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$plantid)
head(flowers)
```
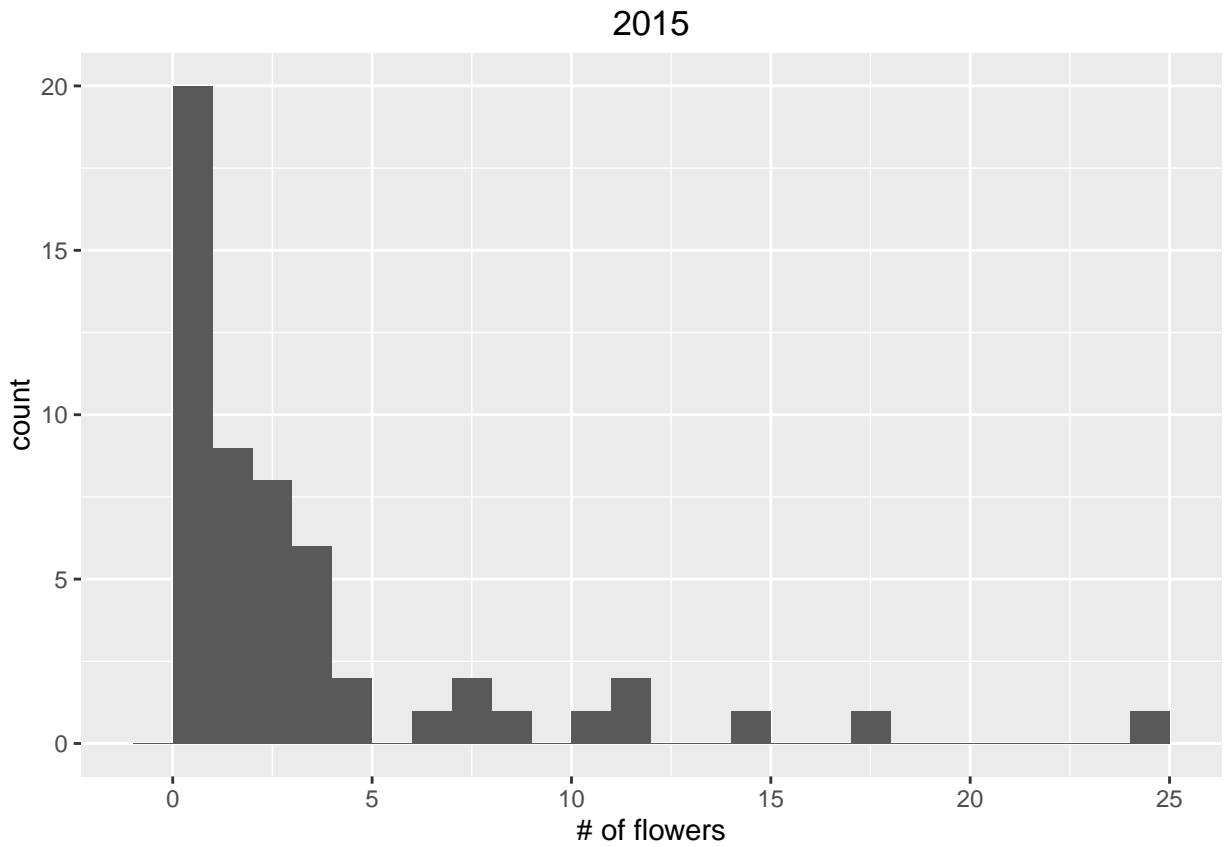
```
##   plot treatment plantid year15 year16 total
## 1  CC6         C   CC6-1      0      6     6
## 2  CC6         C  CC6-10      1      8     9
## 3  CC6         C   CC6-9     10      