TotalFlowers.R

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```r
library(lme4)
```

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

```r
library(lsmeans)
```

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

```
## Loading required package: estimability
```

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

```r
library(ggplot2)
library(blmeco)
```

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

```
## Loading required package: MASS
```

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

#Create df
flowers <- read.csv("nectar analysis/data files/raw data/Balsamroot phenology/TotalFlowersPerPlant.csv"

flowers$total <- apply(flowers[4:5], 1, sum)
names(flowers)[4:5] <- c("year15", "year16")
flowers$plot <- as.factor(flowers$plot)
flowers$treatment <- as.factor(flowers$treatment)
flowers$plantid <- as.factor(flowers$plantid)
head(flowers)
```
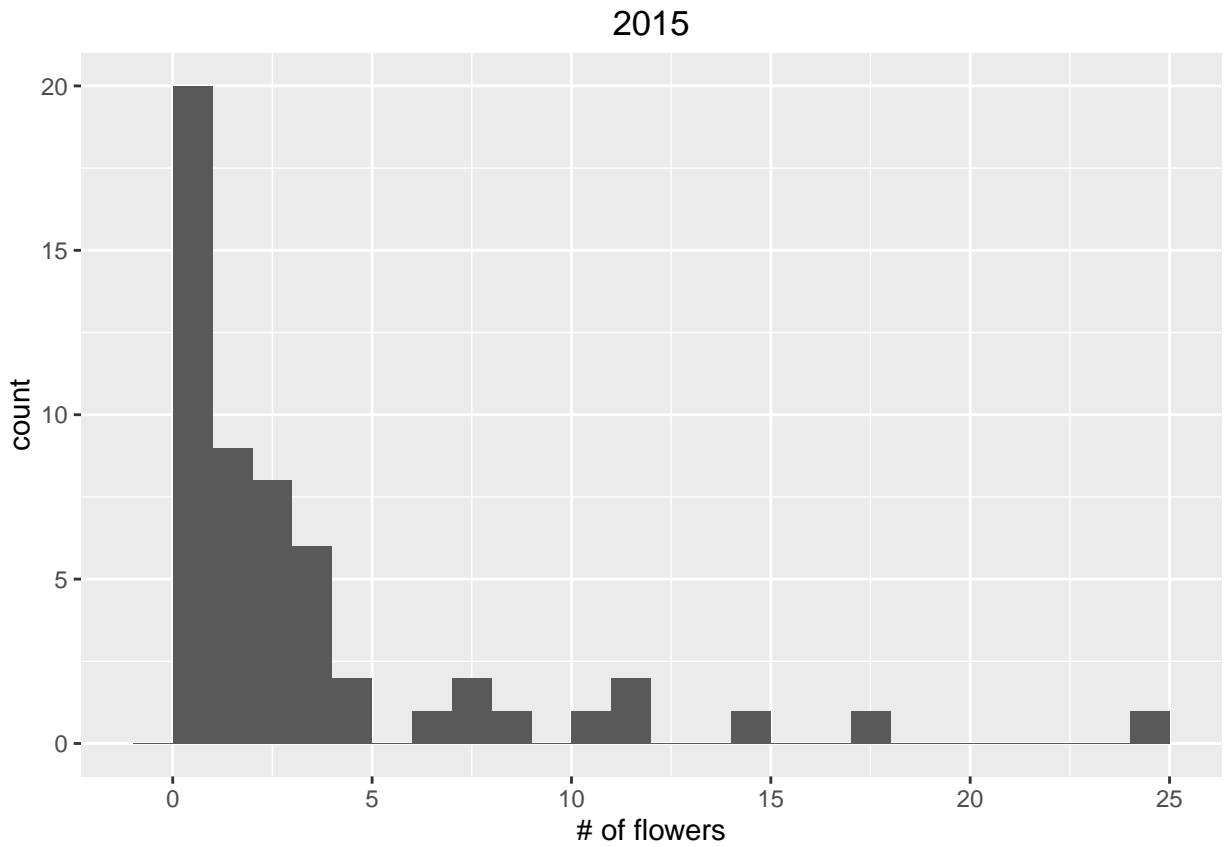
```
##   plot treatment plantid year15 year16 total
## 1  CC6         C   CC6-1      0      6     6
## 2  CC6         C  CC6-10      1      8     9
## 3  CC6         C   CC6-9     10      4    14
## 4  CH5         H   CH5-2      3      8    11
## 5  CH5         H   CH5-3      0      7     7
## 6  CH5         H   CH5-4      1     10    11
```
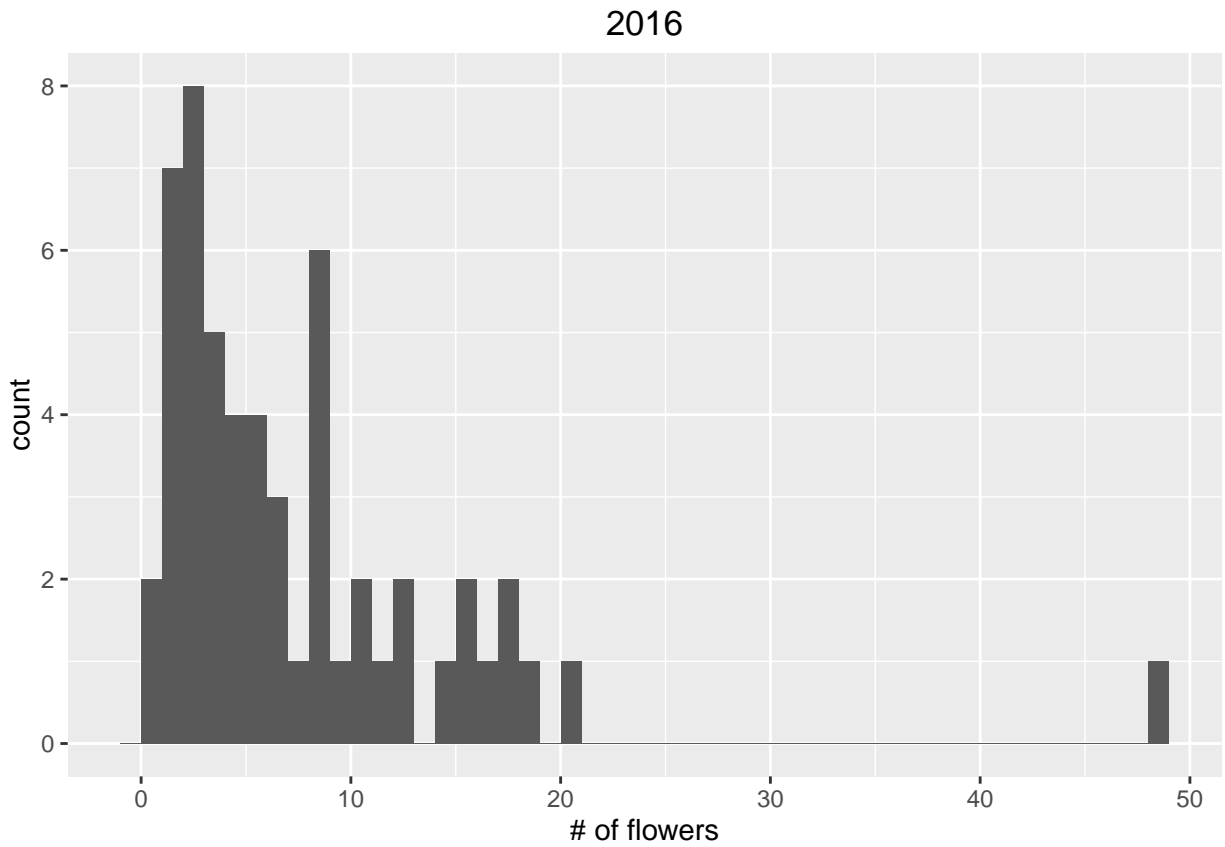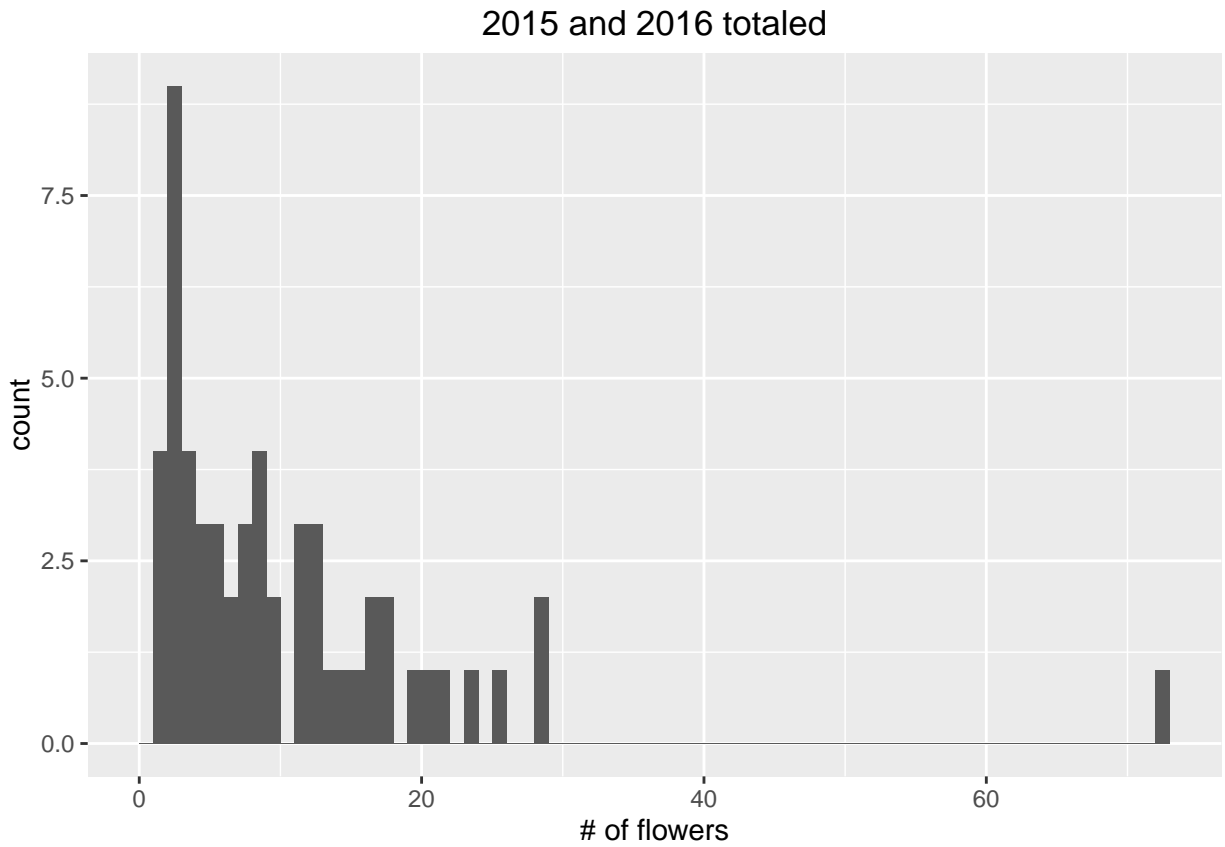
```r
#Data exploration
qplot(flowers$year15, binwidth = 1, xlab = "# of flowers", main = "2015")
```
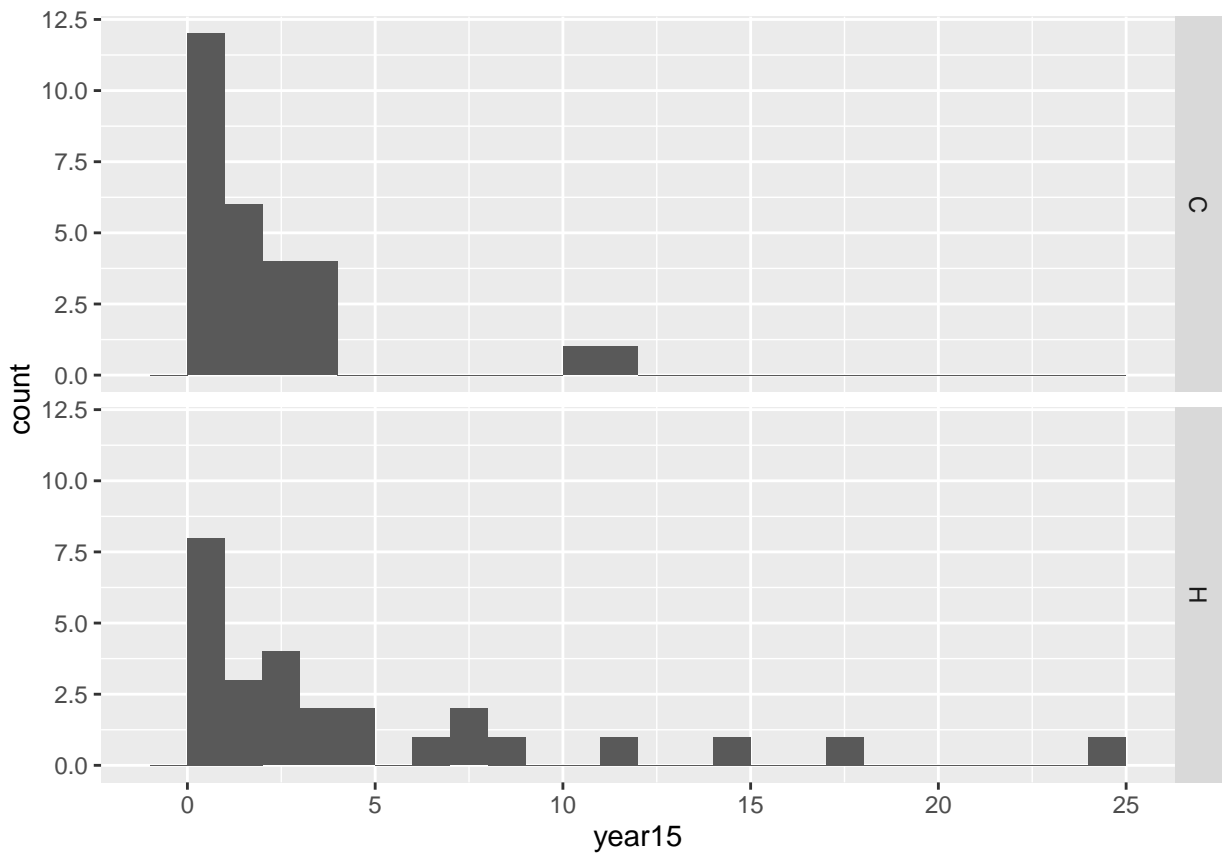
2015

```
qplot(flowers$year16, binwidth = 1, xlab = "# of flowers", main = "2016")
```
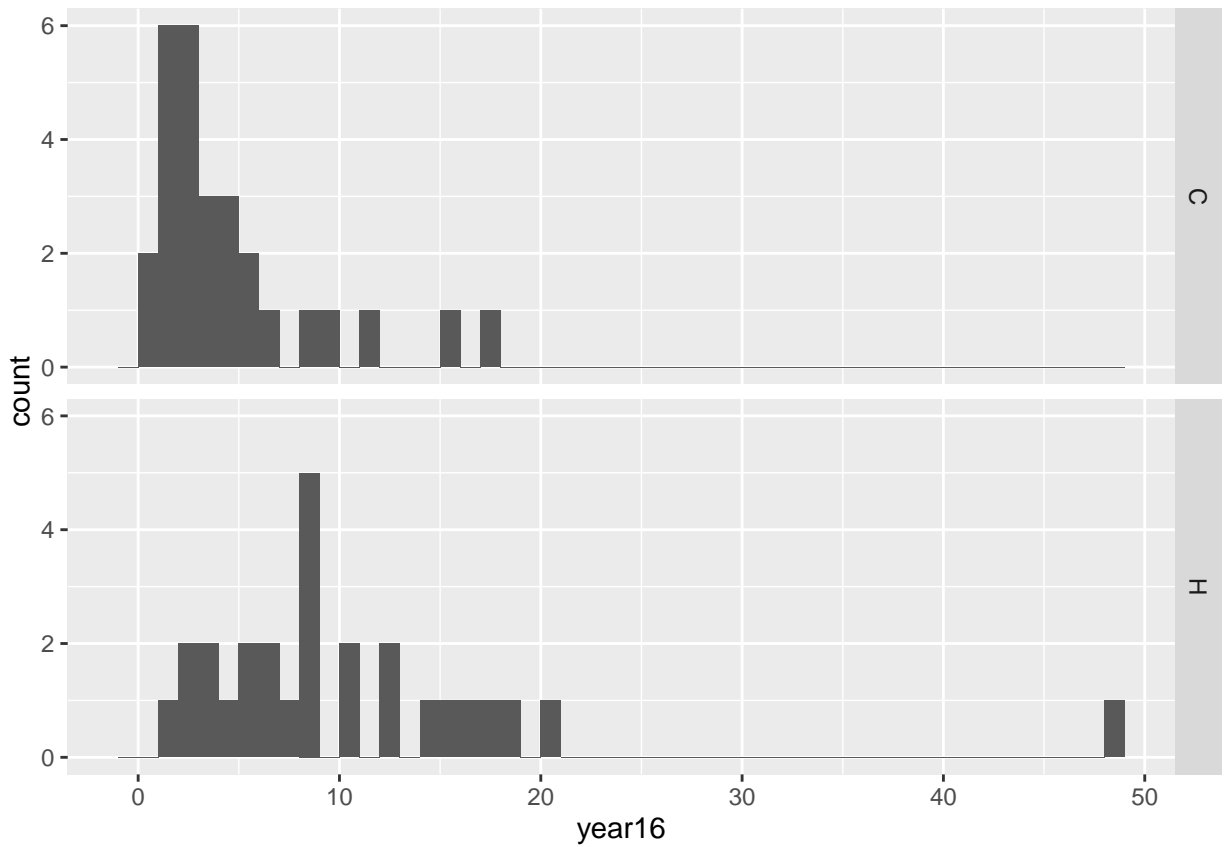
2016

```
qplot(flowers$total, binwidth = 1, xlab = "# of flowers", main = "2015 and 2016 totaled")
```
