STAT 206 Homework 7

Due Monday, November 20, 5:00 PM

General instructions for homework: Homework must be completed as an R Markdown file. Be sure to include your name in the file. Give the commands to answer each question in its own code block, which will also produce plots that will be automatically embedded in the output file. Each answer must be supported by written statements as well as any code used. (Examining your various objects in the "Environment" section of RStudio is insufficient – you must use scripted commands.)

Part I - Beverton-Holt model

The dataset at [http://www.faculty.ucr.edu/~jflegal/fish.txt] contains 40 annual counts of the numbers of spawners `S` and recruits `R` in a salmon population. The units are thousands of fish. Spawners are fish that are laying eggs. Spawners die after laying eggs. Recruits are fish that enter the catchable population.

The classic **Beverton-Holt** model for the relationship between spawners and recruits is

$$R = \frac{1}{\beta_1 + \beta_2/S} \ , \quad \beta_1 > 0, \beta_2 > 0$$

where R and S are the number of recruits and spawners respectively.

Consider the problem of maintaining a sustainable fishery. The total population abundance will only stabilize if $R = S$. The total population will decline if fewer recruits are produced than the number of spawners who died producing them. If too many recruits are produced, the population will also decline eventually because there is not enough food for them all. Thus, only a balanced level of recruits can be sustained indefinitely in a stable population. This stable population level is the point where the 45° line intersects the curve relating R and S. In other words, it is the N such that

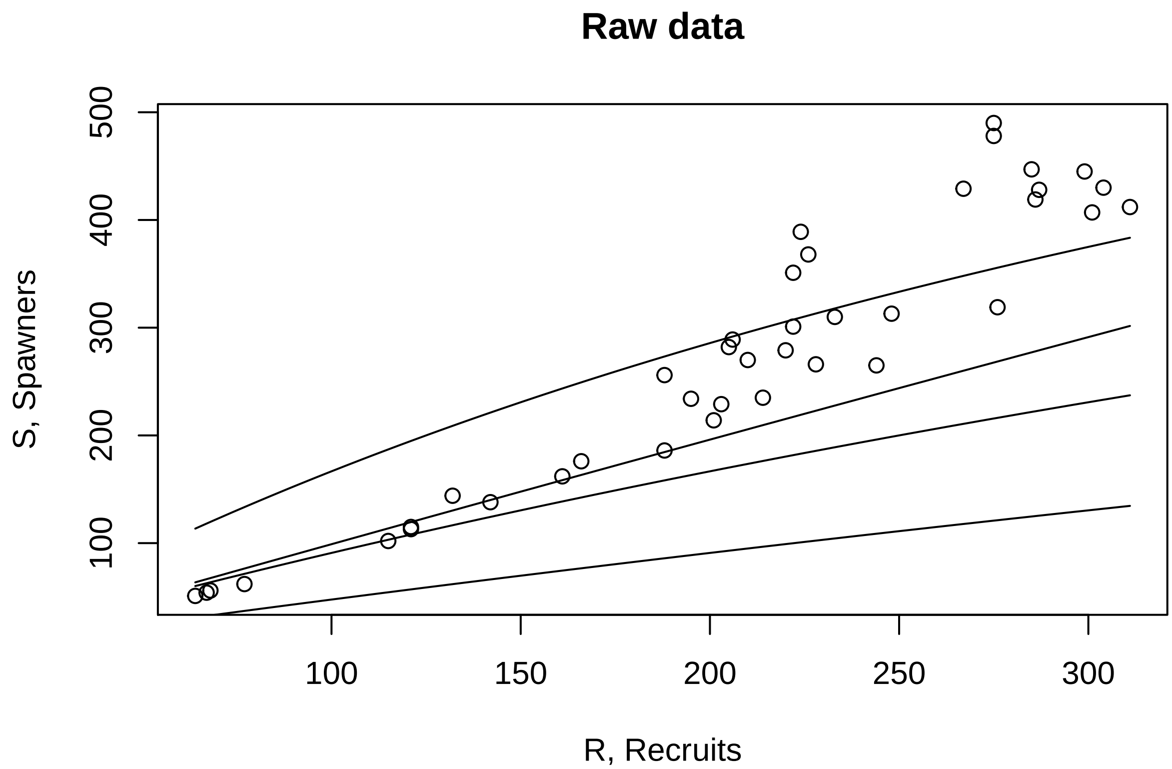
$$N = \frac{1}{\beta_1 + \beta_2/N}.$$

Solving for N we see that the stable population level is $N = (1 - \beta_2)/\beta_1$.

