BuckwheatDataExplore_2015_v1.R

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Tue Sep 27 17:49:35 2016

```r
library(ggplot2)
library(GGally)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:GGally':
##
##     nasa
```

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

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

```r
library(mvnormtest)
library(HH)
```

```
## Loading required package: lattice
```

```
## Loading required package: grid
```

```
## Loading required package: latticeExtra
```

```
## Loading required package: RColorBrewer
```

```
##
## Attaching package: 'latticeExtra'
```

```
## The following object is masked from 'package:ggplot2':
##
##     layer
```

```
## Loading required package: multcomp
```

```
## Loading required package: mvtnorm
```

```
## Loading required package: survival
```

```
## Loading required package: TH.data

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select

##
## Attaching package: 'TH.data'

## The following object is masked from 'package:MASS':
##
##     geyser

## Loading required package: gridExtra
```

```r
library(Rcmdr)
```

```
## Warning: package 'Rcmdr' was built under R version 3.2.5

## Loading required package: splines

## Loading required package: RcmdrMisc

## Warning: package 'RcmdrMisc' was built under R version 3.2.5

## Loading required package: car

## Warning: package 'car' was built under R version 3.2.5

##
## Attaching package: 'car'

## The following objects are masked from 'package:HH':
##
##     logit, vif

## Loading required package: sandwich

## The Commander GUI is launched only in interactive sessions
```

```r
library(nlme)
```

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

## The following object is masked from 'package:dplyr':
##
##     collapse
```

```r
# Create the  data frames

##Read in the data

setwd("D:/Iowa State University/Debinski Lab/Nectar data/Nectar analysis for manuscript")

  # Buckwheat volume, 2015-2016

volume.buck <- read.csv("Nectar_Vol_Buck.csv", header = T)
volume.buck <- data.frame(volume.buck[,1:7])
volume.buck$Date.Factor <- as.factor(volume.buck$Date.Factor)
volume.buck$Year.Factor <- as.factor(volume.buck$Year.Factor) # 1 = 2015, 2 = 2016
volume.buck$Heat <- as.factor(volume.buck$Heat) # 0 = control, 1 = heat treatment
volume.buck$Sample.Round <- as.factor(volume.buck$Sample.Round)
volume.buck$trans.vol <- log10(volume.buck$Volume)  #this doesn't work
head(volume.buck)
```

```
##        Date Date.Factor Year.Factor Plot Sample.Round Heat    Volume
## 1 6/18/2015           1           1  EC3            1    0 0.49090909
## 2 6/18/2015           1           1  EC3            2    0 0.05454545
## 3 6/18/2015           1           1  EC3            3    0 0.47272727
## 4 6/18/2015           1           1  EC3            4    0 0.20000000
## 5 6/18/2015           1           1  EC3            5    0 0.52727273
## 6 6/18/2015           1           1  EC3            6    0 0.16363636
##    trans.vol
## 1 -0.3089989
## 2 -1.2632414
## 3 -0.3253893
## 4 -0.6989700
## 5 -0.2779647
## 6 -0.7861202
```

```r
  # Buckwheat sugar, 2015-2016

sugar.buck <- read.csv("Nectar_BRIX_Buck.csv", header = T, col.names = c("Date", "Date.Factor", "Year.Fa
sugar.buck <- data.frame(sugar.buck[,1:7])
sugar.buck$Date.Factor <- as.factor(sugar.buck$Date.Factor)
sugar.buck$Year.Factor <- as.factor(sugar.buck$Year.Factor)
sugar.buck$Heat <- as.factor(sugar.buck$Heat)
sugar.buck$Mass <- as.numeric(sugar.buck$Mass)
sugar.buck$BRIX <- as.numeric(sugar.buck$BRIX)
sugar.buck$trans.mass <- (sugar.buck$Mass^(1/3))
sugar.buck$trans.conc <- (sugar.buck$BRIX^(2))
head(sugar.buck)
```

```
##        Date Date.Factor Year.Factor Plot Heat BRIX Mass trans.mass
## 1 6/18/2015           1           1  EC3    0   20    3   1.442250
## 2 6/18/2015           1           1  EC3    0   23  146   5.265637
## 3 6/18/2015           1           1  EC3    0   25  193   5.778997
## 4 6/18/2015           1           1  EC3    0   25   64   4.000000
## 5 6/18/2015           1           1  EC3    0   25  210   5.943922
## 6 6/18/2015           1           1  EC3    0   26   48   3.634241
##    trans.conc
```

```
## 1          400
## 2          529
## 3          625
## 4          625
## 5          625
## 6          676
```

```
volume.buck2015 <- as.data.frame(volume.buck[volume.buck$Year.Factor == "1",])
sugar.buck2015 <- as.data.frame(sugar.buck[sugar.buck$Year.Factor == "1",])
```

```
#Data summaries
```

```
summary(volume.buck2015)
```

```
##         Date        Date.Factor  Year.Factor      Plot      Sample.Round
##   6/23/2015: 45    6      : 45   1:415     WSR10  : 47    1      : 12
##   6/22/2015: 42    5      : 42   2:  0     WH12   : 44    2      : 12
##   6/24/2015: 38    7      : 38             EH4    : 42    3      : 12
##   6/21/2015: 37    4      : 37             CH5    : 39    4      : 12
##   6/30/2015: 35    13     : 35             WHSR9  : 39    5      : 12
##   6/25/2015: 31    8      : 31             EC3    : 38    6      : 12
##   (Other)  :187    (Other):187            (Other):166    (Other):343
##   Heat        Volume            trans.vol
##   0:208   Min.   :0.01818   Min.   :-1.7404
##   1:207   1st Qu.:0.21818   1st Qu.:-0.6612
##           Median :0.36364   Median :-0.4393
##           Mean   :0.44338   Mean   :-0.4570
##           3rd Qu.:0.54545   3rd Qu.:-0.2632
##           Max.   :1.96875   Max.   : 0.2942
##
```

```
summarize(group_by(volume.buck2015, Heat), meanVol = mean(Volume), sdVolume = sd(Volume))
```

```
## Source: local data frame [2 x 3]
##
##     Heat   meanVol   sdVolume
##   (fctr)     (dbl)      (dbl)
## 1      0 0.5218675 0.3693587
## 2      1 0.3645161 0.2706726
```

```
summary(sugar.buck2015)
```

```
##         Date        Date.Factor  Year.Factor      Plot       Heat
##   6/23/2015: 45    6      : 45   1:416     WSR10  : 47    0:208
##   6/22/2015: 42    5      : 42   2:  0     WH12   : 44    1:208
##   6/24/2015: 38    7      : 38             EH4    : 42
##   6/21/2015: 37    4      : 37             WHSR9  : 40
##   6/30/2015: 35    13     : 35             CH5    : 39
##   6/25/2015: 31    8      : 31             EC3    : 38
##   (Other)  :188    (Other):188            (Other):166
##       BRIX          Mass          trans.mass       trans.conc
##   Min.   : 2.0   Min.   : 1.0   Min.   :1.000   Min.   :   4
```

```
##   1st Qu.:46.0    1st Qu.:195.8    1st Qu.:5.806    1st Qu.:2116
##   Median :53.0    Median :276.5    Median :6.515    Median :2809
##   Mean   :50.6    Mean   :263.2    Mean   :6.244    Mean   :2778
##   3rd Qu.:60.0    3rd Qu.:342.2    3rd Qu.:6.995    3rd Qu.:3600
##   Max.   :76.0    Max.   :425.0    Max.   :7.518    Max.   :5776
##
```

