

dataexplore.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")
```

```
balsvol15 <- read.csv("nectar analysis/Bals 15 vol no outliers/balsvol15sub.csv", header = T)
balsvol16 <- read.csv("nectar analysis/data files/balsvol16.csv", header = T)
balsvolboth <- rbind(balsvol15,balsvol16)
```

#Data summaries

```
summary(balsvol15)
```

##	date	plot	treatment	plant	volume
##	2015-06-08:21	CHSR8 :19	C:30	CC6-9 : 9	Min. :0.01818
##	2015-06-11:18	CH5 :15	H:60	CHSR8-4: 9	1st Qu.:0.16364
##	2015-06-03:17	CC6 :11		CH5-6 : 7	Median :0.40000
##	2015-06-06:12	EH4 :11		CHSR8-6: 6	Mean :0.46525
##	2015-06-10:10	WHSR9 : 9		EHSR1-2: 6	3rd Qu.:0.60000
##	2015-06-02: 6	EHSR1 : 6		CH5-7 : 4	Max. :2.25455
##	(Other) : 6	(Other):19		(Other):49	

```
summary(balsvol16)
```

##	date	plot	treatment	plant	volume
##	2016-06-05:19	CC6 :19	C:85	EC3-3 : 8	Min. :0.01818
##	2016-06-06:34	CHSR8 :19	H:83	WHSR9-2: 8	1st Qu.:0.07273
##	2016-06-07:45	CH5 :18		CC6-10 : 7	Median :0.12727
##	2016-06-08:60	EHSR1 :16		CH5-2 : 6	Mean :0.15942
##	2016-06-16:10	CSR7 :15		EC3-1 : 6	3rd Qu.:0.20000
##		EH4 :15		EHSR1-1: 6	Max. :0.85455
##		(Other):66		(Other):127	

```
summary(balsvolboth)
```

```
##           date      plot  treatment    plant      volume
## 2016-06-08:60 CHSR8 :38 C:115    CHSR8-4: 12 Min.    :0.01818
## 2016-06-07:45 CH5   :33 H:143    CHSR8-6: 10 1st Qu.:0.09091
## 2016-06-06:34 CC6   :30          EHSR1-2: 10 Median  :0.16364
## 2015-06-08:21 EH4   :26          CC6-9  : 9 Mean    :0.26610
## 2016-06-05:19 WHSR9 :24          CHSR8-2: 9 3rd Qu.:0.32727
## 2015-06-11:18 EHSR1 :22          EC3-3  : 9 Max.    :2.25455
## (Other)      :61 (Other):85          (Other):199
```

```
summarize(group_by(balsvol15, treatment), meanVol = mean(volume), sdVolume = sd(volume))
```