1. Make a scatterplot of the data and overlay the Beverton-Holt curve for a couple different choices of β_1 and β_2.

```
#From some guessing I've found that beta1 needs to be close to 0 and beta2 needs to be realtively much
#larger to get that lines to follow the curve at all

data = read.table( file = "http://www.faculty.ucr.edu/~jflegal/fish.txt", header = TRUE)
#data

beta1 = .001
beta2 = 1
fun = function(x) {
  1 / (beta1 + (beta2 / x))
}

plot(data, main = "Raw data", xlab = "R, Recruits", ylab = "S, Spawners")
curve(fun, add = TRUE)
beta1 = .001
beta2 = 2
curve(fun, add = TRUE)
```

```r
beta1 = .0001
beta2 = 1
curve(fun, add = TRUE)
beta1 = .001
beta2 = .5
curve(fun, add = TRUE)
```

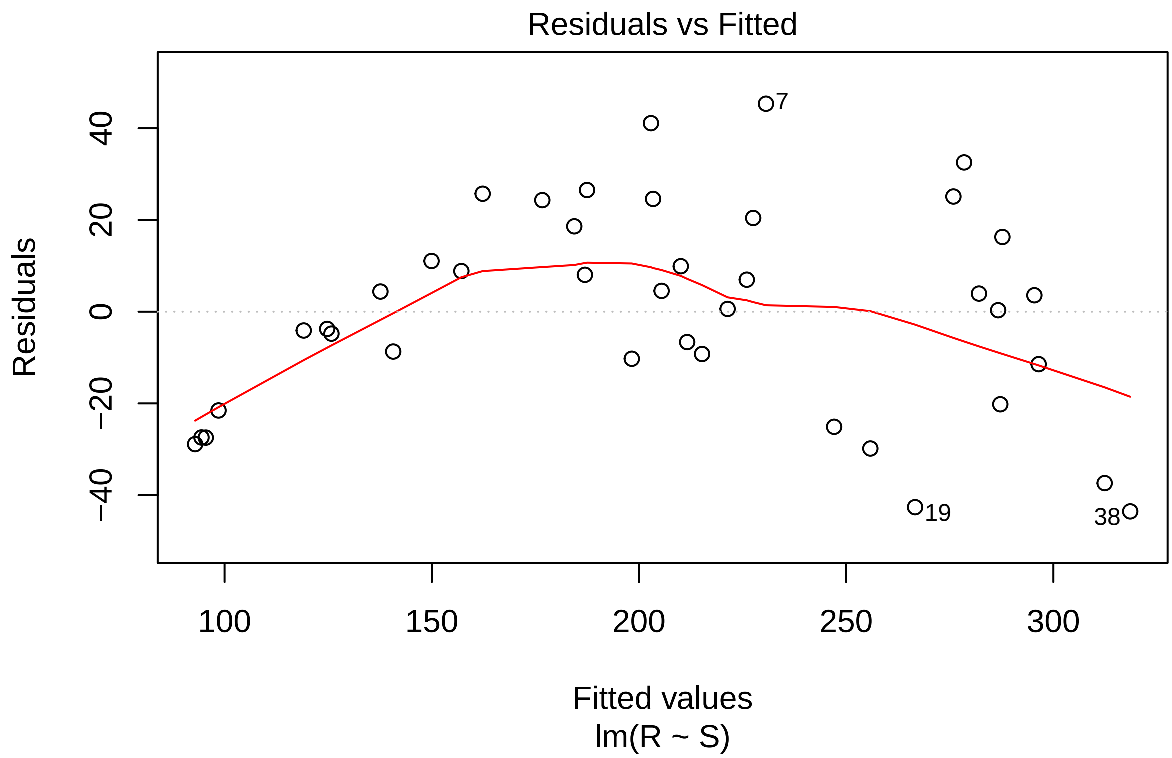


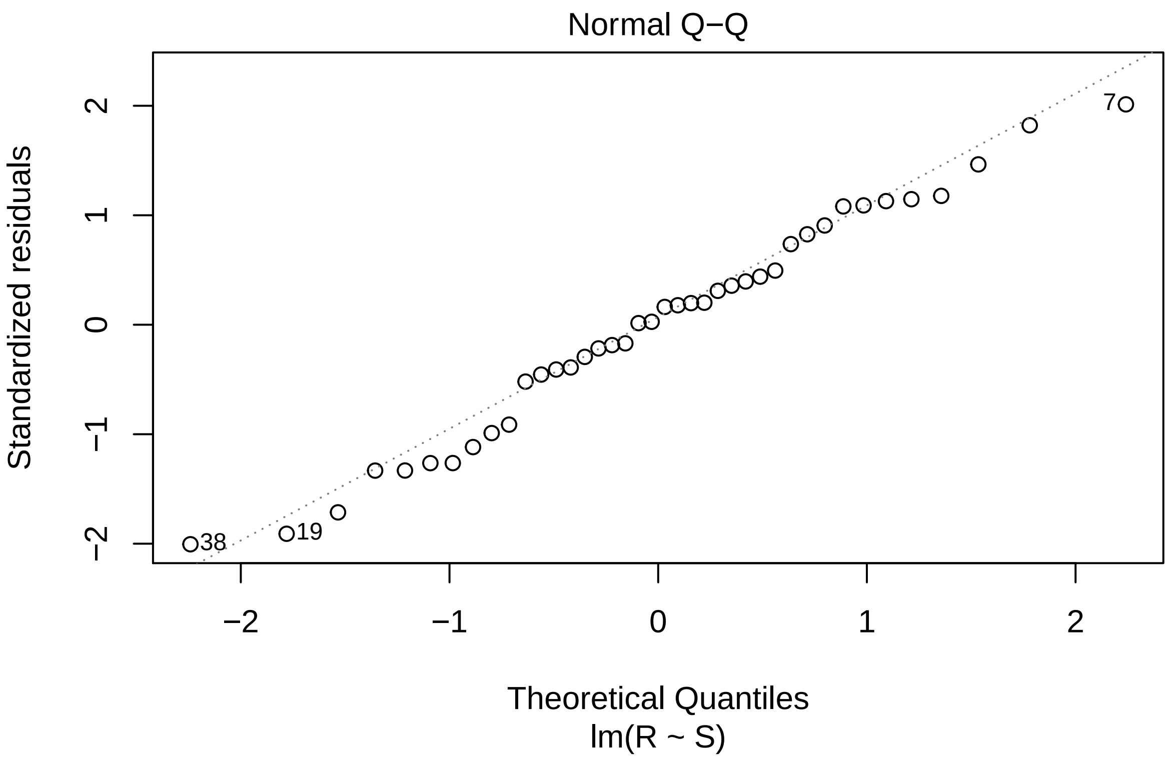
2. The Beverton-Holt model can be found by transforming $R \mapsto (1/R)$ and and $S \mapsto (1/S)$. That is,