4    14
## 4  CH5         H   CH5-2      3      8    11
## 5  CH5         H   CH5-3      0      7     7
## 6  CH5         H   CH5-4      1     10    11
```
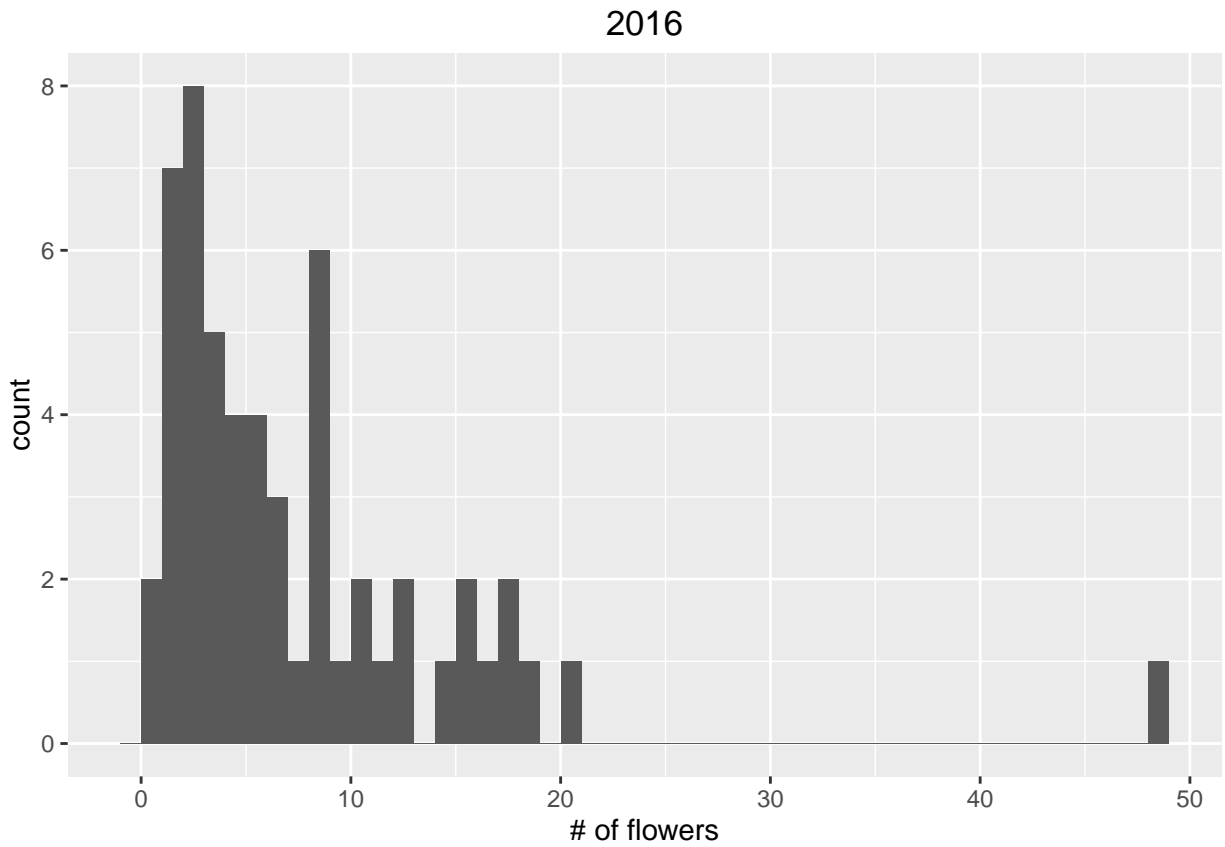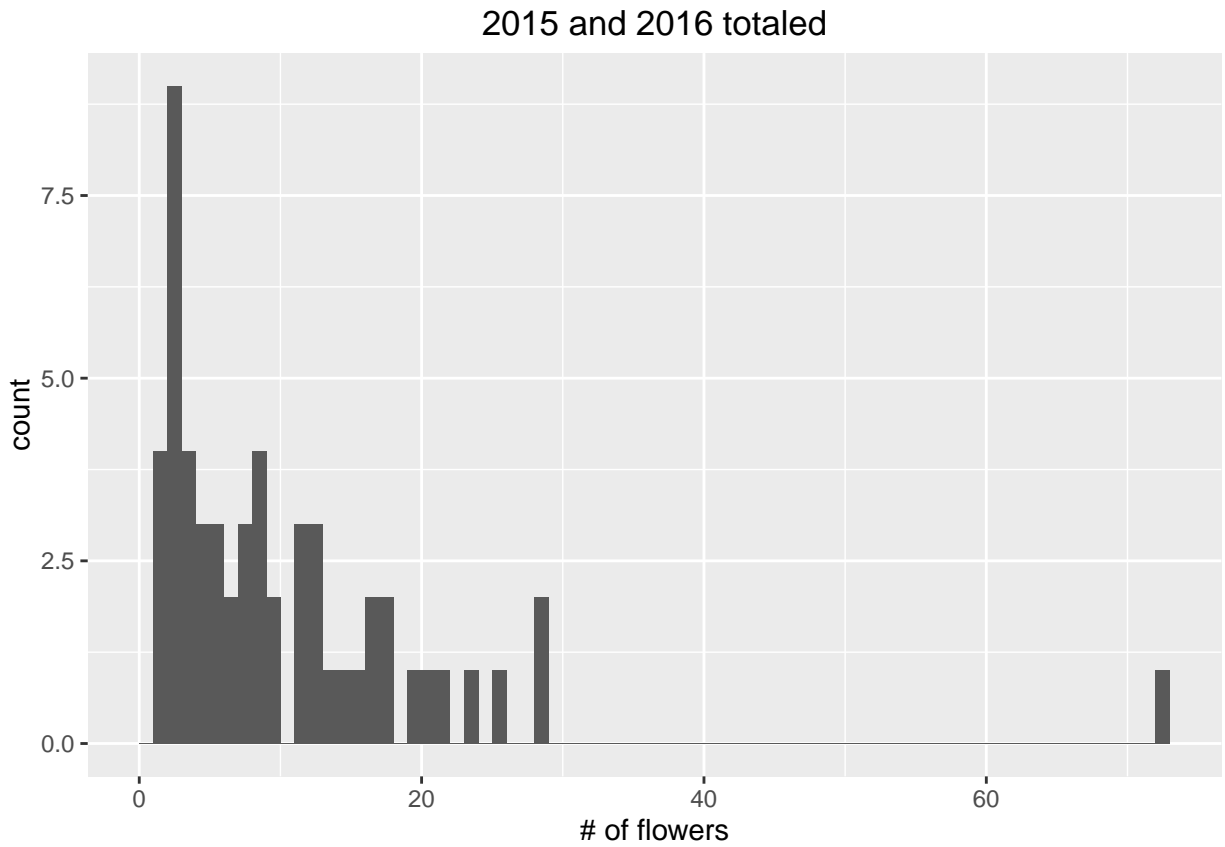
```r
#Data exploration
qplot(flowers$year15, binwidth = 1, xlab = "# of flowers", main = "2015")