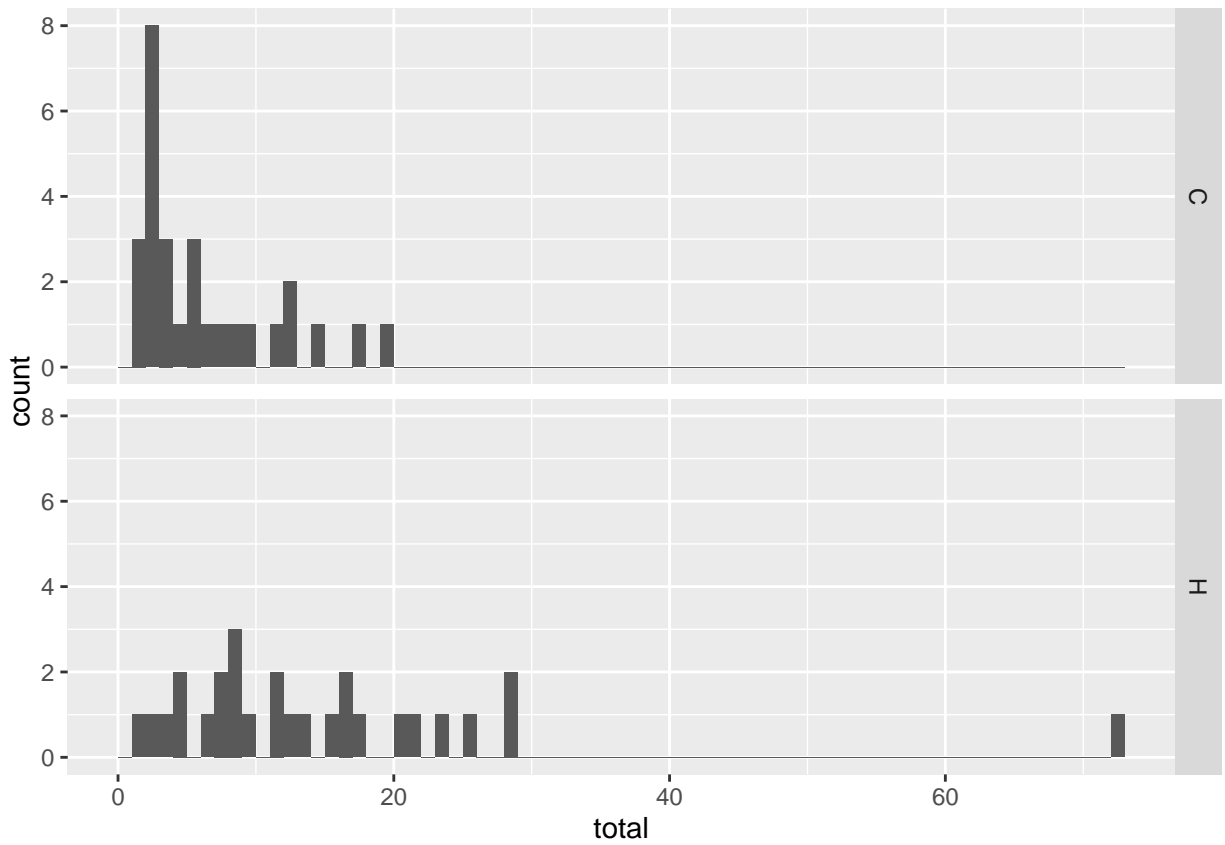
2015 and 2016 totaled


```r
ggplot(flowers, aes(x = year15)) + geom_histogram(binwidth = 1) + facet_grid(treatment~.)
```
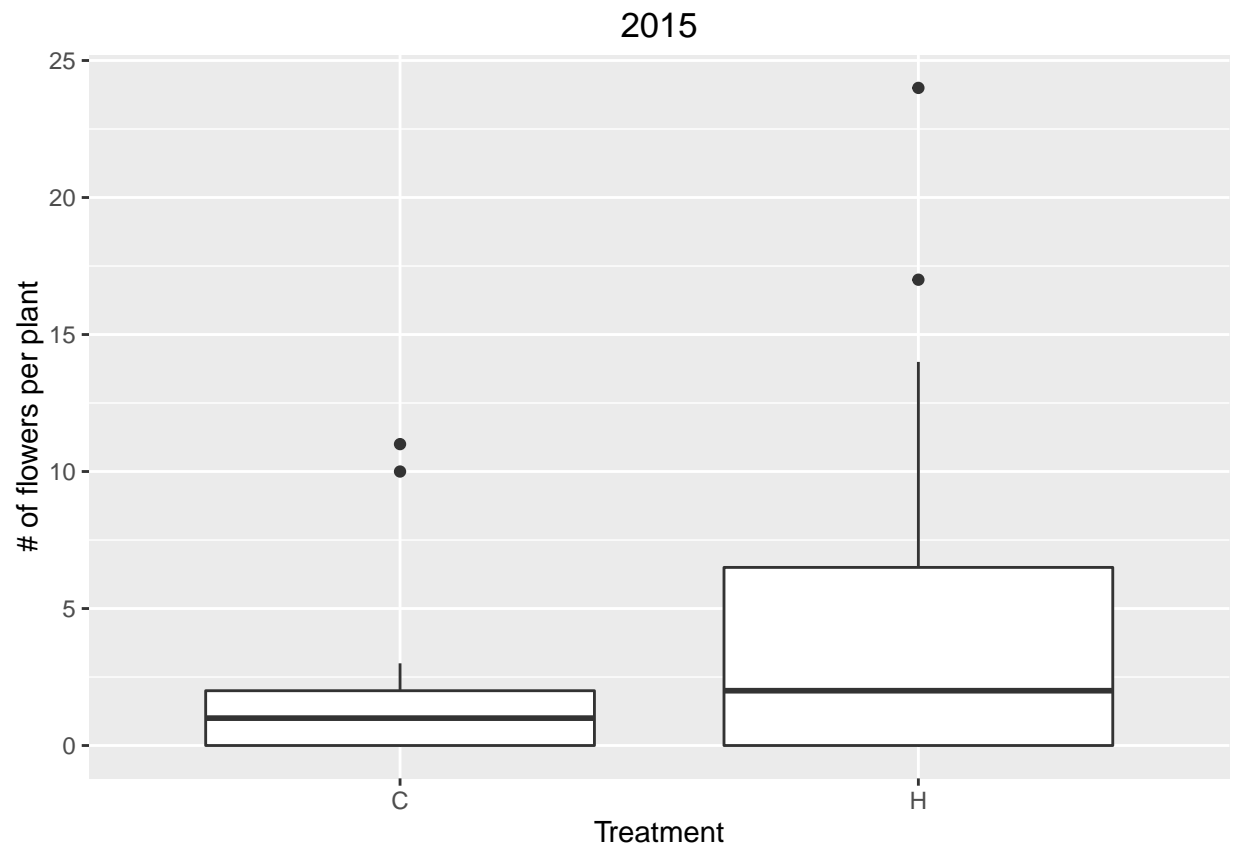
```
ggplot(flowers, aes(x = year16)) + geom_histogram(binwidth = 1) + facet_grid(treatment~.)
```
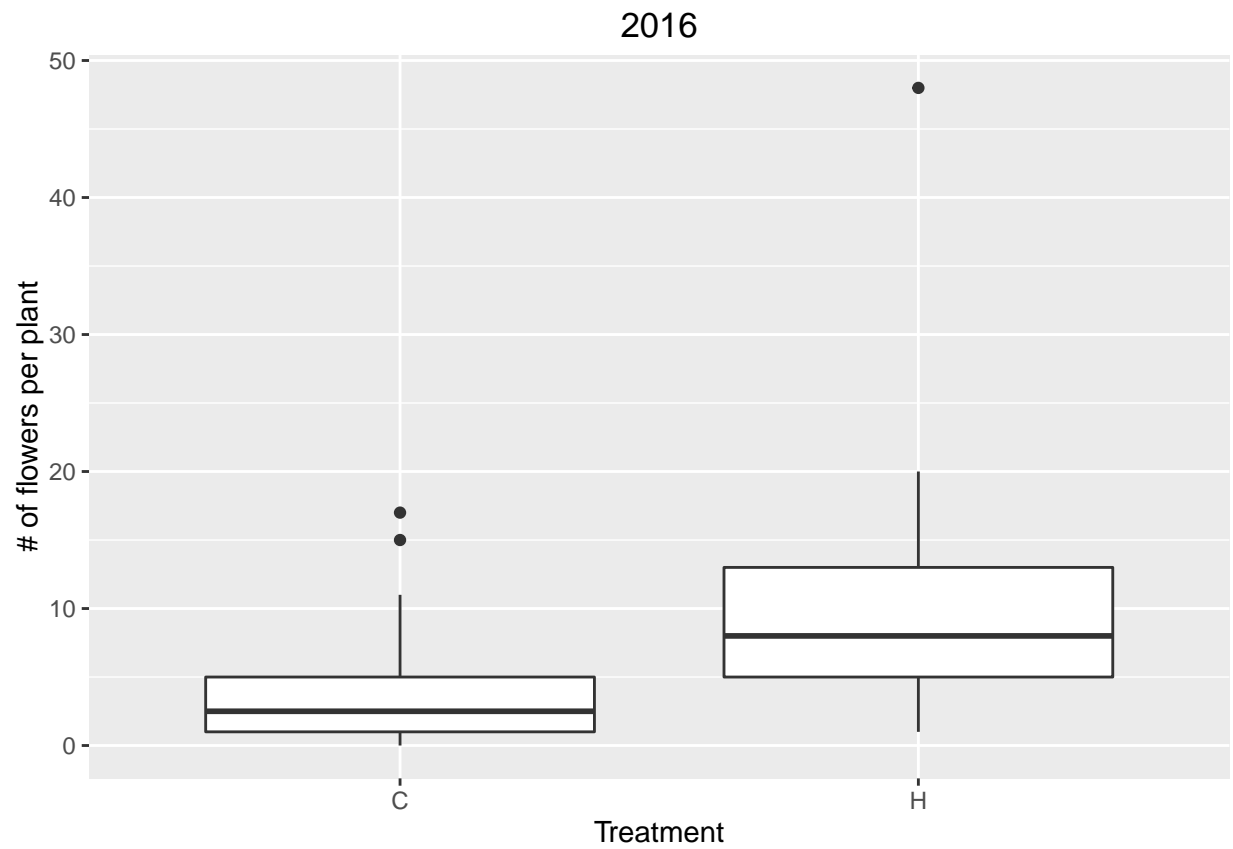
```
ggplot(flowers, aes(x = total)) + geom_histogram(binwidth = 1) + facet_grid(treatment~.)
```
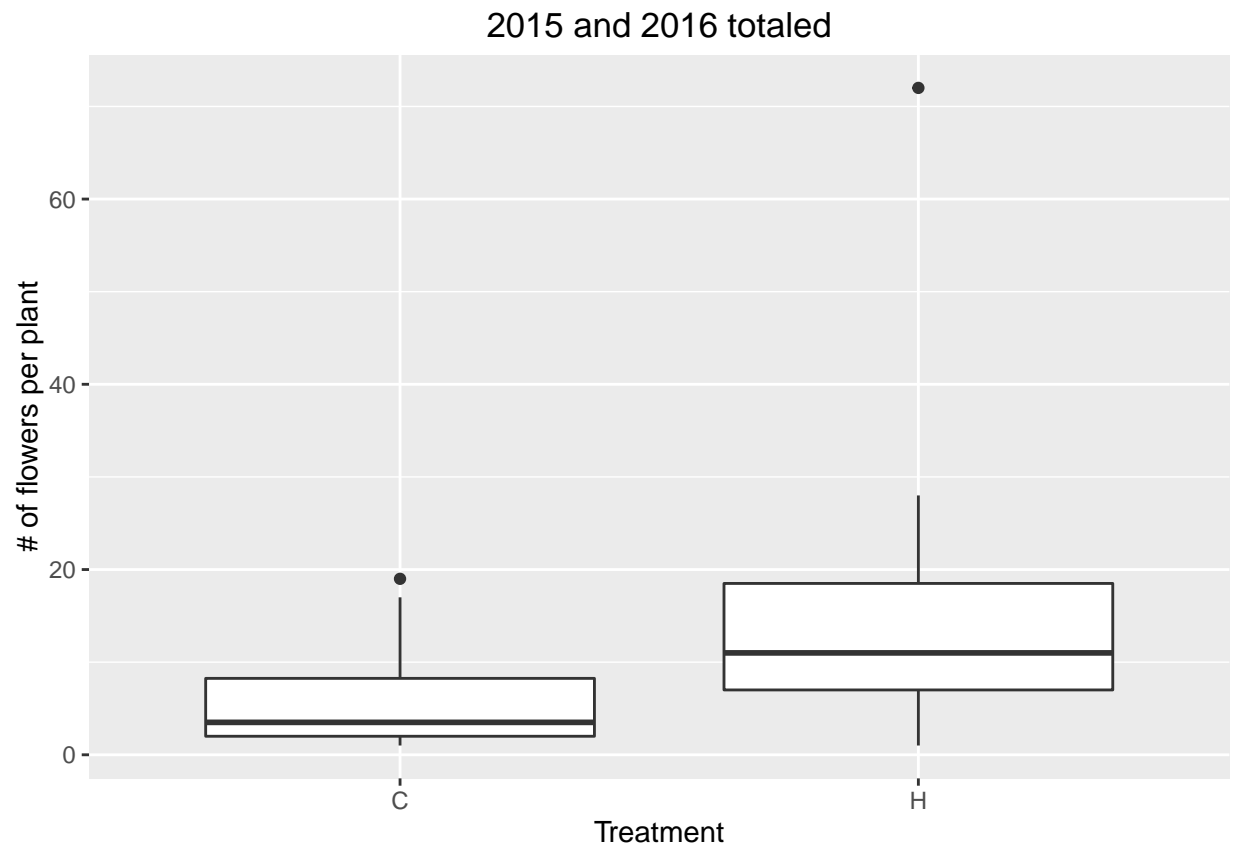
```
qplot(flowers$treatment, flowers$year15, geom = "boxplot", xlab = "Treatment", ylab = "# of flowers per
```

```
qplot(flowers$treatment, flowers$year16, geom = "boxplot", xlab = "Treatment", ylab = "# of flowers per
```
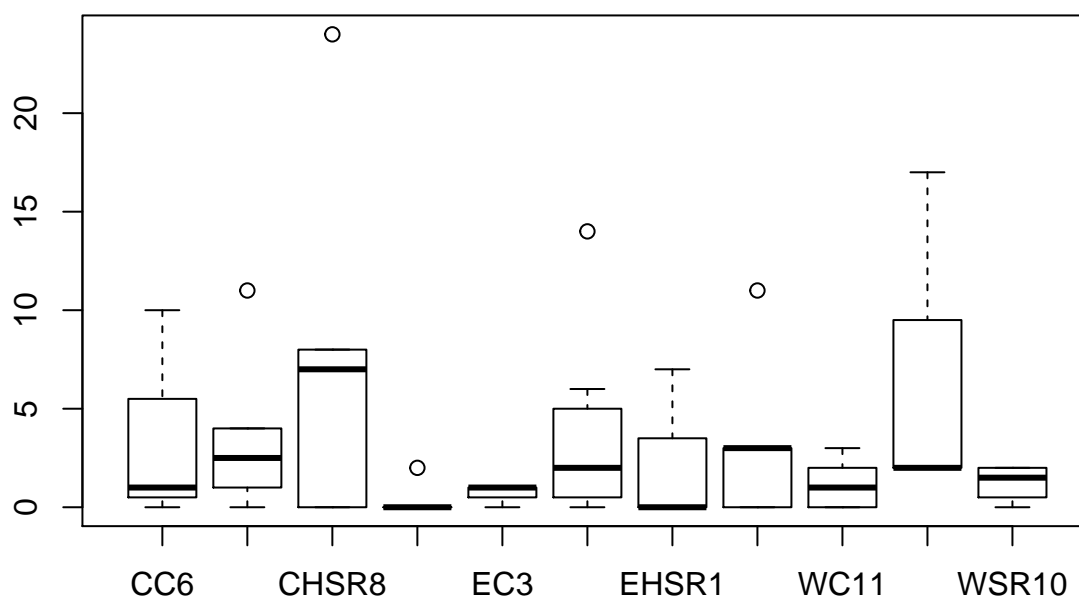
2016

```
qplot(flowers$treatment, flowers$total, geom = "boxplot", xlab = "Treatment", ylab = "# of flowers per
```