```
## Source: local data frame [2 x 3]
##
##   treatment  meanVol  sdVolume
##   (fctr)      (dbl)      (dbl)
## 1          C 0.5339394 0.3988723
## 2          H 0.4309091 0.4172536
```

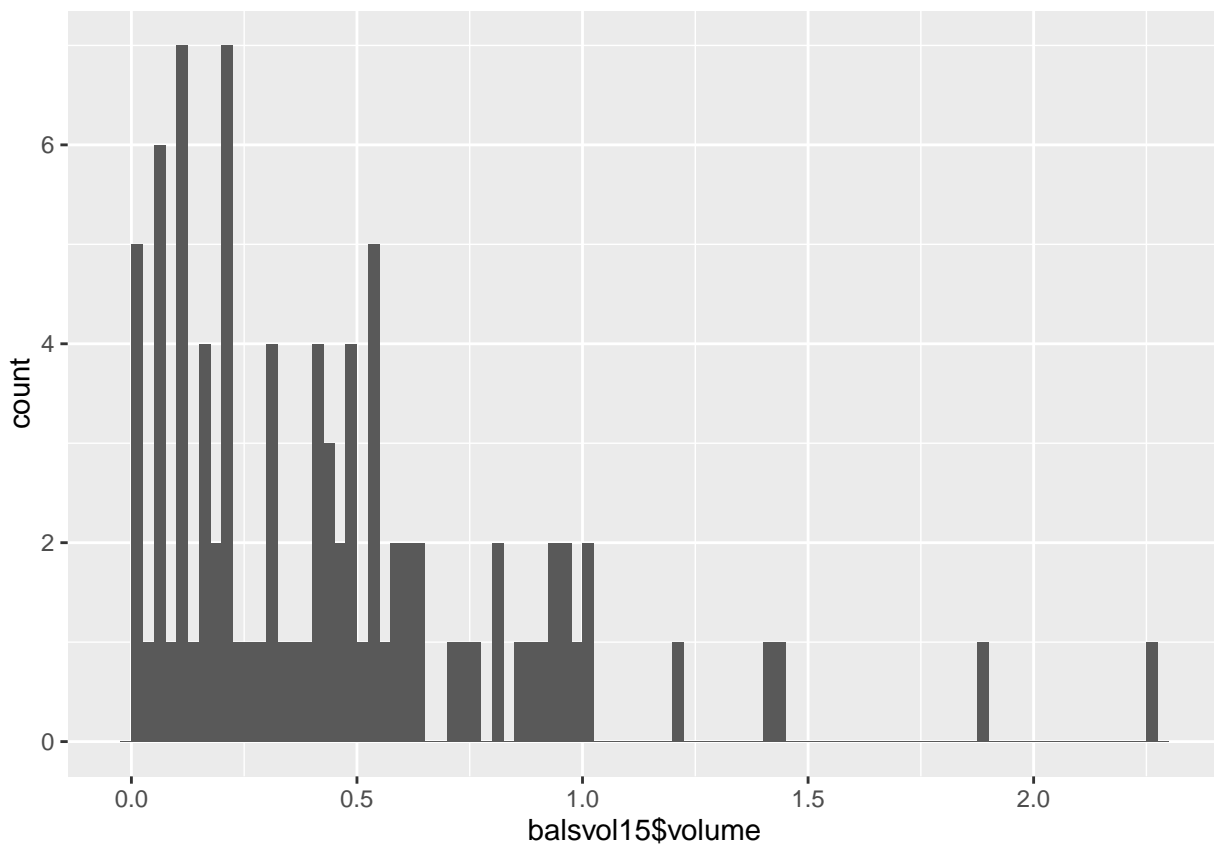
```
summarize(group_by(balsvol16, treatment), meanVol = mean(volume), sdVolume = sd(volume))
```