```
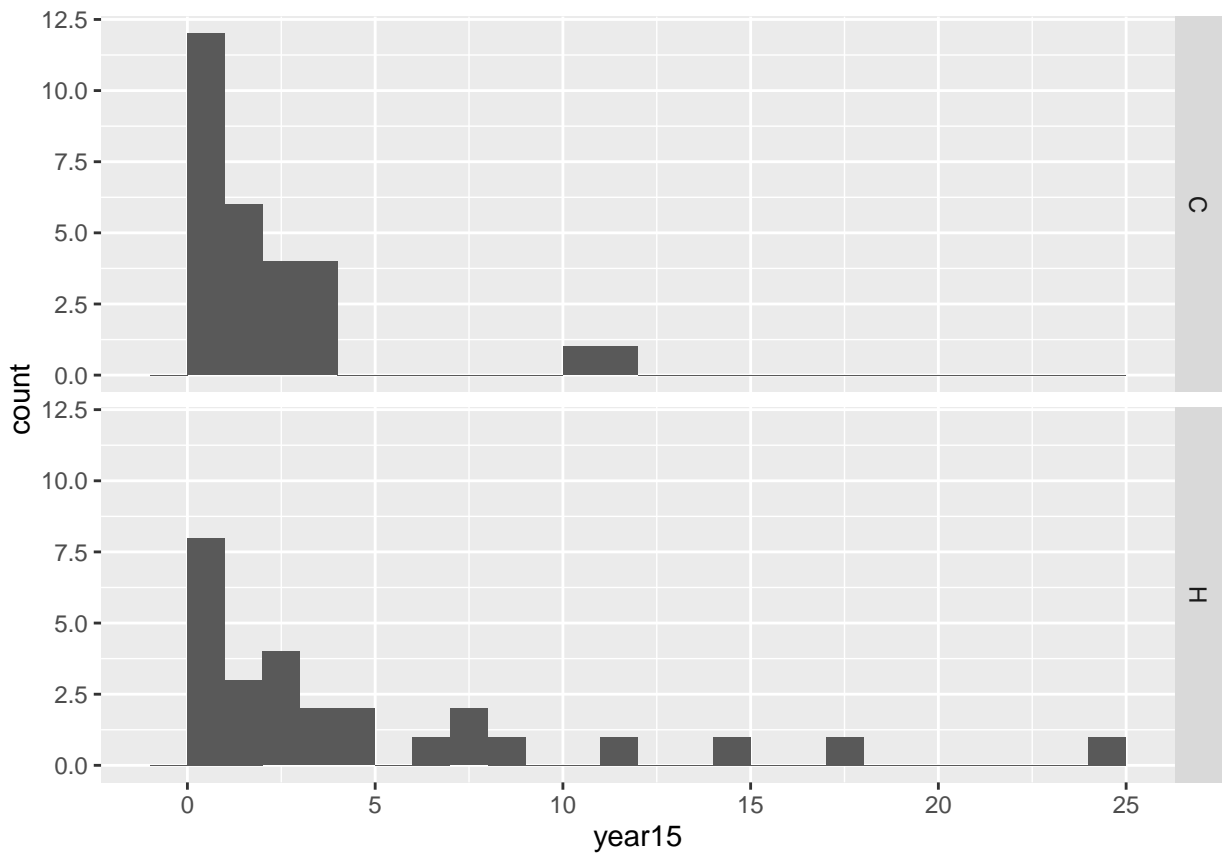
2015


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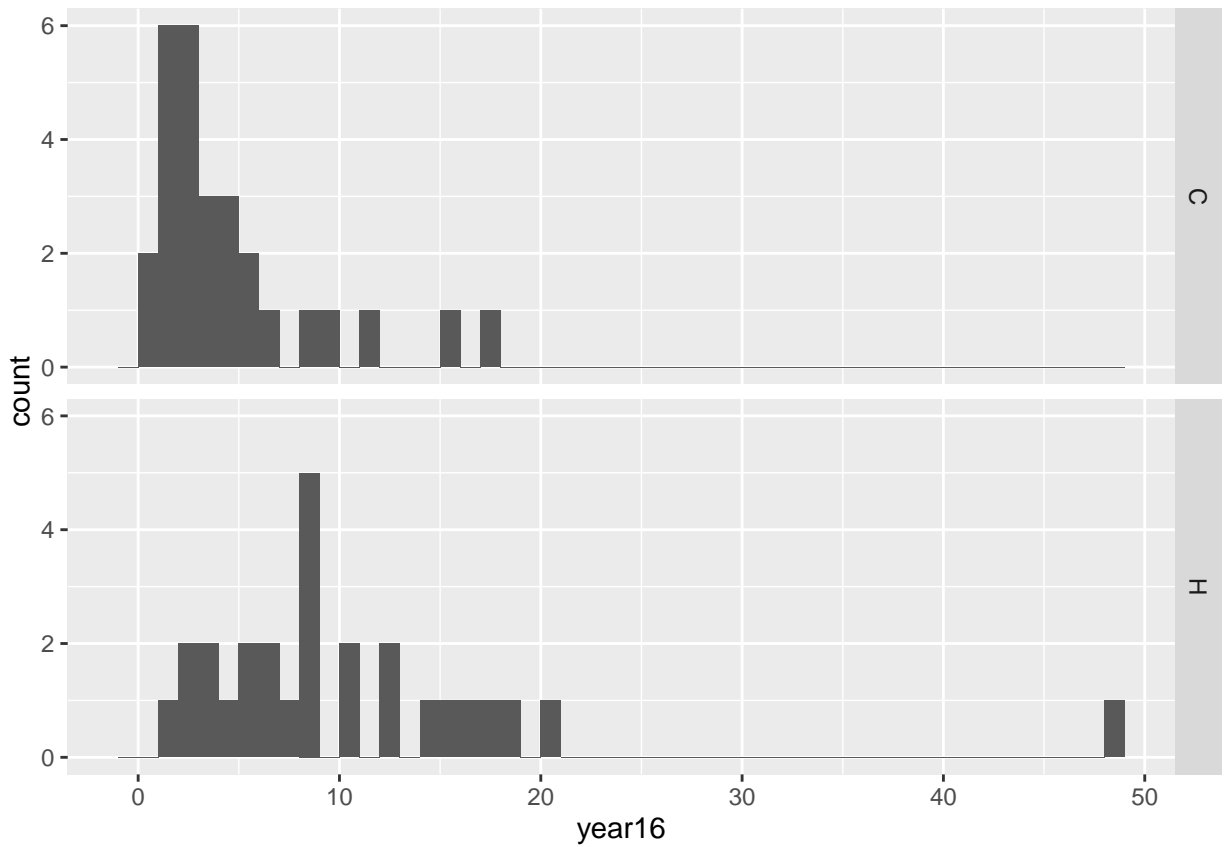
2016

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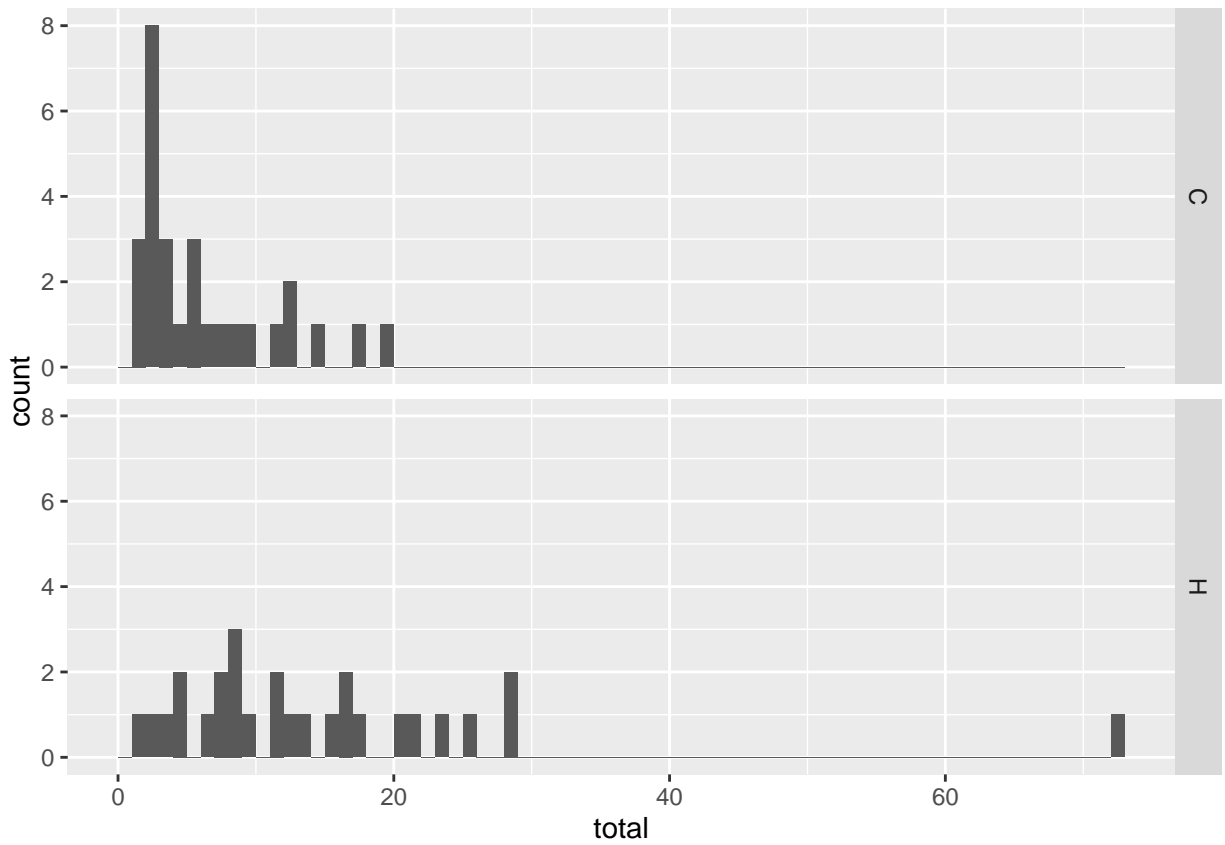
2015 and 2016 totaled