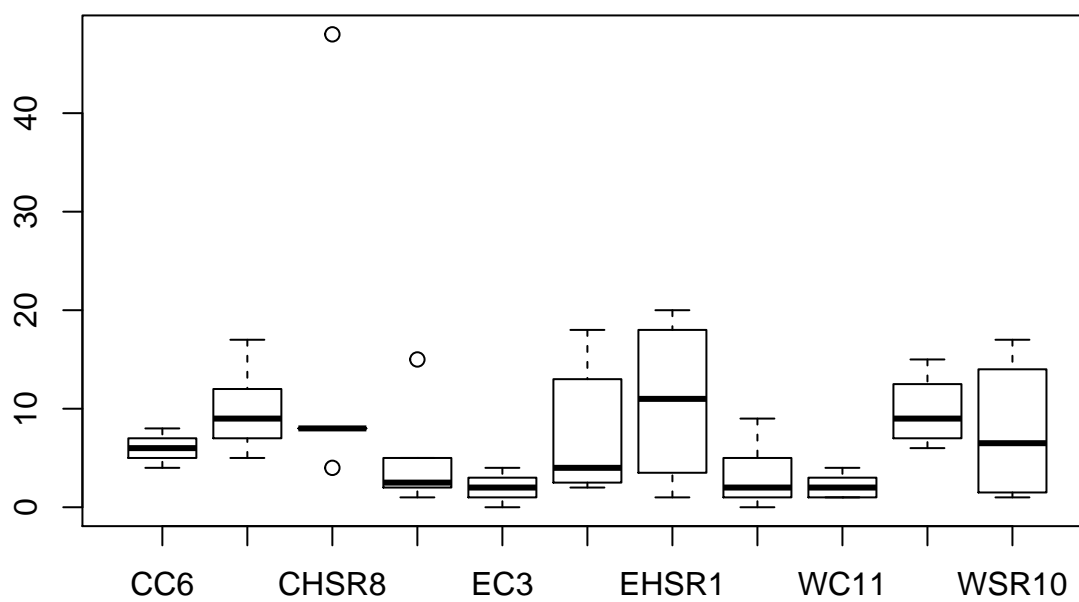## 2015 and 2016 totaled


```
plot(flowers$plot, flowers$year15, main = "2015")
```
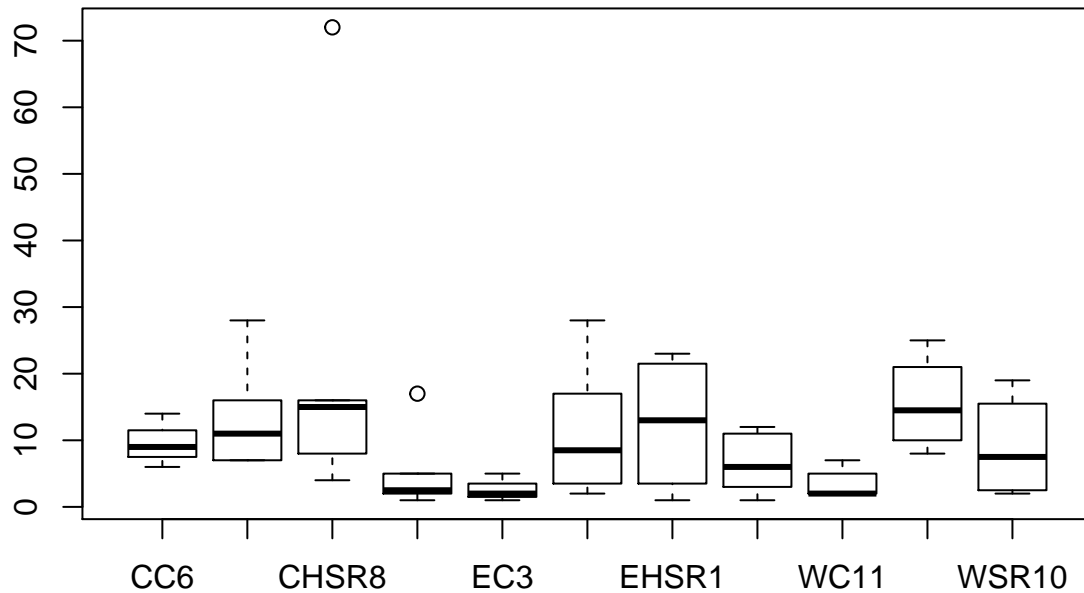
2015


```
plot(flowers$plot, flowers$year16, main = "2016")
```

