BalsamModsDiag.R

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```r
library(ggplot2)
library(lme4)
```

```
## Loading required package: Matrix
```

```r
library(nlme)
```

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

```
## The following object is masked from 'package:lme4':
##
##     lmList
```

```r
library(lubridate)
```

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

```
##
## Attaching package: 'lubridate'
```

```
## The following object is masked from 'package:base':
##
##     date
```

```r
library(influence.ME)
```

```
## Warning: package 'influence.ME' was built under R version 3.2.5
```

```
##
## Attaching package: 'influence.ME'
```

```
## The following object is masked from 'package:stats':
##
##     influence
```

```r
setwd("D:/Iowa State University/Debinski Lab/Nectar data/MAL")

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)
balsvolboth$year <- as.factor(year(balsvolboth$date))
```
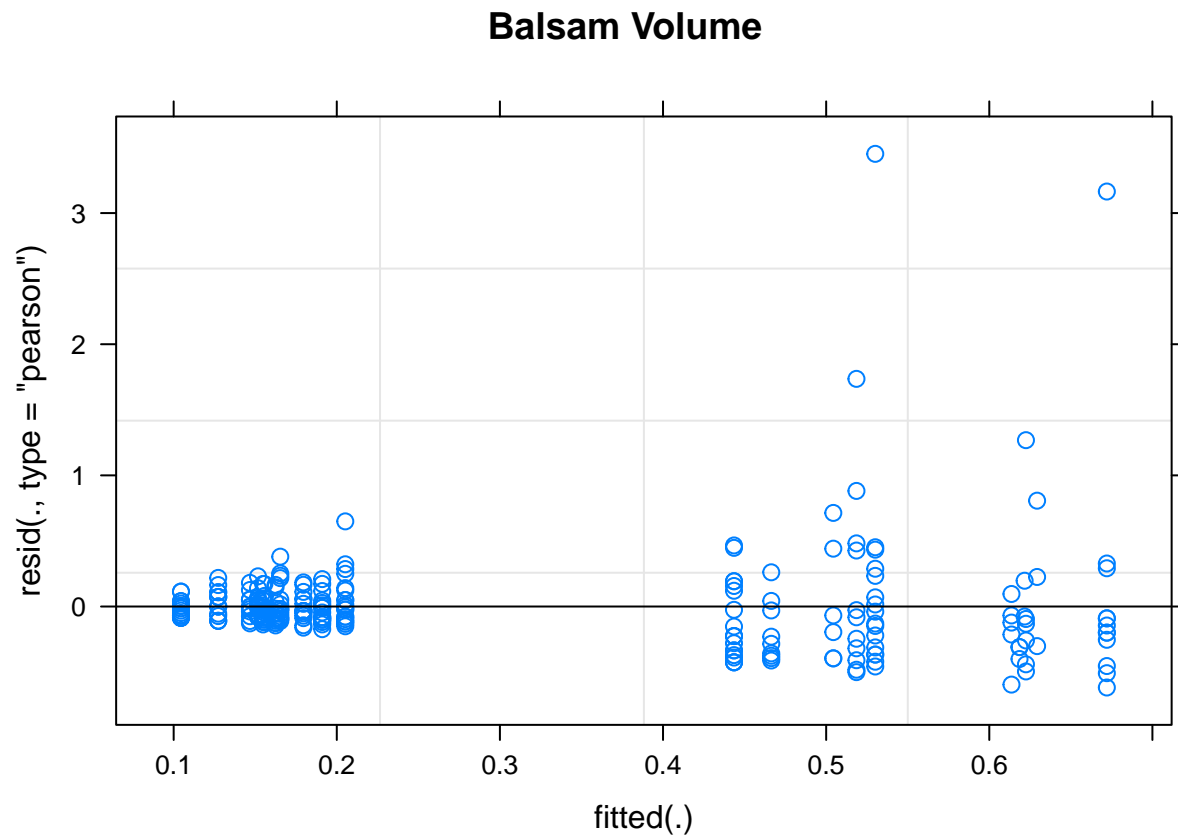
```
balssug15 <- read.csv("nectar analysis/data files/balssugar15.csv", header = T)
balssug16 <- read.csv("nectar analysis/data files/balssugar16.csv", header = T)
balssugboth <- rbind(balssug15,balssug16)
balssugboth$year <- as.factor(year(balssugboth$date))