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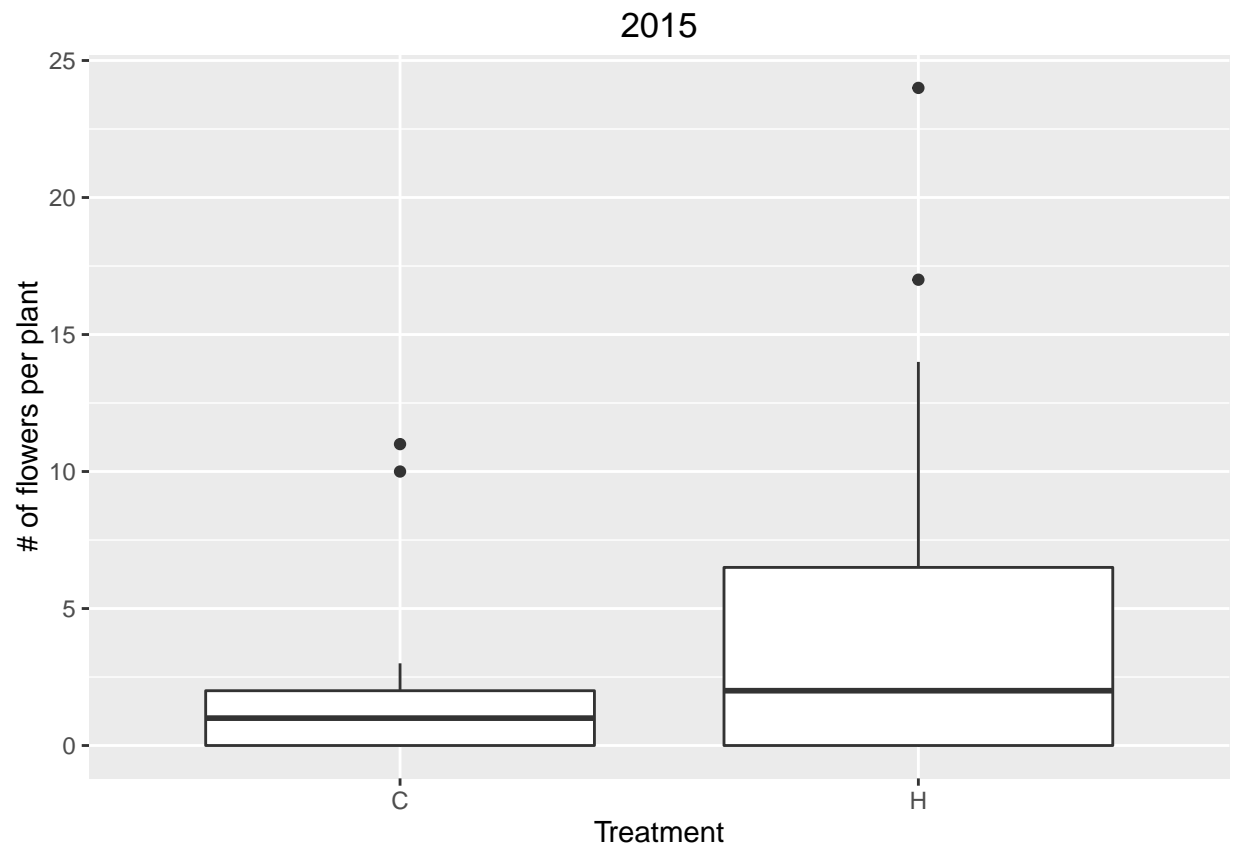
```
ggplot(flowers, aes(x = year16)) + geom_histogram(binwidth = 1) + facet_grid(treatment~.)
```
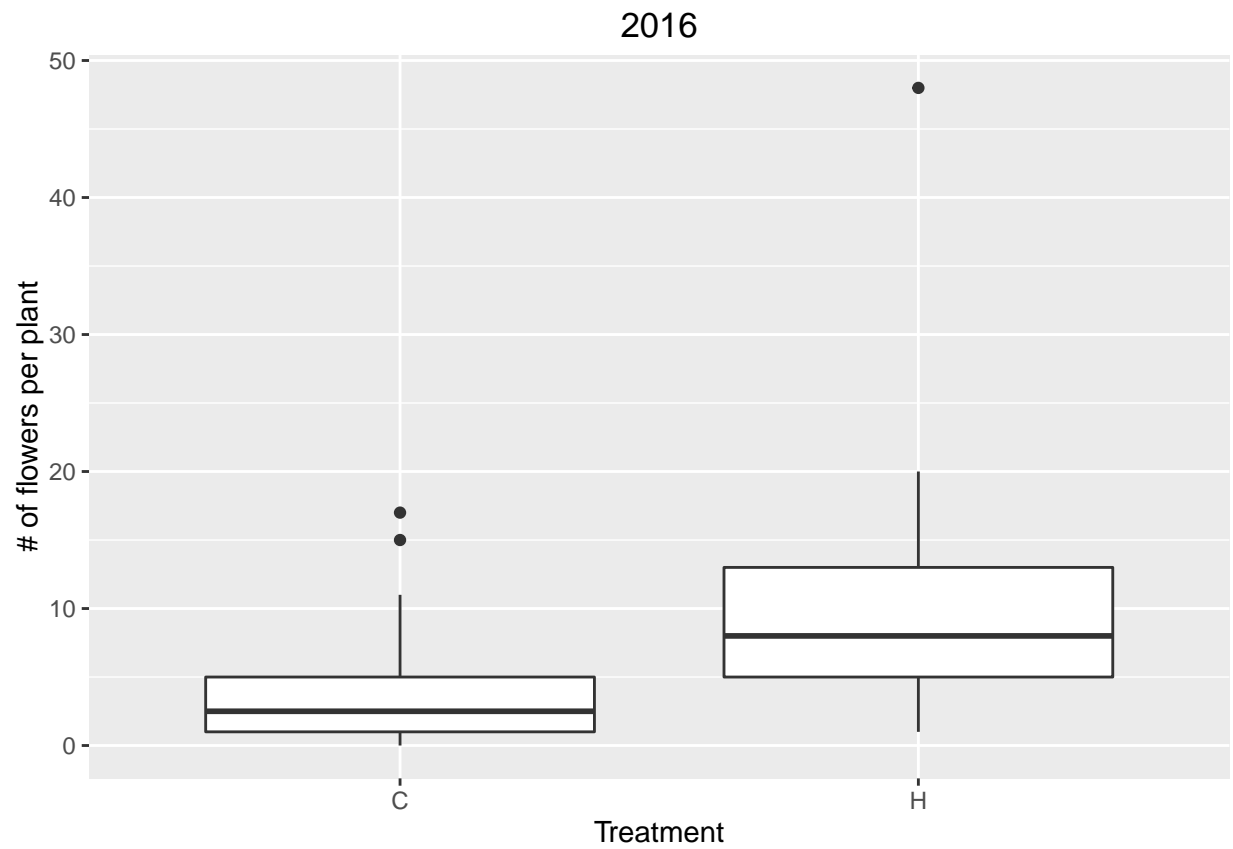
```
ggplot(flowers, aes(x = total)) + geom_histogram(binwidth = 1) + facet_grid(treatment~.)