2016


```r
plot(flowers$plot, flowers$total, main = "2015 and 2016 totaled")
```

2015 and 2016 totaled


```r
# models
  #2015
mod15 <- glmer(year15 ~ treatment + (1|plantid), data = flowers, family = poisson)
dispersion_glmer(mod15)
```
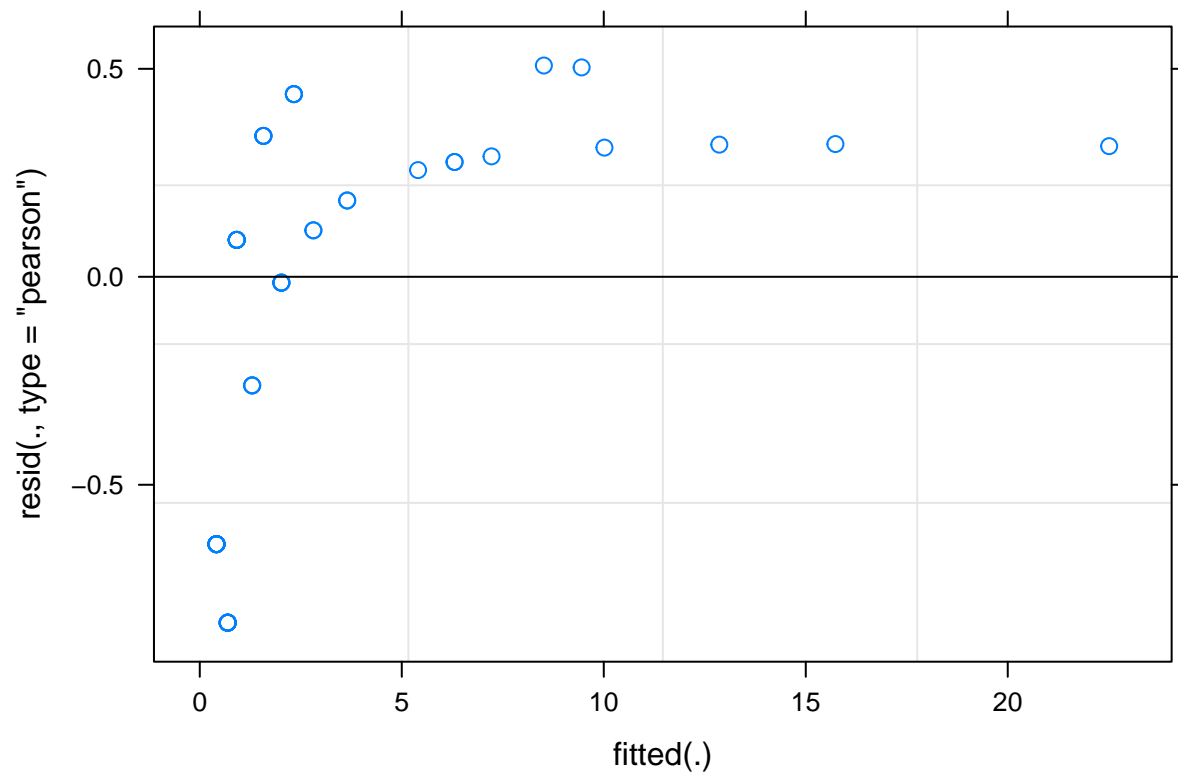
```
## [1] 1.028229
```

```r
summary(mod15)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: year15 ~ treatment + (1 | plantid)
##    Data: flowers
##
##      AIC      BIC   logLik deviance df.resid
##    242.5    248.5   -118.2    236.5       52
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -0.83161 -0.64280  0.08875  0.30003  0.50793
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  plantid (Intercept) 1.596    1.263
## Number of obs: 55, groups:  plantid, 55
##
```
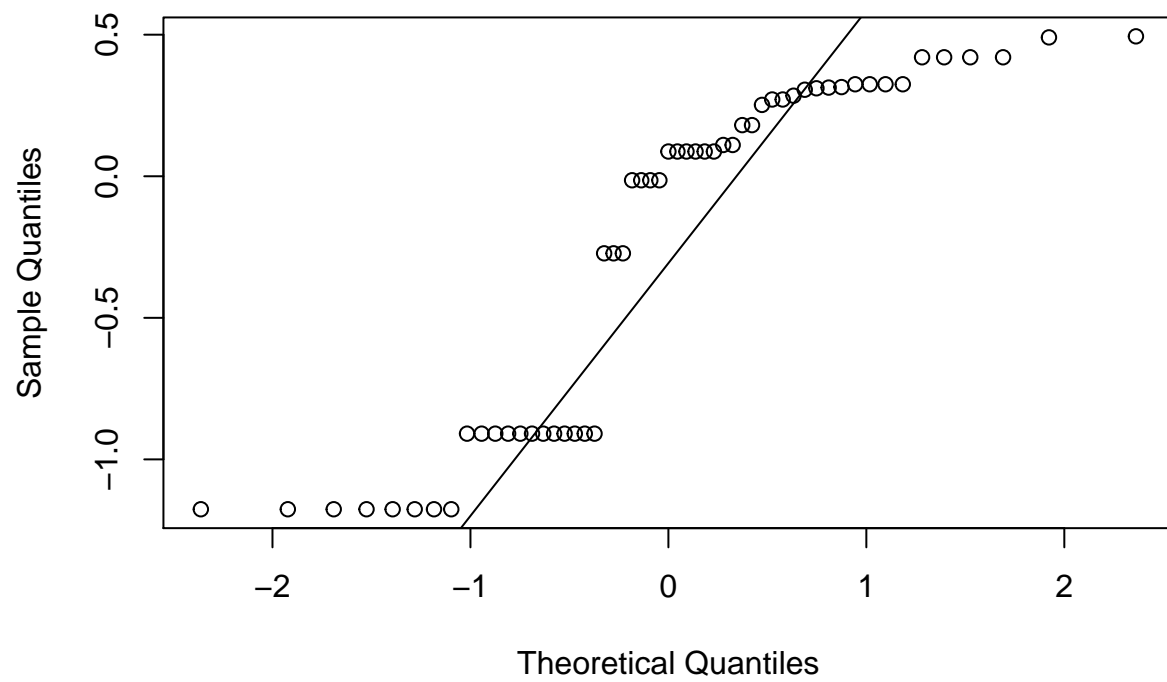
```
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.2243     0.3379  -0.664   0.5069
## treatmentH    0.9595     0.4236   2.265   0.0235 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr)
## treatmentH -0.711
```
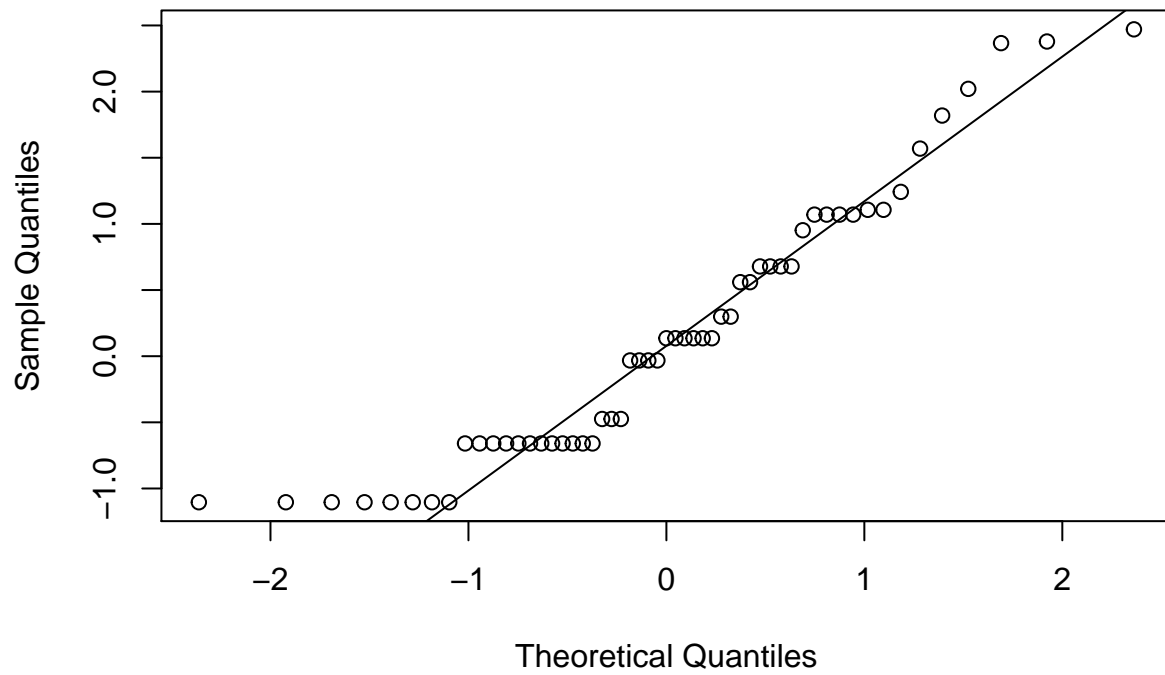
```
plot(mod15)
```



```
qqnorm(resid(mod15), main="normal qq-plot, residuals")
qqline(resid(mod15))
```

