BuckwheatDataExplore_v1.R

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```
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
```

```
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.F
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
```

```
#Data summaries
```

```
summary(volume.buck)
```

```
##          Date       Date.Factor  Year.Factor       Plot        Sample.Round
##  6/24/2016: 70    15     : 70    1:415      WSR10  : 98    1       : 12
##  6/23/2016: 65    14     : 65    2:376      WH12   : 86    2       : 12
##  6/25/2016: 58    16     : 58               WHSR9  : 84    3       : 12
##  6/27/2016: 56    18     : 56               CC6    : 74    4       : 12
##  6/29/2016: 54    19     : 54               CH5    : 69    5       : 12
##  6/26/2016: 51    17     : 51               EH4    : 67    6       : 12
##  (Other)  :437    (Other):437              (Other):313    (Other):719
##  Heat         Volume           trans.vol
##  0:399   Min.    :0.01515   Min.    :-1.8195
##  1:392   1st Qu.:0.07576    1st Qu.:-1.1206
##          Median :0.16364    Median :-0.7861
##          Mean    :0.27276   Mean    :-0.7961
##          3rd Qu.:0.38182    3rd Qu.:-0.4181
##          Max.    :1.96875   Max.    : 0.2942
##
```

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

```
## Source: local data frame [2 x 3]
##
##     Heat    meanVol   sdVolume
##    (fctr)     (dbl)      (dbl)
## 1       0 0.3143729 0.3460375
## 2       1 0.2304042 0.2447087
```

```
summary(sugar.buck)
```

```
##          Date       Date.Factor  Year.Factor       Plot      Heat
##  6/24/2016: 58    15     : 58    1:416      WSR10  : 90    0:350
##  6/23/2016: 49    14     : 49    2:296      WHSR9  : 80    1:362
##  6/27/2016: 48    18     : 48               WH12   : 78
##  6/23/2015: 45    6      : 45               CC6    : 71
##  6/29/2016: 44    19     : 44               EH4    : 63
##  6/22/2015: 42    5      : 42               CH5    : 60
##  (Other)  :426    (Other):426              (Other):270
##       BRIX          Mass           trans.mass       trans.conc
##  Min.    : 2.00   Min.    :  1.00   Min.    :1.000   Min.    :   4
##  1st Qu.:48.00    1st Qu.: 73.75    1st Qu.:4.194    1st Qu.:2304
##  Median :55.00    Median :166.50    Median :5.501    Median :3025
##  Mean    :53.33   Mean    :186.62   Mean    :5.341   Mean    :3008
```

```
## 3rd Qu.:62.00    3rd Qu.:299.25    3rd Qu.:6.689    3rd Qu.:3844
## Max.    :76.00    Max.    :425.00   Max.    :7.518   Max.    :5776
##
```
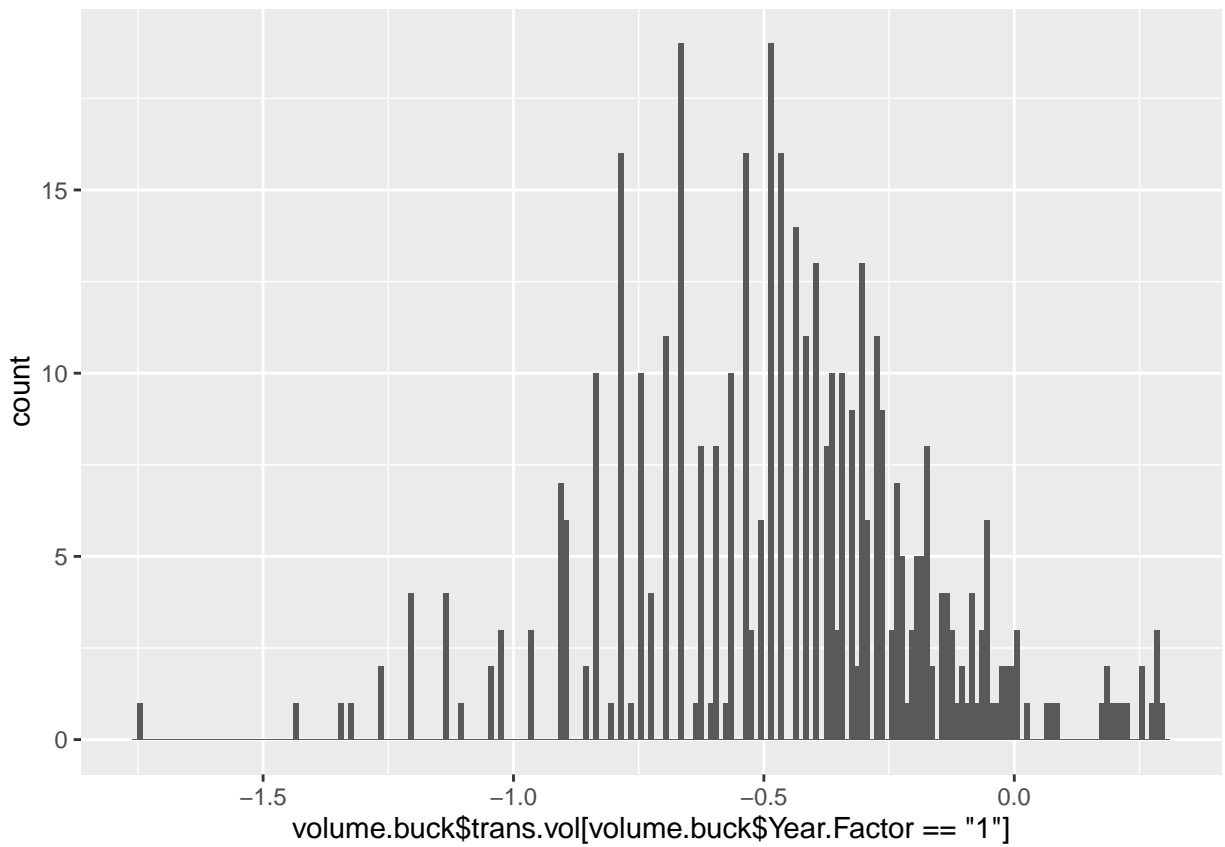
```
summarize(group_by(sugar.buck, Heat), meanBRIX = mean(BRIX), meanMass = mean(Mass), sdBRIX = sd(BRIX), :
```

