

BalsamrootModels_v1.R

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Wed Sep 28 22:11:07 2016

```
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

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

```

```

library(nlme)

##
## Attaching package: 'nlme'

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

```

```
#####
### 2015-2016 data ###
#####

# Create the data frames

##Read in the data

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

# Balsamroot volume, 2015-2016

volume.balsam <- read.csv("Nectar_Vol_Balsam.csv", header = T, col.names = c("Date", "Date.Factor", "Year.Factor", "Plot", "Heat", "Plant", "Volume", "log.vol"))
volume.balsam <- data.frame(volume.balsam[,1:7])
volume.balsam$Date.Factor <- as.factor(volume.balsam$Date.Factor)
volume.balsam$Year.Factor <- as.factor(volume.balsam$Year.Factor) # 1 = 2015, 2 = 2016
volume.balsam$Heat <- as.factor(volume.balsam$Heat) # 0 = control, 1 = heat
volume.balsam$Plant <- as.factor(paste(volume.balsam$Plot, volume.balsam$Plant, sep="-"))
volume.balsam$Plot <- as.factor(volume.balsam$Plot)
volume.balsam$log.vol <- log(volume.balsam$Volume)
head(volume.balsam)
```

```
##      Date Date.Factor Year.Factor Plot Heat Plant Volume log.vol
## 1 6/2/2015          1          1 WHSR9  1 WHSR9-2 0.4363636 -0.8292794
## 2 6/2/2015          1          1 WHSR9  1 WHSR9-1 0.7272727 -0.3184537
## 3 6/2/2015          1          1 WSR10  0 WSR10-9 0.3636364 -1.0116009
## 4 6/2/2015          1          1 WSR10  0 WSR10-1 0.4909091 -0.7114963
## 5 6/2/2015          1          1 WSR10  0 WSR10-1 0.5272727 -0.6400374
## 6 6/2/2015          1          1 WSR10  0 WSR10-9 1.8909091  0.6370577
```

```
# Balsamroot sugar, 2015-2016

sugar.balsam <- read.csv("Nectar_BRIX_Balsam.csv", header = T, col.names = c("Date", "Date.Factor", "Year.Factor", "Plot", "Heat", "Plant", "BRIX", "Mass"))
sugar.balsam <- data.frame(sugar.balsam[,1:8])
sugar.balsam$Date.Factor <- as.factor(sugar.balsam$Date.Factor)
sugar.balsam$Year.Factor <- as.factor(sugar.balsam$Year.Factor)
sugar.balsam$Heat <- as.factor(sugar.balsam$Heat)
sugar.balsam$Plant <- as.factor(paste(sugar.balsam$Plot, sugar.balsam$Plant, sep="-"))
sugar.balsam$Plot <- as.factor(sugar.balsam$Plot)
sugar.balsam$log.mass <- log(sugar.balsam$Mass)
head(sugar.balsam)
```

```
##      Date Date.Factor Year.Factor Plot Heat Plant BRIX Mass
## 1 6/2/2015          1          1 WSR10  0 WSR10-6 12 0.07079273
## 2 6/2/2015          1          1 WSR10  0 WSR10-4 22 0.10028000
## 3 6/2/2015          1          1 WSR10  0 WSR10-6 42 0.10874182
## 4 6/2/2015          1          1 WHSR9  1 WHSR9-4 18 0.12281818
## 5 6/2/2015          1          1 WHSR9  1 WHSR9-4 27 0.19911818
## 6 6/2/2015          1          1 WSR10  0 WSR10-2 29 0.20286000
##      log.mass
## 1 -2.647999
## 2 -2.299789
## 3 -2.218779
```

```
## 4 -2.097050
## 5 -1.613857
## 6 -1.595239
```

