Honeysuckle Density	Species Richness
24	6
5	12
13	3
31	2
20	10
4	8
13	15
4	20

```
dat <- read.csv("data.csv")
dat
```

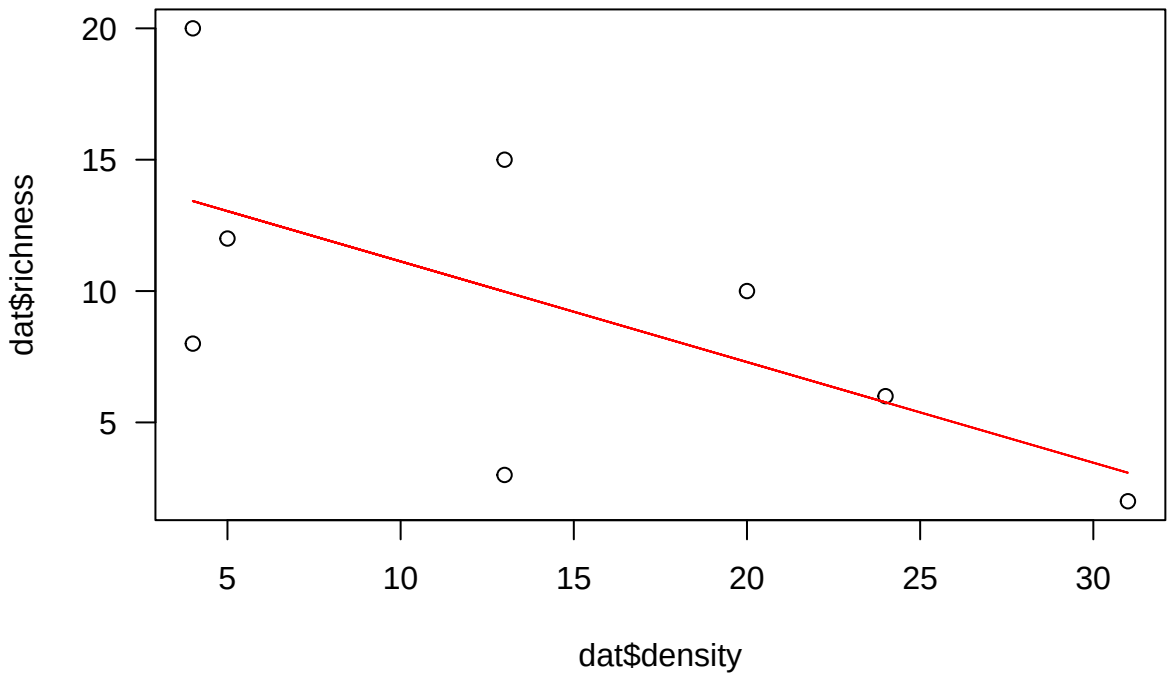
```
##   density richness
## 1      24        6
## 2       5       12
## 3      13        3
## 4      31        2
## 5      20       10
## 6       4        8
## 7      13       15
## 8       4       20
```

Analyze the data set. Do a linear regression of Species Richness on Honeysuckle Density.