```
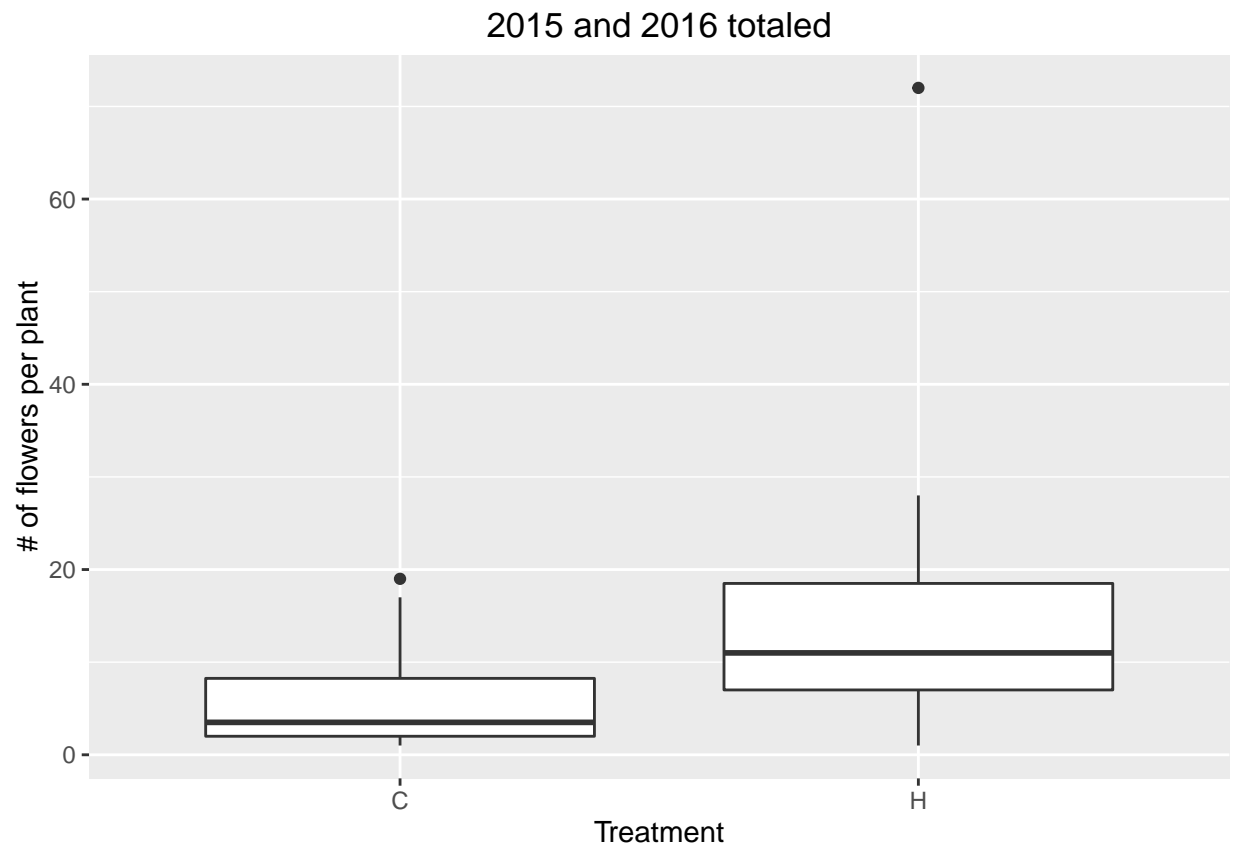
```
qplot(flowers$treatment, flowers$year15, geom = "boxplot", xlab = "Treatment", ylab = "# of flowers per
```

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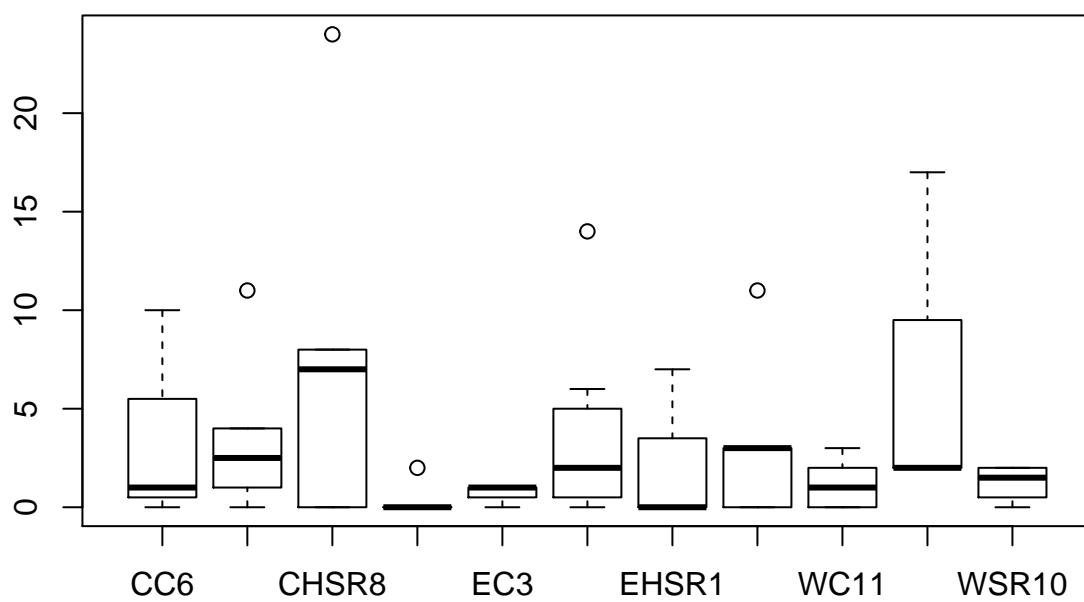
2016

of flowers per plant

Treatment

```
qplot(flowers$treatment, flowers$total, geom = "boxplot", xlab = "Treatment", ylab = "# of flowers per
```
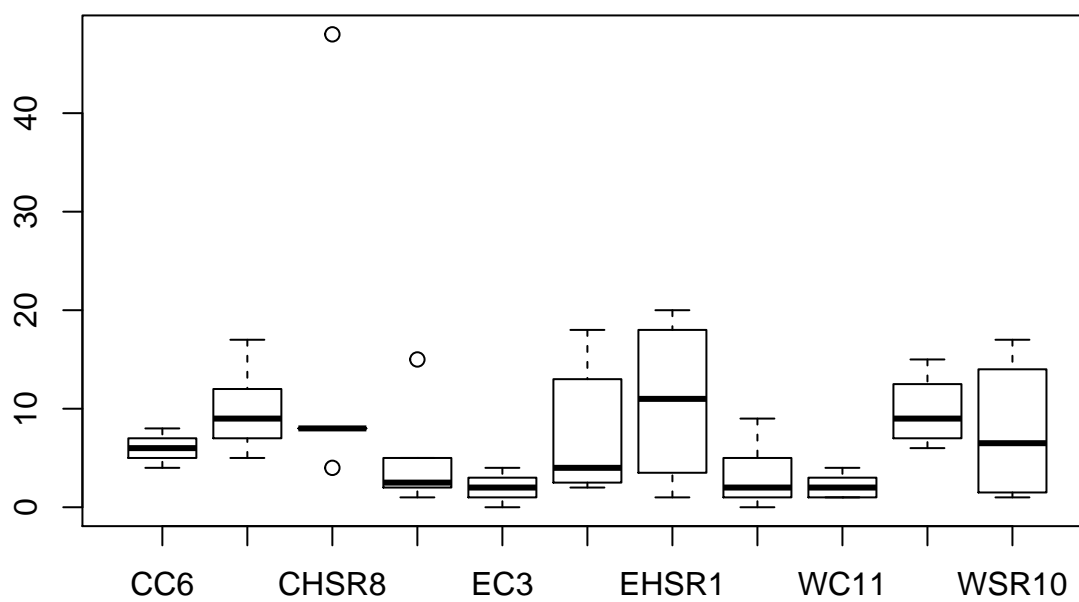
2015 and 2016 totaled

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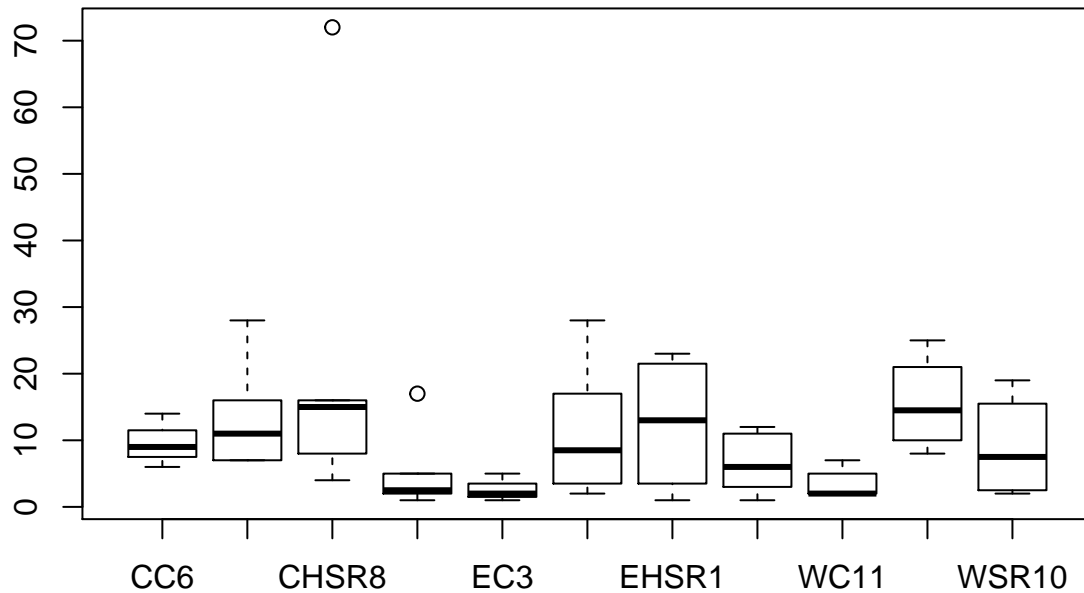
2015


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

2016


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

2015 and 2016 totaled


```
# models
  #2015
mod15 <- glmer(year15 ~ treatment + (1|plantid) + (1|plot), data = flowers, family = poisson)