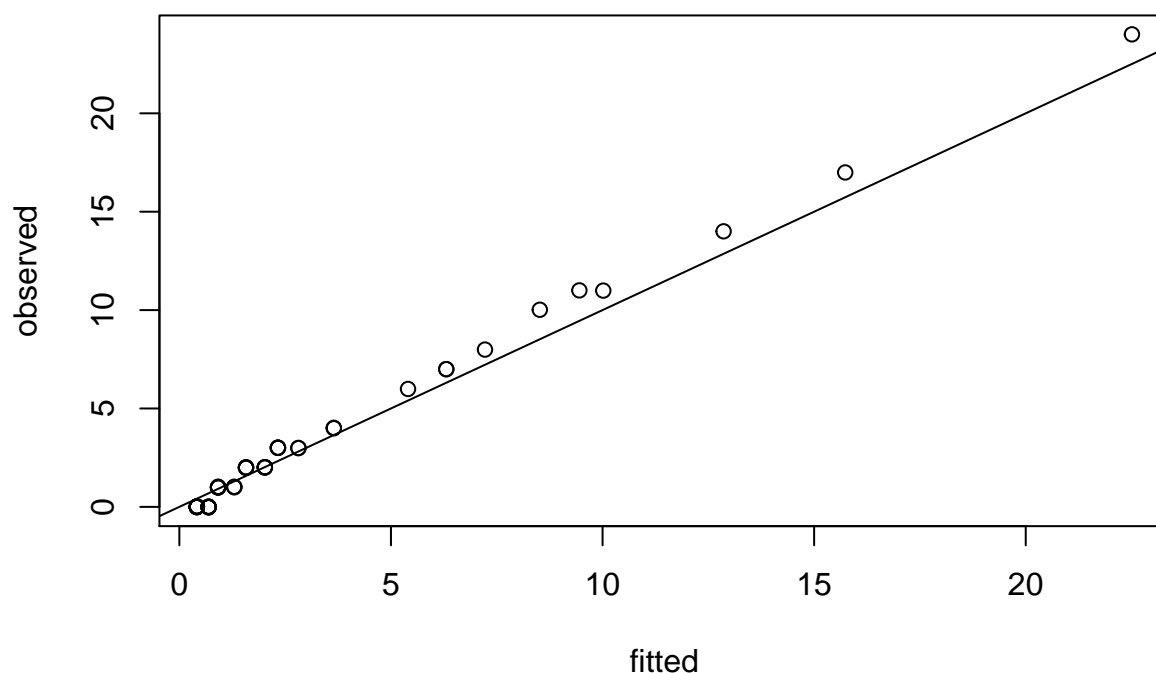## normal qq–plot, residuals


```r
qqnorm(ranef(mod15)$plantid[,1])
qqline(ranef(mod15)$plantid[,1])
```

Normal Q–Q Plot


```r
plot(fitted(mod15), jitter(flowers$year15,0.1), xlab = "fitted", ylab = "observed", main = "2015")  #fi
abline(0,1)
```