```r
summarize(group_by(sugar.buck2015, Heat), meanBRIX = mean(BRIX), meanMass = mean(Mass), sdBRIX = sd(BRI
```

```
## Source: local data frame [2 x 5]
##
##     Heat meanBRIX meanMass   sdBRIX    sdMass
##   (fctr)    (dbl)    (dbl)    (dbl)     (dbl)
## 1      0 45.91827 270.1875 15.59908 106.57631
## 2      1 55.28365 256.2981 12.21076  97.36523
```

```r
qplot(volume.buck2015$trans.vol, binwidth = 0.01)
```
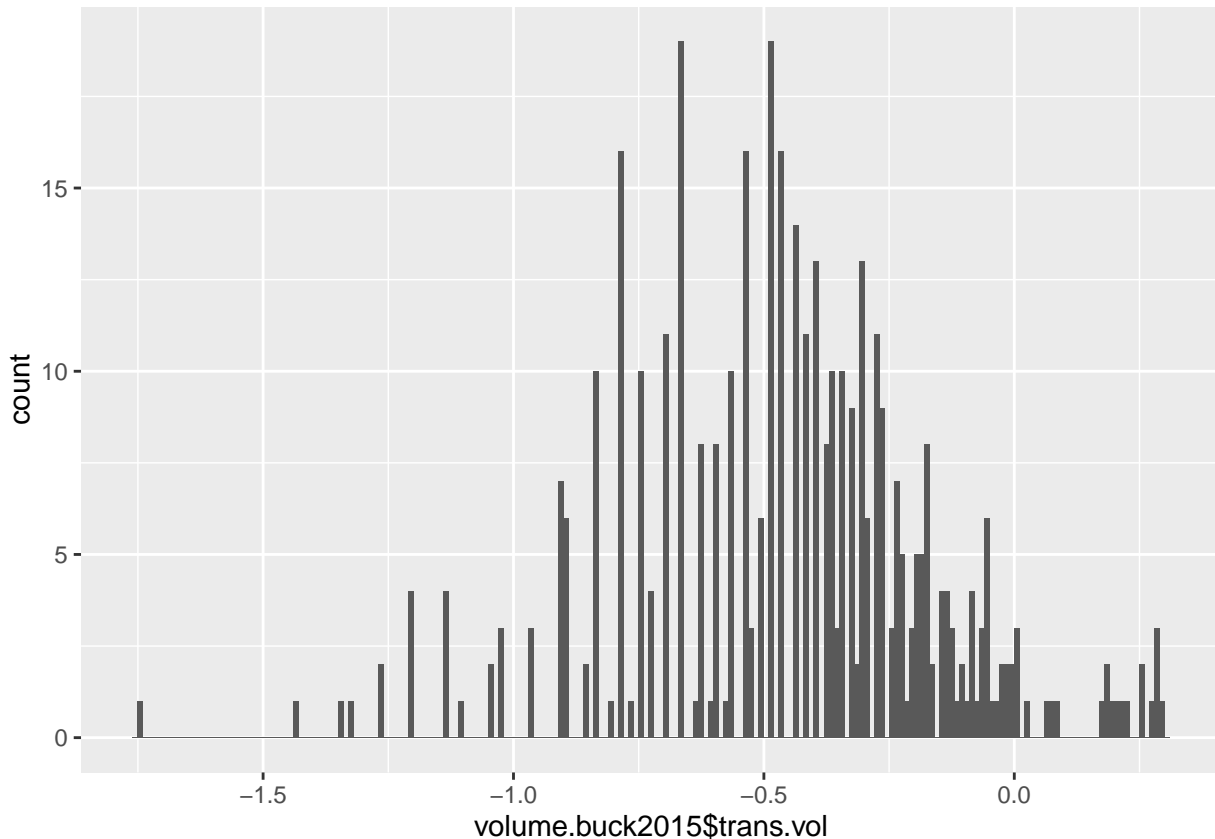