modvol <- lmer(volume ~ treatment * year + (1|plot/plant), data = balsvolboth)
plot(modvol, main = "Balsam Volume")
```
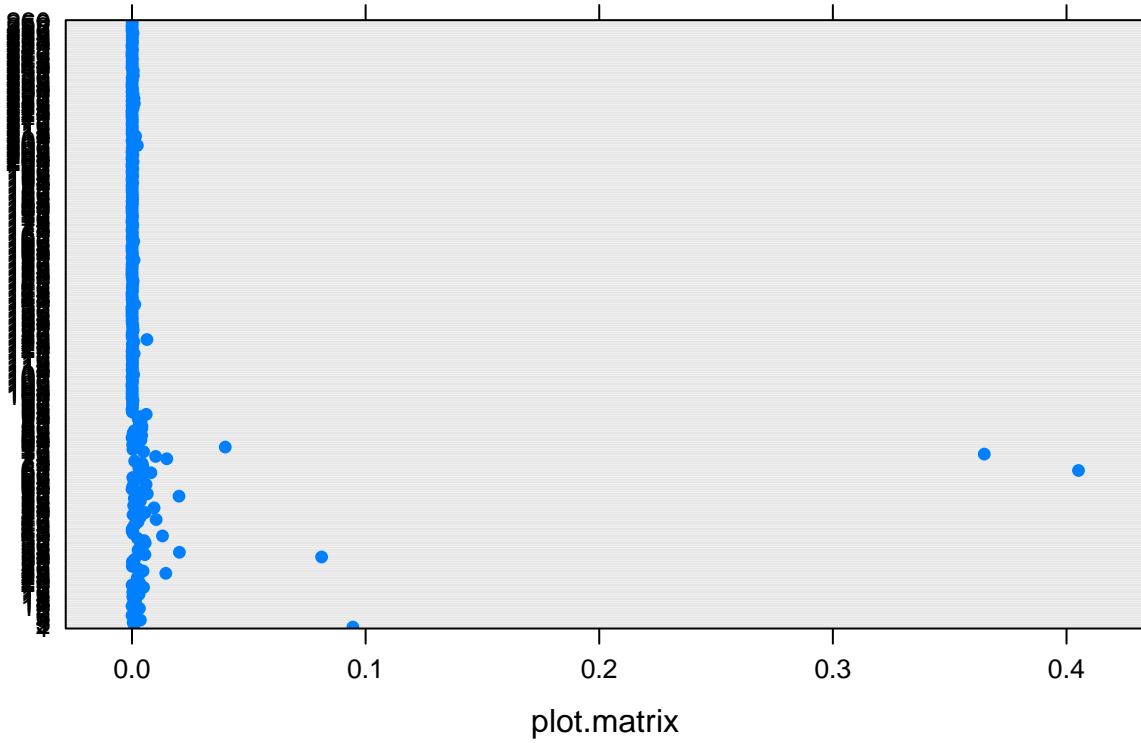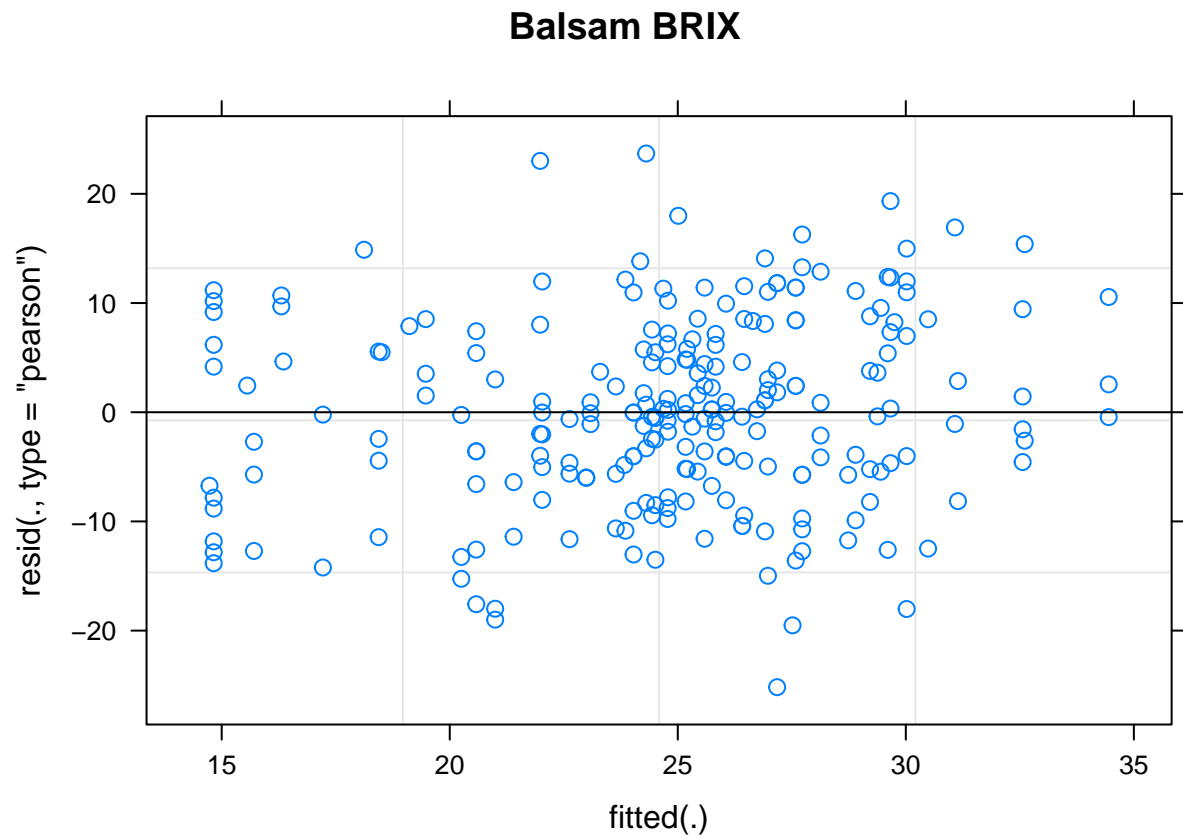
Balsam Volume