```
## Source: local data frame [2 x 3]
##
##   treatment  meanVol  sdVolume
##   (fctr)      (dbl)      (dbl)
## 1          C 0.1659893 0.1328342
## 2          H 0.1526835 0.1127952
```

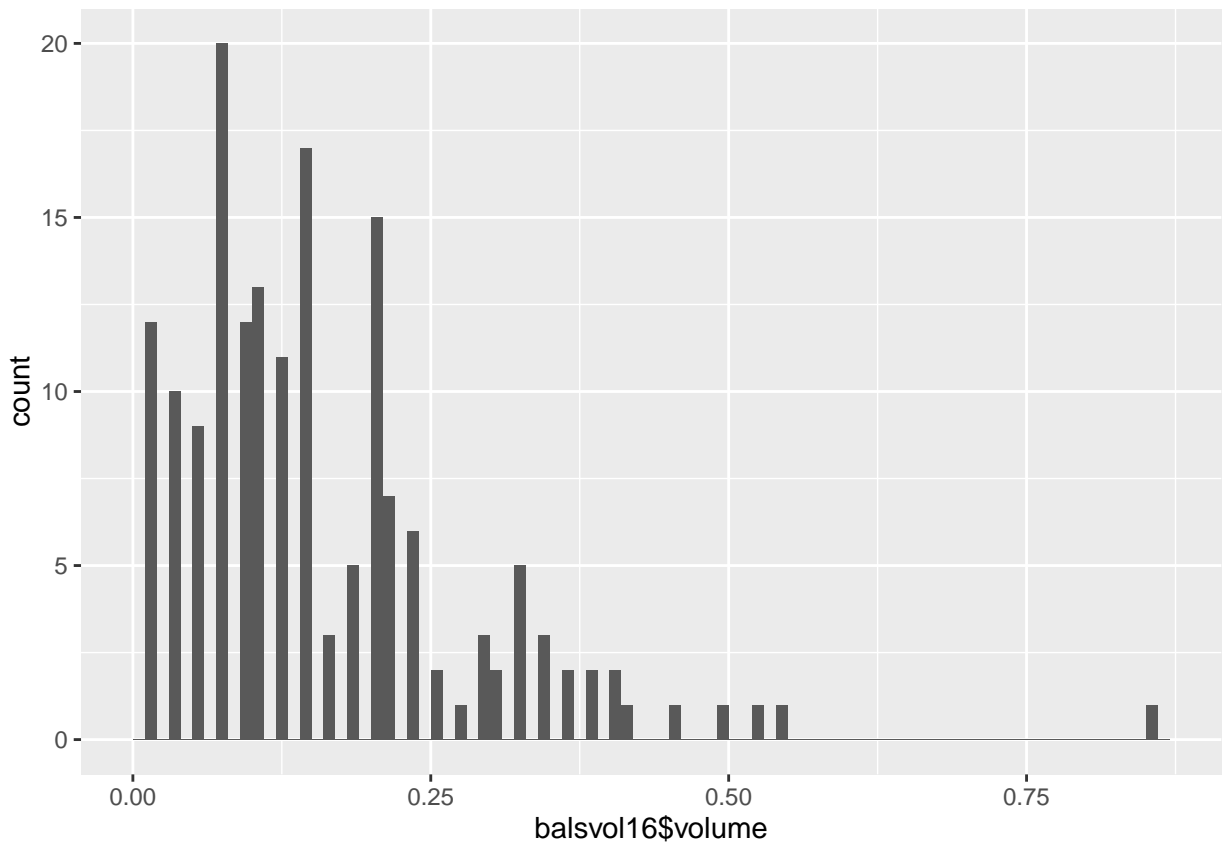
```
summarize(group_by(balsvolboth, treatment), meanVol = mean(volume), sdVolume = sd(volume))
```