```
library(graphics)
dat$richness ~ dat$density
```

```
## dat$richness ~ dat$density
```

```
plot(dat$richness ~ dat$density, las = 1)
regression <- lm(richness ~ density, data = dat)
lines(dat$density, predict(regression), col = "red")
```




```
anova(regression)
```

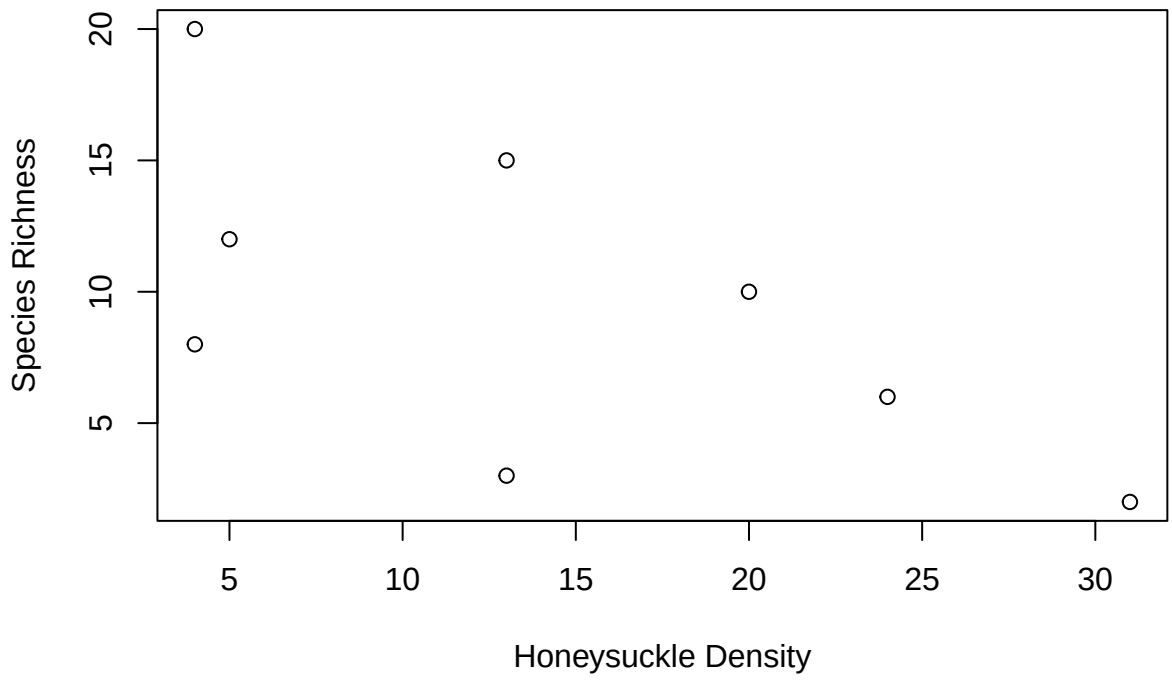
```
## Analysis of Variance Table
##
## Response: richness
##           Df Sum Sq Mean Sq F value  Pr(>F)
## density    1  103.8 103.804  3.9874 0.09283 .
## Residuals  6  156.2  26.033
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(regression)