```
## Source: local data frame [2 x 5]
##
##      Heat meanBRIX meanMass  sdBRIX   sdMass
##   (fctr)    (dbl)    (dbl)   (dbl)    (dbl)
## 1      0 50.32571 194.5971 14.1647 127.3623
## 2      1 56.24309 178.9171 10.5040 120.4917
```
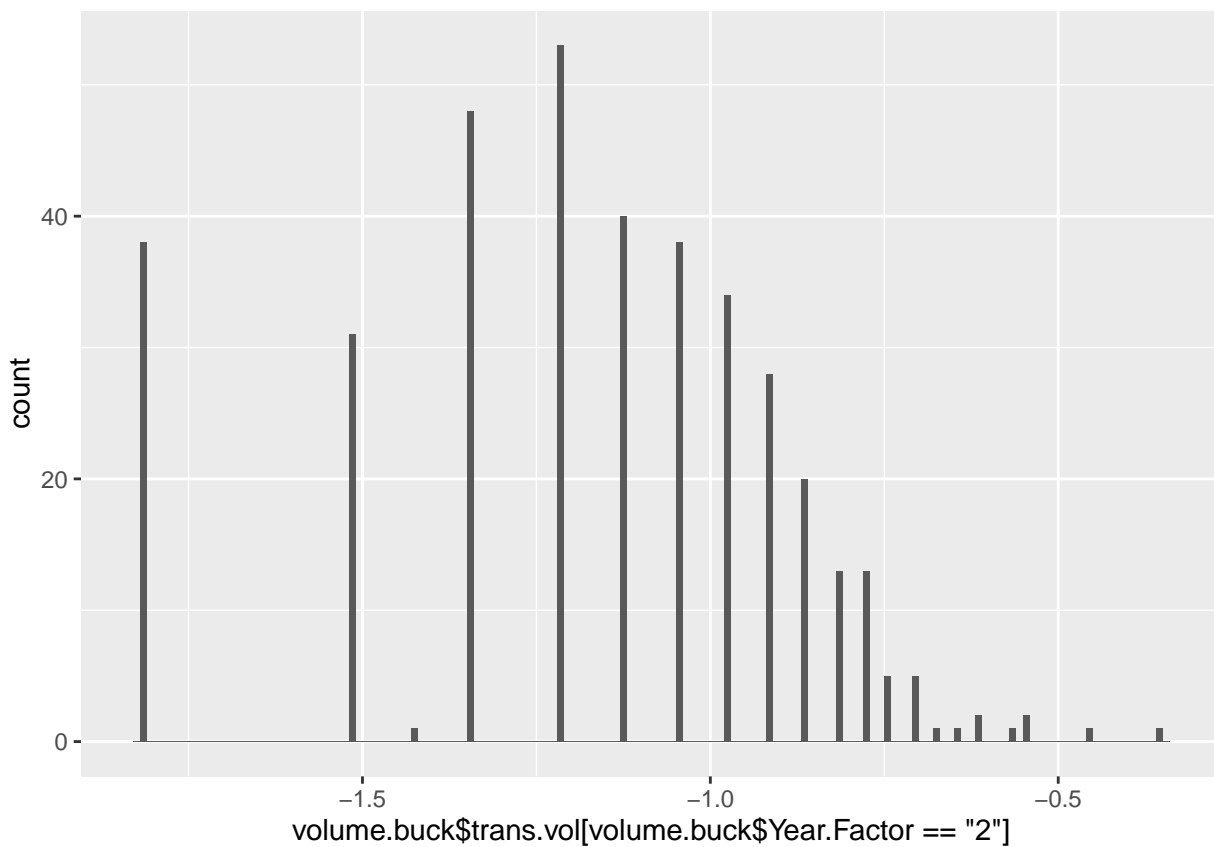
```
qplot(volume.buck$trans.vol, binwidth = 0.01)
```
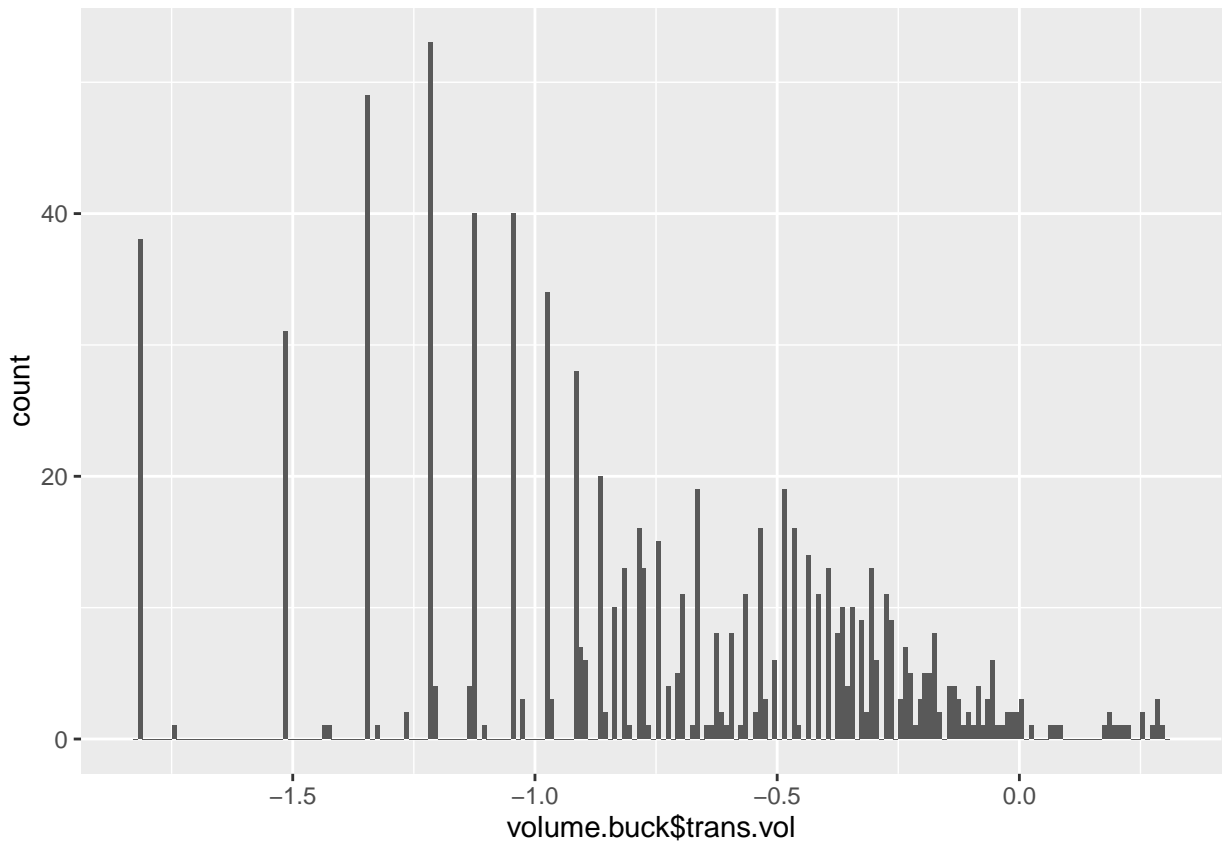