```
## Source: local data frame [2 x 3]
##
##   treatment  meanVol  sdVolume
##   (fctr)      (dbl)      (dbl)
## 1          C 0.2619763 0.2825031
## 2          H 0.2694215 0.3141162
```

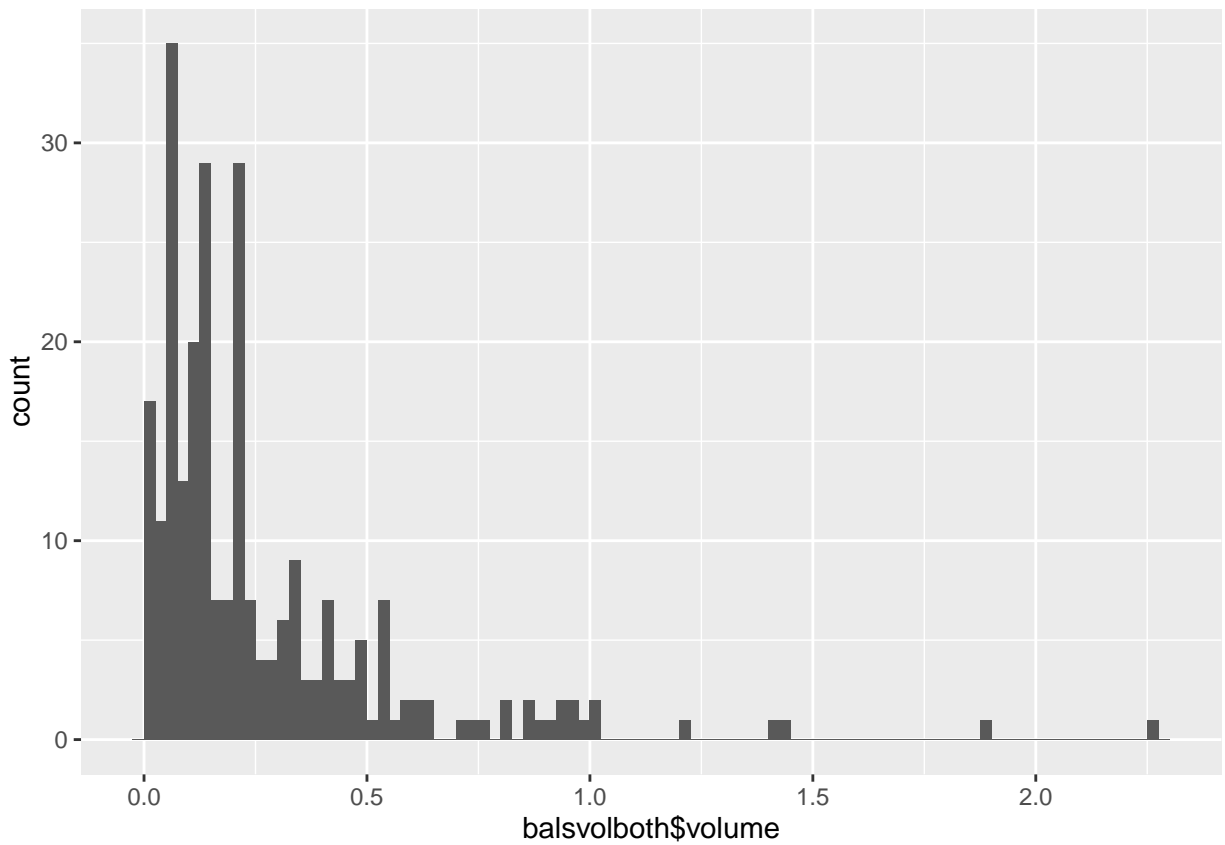