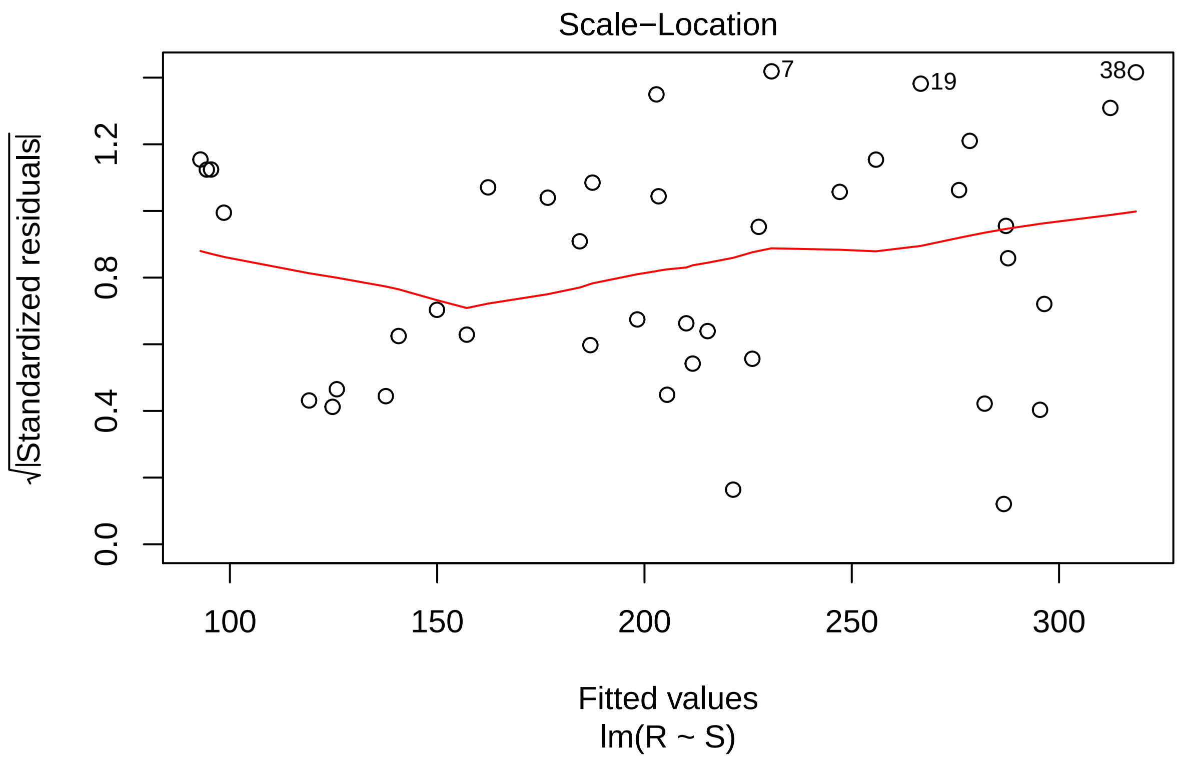
$$(1/R) = \beta_1 + \beta_2(1/S).$$

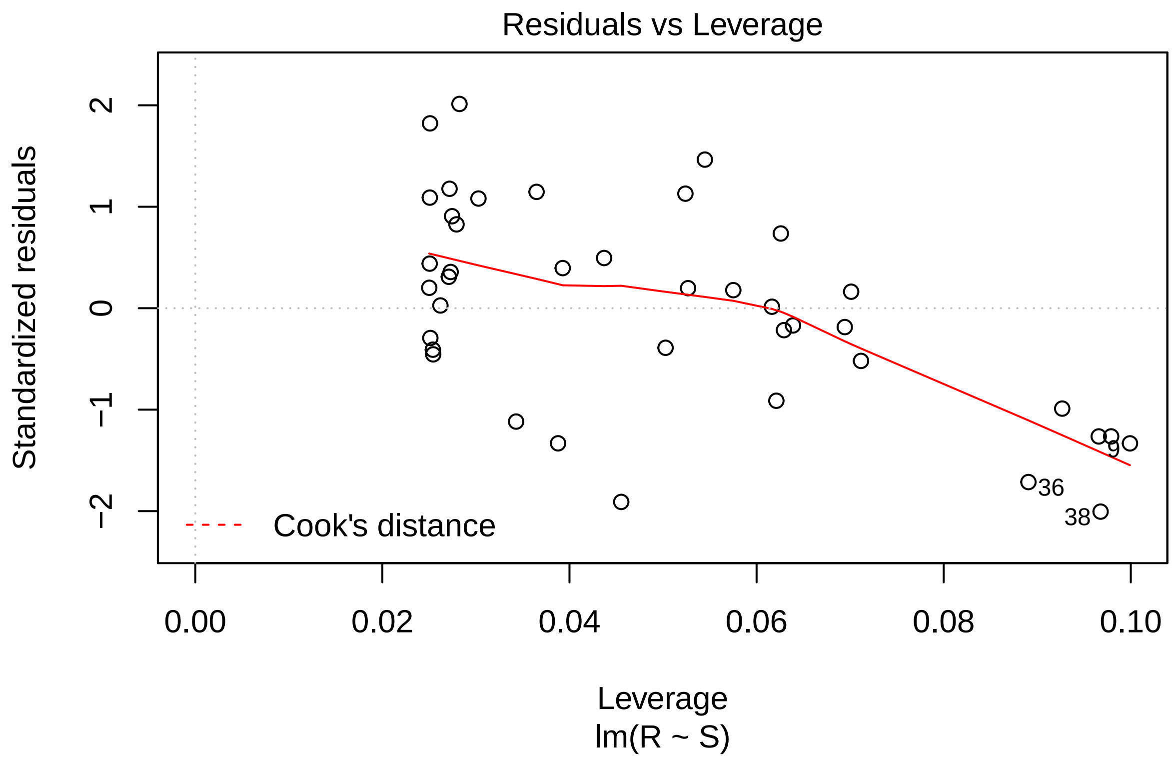
This is a linear model with response variable $(1/R)$ and covariate $(1/S)$. Use least squares regression to fit this model to the fish dataset.

```r
beta1 = .001
beta2=.5
l_fun = function(x) {
  beta1 + (beta2 / (1/x))
}

model = lm(R ~ S, data)

plot(model)
```


Residuals vs Fitted