```
qplot(volume.buck$trans.vol[volume.buck$Year.Factor == "1"], binwidth = 0.01)
```

```
qplot(volume.buck$trans.vol[volume.buck$Year.Factor == "2"], binwidth = 0.01)
```
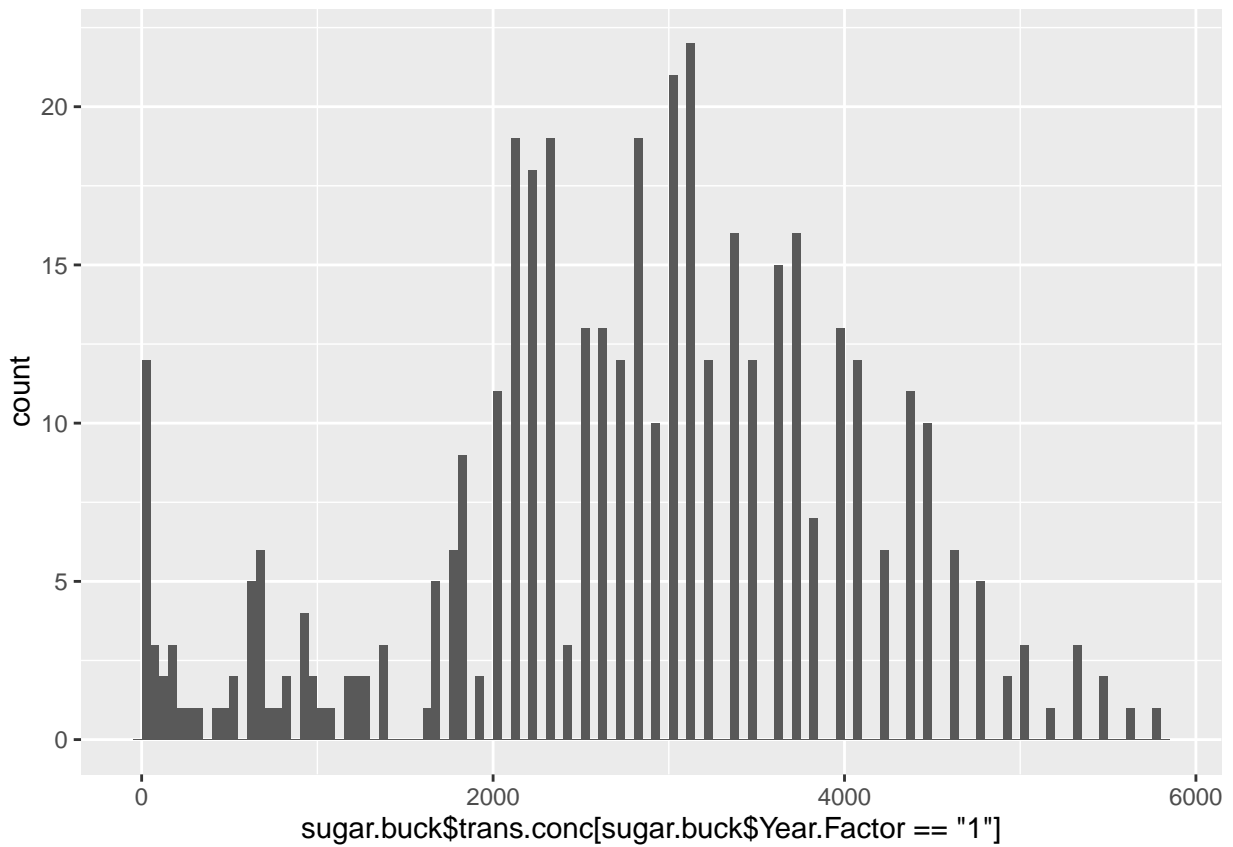
```
qplot(sugar.buck$trans.conc, binwidth = 50)