```
qplot(balsvol15$volume, binwidth = .025)
```



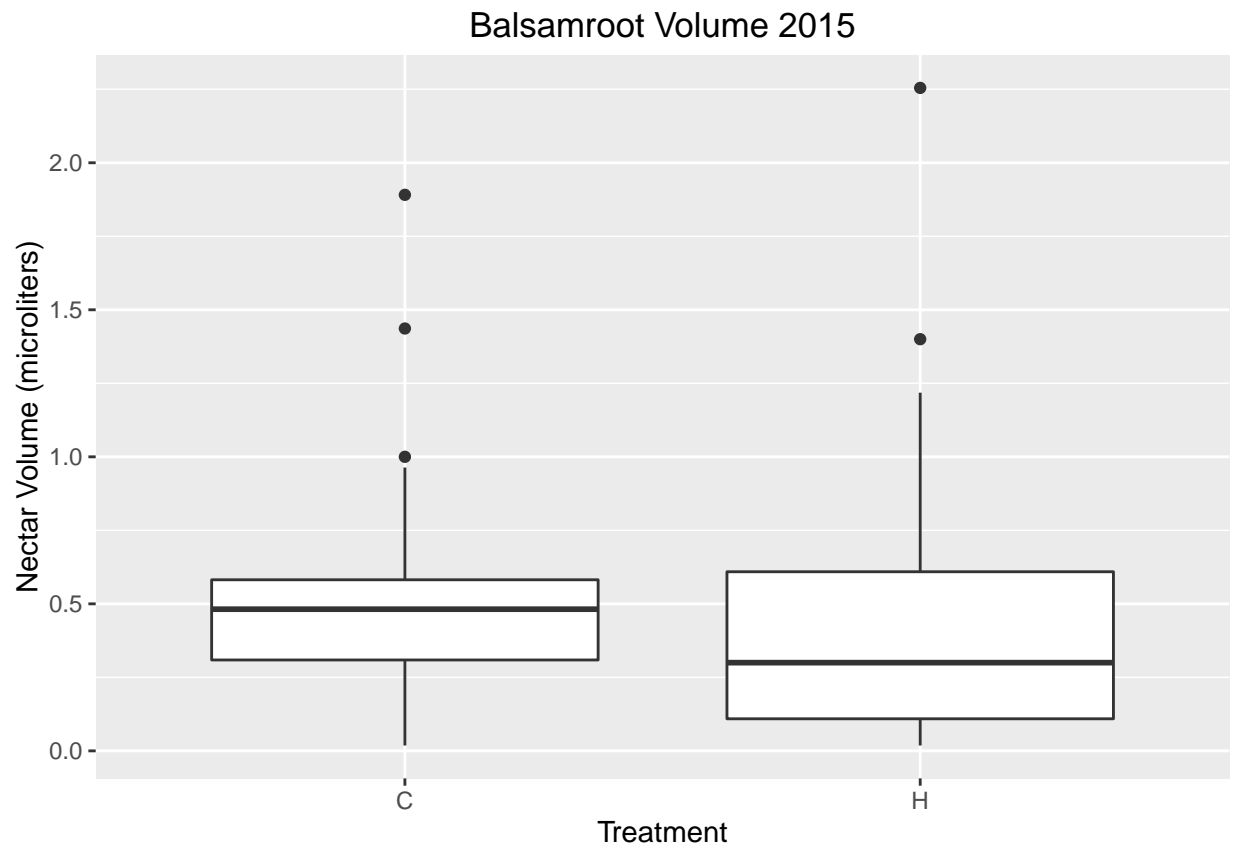
```
qplot(balsvol16$volume, binwidth = .01)
```



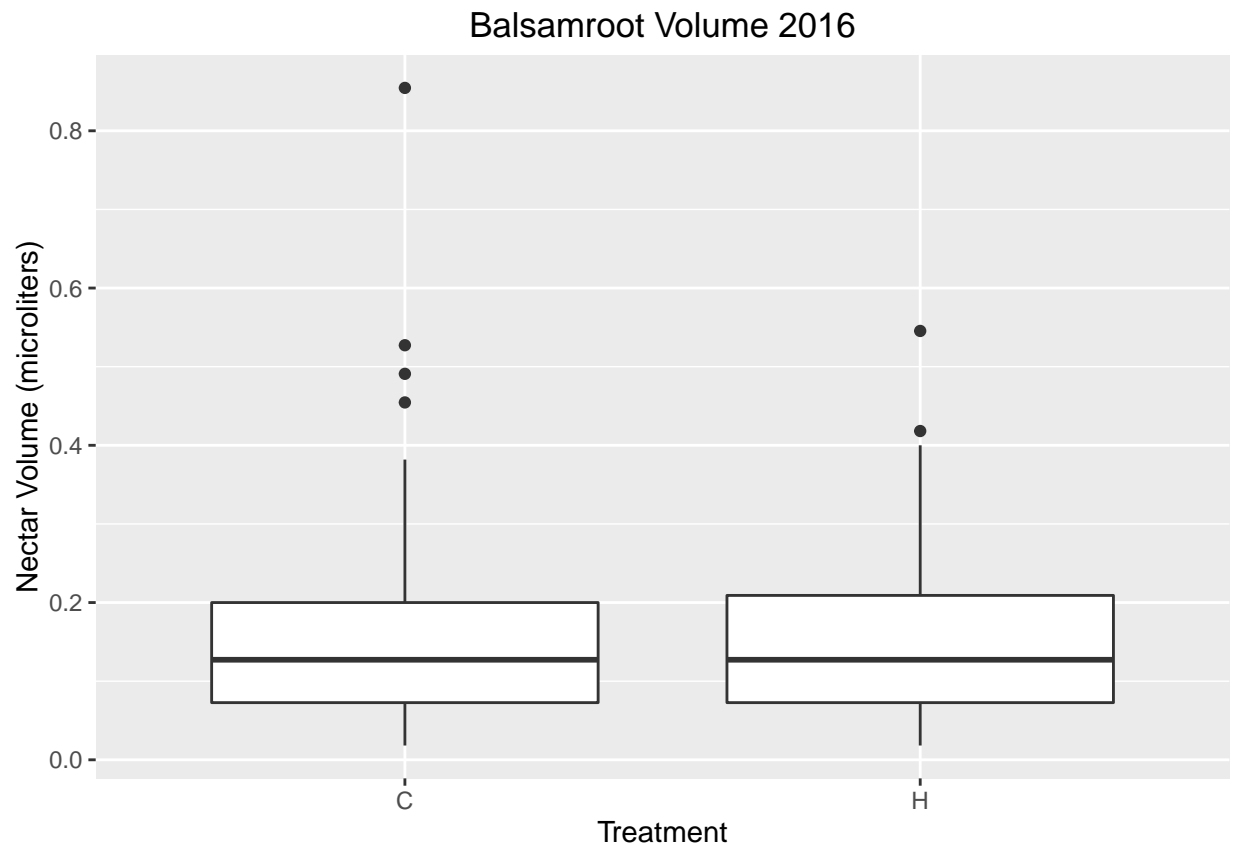
```
qplot(balsvolboth$volume, binwidth = .025)