2015


```
#2016
mod16 <- glmer(year16 ~ treatment + (1|plantid), data = flowers, family = poisson)
dispersion_glmer(mod16)
```
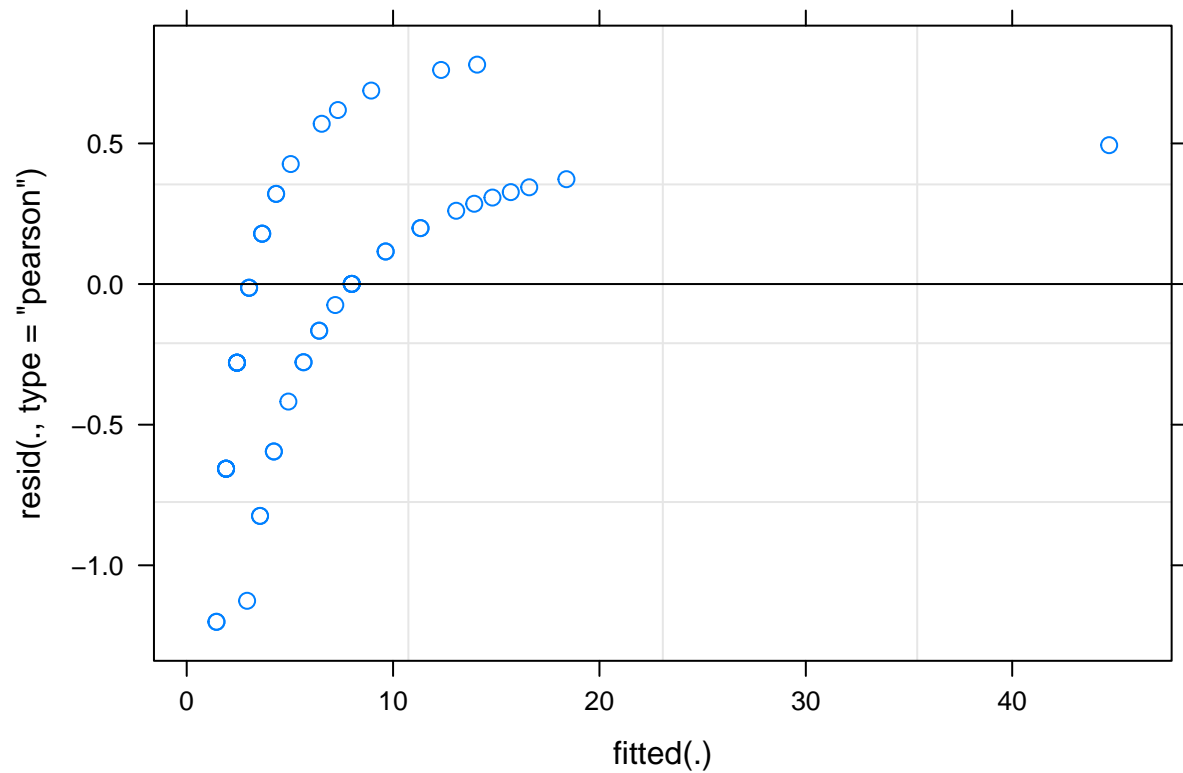
```
## [1] 1.003602
```

```
summary(mod16)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: year16 ~ treatment + (1 | plantid)
##    Data: flowers
##
##      AIC      BIC   logLik deviance df.resid
##    319.5    325.6   -156.8    313.5       52
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.20095 -0.34879 -0.01323  0.27307  0.78018
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  plantid (Intercept) 0.5214   0.7221
## Number of obs: 55, groups:  plantid, 55
##
## Fixed effects:
```
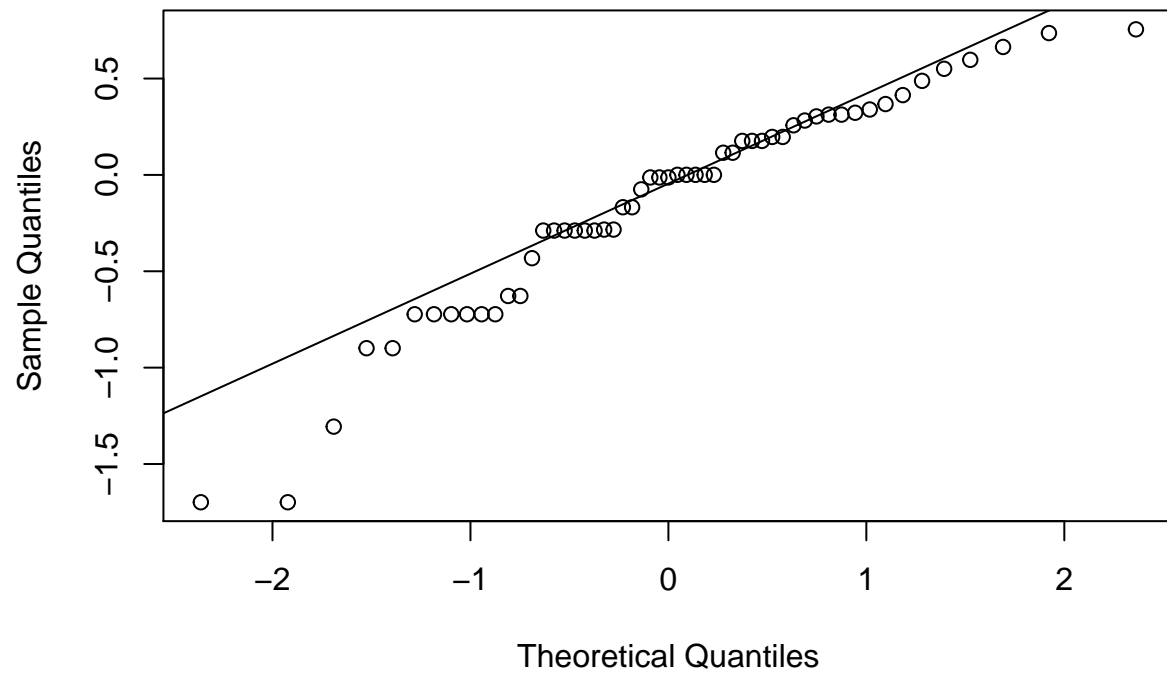
```
##            Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.1182      0.1795    6.228 4.71e-10 ***
## treatmentH    0.9603      0.2350    4.087 4.38e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr)
## treatmentH -0.742
```
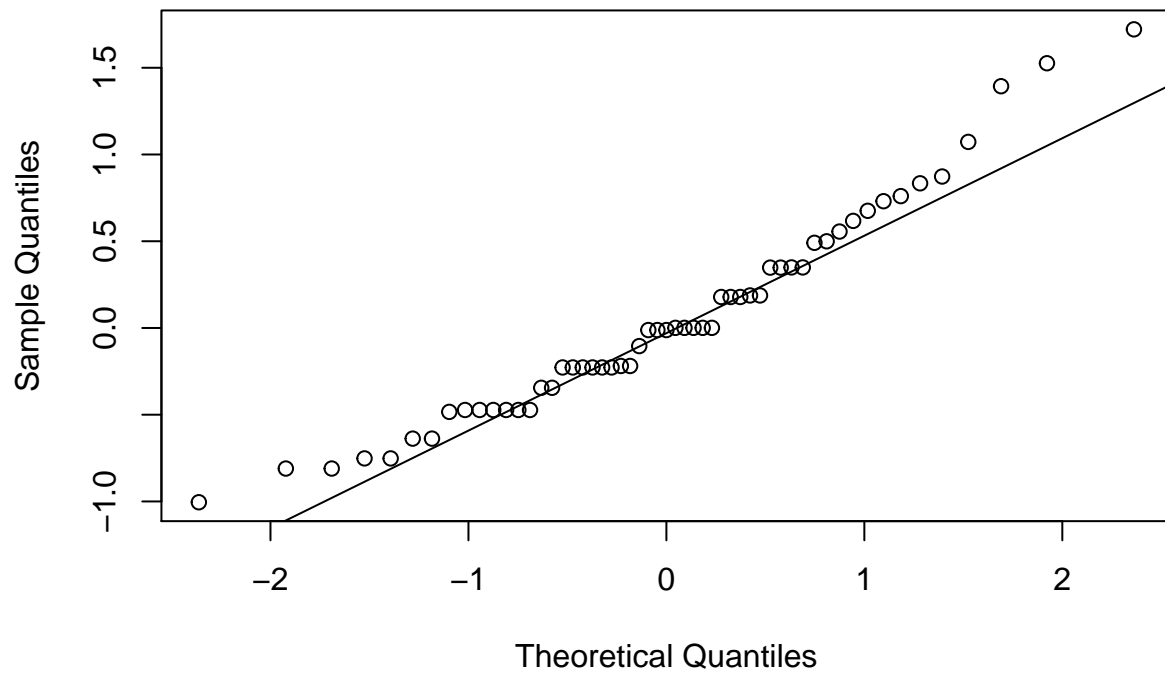
```r
plot(mod16)
```



```r
qqnorm(resid(mod16), main="normal qq-plot, residuals")
qqline(resid(mod16))
```

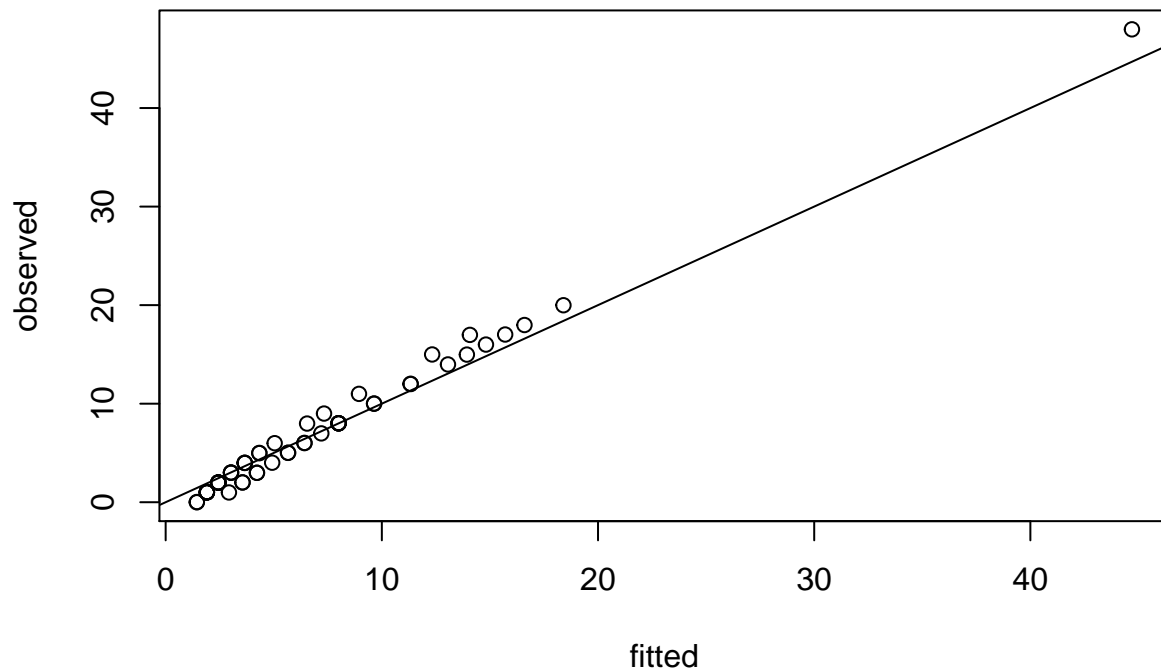## normal qq−plot, residuals


```r
qqnorm(ranef(mod16)$plantid[,1])
qqline(ranef(mod16)$plantid[,1])
```

Normal Q–Q Plot


```r
plot(fitted(mod16), jitter(flowers$year16,0.1), xlab = "fitted", ylab = "observed", main = "2016")  #fi
abline(0,1)
```

2016


```
  #2015 plus 2016
modtot <- glmer(total ~ treatment + (1|plantid), data = flowers, family = poisson)
dispersion_glmer(modtot)
```