Models

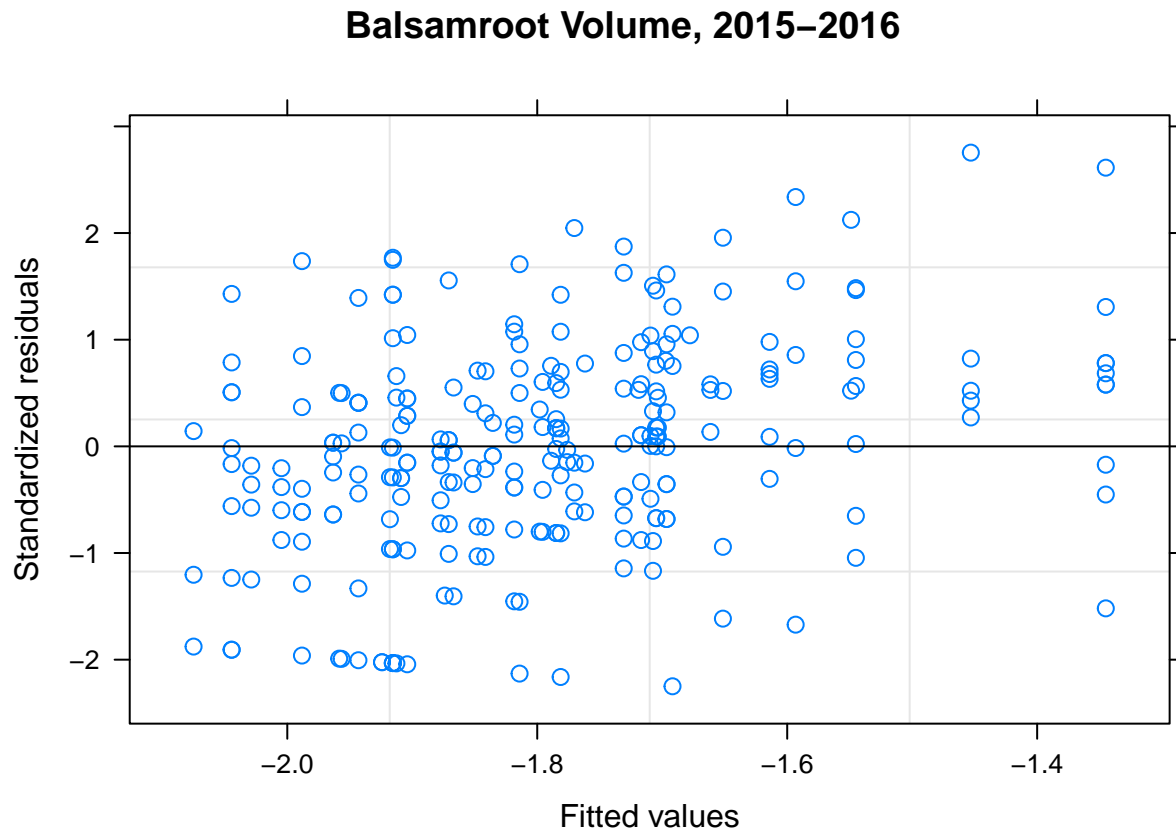
```
vol.balsam.mod <- lme(log.vol ~ Heat, random = ~1 | Plant, data = volume.balsam)
vol.balsam.mod
```

```
## Linear mixed-effects model fit by REML
## Data: volume.balsam
## Log-restricted-likelihood: -386.2819
## Fixed: log.vol ~ Heat
## (Intercept)      Heat1
## -1.76152763 -0.07724062
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev:    0.2876561 1.029337
##
## Number of Observations: 260
## Number of Groups: 53
```

```
summary(vol.balsam.mod)
```

```
## Linear mixed-effects model fit by REML
## Data: volume.balsam
##      AIC      BIC    logLik
##  780.5639 794.7757 -386.2819
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev:    0.2876561 1.029337
##
## Fixed effects: log.vol ~ Heat
##      Value Std.Error DF   t-value p-value
## (Intercept) -1.7615276 0.1141905 207 -15.426223  0.0000
## Heat1       -0.0772406 0.1557420  51  -0.495953  0.6221
## Correlation:
## (Intr)
## Heat1 -0.733
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -2.24958580 -0.61556347  0.02365072  0.58544978  2.75400200
##
## Number of Observations: 260
## Number of Groups: 53
```

```
plot(vol.balsam.mod, main = "Balsamroot Volume, 2015-2016")
```



```
conc.balsam.mod <- lme(BRIX ~ Heat, random = ~1 | Plant, data = sugar.balsam)
conc.balsam.mod
```