```



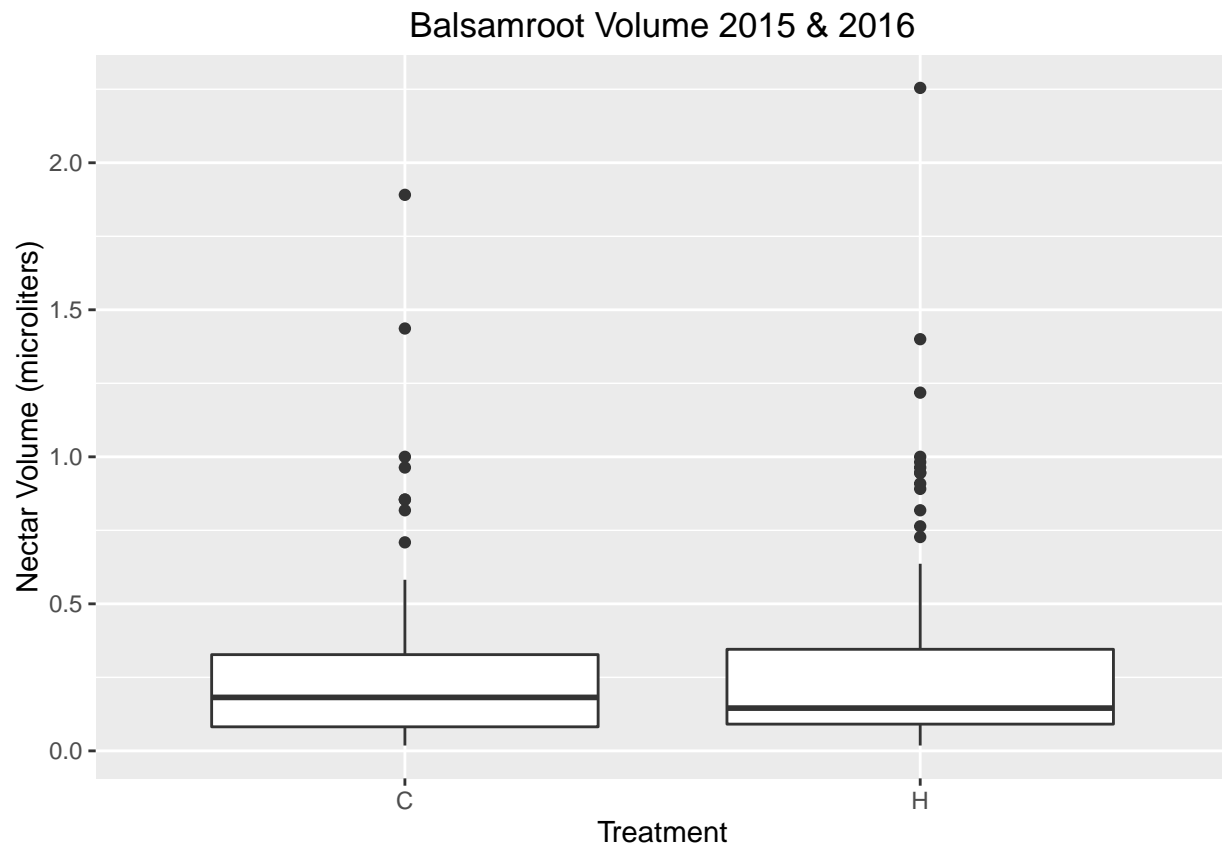
```
ggplot(balsvol15, aes(x=treatment, y=volume)) + geom_boxplot() +  
  xlab("Treatment") +  
  ylab("Nectar Volume (microliters)") + ggtitle("Balsamorhiza Volume 2015")
```