```

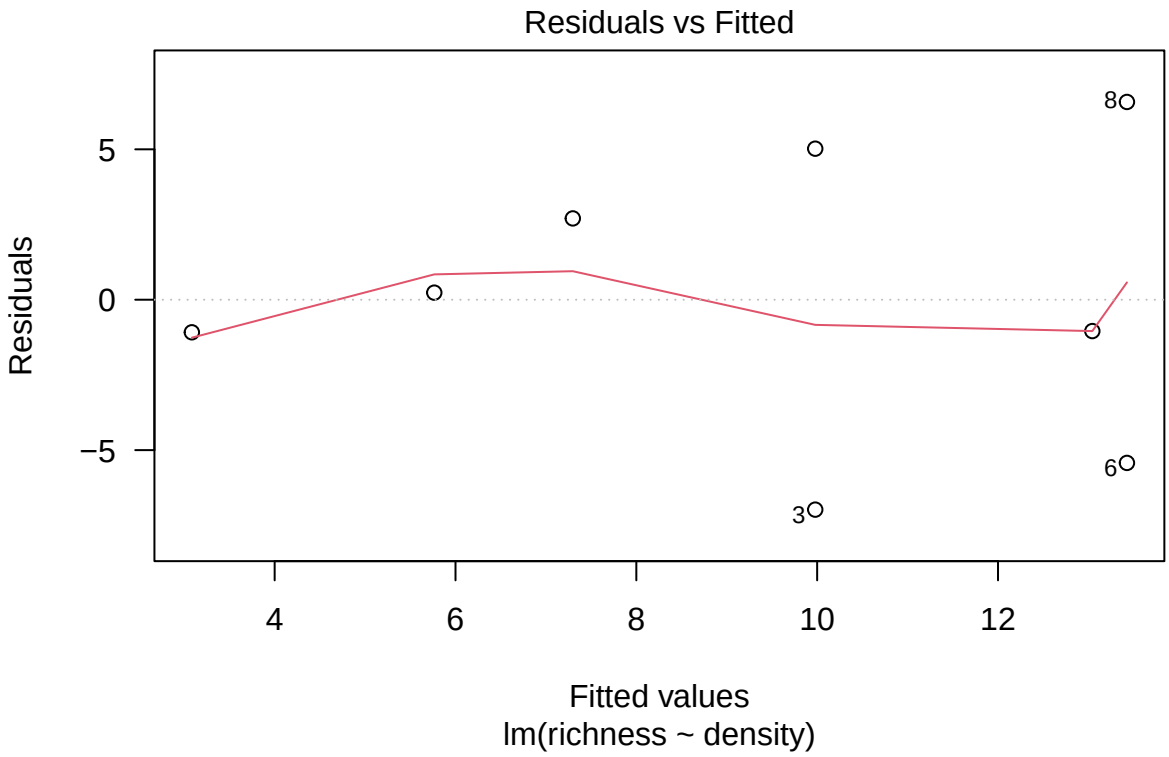
```
##
## Call:
## lm(formula = richness ~ density, data = dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.9788 -2.1696 -0.4042  3.2822  6.5739
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  14.9583     3.2750   4.567  0.00382 **
## density      -0.3830     0.1918  -1.997  0.09283 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

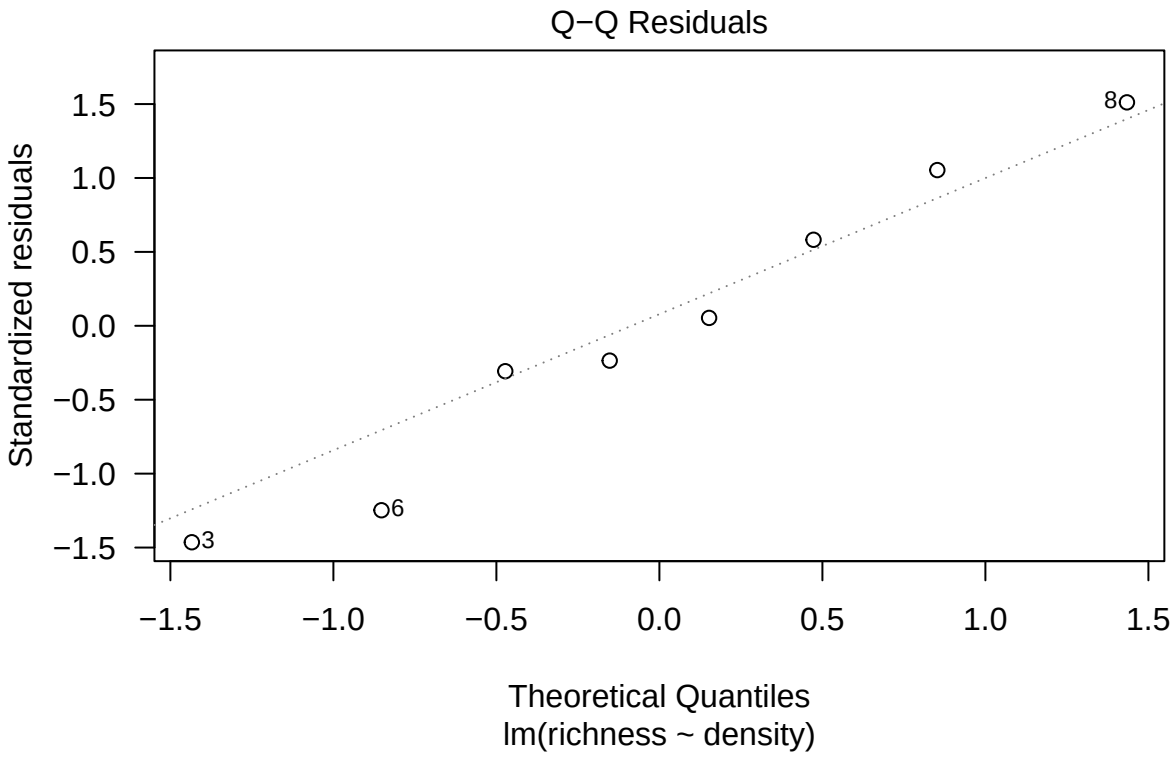
```