```
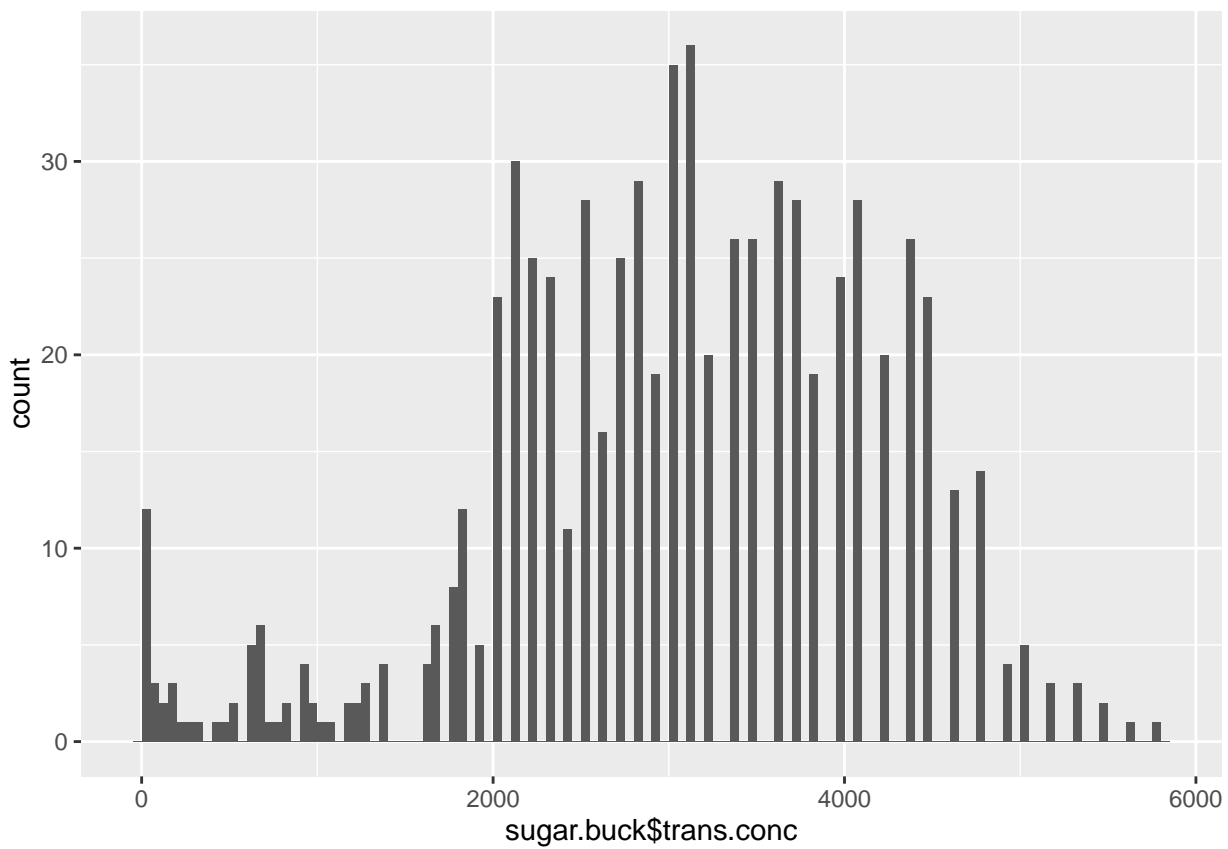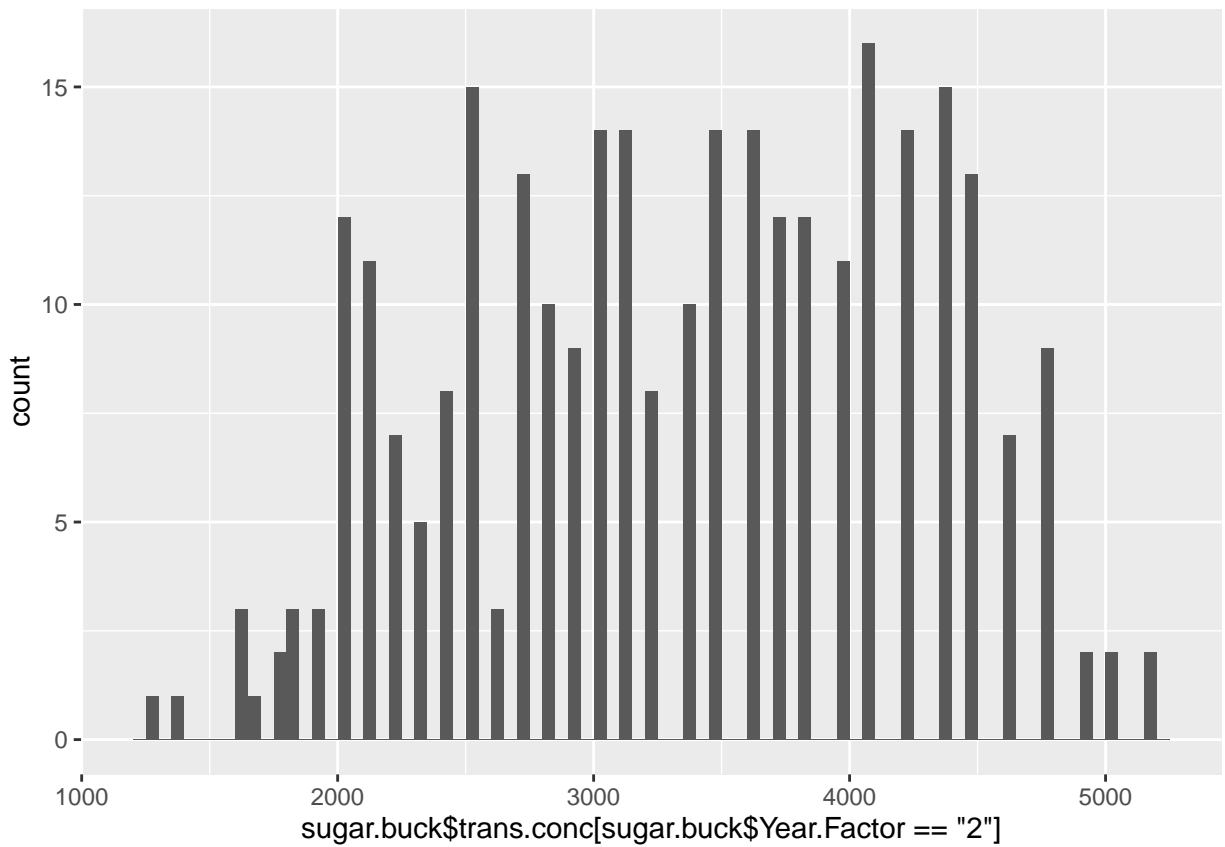
```r
qplot(sugar.buck$trans.conc[sugar.buck$Year.Factor == "1"], binwidth = 50)
```
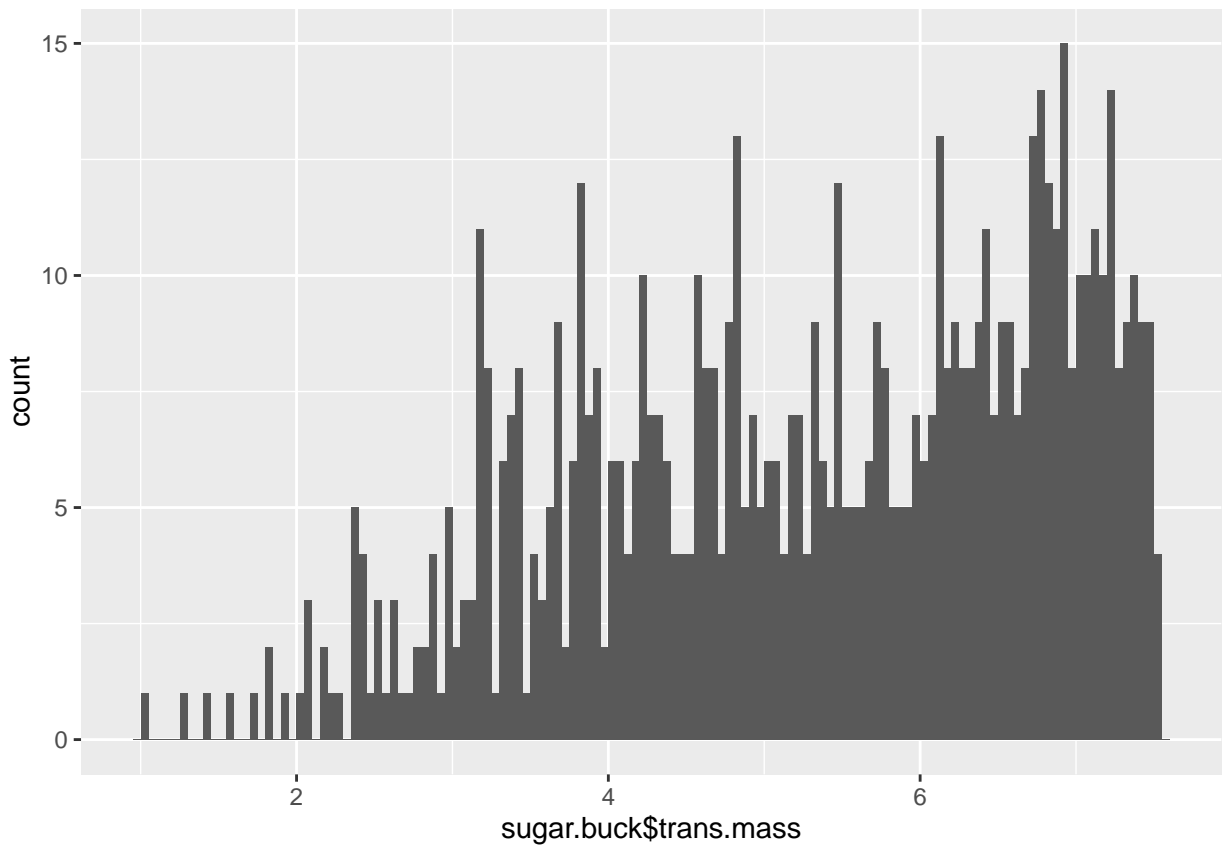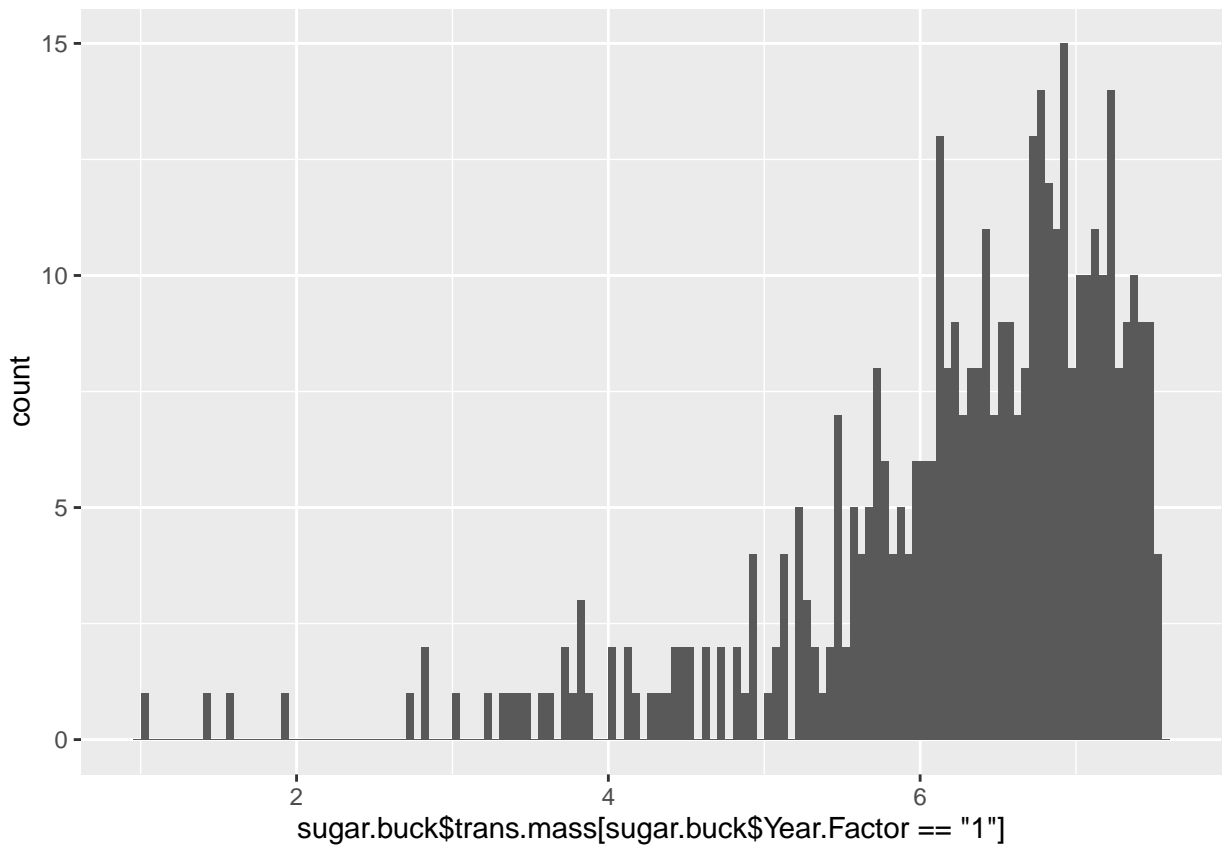