```r
qplot(volume.buck2015$trans.vol[volume.buck2015$Year.Factor == "1"], binwidth = 0.01)
```
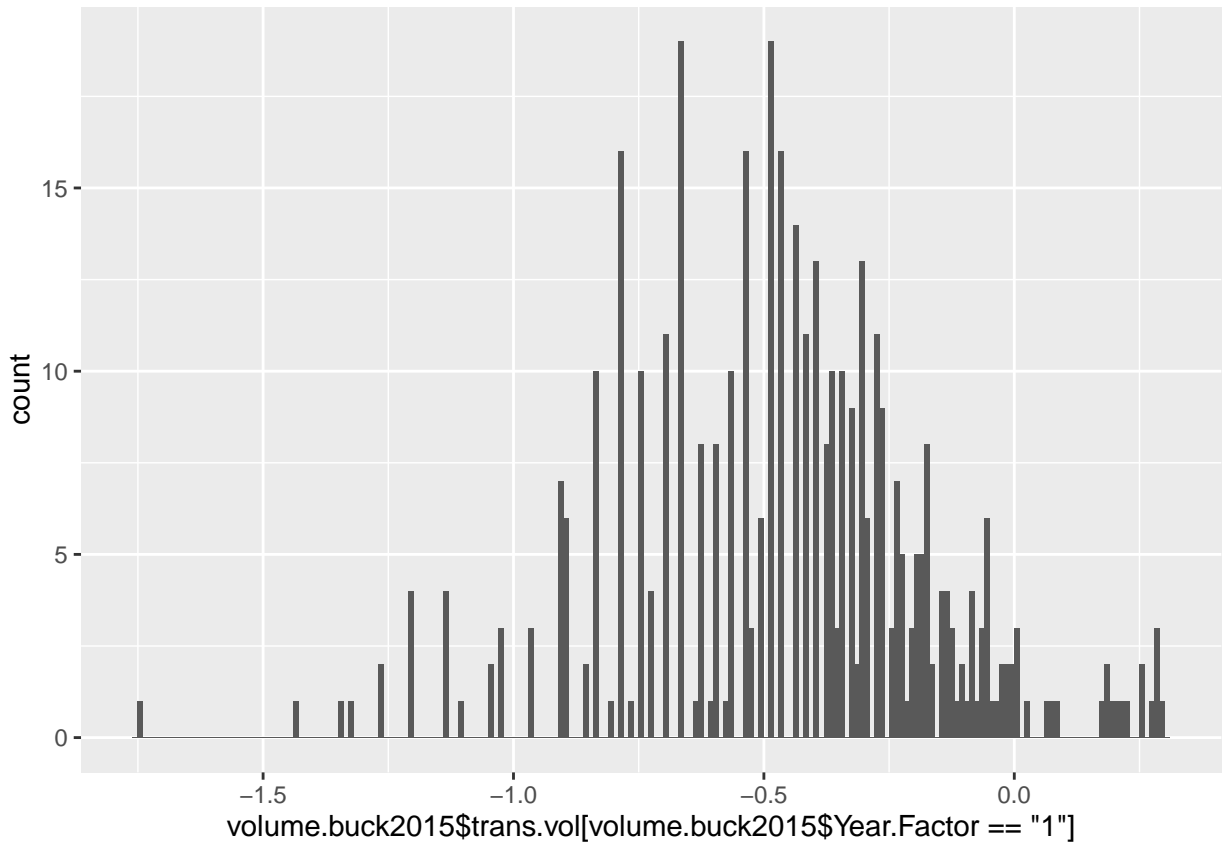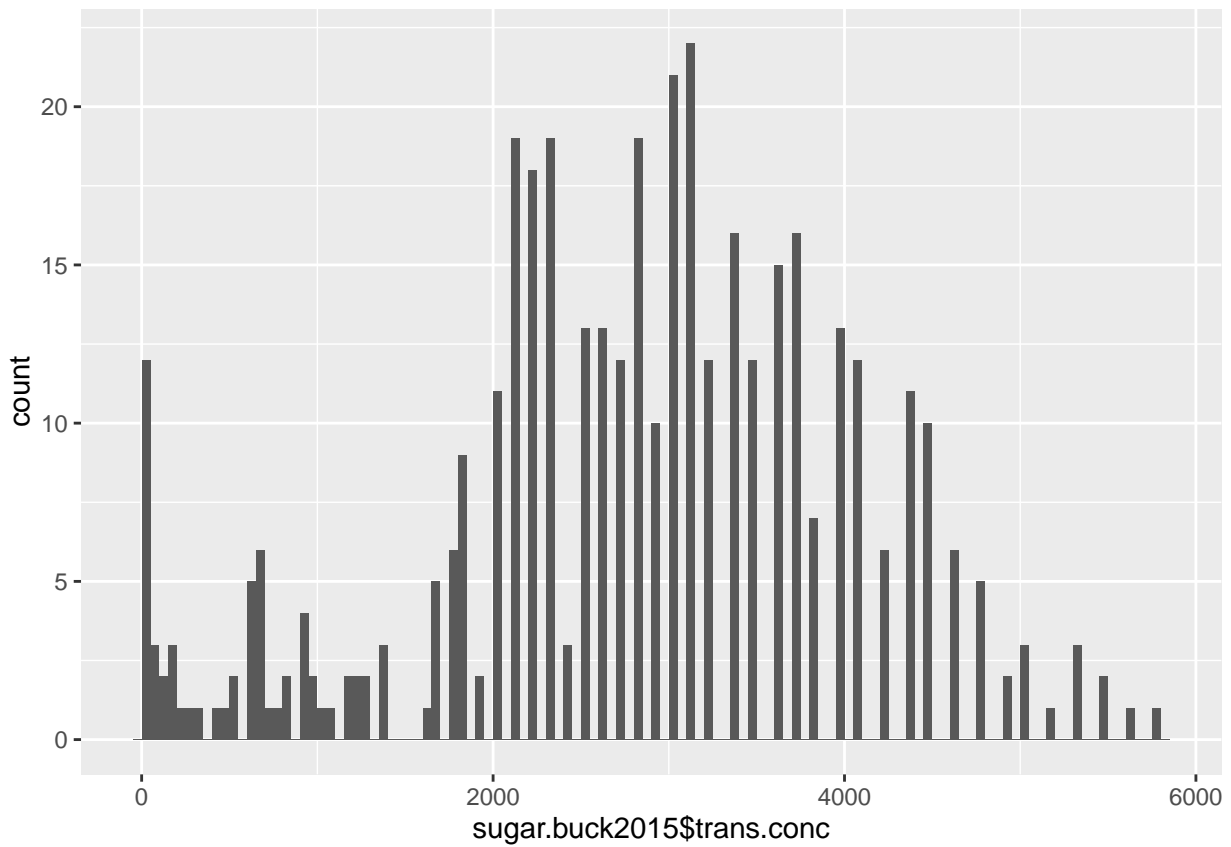
```
qplot(volume.buck2015$trans.vol[volume.buck2015$Year.Factor == "2"], binwidth = 0.01)
```
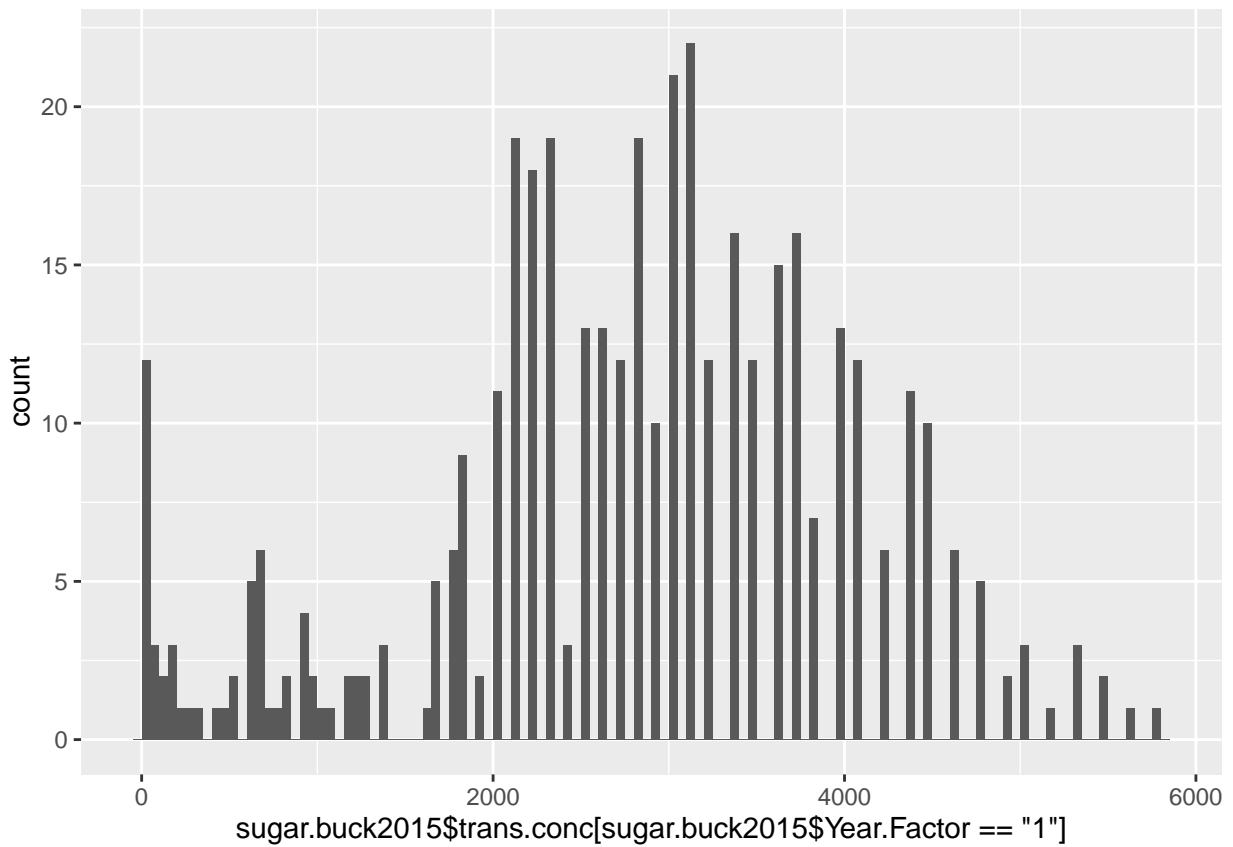
volume.buck2015$trans.vol[volume.buck2015$Year.Factor == "2"]