##
## Residual standard error: 5.102 on 6 degrees of freedom
## Multiple R-squared:  0.3992, Adjusted R-squared:  0.2991
## F-statistic: 3.987 on 1 and 6 DF,  p-value: 0.09283
```

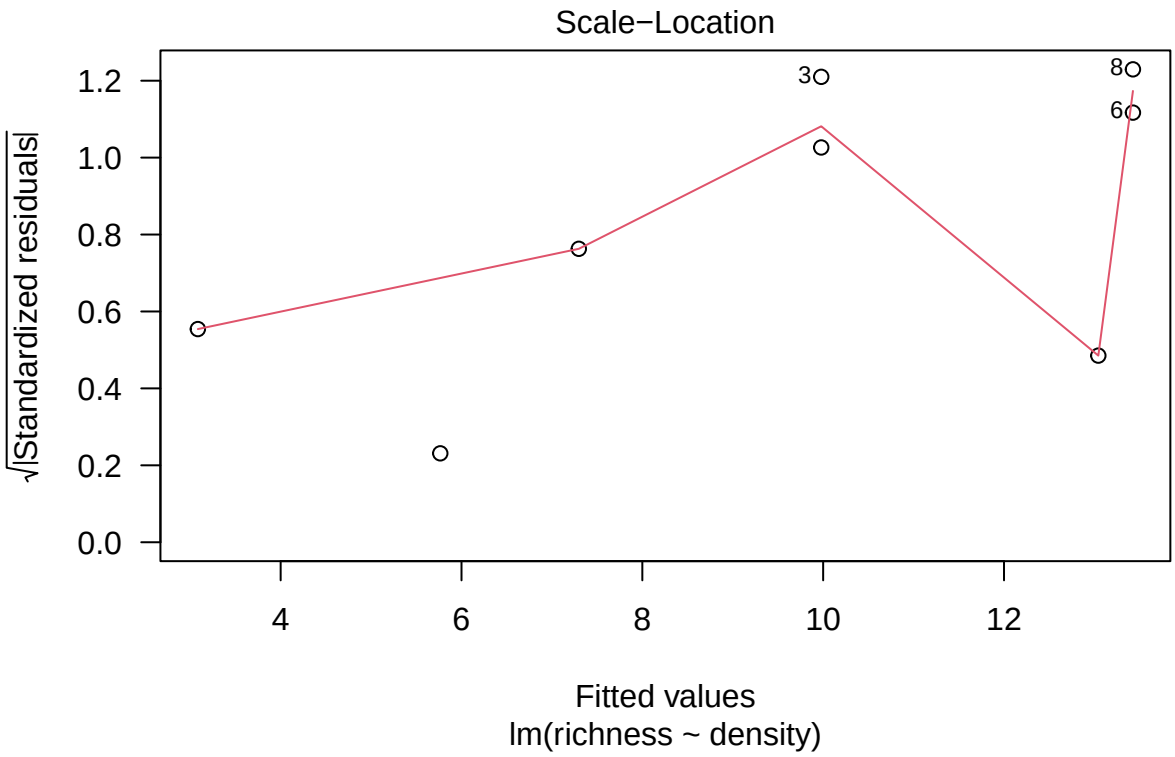
```r
plot(
  richness ~ density,
  data = dat,
  xlab = "Honeysuckle Density",
  ylab = "Species Richness"
)
```

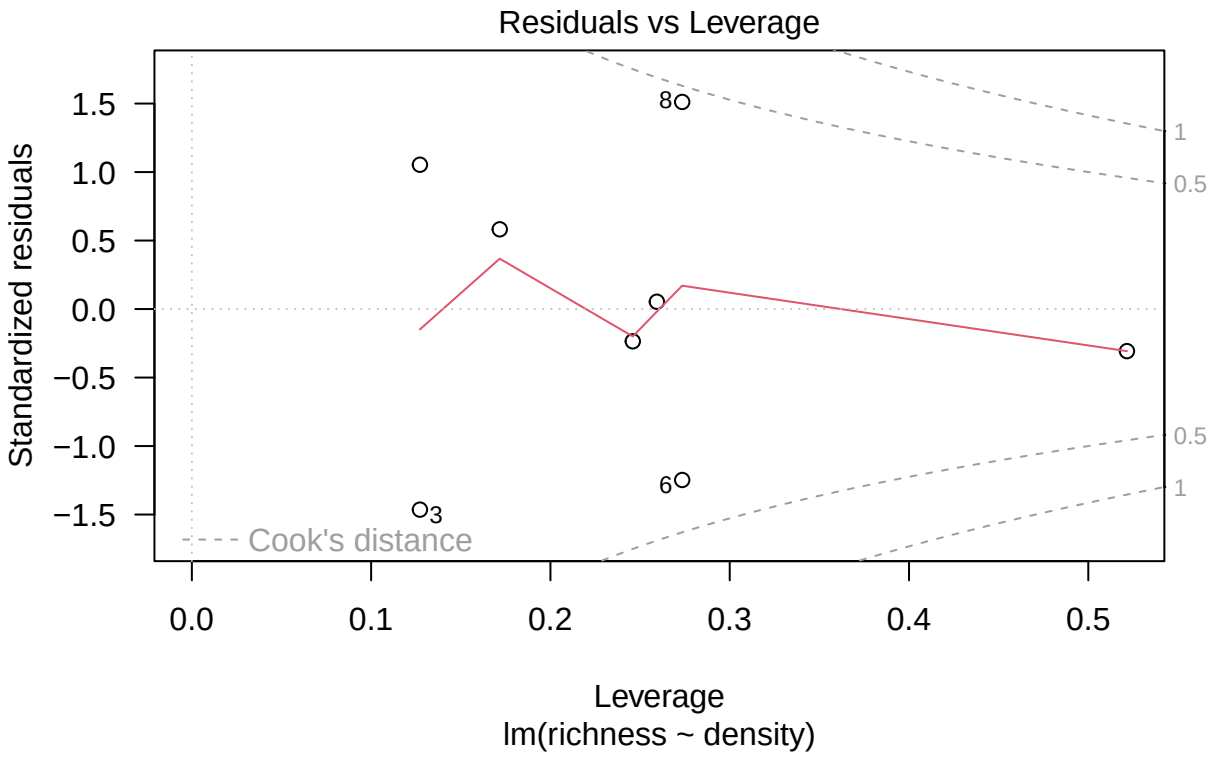



```r
plot(regression, las = 1)
```


Residuals vs Fitted
Residuals
5
0
−5
8
3
6
4
6
8
10
12
Fitted values
lm(richness ~ density)


Q−Q Residuals
Standardized residuals
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
8
6
3
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Theoretical Quantiles
lm(richness ~ density)


Scale−Location
√|Standardized residuals|
1.2
1.0
0.8
0.6
0.4
0.2
0.0
3
8
6
4
6
8
10
12
Fitted values
lm(richness ~ density)


Residuals vs Leverage
Standardized residuals
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
8
3
6
1
0.5
0.5
1
Cook's distance
0.0
0.1
0.2
0.3
0.4
0.5
Leverage
lm(richness ~ density)