```
qplot(sugar.buck$trans.conc[sugar.buck$Year.Factor == "2"], binwidth = 50)
```
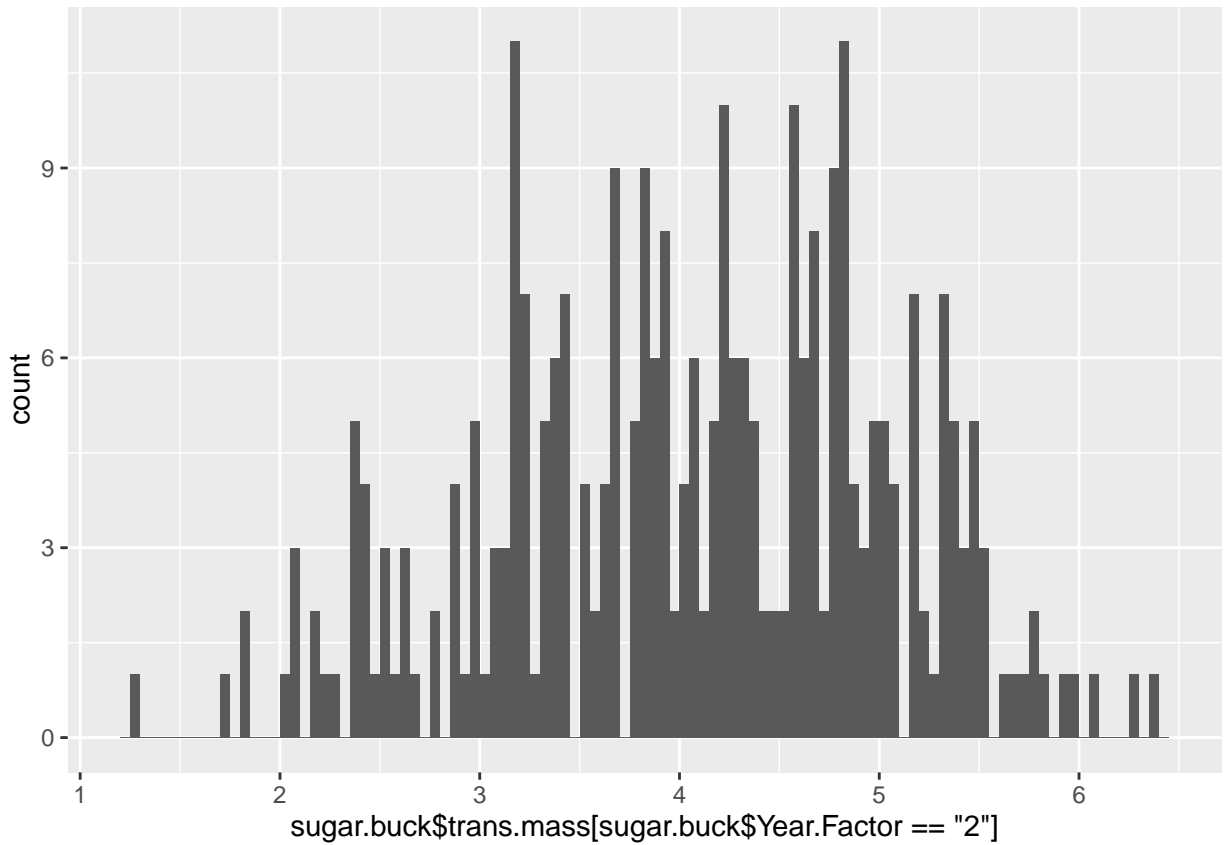
```
qplot(sugar.buck$trans.mass, binwidth = .05)
```
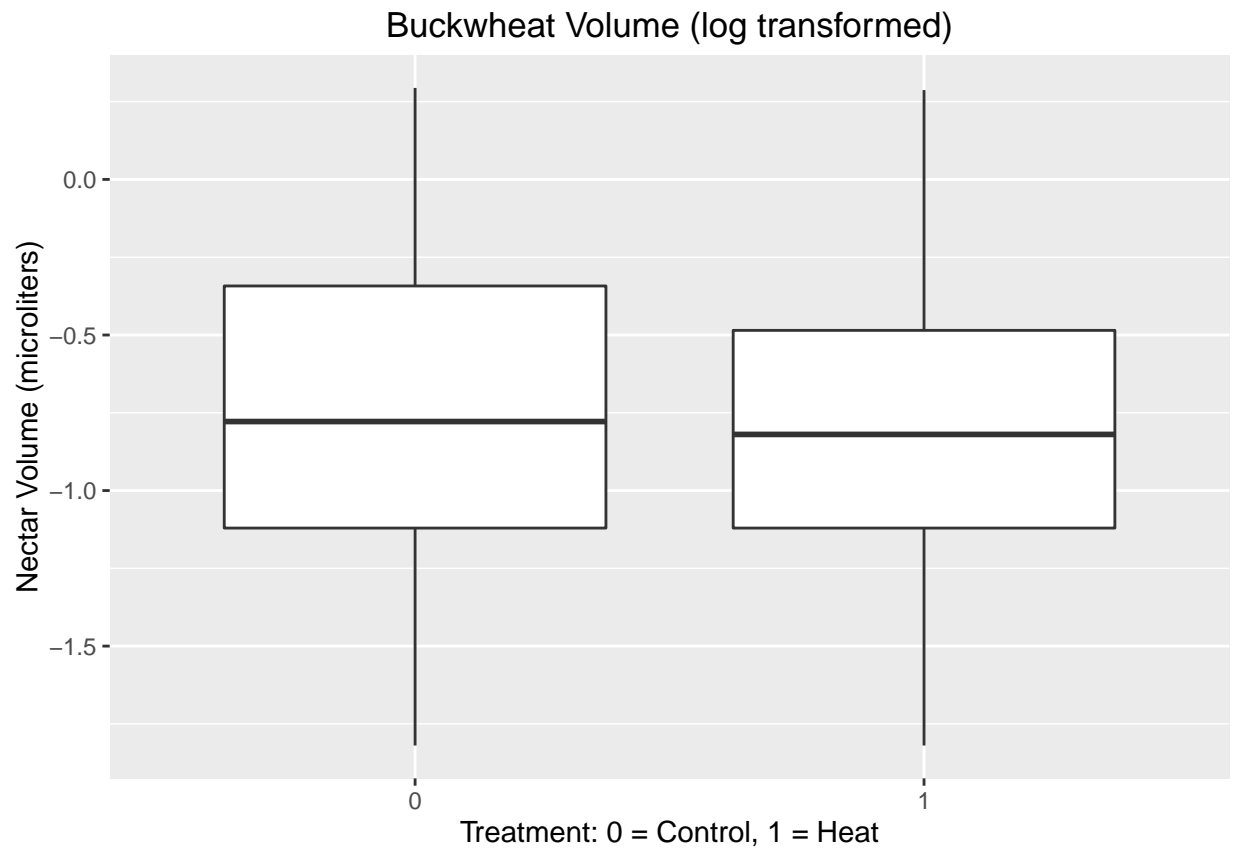
```r