```
qplot(sugar.buck2015$trans.conc, binwidth = 50)
```

```r
qplot(sugar.buck2015$trans.conc[sugar.buck2015$Year.Factor == "1"], binwidth = 50)
```
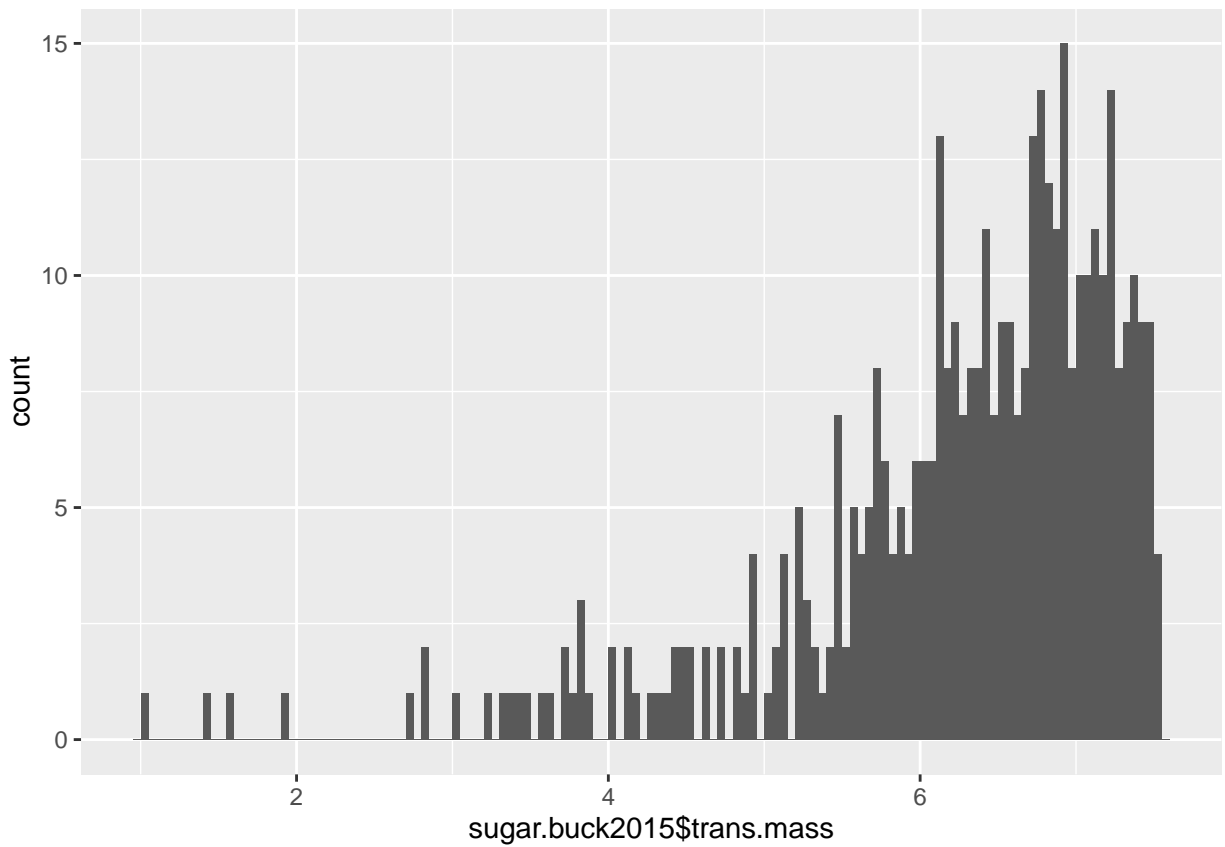
```r
qplot(sugar.buck2015$trans.conc[sugar.buck2015$Year.Factor == "2"], binwidth = 50)
```
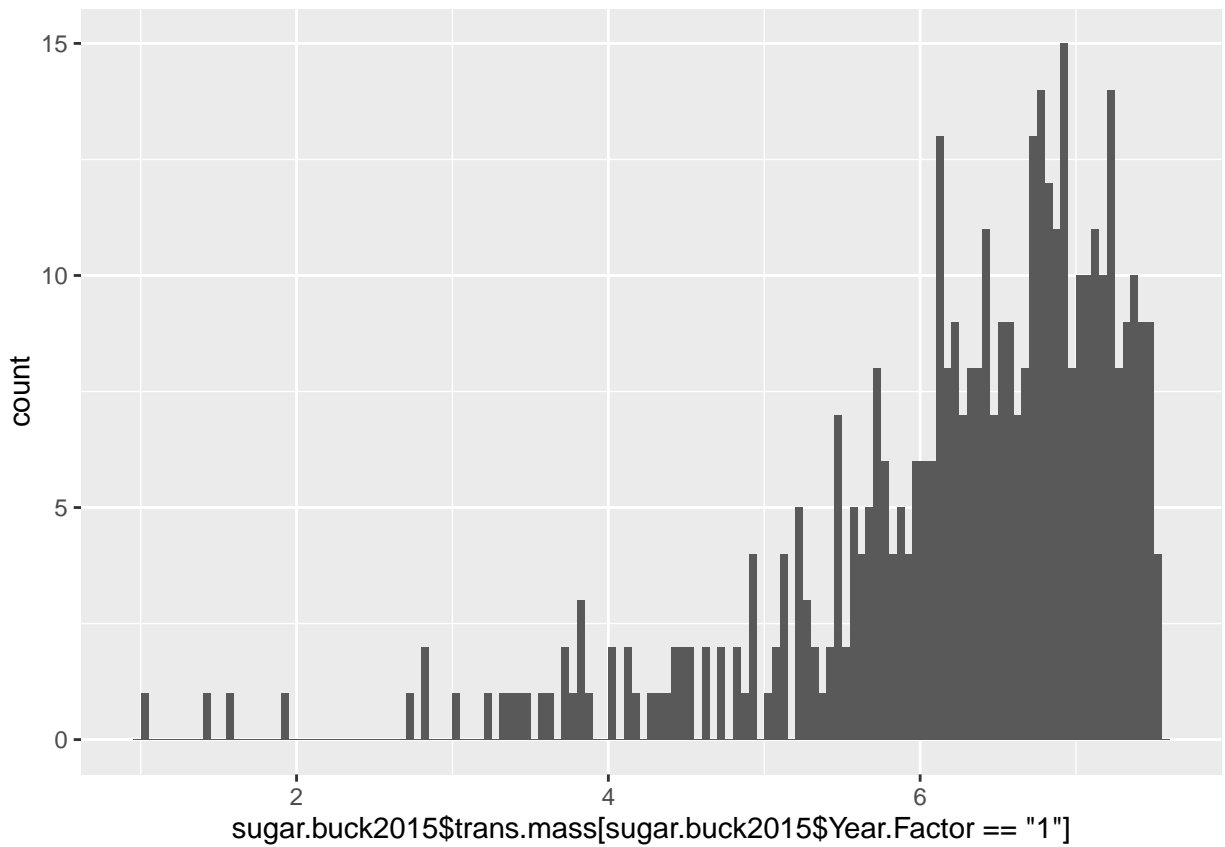
count

sugar.buck2015$trans.conc[sugar.buck2015$Year.Factor == "2"]

```
qplot(sugar.buck2015$trans.mass, binwidth = .05)
```

```
qplot(sugar.buck2015$trans.mass[sugar.buck2015$Year.Factor == "1"], binwidth = .05)
```

count

sugar.buck2015$trans.mass[sugar.buck2015$Year.Factor == "1"]