Residuals
40
20
0
−20
−40
7
19
38
100
150
200
250
300
Fitted values
lm(R ~ S)


Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(R ~ S)
−2
−1
0
1
2
38
19
7


Scale−Location
7
19
38
0.0
0.4
0.8
1.2
√|Standardized residuals|
100
150
200
250
300
Fitted values
lm(R ~ S)



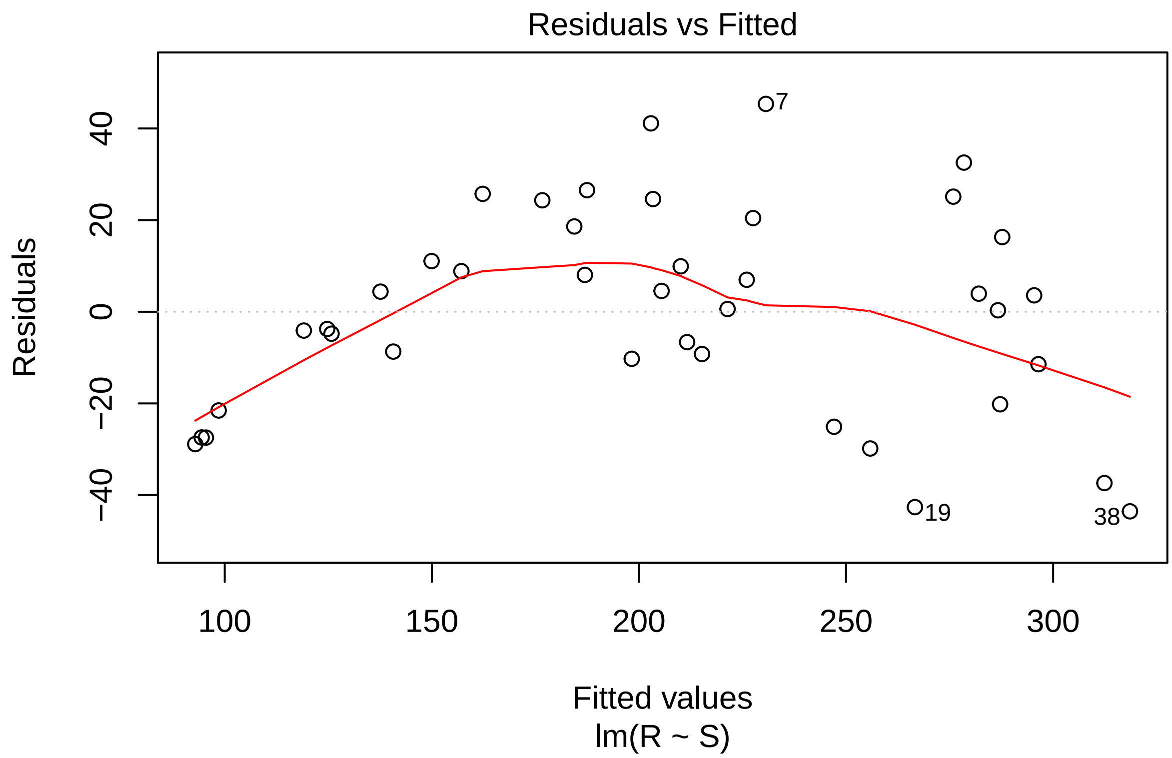
3. Find an estimate for the stable population level, where $R = S$ in the Beverton-Holt model.

