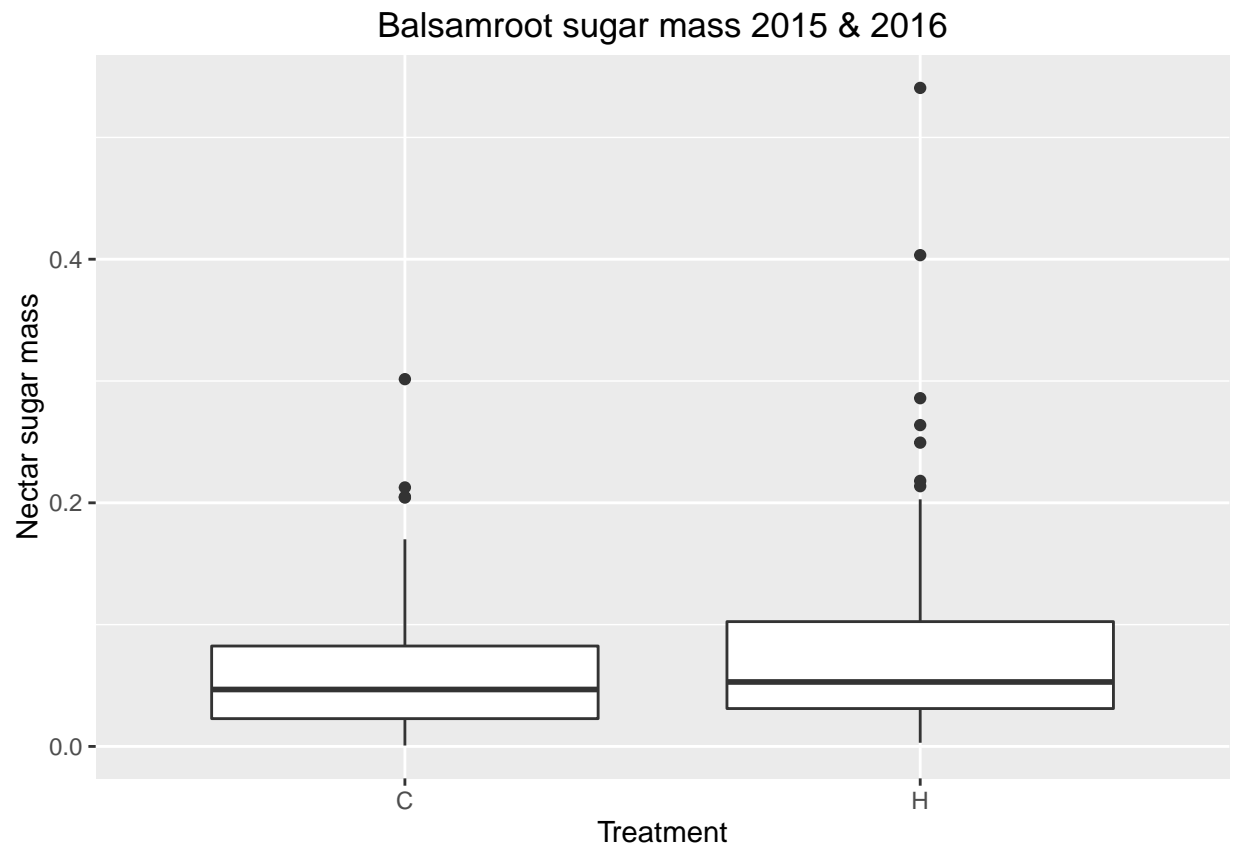

```r
balsvol15 <- read.csv("nectar analysis/data files/balsvol15.csv", header = T)
balsvol16 <- read.csv("nectar analysis/data files/balsvol16.csv", header = T)
balsvolboth <- rbind(balsvol15,balsvol16)

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

Balsamroot Volume 2015 & 2016