```
inflvol <- influence(modvol, obs = T)
plot(inflvol, which = "cook", main = "Balsam Volume")
```

Balsam Volume

plot.matrix
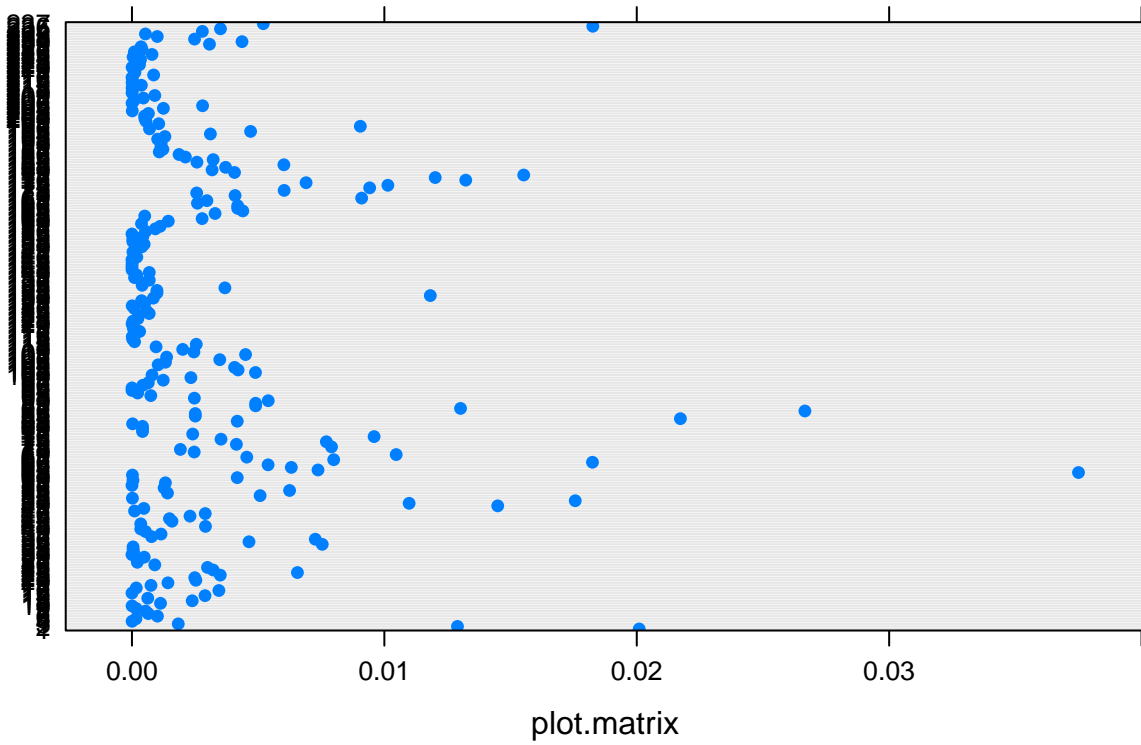
```
modBRIX <- lmer(BRIX ~ treatment * year + (1|plot/plant), data = balssugboth)
plot(modBRIX, main = "Balsam BRIX")
```
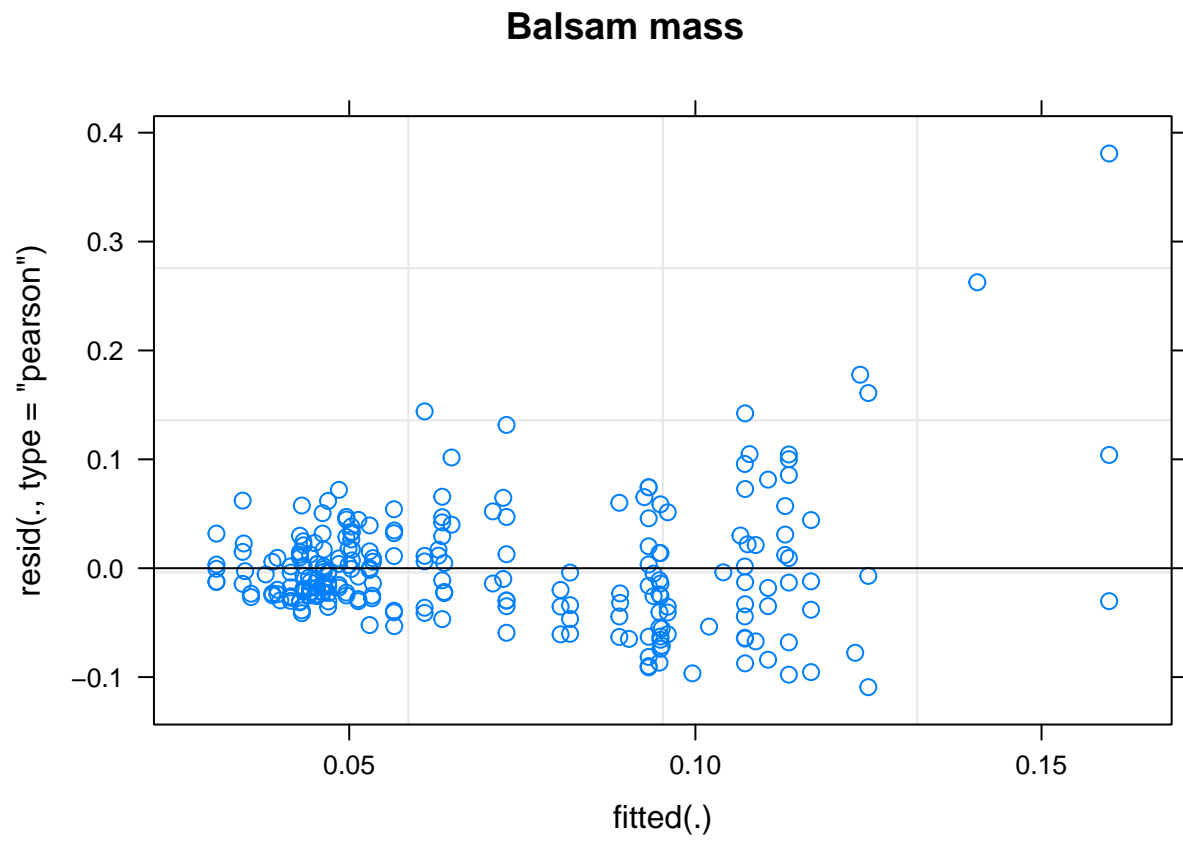
Balsam BRIX


```
inflBRIX <- influence(modBRIX, obs = T)
plot(inflBRIX, which = "cook", main = "Balsam BRIX")
```

Balsam BRIX

plot.matrix

```
modmass <- lmer(mass ~ treatment * year + (1|plot/plant), data = balssugboth)
plot(modmass, main = "Balsam mass")
```

Balsam mass


```
inflmass <- influence(modmass, obs = T)
plot(inflmass, which = "cook", main = "Balsam mass")
```

Balsam mass

plot.matrix