qplot(sugar.buck$trans.mass[sugar.buck$Year.Factor == "1"], binwidth = .05)
```

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

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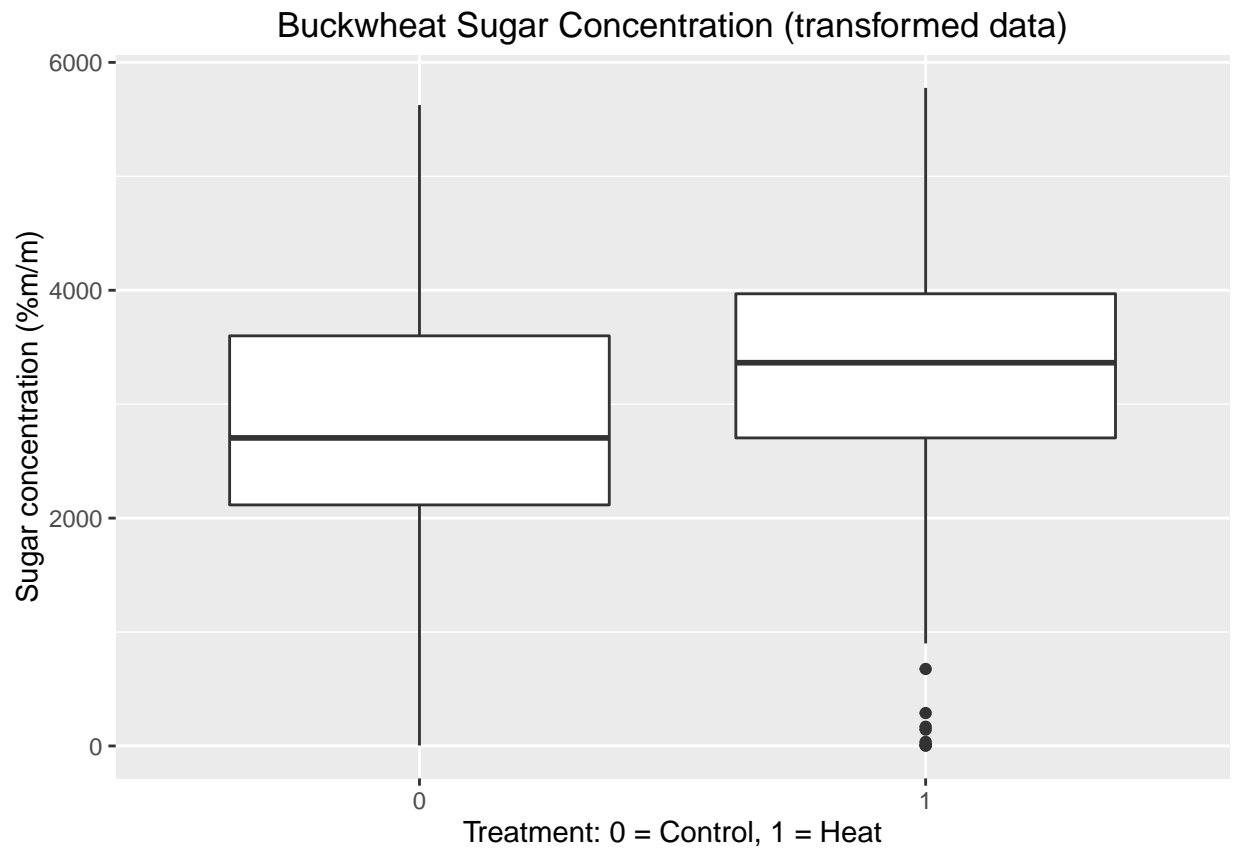
```