```
ggplot(balsvol16, aes(x=treatment, y=volume)) + geom_boxplot() +  
  xlab("Treatment") +  
  ylab("Nectar Volume (microliters)") + ggtitle("Balsamroot Volume 2016")
```



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



Homoscedastic?

```
var15C <- sd(balsvol15$volume[balsvol15$treatment=="C"])^2
var15H <- sd(balsvol15$volume[balsvol15$treatment=="H"])^2
ratio15 <- var15H/var15C
ratio15
```

```
## [1] 1.09429
```

```
var16C <- sd(balsvol16$volume[balsvol16$treatment=="C"])^2
var16H <- sd(balsvol16$volume[balsvol16$treatment=="H"])^2
ratio16 <- var16C/var16H
ratio16
```

```
## [1] 1.38688
```

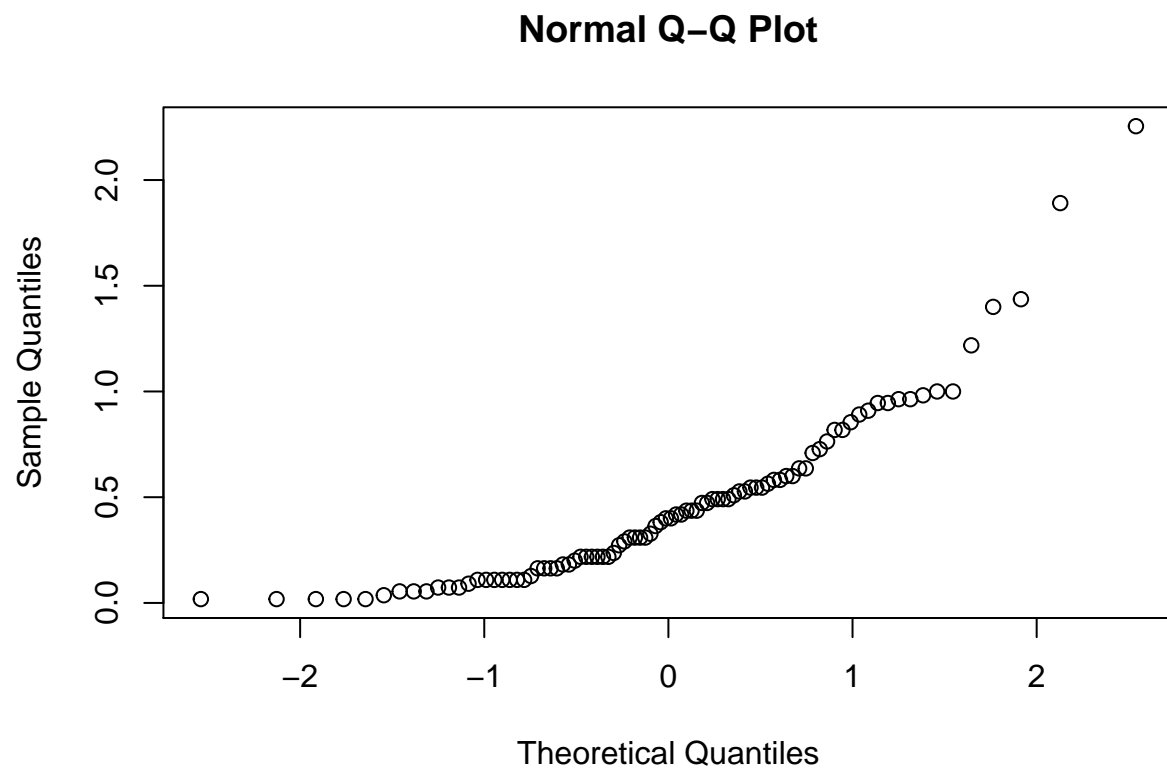
```
varbothC <- sd(balsvolboth$volume[balsvolboth$treatment=="C"])^2
varbothH <- sd(balsvolboth$volume[balsvolboth$treatment=="H"])^2
ratioboth <- varbothH/varbothC
ratioboth
```