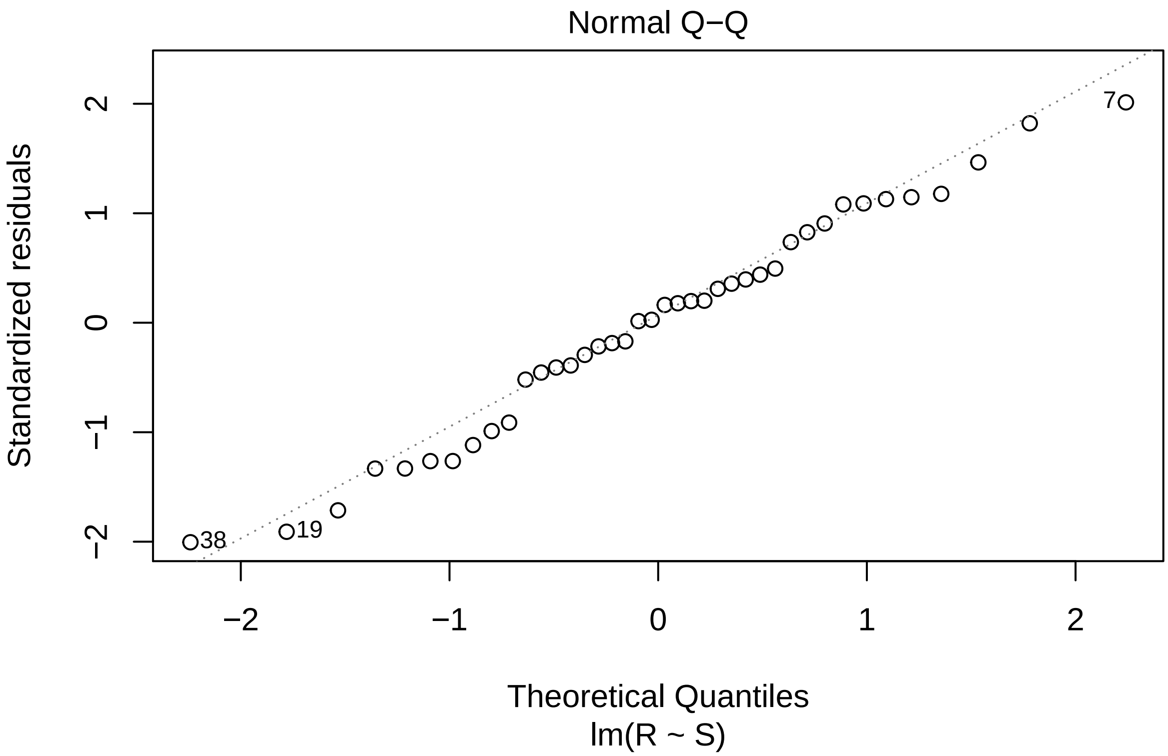
```
#Using abline I have added at 45 degree line. Where this line and the fitted line meet is where
#the population is stable. That appears to be around (.06, 0)

beta1 = .005
beta2=.1
l_fun = function(x) {
  beta1 + (beta2 / (1/x))
}



model = lm(R ~ S, data)
summary(model)
```