[1] 0.987772

```
summary(modtot)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: total ~ treatment + (1 | plantid)
##    Data: flowers
##
##      AIC      BIC   logLik deviance df.resid
##    355.3    361.4   -174.7    349.3       52
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.24692 -0.49050 -0.00174  0.25243  0.59549
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  plantid (Intercept) 0.5447   0.7381
## Number of obs: 55, groups:  plantid, 55
##
## Fixed effects:
```
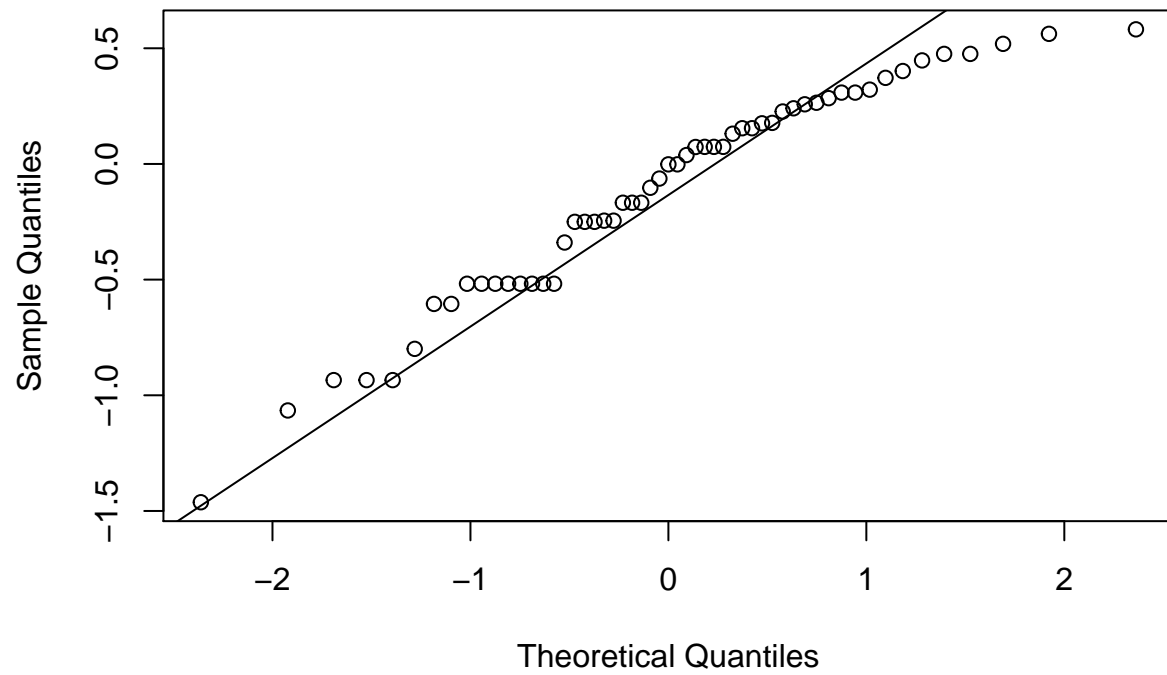
```
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.4873      0.1699   8.753  < 2e-16 ***
## treatmentH    0.9143      0.2282   4.006 6.17e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr)
## treatmentH -0.730
```
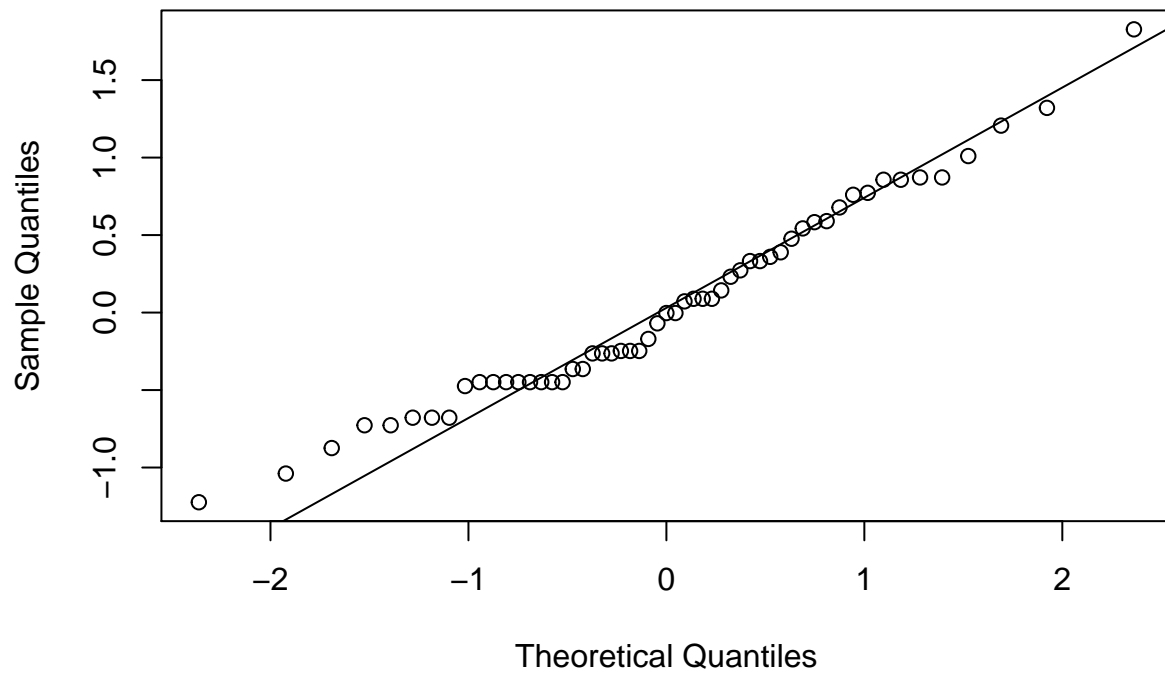
```r
plot(modtot)
```
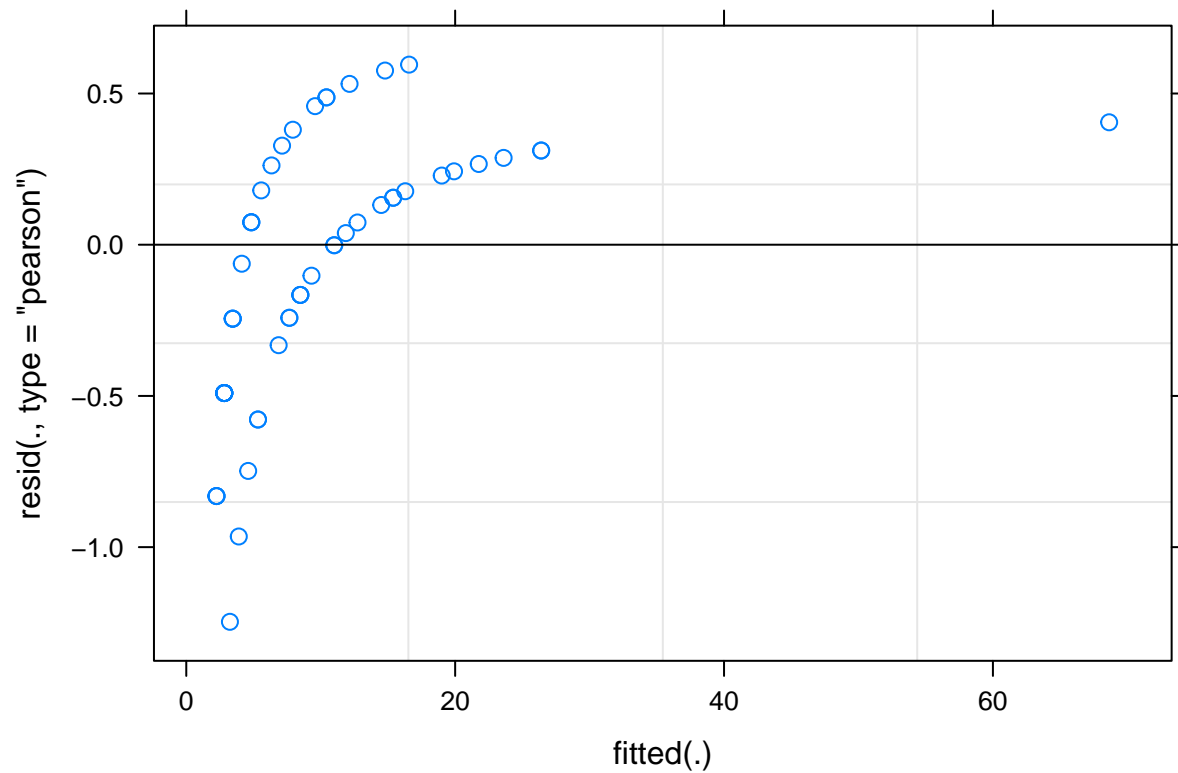


```r
qqnorm(resid(modtot), main="normal qq-plot, residuals")
qqline(resid(modtot))
```

normal qq−plot, residuals


```r
qqnorm(ranef(modtot)$plantid[,1])
qqline(ranef(modtot)$plantid[,1])
```

Normal Q–Q Plot


```
plot(fitted(modtot), jitter(flowers$total,0.1), xlab = "fitted", ylab = "observed", main = "2015 and 20
abline(0,1)
```

2015 and 2016