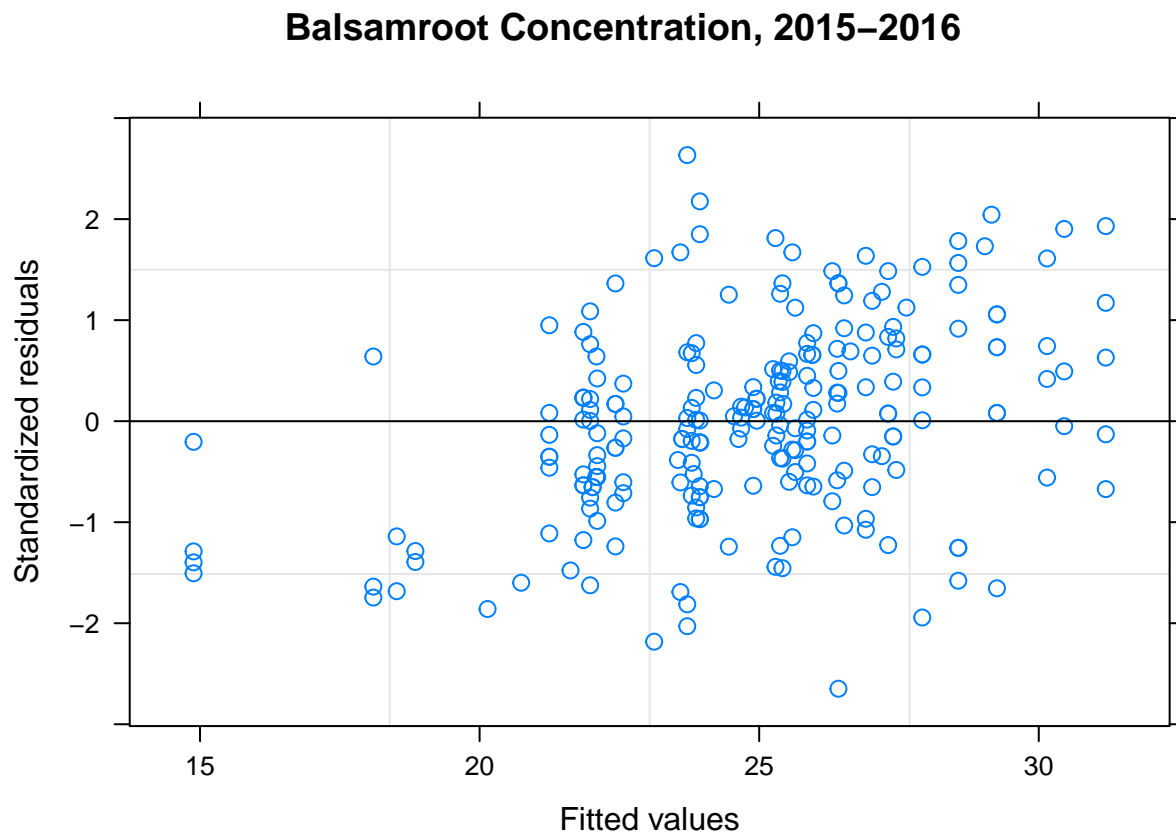
```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam
## Log-restricted-likelihood: -879.4542
## Fixed: BRIX ~ Heat
## (Intercept)      Heat1
## 24.4355773    0.6021936
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev:    4.614124 9.220047
##
## Number of Observations: 237
## Number of Groups: 69
```

```
summary(conc.balsam.mod)
```

```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam
```

```
##           AIC      BIC    logLik
##  1766.908 1780.747 -879.4542
##
## Random effects:
## Formula: ~1 | Plant
##      (Intercept) Residual
## StdDev:    4.614124 9.220047
##
## Fixed effects: BRIX ~ Heat
##              Value Std.Error DF   t-value p-value
## (Intercept) 24.435577  1.258188 168  19.421246  0.0000
## Heat1        0.602194  1.725908  67   0.348914  0.7282
## Correlation:
##      (Intr)
## Heat1 -0.729
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -2.64829218 -0.60645502  0.01368413  0.64851656  2.63402492
##
## Number of Observations: 237
## Number of Groups: 69
```

```
plot(conc.balsam.mod, main = "Balsamroot Concentration, 2015-2016")
```



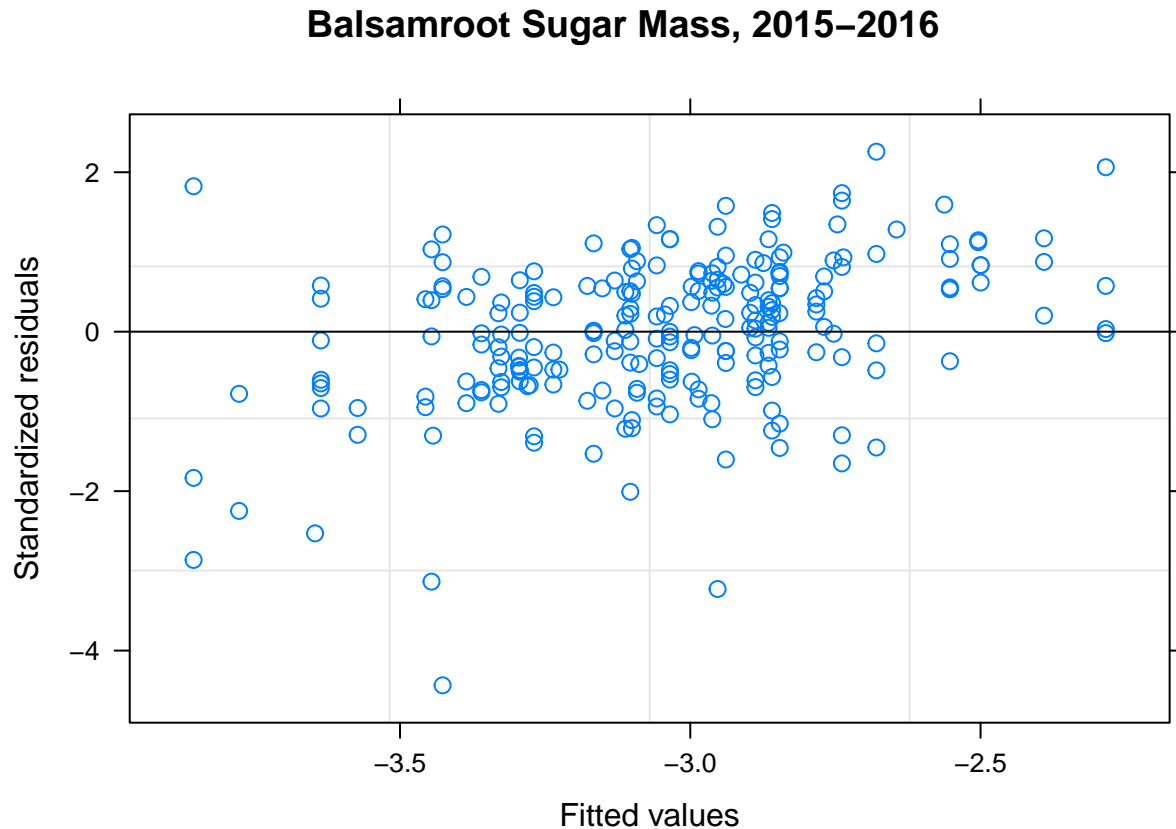
```
mass.balsam.mod <- lme(log.mass ~ Heat, random = ~1 | Plant, data = sugar.balsam)
mass.balsam.mod
```

```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam
## Log-restricted-likelihood: -323.7359
## Fixed: log.mass ~ Heat
## (Intercept)      Heat1
## -3.1003060    0.1189689
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev:    0.4741969 0.8554693
##
## Number of Observations: 237
## Number of Groups: 69
```

```
summary(mass.balsam.mod)
```

```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam
##      AIC      BIC    logLik
## 655.4717 669.3101 -323.7359
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev:    0.4741969 0.8554693
##
## Fixed effects: log.mass ~ Heat
##              Value Std.Error DF   t-value p-value
## (Intercept) -3.1003060 0.1226520 168 -25.277264  0.0000
## Heat1        0.1189689 0.1684721  67   0.706164  0.4825
## Correlation:
## (Intr)
## Heat1 -0.728
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -4.43568355 -0.56834625  0.04871242  0.61587880  2.25779805
##
## Number of Observations: 237
## Number of Groups: 69
```

```
plot(mass.balsam.mod, main = "Balsamroot Sugar Mass, 2015-2016")
```



```
#####
### 2016 only data ###
#####

volume.balsam2016 <- as.data.frame(volume.balsam[volume.balsam$Year.Factor == "2",])
sugar.balsam2016 <- as.data.frame((sugar.balsam[sugar.balsam$Year.Factor == "2",]))

vol.2016.mod <- lme(log.vol ~ Heat, random = ~1 | Plant, data = volume.balsam2016)
vol.2016.mod

## Linear mixed-effects model fit by REML
## Data: volume.balsam2016
## Log-restricted-likelihood: -207.5581
## Fixed: log.vol ~ Heat
## (Intercept)      Heat1
## -2.0930138 -0.1330206
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev: 0.3283418 0.7713958
##
## Number of Observations: 168
```