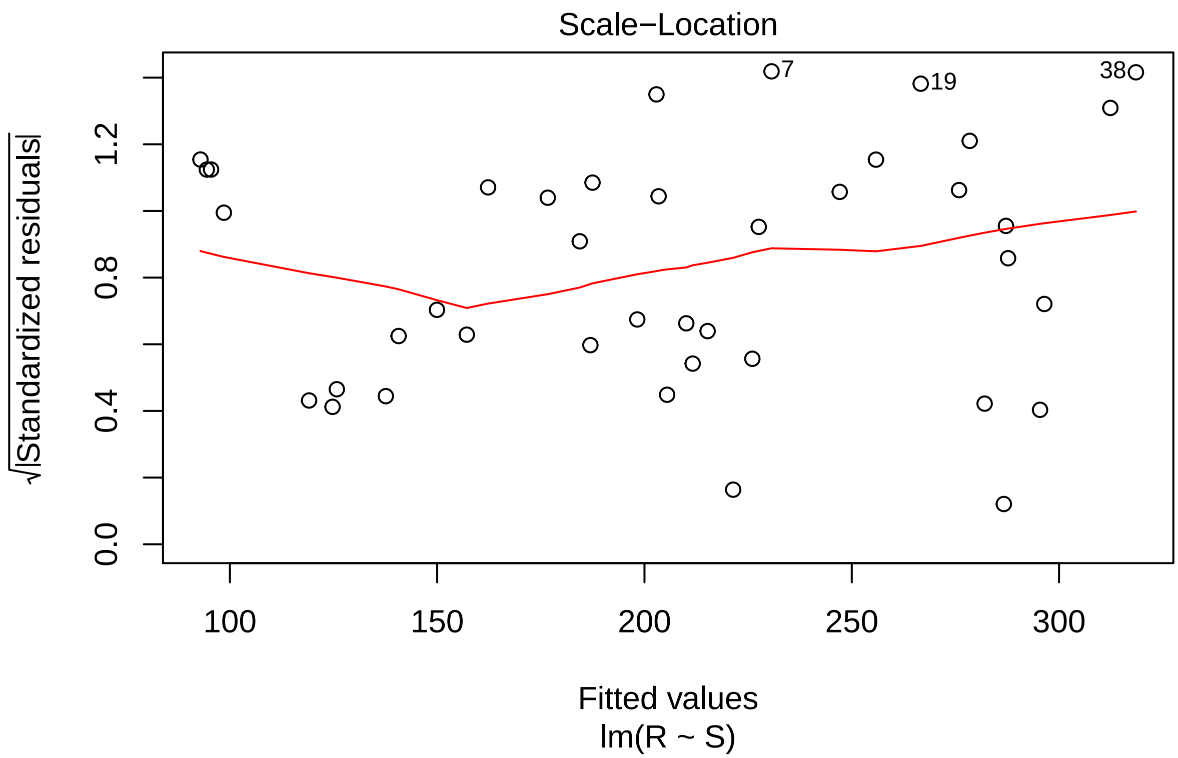
```
##
## Call:
## lm(formula = R ~ S, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -43.548 -13.631   2.094  16.875  45.352
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  66.6706     8.4996   7.844 1.83e-09 ***
```

```
## S              0.5140     0.0282  18.231  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 22.85 on 38 degrees of freedom
## Multiple R-squared:  0.8974, Adjusted R-squared:  0.8947
## F-statistic: 332.4 on 1 and 38 DF,  p-value: < 2.2e-16
```