ggplot(sugar.buck, aes(x=Heat, y=trans.mass)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Sugar mass (mg)") + ggtitle("Buckwheat Sugar Mass (transformed data)")
```

Buckwheat Sugar Mass (transformed data)
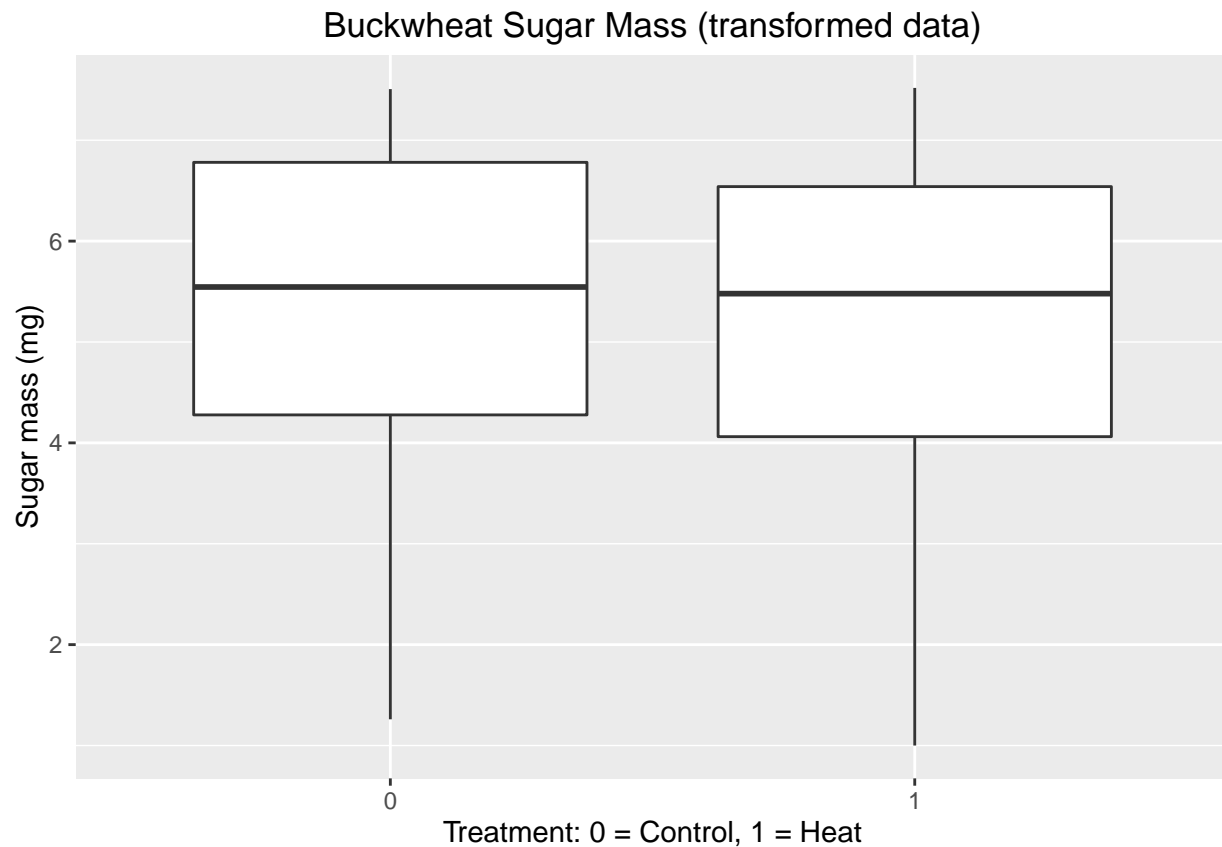