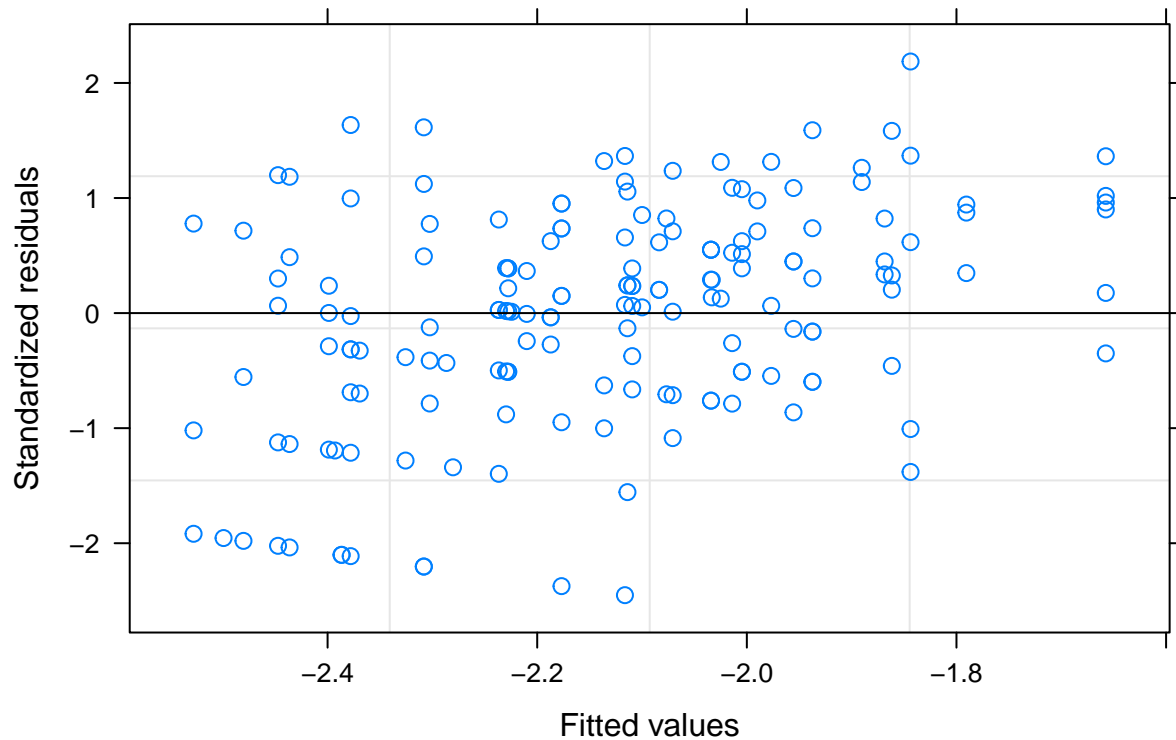
```
## Number of Groups: 47
```

```
summary(vol.2016.mod)
```

```
## Linear mixed-effects model fit by REML
## Data: volume.balsam2016
##      AIC      BIC    logLik
##  423.1162 435.5641 -207.5581
##
## Random effects:
## Formula: ~1 | Plant
##      (Intercept) Residual
## StdDev:   0.3283418 0.7713958
##
## Fixed effects: log.vol ~ Heat
##              Value Std.Error DF   t-value p-value
## (Intercept) -2.0930138 0.1126450 121 -18.580620  0.0000
## Heat1       -0.1330206 0.1581196  45  -0.841266  0.4046
## Correlation:
##      (Intr)
## Heat1 -0.712
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -2.4514416 -0.5483168  0.1312750  0.7101137  2.1864722
##
## Number of Observations: 168
## Number of Groups: 47
```

```
plot(vol.2016.mod, main = "Balsamroot Volume (log transformed), 2016 only")
```