```r
qplot(sugar.buck2015$trans.mass[sugar.buck2015$Year.Factor == "2"], binwidth = .05)
```

count

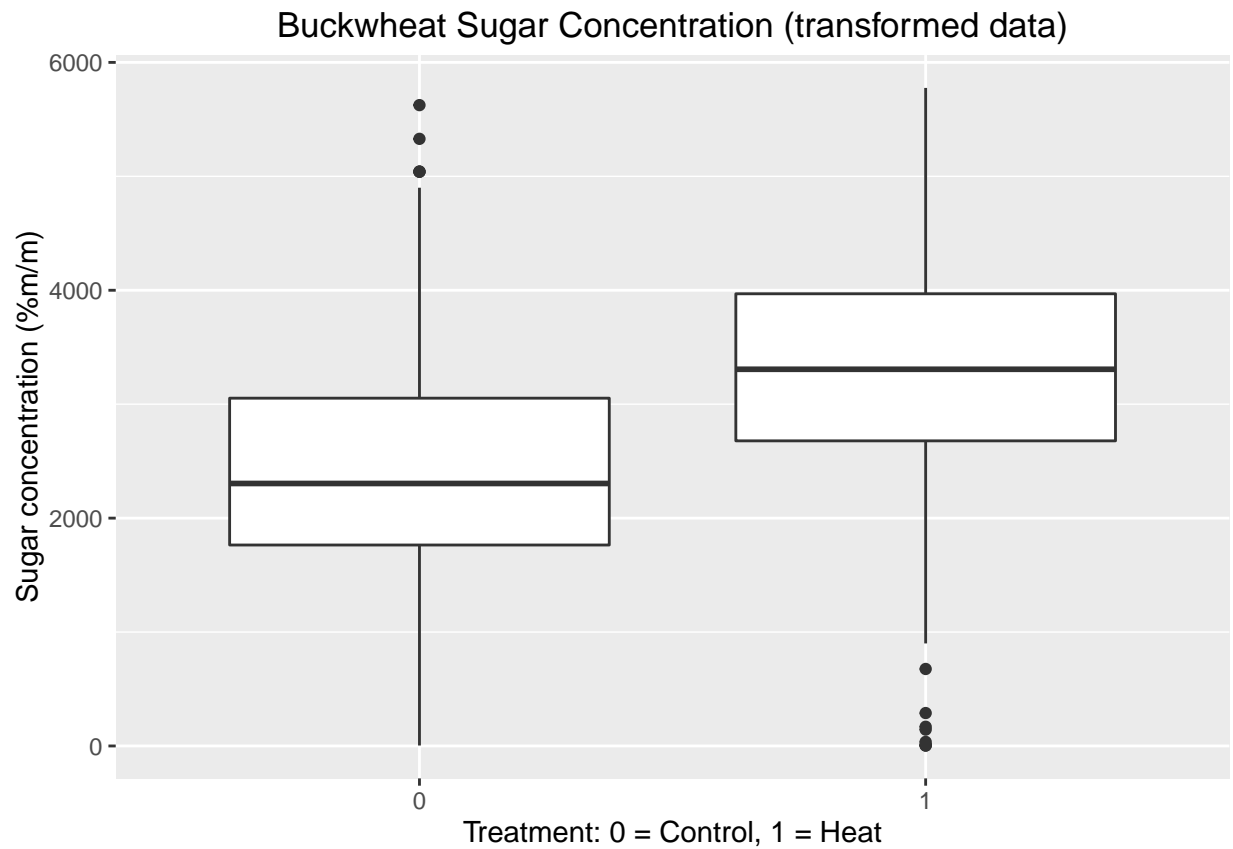sugar.buck2015$trans.mass[sugar.buck2015$Year.Factor == "2"]

```
#Volume
ggplot(volume.buck2015, aes(x=Heat, y=trans.vol)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Nectar Volume (microliters)") + ggtitle("Buckwheat Volume (log transformed)")
```

Buckwheat Volume (log transformed)
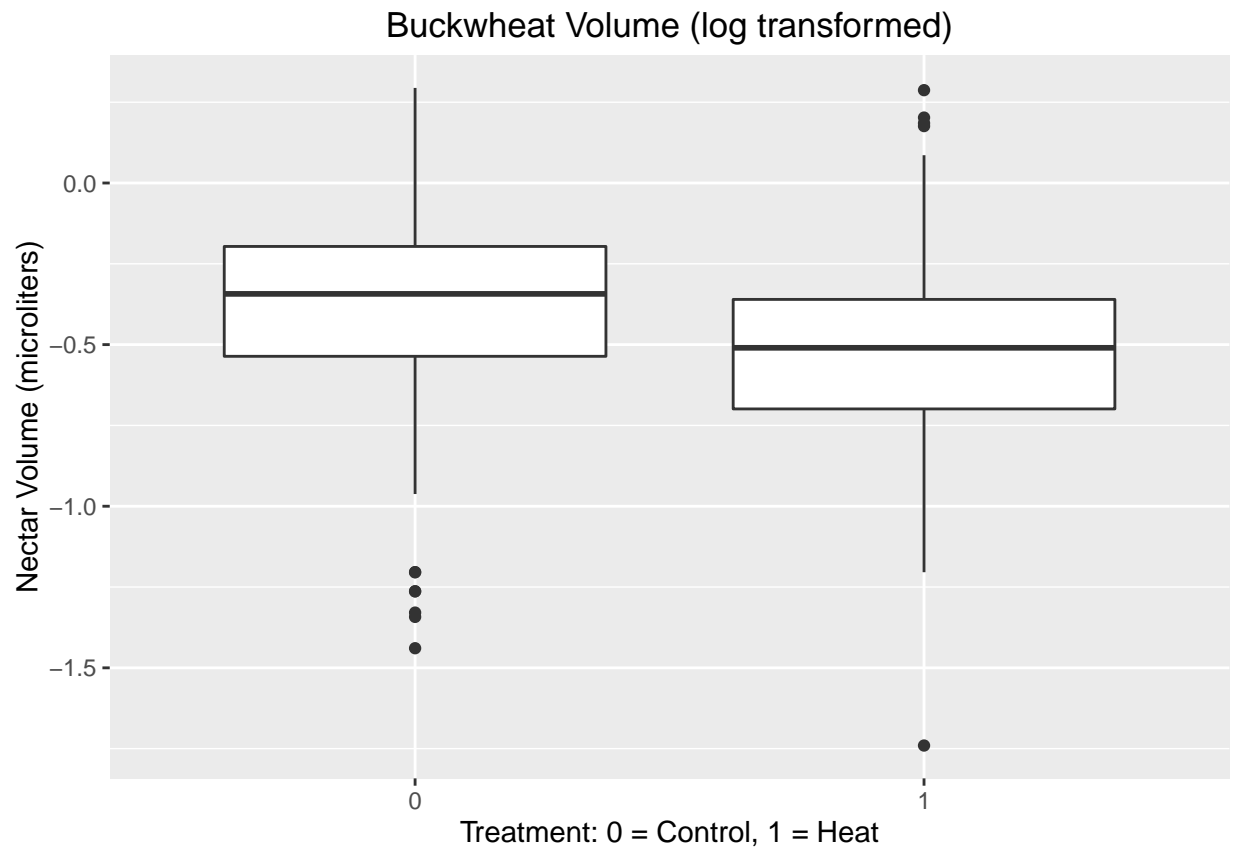