```r
# Test normality for volume by treatment
shapiro.test(as.matrix(volume.buck[volume.buck[,6] == "0", 8])) #control
```

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(volume.buck[volume.buck[, 6] == "0", 8])
## W = 0.97402, p-value = 1.466e-06
```

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

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(volume.buck[volume.buck[, 6] == "1", 8])
## W = 0.98575, p-value = 0.0006724
```

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

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.buck[sugar.buck[, 5] == "0", 9])
## W = 0.97898, p-value = 5.462e-05
```

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

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.buck[sugar.buck[, 5] == "1", 9])
## W = 0.9749, p-value = 6.308e-06
```

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

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.buck[sugar.buck[, 5] == "0", 8])
## W = 0.94445, p-value = 3.48e-10
```

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

```
##
##  Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.buck[sugar.buck[, 5] == "1", 8])
## W = 0.95438, p-value = 3.698e-09
```

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

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value  Pr(>F)
## group  97  1.3996 0.01008 *
##       693
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value    Pr(>F)
## group   1  12.396 0.0004578 ***
##       710
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.0229 0.8796
##       710
```

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

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  volume.buck[, 8] and volume.buck[, 5]
## Fligner-Killeen:med chi-squared = 121.89, df = 97, p-value =
## 0.04453
```

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

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  sugar.buck[, 9] and sugar.buck[, 5]
## Fligner-Killeen:med chi-squared = 9.6306, df = 1, p-value =
## 0.001914
```

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

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  sugar.buck[, 8] and sugar.buck[, 5]
## Fligner-Killeen:med chi-squared = 0.030029, df = 1, p-value =
## 0.8624
```
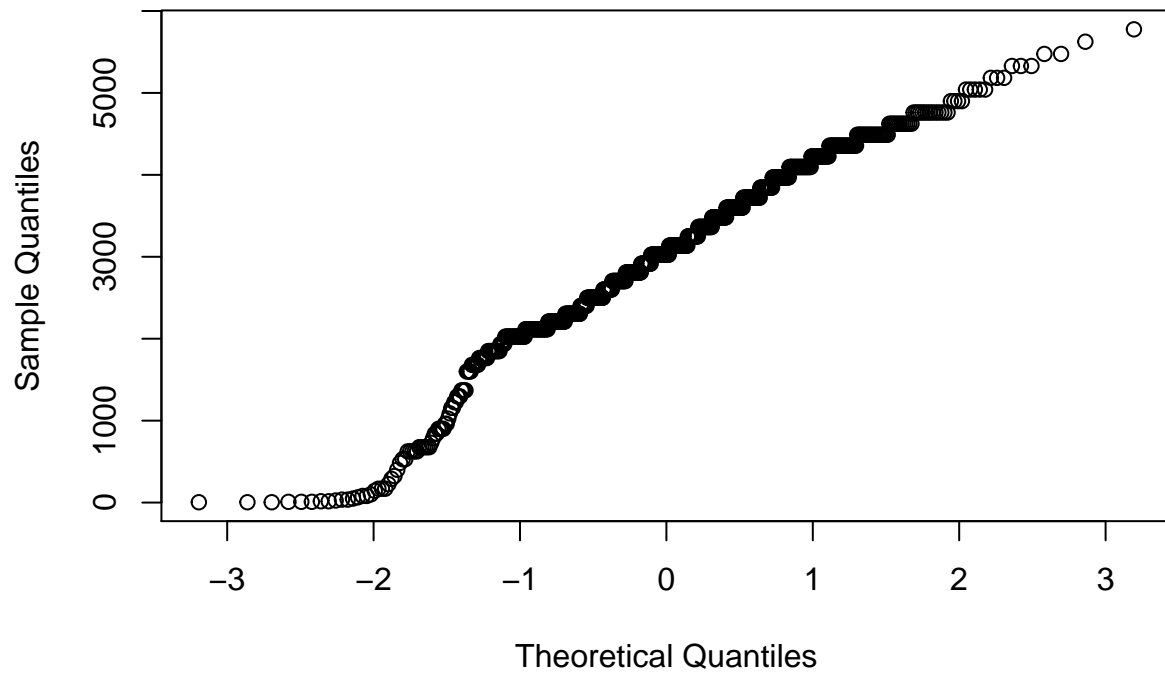
```r
qqnorm(volume.buck$trans.vol)
```

Normal Q–Q Plot
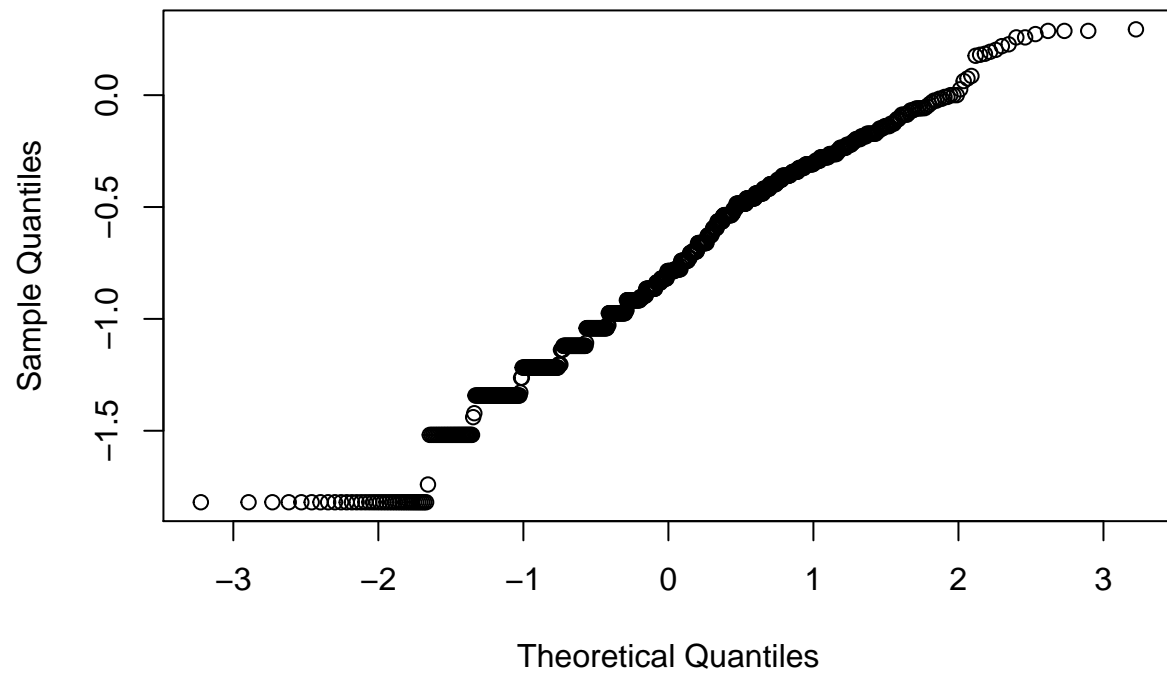

```r
qqnorm(sugar.buck$trans.conc)
```

Normal Q–Q Plot


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

Normal Q−Q Plot