Balsamroot Volume (log transformed), 2016 only



```
conc.2016.mod <- lme(BRIX ~ Heat, random = ~1 | Plant, data = sugar.balsam2016)
conc.2016.mod
```

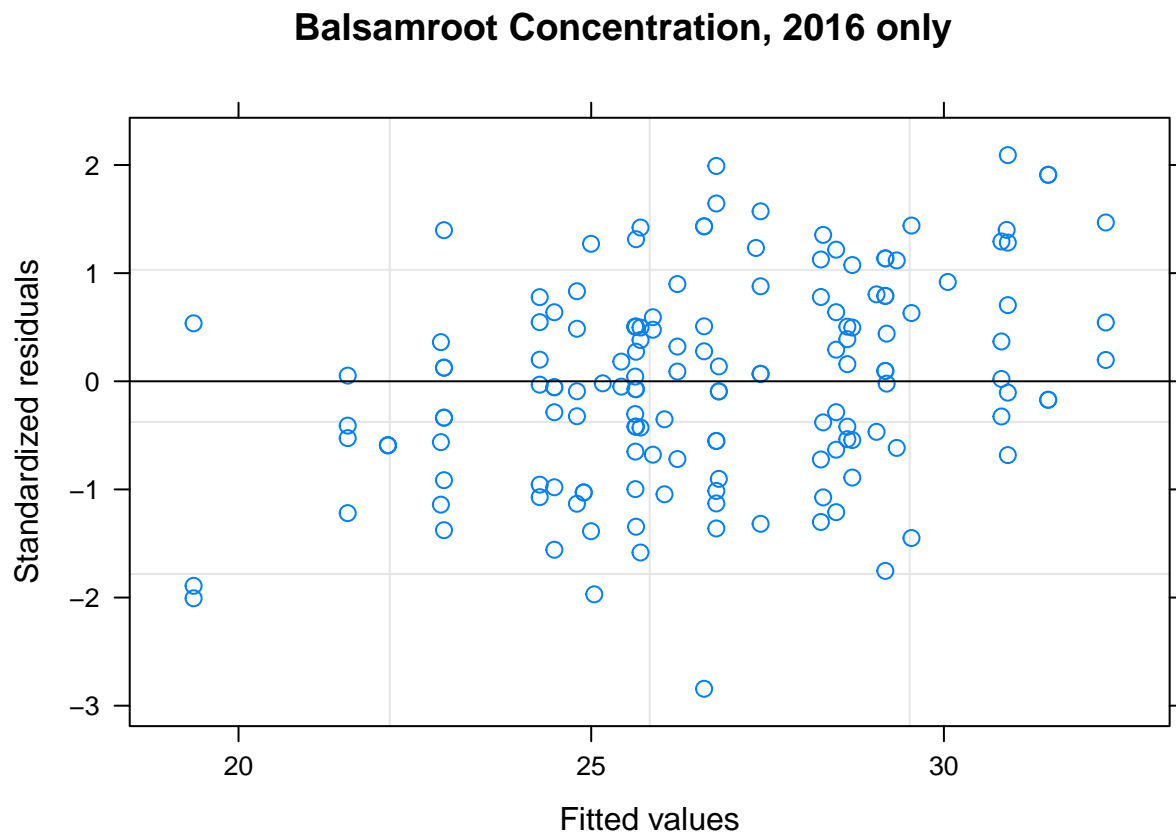
```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam2016
## Log-restricted-likelihood: -547.7116
## Fixed: BRIX ~ Heat
## (Intercept)      Heat1
##    25.19662     3.26481
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev:    3.873996 8.650767
##
## Number of Observations: 151
## Number of Groups: 44
```

```
summary(conc.2016.mod)
```

```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam2016
##      AIC      BIC    logLik
## 1103.423 1115.439 -547.7116
##
```

```
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev: 3.873996 8.650767
##
## Fixed effects: BRIX ~ Heat
## Value Std.Error DF t-value p-value
## (Intercept) 25.19662 1.333589 107 18.893840 0.0000
## Heat1 3.26481 1.887999 42 1.729243 0.0911
## Correlation:
## (Intr)
## Heat1 -0.706
##
## Standardized Within-Group Residuals:
## Min Q1 Med Q3 Max
## -2.8437031 -0.6039320 -0.0189322 0.6118382 2.0916004
##
## Number of Observations: 151
## Number of Groups: 44
```

```
plot(conc.2016.mod, main = "Balsamroot Concentration, 2016 only")
```



```
mass.2016.mod <- lme(log.mass ~ Heat, random = ~1 | Plant, data = sugar.balsam2016)
mass.2016.mod
```

```
## Linear mixed-effects model fit by REML
```