```
## [1] 1.23633
```



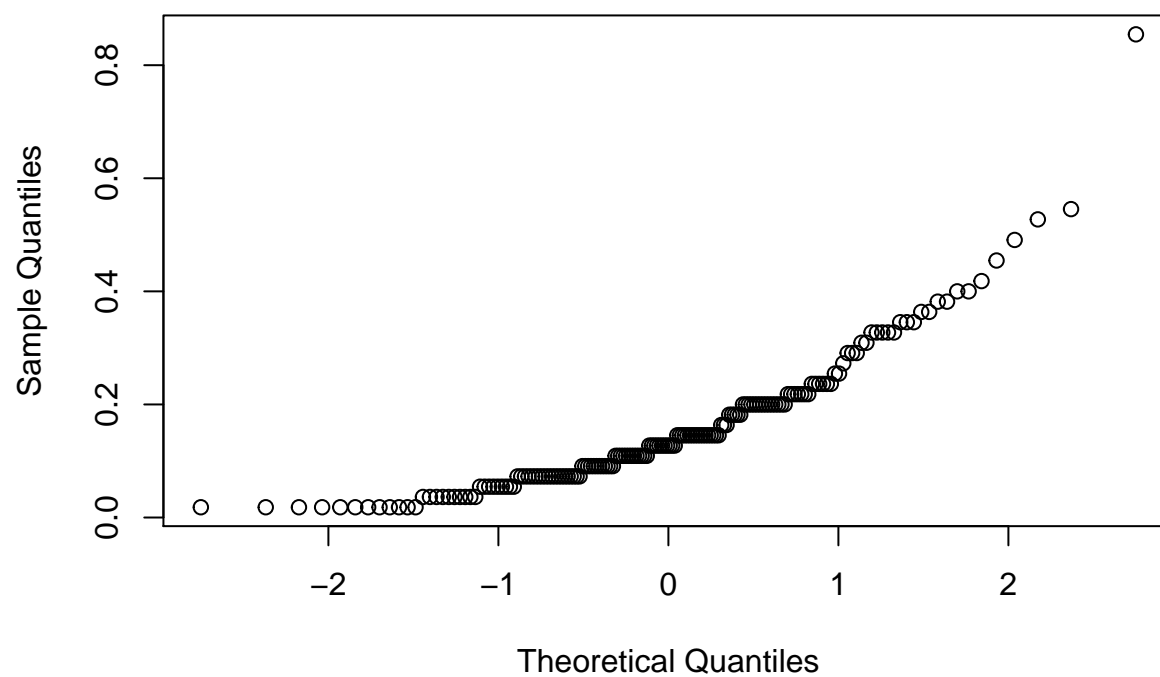
```
# Q-Q plots
```

```
qqnorm(balsvol15$volume)
```



```
qqnorm(balsvol16$volume)
```

Normal Q-Q Plot



```
qqnorm(balsvolboth$volume)
```

Normal Q-Q Plot