```
ggplot(volume.buck2015, aes(x=Heat, y=Volume)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Nectar Volume (microliters)") + ggtitle("Buckwheat Volume (untransformed)")
```
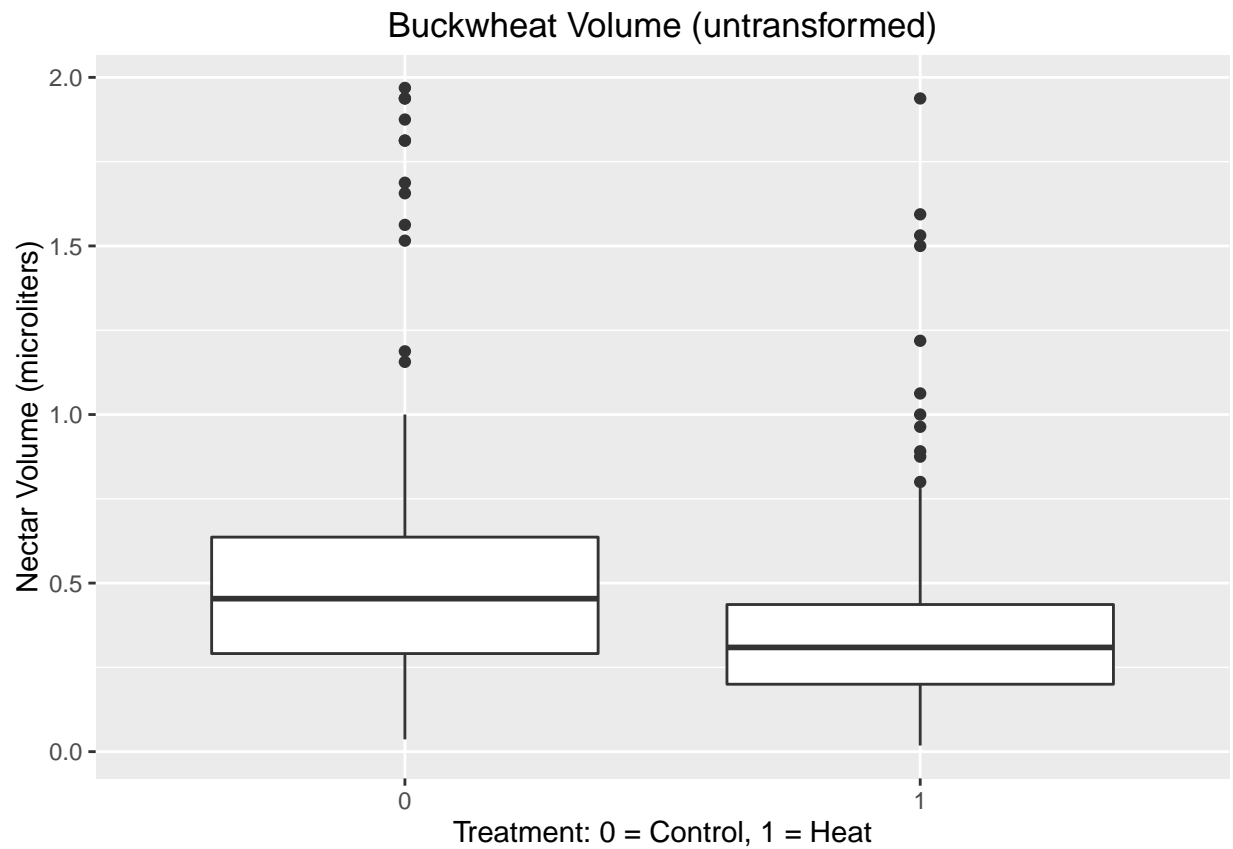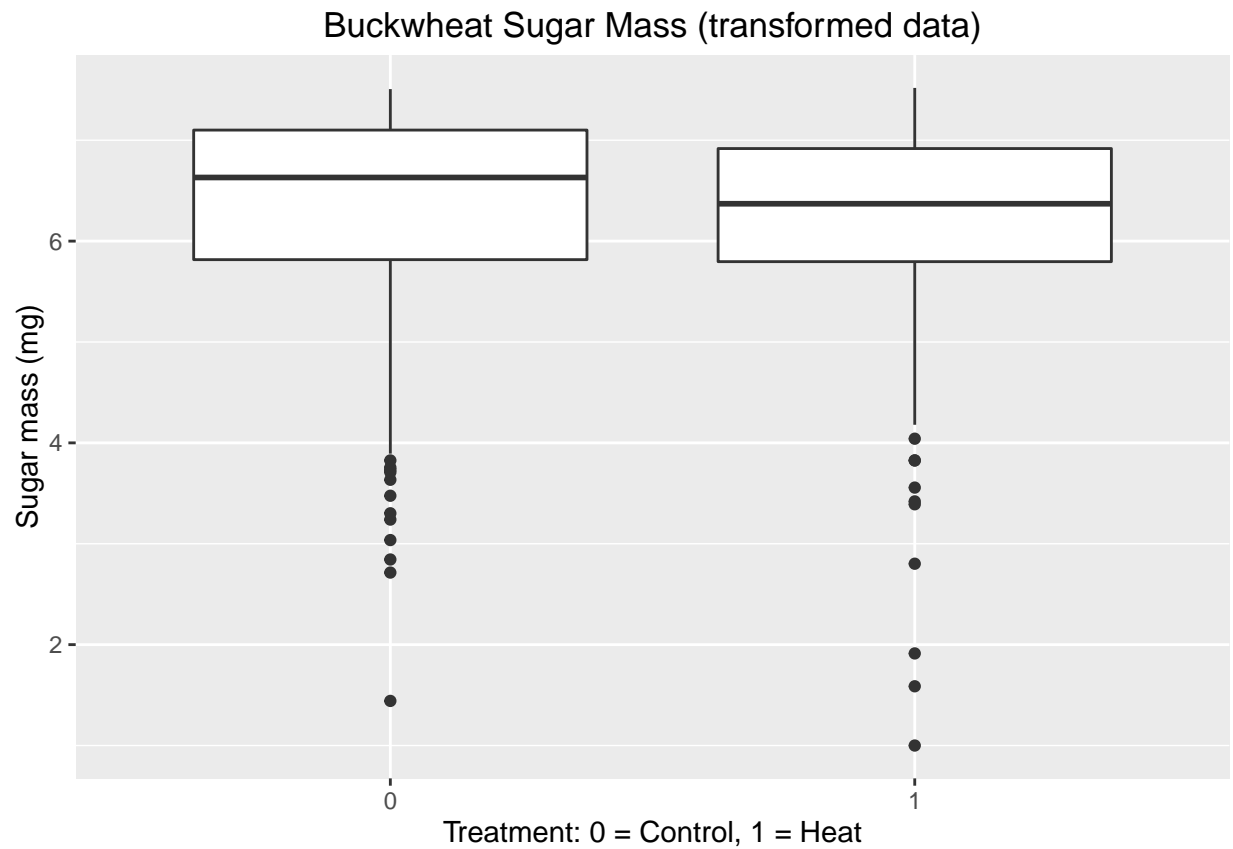
```
ggplot(sugar.buck2015, aes(x=Heat, y=trans.conc)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Sugar concentration (%m/m)") + ggtitle("Buckwheat Sugar Concentration (transformed data)")
```

## Buckwheat Sugar Concentration (transformed data)