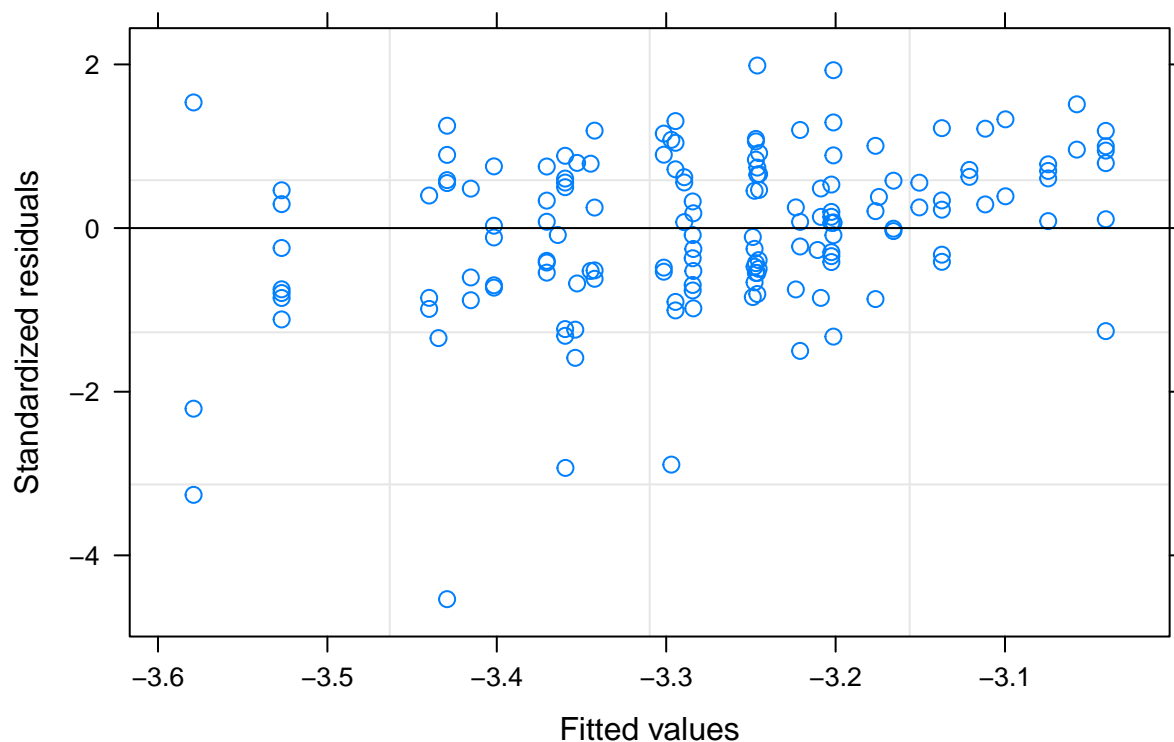
```
## Data: sugar.balsam2016
## Log-restricted-likelihood: -193.2742
## Fixed: log.mass ~ Heat
## (Intercept)      Heat1
## -3.3592592    0.1635761
##
## Random effects:
## Formula: ~1 | Plant
##      (Intercept) Residual
## StdDev:    0.216143 0.8360971
##
## Number of Observations: 151
## Number of Groups: 44
```

```
summary(mass.2016.mod)
```

```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam2016
##      AIC      BIC    logLik
## 394.5485 406.5643 -193.2742
##
## Random effects:
## Formula: ~1 | Plant
##      (Intercept) Residual
## StdDev:    0.216143 0.8360971
##
## Fixed effects: log.mass ~ Heat
##              Value Std.Error DF   t-value p-value
## (Intercept) -3.359259 0.1070051 107 -31.393439  0.0000
## Heat1        0.163576 0.1539085  42   1.062814  0.2939
## Correlation:
##      (Intr)
## Heat1 -0.695
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -4.53522618 -0.54644246  0.08487672  0.67872904  1.98670435
##
## Number of Observations: 151
## Number of Groups: 44
```

```
plot(mass.2016.mod, main = "Balsamroot Mass (log transformed), 2016 only")
```

Balsamroot Mass (log transformed), 2016 only



```
#####
### 2015 only data ###
#####

volume.balsam2015 <- as.data.frame(volume.balsam[volume.balsam$Year.Factor == "1",])
sugar.balsam2015 <- as.data.frame((sugar.balsam[sugar.balsam$Year.Factor == "1",]))

vol.2015.mod <- lme(log.vol ~ Heat, random = ~1 | Plant, data = volume.balsam2015)
vol.2015.mod
```

```
## Linear mixed-effects model fit by REML
## Data: volume.balsam2015
## Log-restricted-likelihood: -143.9377
## Fixed: log.vol ~ Heat
## (Intercept)      Heat1
## -0.8608383 -0.4662115
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev: 0.05041809 1.147492
##
## Number of Observations: 92
## Number of Groups: 29
```

```
Anova(vol.2015.mod)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: log.vol
##      Chisq Df Pr(>Chisq)
## Heat 3.3604 1    0.06678 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(vol.2015.mod)
```