dispersion_glmer(mod15)
```
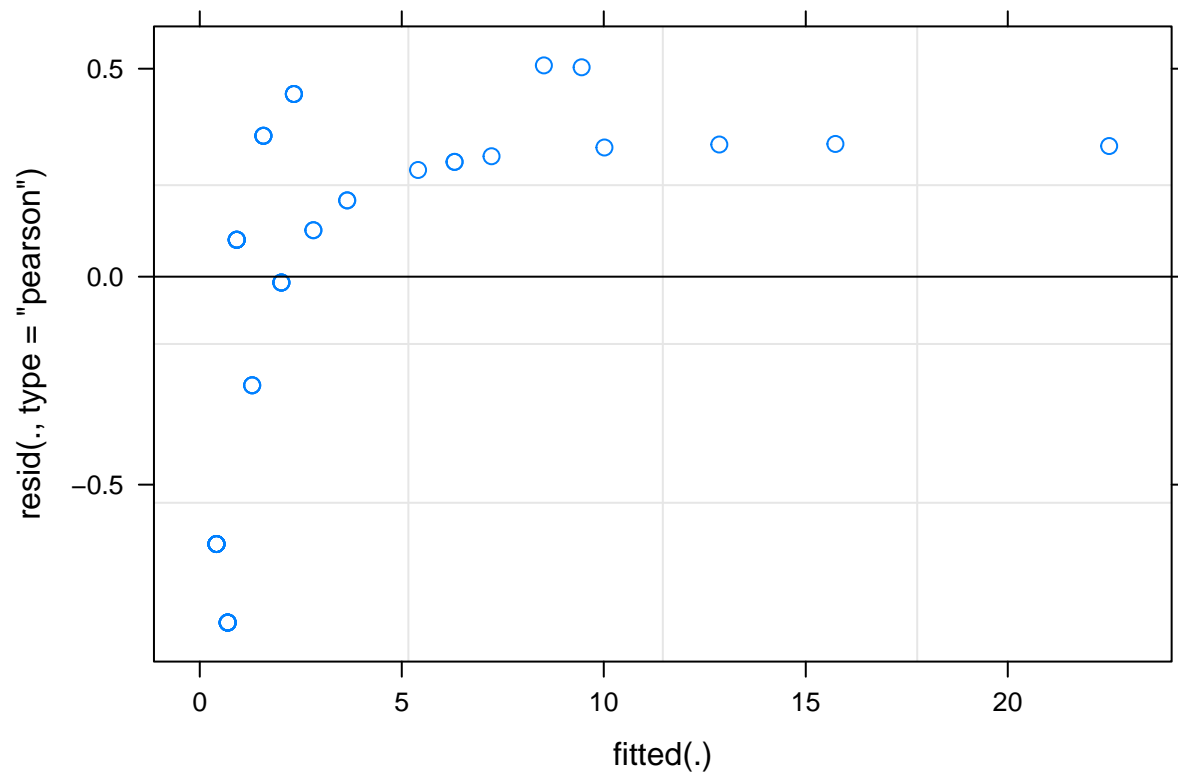
```
## [1] 1.028234
```

```
summary(mod15)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: year15 ~ treatment + (1 | plantid) + (1 | plot)
##    Data: flowers
##
##      AIC      BIC   logLik deviance df.resid
##    244.5    252.5   -118.2    236.5       51
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -0.83161 -0.64280  0.08876  0.30004  0.50794
##
## Random effects:
##  Groups  Name        Variance  Std.Dev.
##  plantid (Intercept) 1.596e+00 1.263e+00
##  plot    (Intercept) 1.049e-10 1.024e-05
## Number of obs: 55, groups:  plantid, 55; plot, 11
```
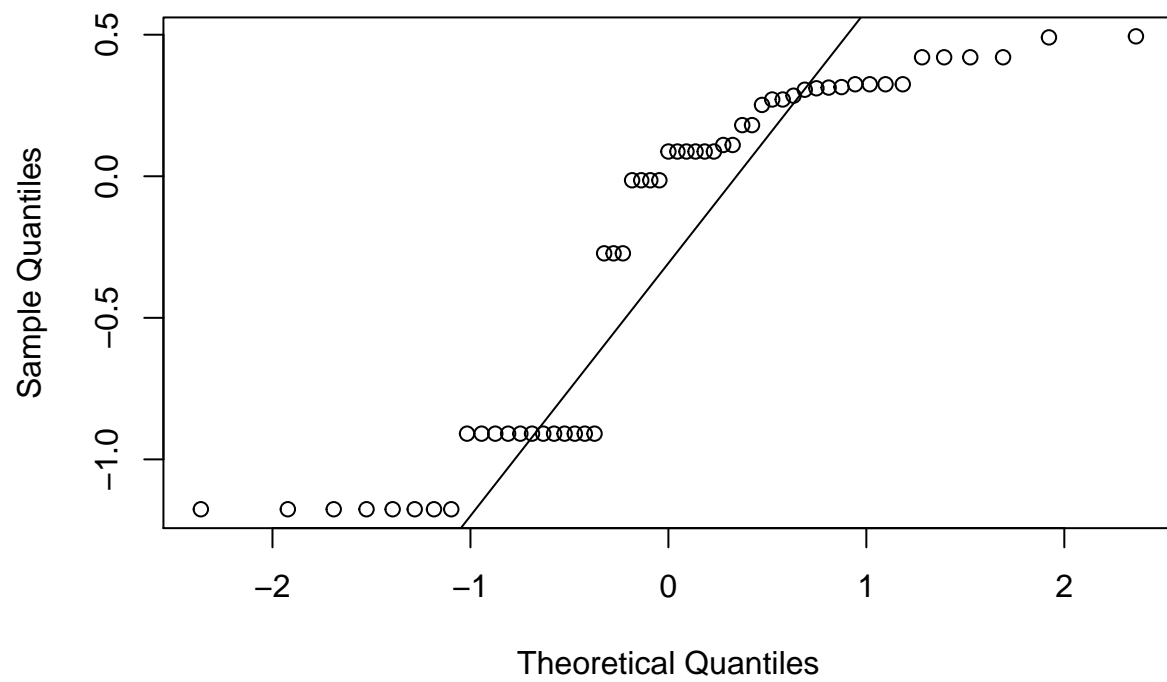
```
## 
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.2243     0.3379  -0.664   0.5069