```
ggplot(sugar.buck2015, aes(x=Heat, y=BRIX)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Sugar concentration (%m/m)") + ggtitle("Buckwheat Sugar Concentration (untransformed data)")
```

Buckwheat Sugar Concentration (untransformed data)
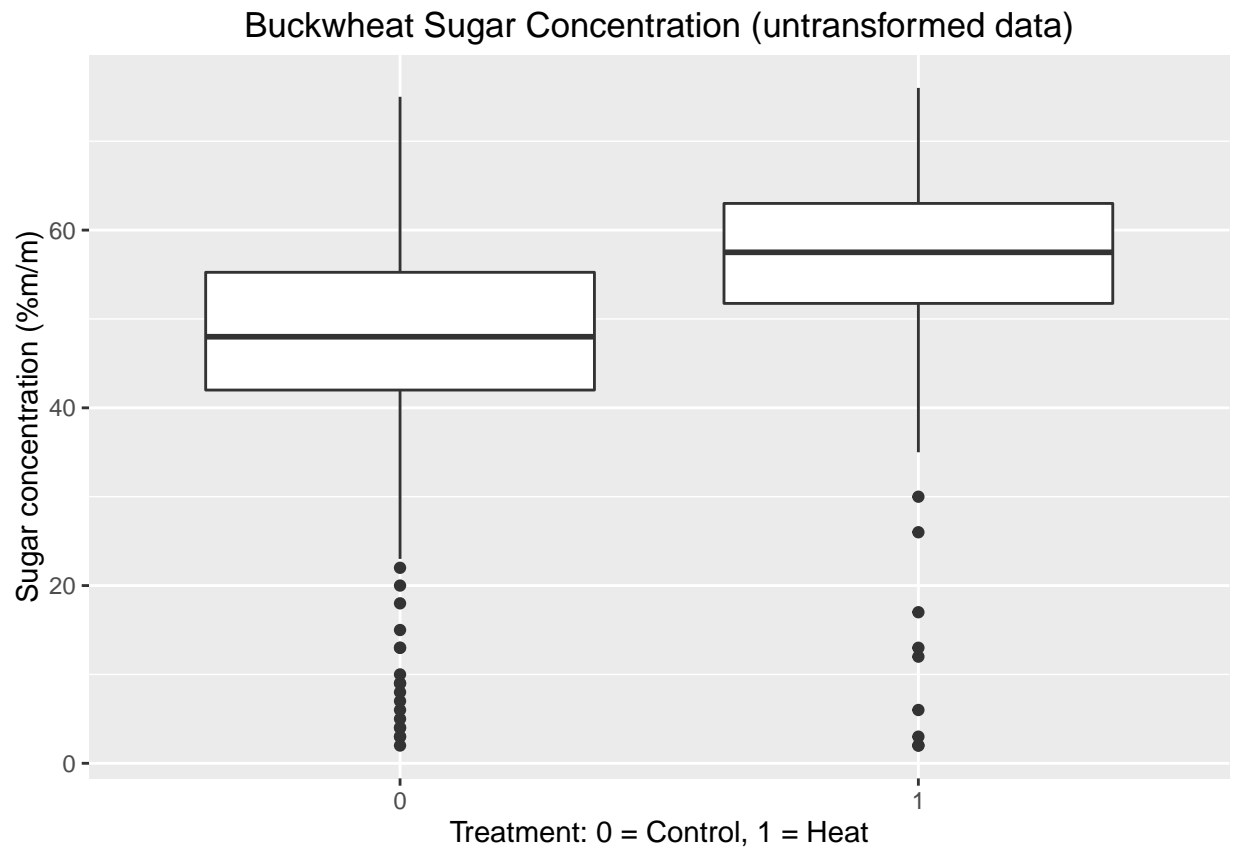

```
ggplot(sugar.buck2015, aes(x=Heat, y=trans.mass)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Sugar mass (mg)") + ggtitle("Buckwheat Sugar Mass (transformed data)")
```

Buckwheat Sugar Mass (transformed data)


```
ggplot(sugar.buck2015, aes(x=Heat, y=Mass)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Sugar mass (mg)") + ggtitle("Buckwheat Sugar Mass (untransformed data)")
```

Buckwheat Sugar Mass (untransformed data)
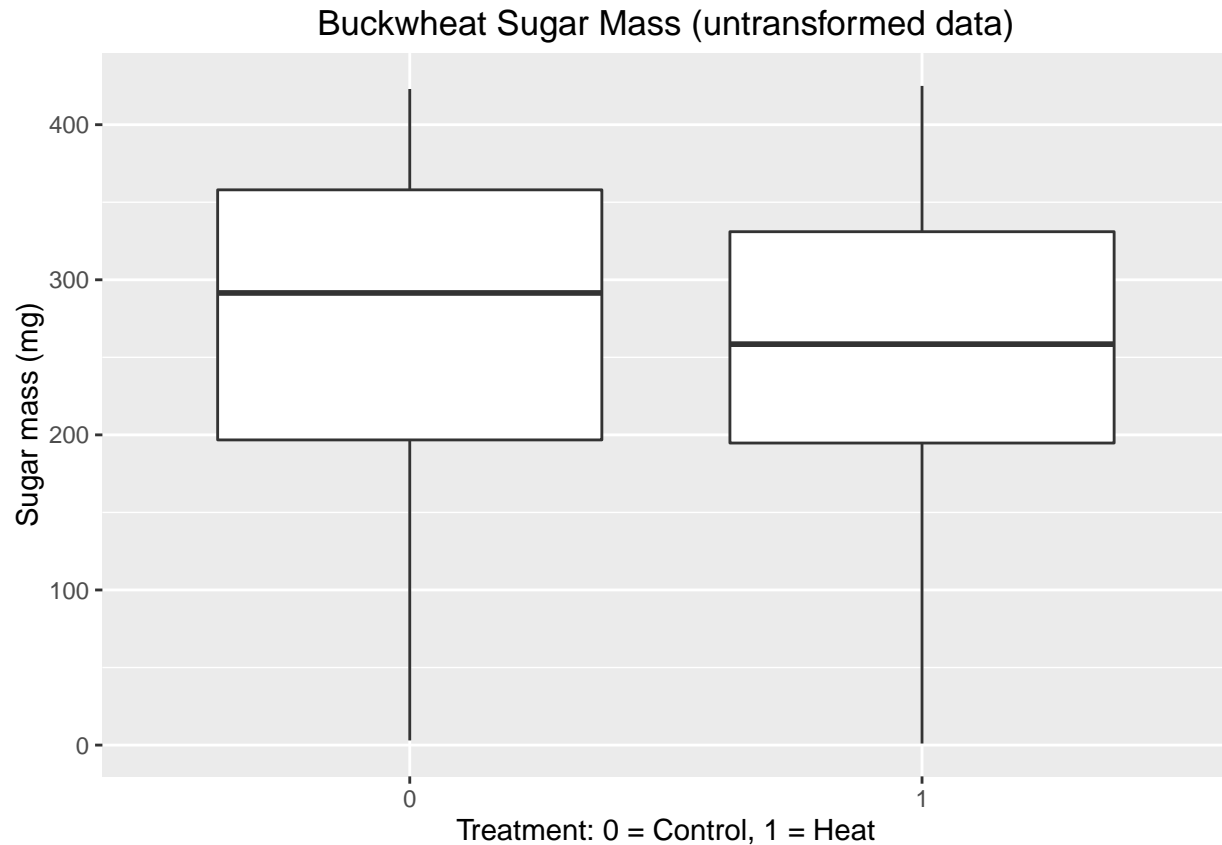

```r
# Test normality for volume by treatment
shapiro.test(as.matrix(volume.buck2015[volume.buck2015[,6] == "0", 8])) #control
```

```
## 
##  Shapiro-Wilk normality test
## 
## data:  as.matrix(volume.buck2015[volume.buck2015[, 6] == "0", 8])
## W = 0.96261, p-value = 2.656e-05
```

```r
shapiro.test(as.matrix(volume.buck2015[volume.buck2015[,6] == "1", 8])) #heat treatment
```

```
## 
##  Shapiro-Wilk normality test
## 
## data:  as.matrix(volume.buck2015[volume.buck2015[, 6] == "1", 8])
## W = 0.98528, p-value = 0.02988
```

```r
# Test normality for sugar concentration by treatment
shapiro.test(as.matrix(sugar.buck2015[sugar.buck2015[,5] == "0", 9])) #control
```

```
## 
##  Shapiro-Wilk normality test
## 
## data:  as.matrix(sugar.buck2015[sugar.buck2015[, 5] == "0", 9])
## W = 0.9737, p-value = 0.0006183
```