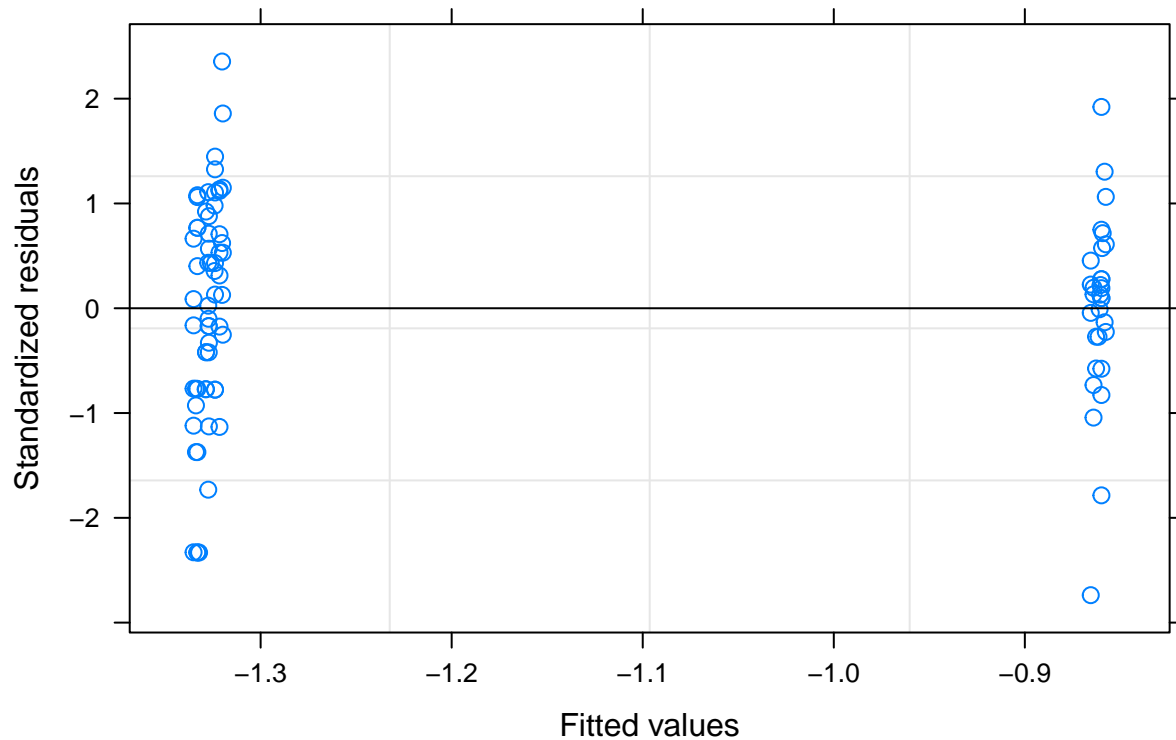
```
##              numDF denDF  F-value p-value
## (Intercept)      1     63 94.71549  <.0001
## Heat            1     27  3.36044  0.0778
```

```
summary(vol.2015.mod) # p-value = 0.0778
```

```
## Linear mixed-effects model fit by REML
## Data: volume.balsam2015
##      AIC      BIC    logLik
## 295.8754 305.8746 -143.9377
##
## Random effects:
## Formula: ~1 | Plant
##      (Intercept) Residual
## StdDev:  0.05041809 1.147492
##
## Fixed effects: log.vol ~ Heat
##              Value Std.Error DF   t-value p-value
## (Intercept) -0.8608383 0.2070830 63 -4.156973  0.0001
## Heat1       -0.4662115 0.2543224 27 -1.833151  0.0778
## Correlation:
##      (Intr)
## Heat1 -0.814
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -2.7380062 -0.6161811  0.1285882  0.6744967  2.3546244
##
## Number of Observations: 92
## Number of Groups: 29
```

```
plot(vol.2015.mod, main = "Balsamroot Volume (log transformed), 2015 only")
```

Balsamroot Volume (log transformed), 2015 only



```
conc.2015.mod <- lme(BRIX ~ Heat, random = ~1 | Plant, data = sugar.balsam2015)
conc.2015.mod
```

```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam2015
## Log-restricted-likelihood: -318.9947
## Fixed: BRIX ~ Heat
## (Intercept)      Heat1
## 22.334385    -0.504886
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev:      6.15416 8.824561
##
## Number of Observations: 86
## Number of Groups: 44
```

```
Anova(conc.2015.mod)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: BRIX
##      Chisq Df Pr(>Chisq)
## Heat 0.0311 1    0.8601
```

```
anova(conc.2015.mod)
```