## treatmentH    0.9595     0.4236   2.265   0.0235 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Correlation of Fixed Effects:
##            (Intr)
## treatmentH -0.711
```
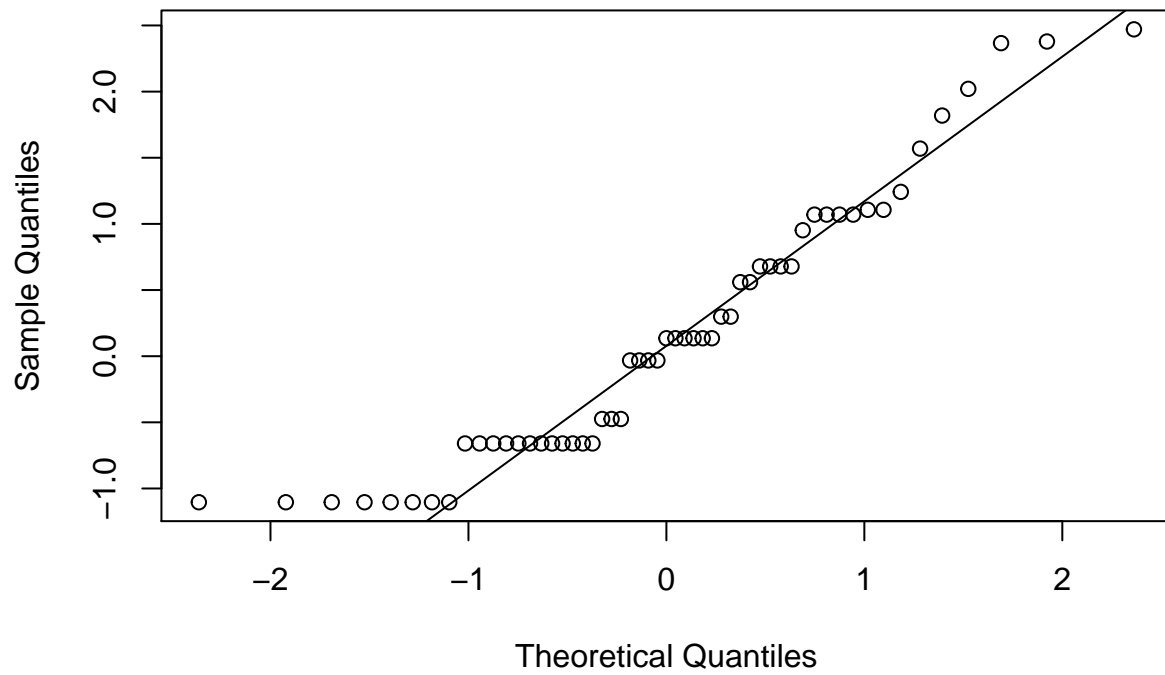
```r
plot(mod15)
```



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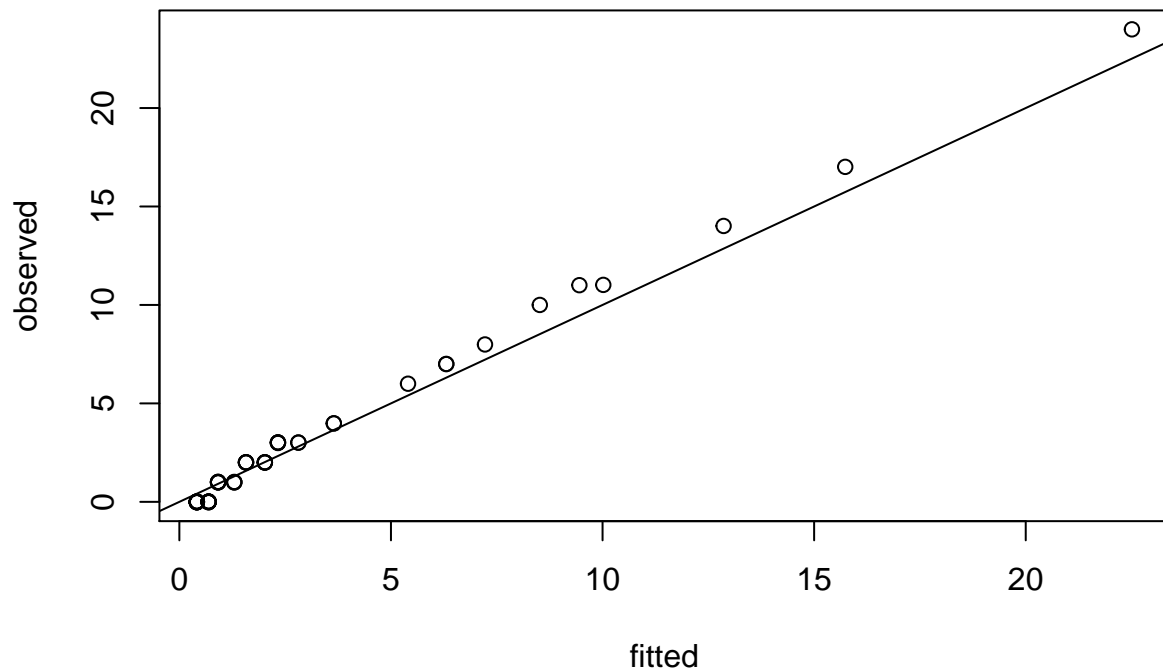
normal qq-plot, residuals


```
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) + (1|plot), data = flowers, family = poisson)
dispersion_glmer(mod16)
```

```
## [1] 1.0036
```

```
summary(mod16)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: year16 ~ treatment + (1 | plantid) + (1 | plot)
##    Data: flowers
##
##      AIC      BIC   logLik deviance df.resid
##    321.5    329.6   -156.8    313.5       51
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.20095 -0.34878 -0.01322  0.27306  0.78018