```r
shapiro.test(as.matrix(sugar.buck2015[sugar.buck2015[,5] == "1", 9])) #heat treatment
```

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.buck2015[sugar.buck2015[, 5] == "1", 9])
## W = 0.96546, p-value = 5.707e-05
```

```r
# Test normality for sugar mass by treatment
shapiro.test(as.matrix(sugar.buck2015[sugar.buck2015[,5] == "0", 8])) #control
```

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.buck2015[sugar.buck2015[, 5] == "0", 8])
## W = 0.84745, p-value = 1.631e-13
```

```r
shapiro.test(as.matrix(sugar.buck2015[sugar.buck2015[,5] == "1", 8])) #heat treatment
```

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.buck2015[sugar.buck2015[, 5] == "1", 8])
## W = 0.84998, p-value = 2.17e-13
```

```r
#Levene test for Homogineity of variances
leveneTest(volume.buck2015[,8],volume.buck2015[,5]) #Volume
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value   Pr(>F)
## group  46  1.8117 0.001578 **
##       368
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
leveneTest(sugar.buck2015[,9],sugar.buck2015[,5]) #Concentration
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  2.6663 0.1033
##       414
```

```r
leveneTest(sugar.buck2015[,8],sugar.buck2015[,5]) #Mass
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.4182 0.5182
##       414
```

```r
#Fligner test for homogineity of variances
fligner.test(volume.buck2015[,8],volume.buck2015[,5]) #Volume
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  volume.buck2015[, 8] and volume.buck2015[, 5]
## Fligner-Killeen:med chi-squared = 69.163, df = 46, p-value =
## 0.01518
```

```r
fligner.test(sugar.buck2015[,9],sugar.buck2015[,5]) #Concentration
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  sugar.buck2015[, 9] and sugar.buck2015[, 5]
## Fligner-Killeen:med chi-squared = 2.8977, df = 1, p-value =
## 0.08871
```

```r
fligner.test(sugar.buck2015[,8],sugar.buck2015[,5]) #Mass
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  sugar.buck2015[, 8] and sugar.buck2015[, 5]
## Fligner-Killeen:med chi-squared = 0.064823, df = 1, p-value =
## 0.799
```
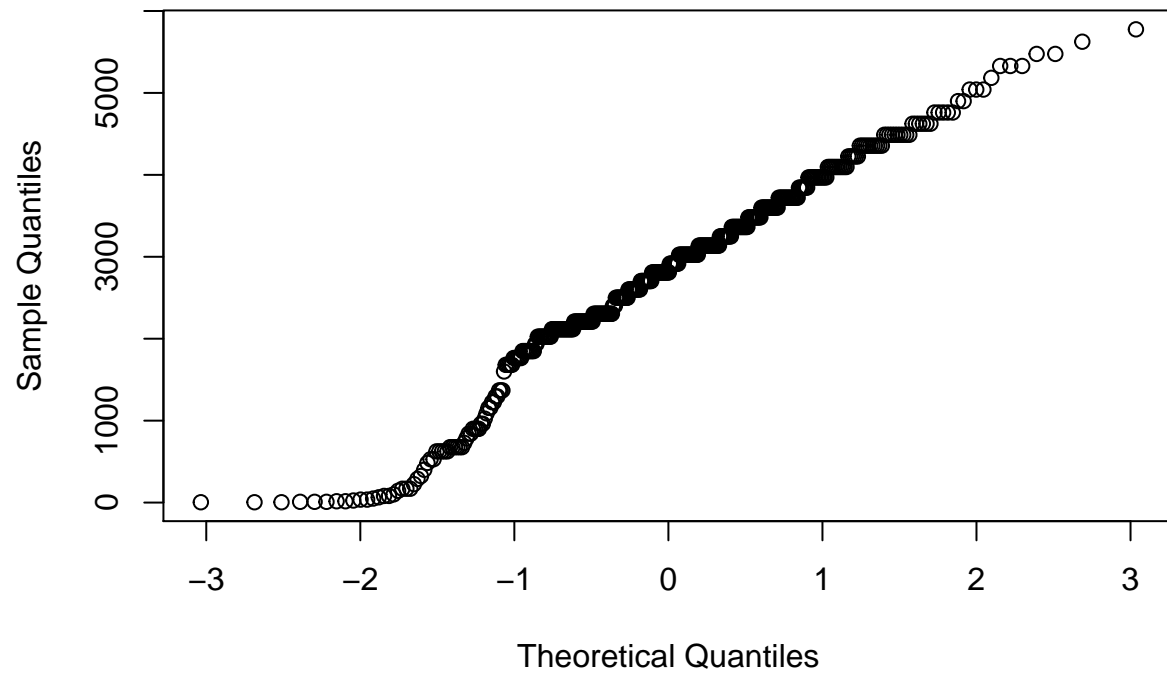
```r
qqnorm(volume.buck2015$trans.vol)
```

Normal Q–Q Plot
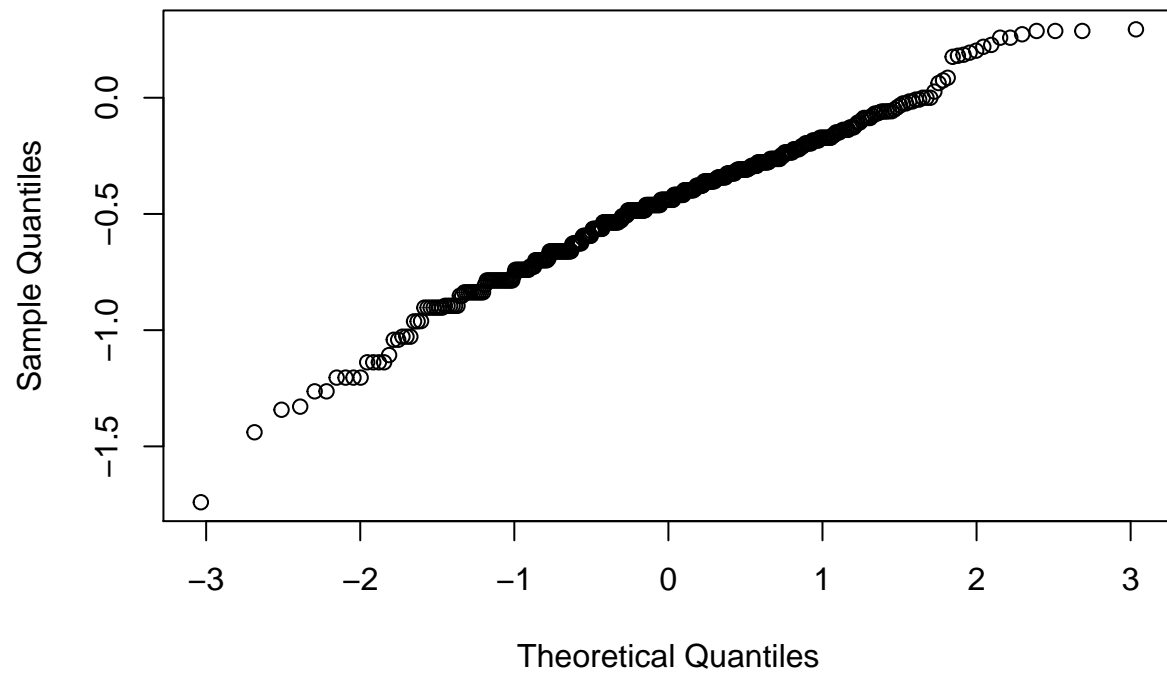

```
qqnorm(sugar.buck2015$trans.conc)
```

Normal Q–Q Plot


```
qqnorm(sugar.buck2015$trans.mass)
```

Normal Q−Q Plot