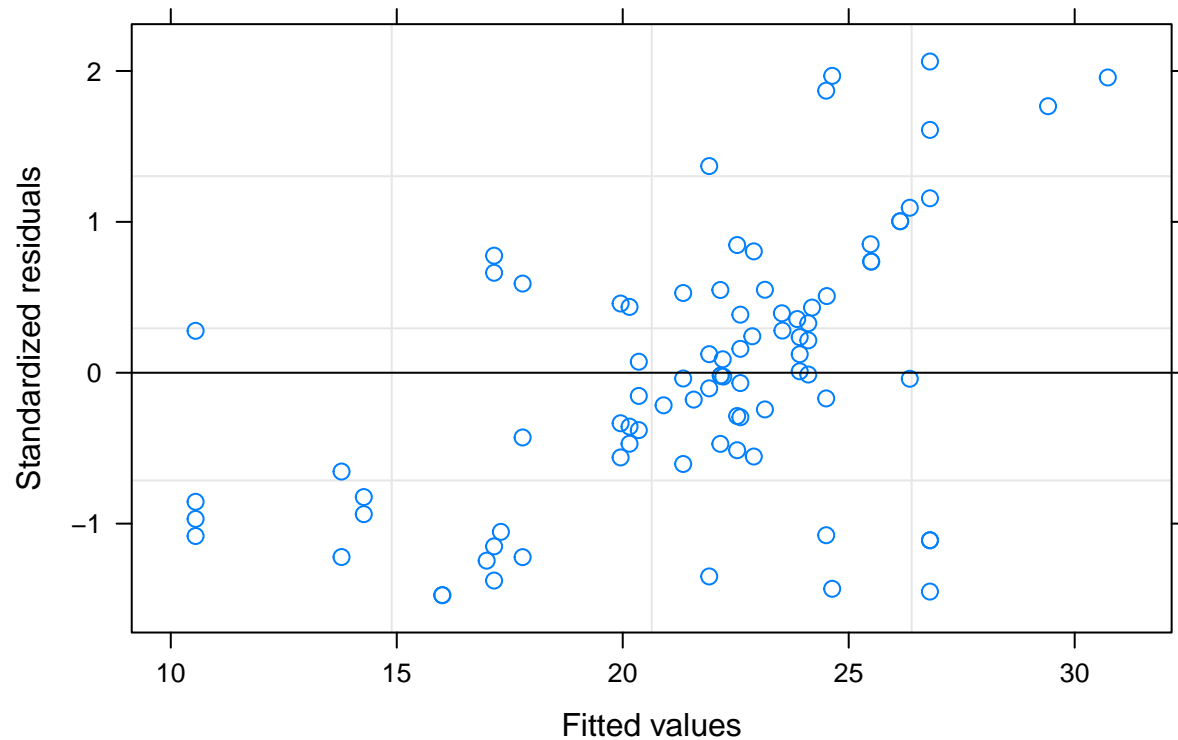
```
##           numDF denDF   F-value p-value
## (Intercept)      1    42 254.24517 <.0001
## Heat            1    42   0.03106  0.861
```

```
summary(conc.2015.mod)
```

```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam2015
##      AIC      BIC    logLik
## 645.9894 655.7126 -318.9947
##
## Random effects:
## Formula: ~1 | Plant
##      (Intercept) Residual
## StdDev:      6.15416 8.824561
##
## Fixed effects: BRIX ~ Heat
##              Value Std.Error DF   t-value p-value
## (Intercept) 22.334385  2.279933 42   9.796071   0.000
## Heat1       -0.504886  2.864982 42  -0.176227   0.861
## Correlation:
##      (Intr)
## Heat1 -0.796
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.47406070 -0.55975374 -0.01920842  0.52332838  2.06270618
##
## Number of Observations: 86
## Number of Groups: 44
```

```
plot(conc.2015.mod, main = "Balsamroot Concentration, 2015 only")
```


Balsamroot Concentration, 2015 only



```
mass.2015.mod <- lme(log.mass ~ Heat, random = ~1 | Plant, data = sugar.balsam2015)
mass.2015.mod
```

```
## Linear mixed-effects model fit by REML
## Data: sugar.balsam2015
## Log-restricted-likelihood: -119.2367
## Fixed: log.mass ~ Heat
## (Intercept)      Heat1
## -2.5405221  -0.1253568
##
## Random effects:
## Formula: ~1 | Plant
## (Intercept) Residual
## StdDev:    0.5577253 0.8236624
##
## Number of Observations: 86
## Number of Groups: 44
```

```
Anova(mass.2015.mod)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: log.mass
##      Chisq Df Pr(>Chisq)
## Heat 0.2258 1    0.6347
```

```
anova(mass.2015.mod)
```

```
##           numDF denDF  F-value p-value
## (Intercept)      1    42 425.2963  <.0001
## Heat            1    42   0.2258  0.6371
```

```
summary(mass.2015.mod)
```

```
## Linear mixed-effects model fit by REML
## Data:  sugar.balsam2015
##      AIC      BIC    logLik
## 246.4734 256.1966 -119.2367
##
## Random effects:
## Formula: ~1 | Plant
##      (Intercept)  Residual
## StdDev:    0.5577253 0.8236624
##
## Fixed effects: log.mass ~ Heat
##              Value Std.Error DF   t-value p-value
## (Intercept) -2.5405221 0.2101224 42 -12.090677  0.0000
## Heat1       -0.1253568 0.2638057 42  -0.475186  0.6371
## Correlation:
##      (Intr)
## Heat1 -0.797
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.2932310 -0.3268951  0.1582288  0.5880608  1.8762142
##
## Number of Observations: 86
## Number of Groups: 44
```

```
plot(mass.2015.mod, main = "Balsamroot Mass (log transformed), 2015 only")
```

Balsamroot Mass (log transformed), 2015 only