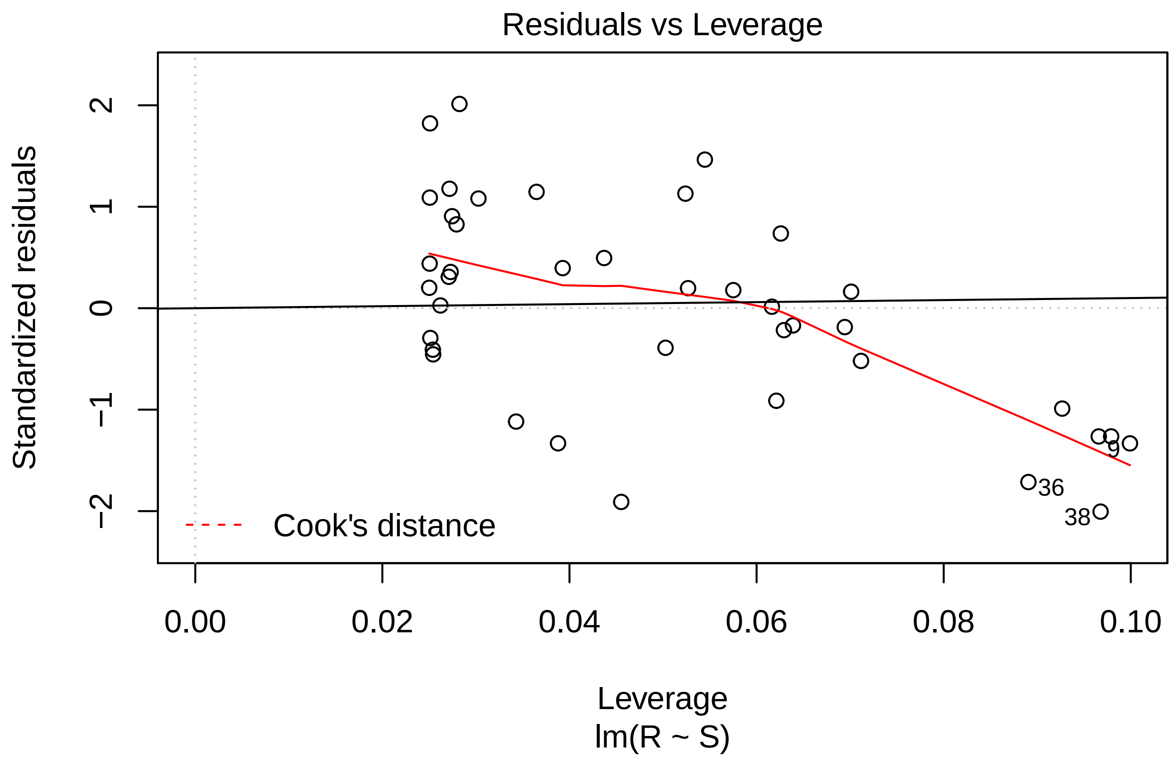
```
plot(model)
```




Normal Q−Q
Standardized residuals
−2
−1
0
1
2
38
19
7
Theoretical Quantiles
lm(R ~ S)




```r
abline(0,1)
test = locator()
```




```
test
```

```
## NULL
```

4. Use the bootstrap to obtain the sampling distribution and standard error for the stable population level. Use the bootstrap to construct a 95% confidence interval for the stable population level.

Part II - Snowfall accumulations

The data set `buffalo` at [http://www.faculty.ucr.edu/~jflegal/buffalo.txt] contains annual snowfall accumulations in Buffalo, NY from 1910 to 1973.

5. Construct kernel density estimates of the data using the Gaussian and Epanechnikov kernels.
6. Compare the estimates for different choices of bandwidth.
7. Is the estimate more influenced by the type of kernel or the bandwidth?