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  plantid (Intercept) 0.5214   0.7221
##  plot    (Intercept) 0.0000   0.0000
## Number of obs: 55, groups:  plantid, 55; plot, 11
##
```
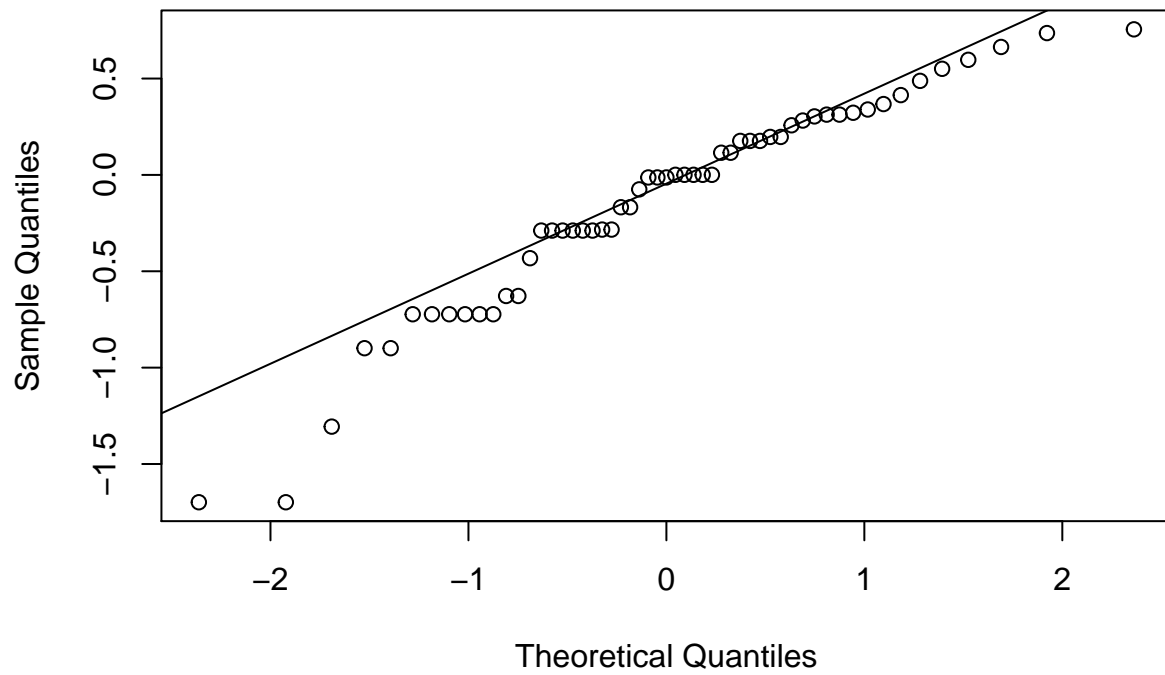
```
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.1182     0.1795   6.228 4.72e-10 ***
## treatmentH    0.9603     0.2350   4.087 4.38e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr)
## treatmentH -0.742
```
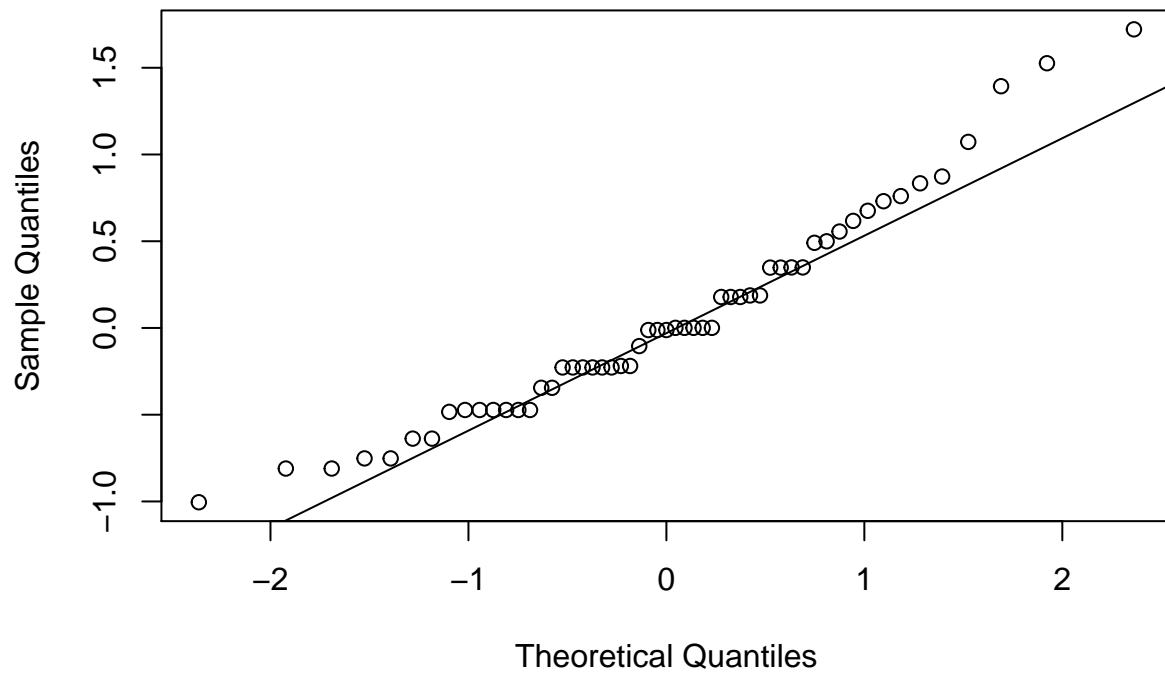
```r
plot(mod16)
```
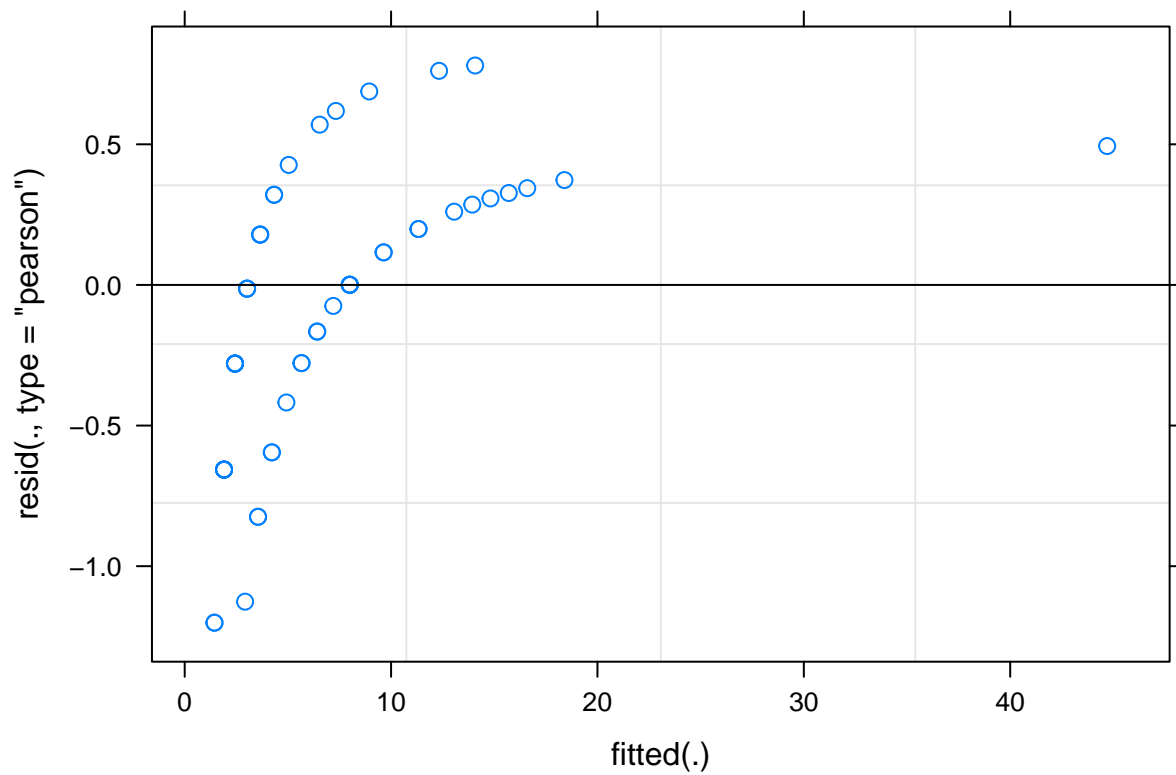


```r
qqnorm(resid(mod16), main="normal qq-plot, residuals")
qqline(resid(mod16))
```

normal qq−plot, residuals


```
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