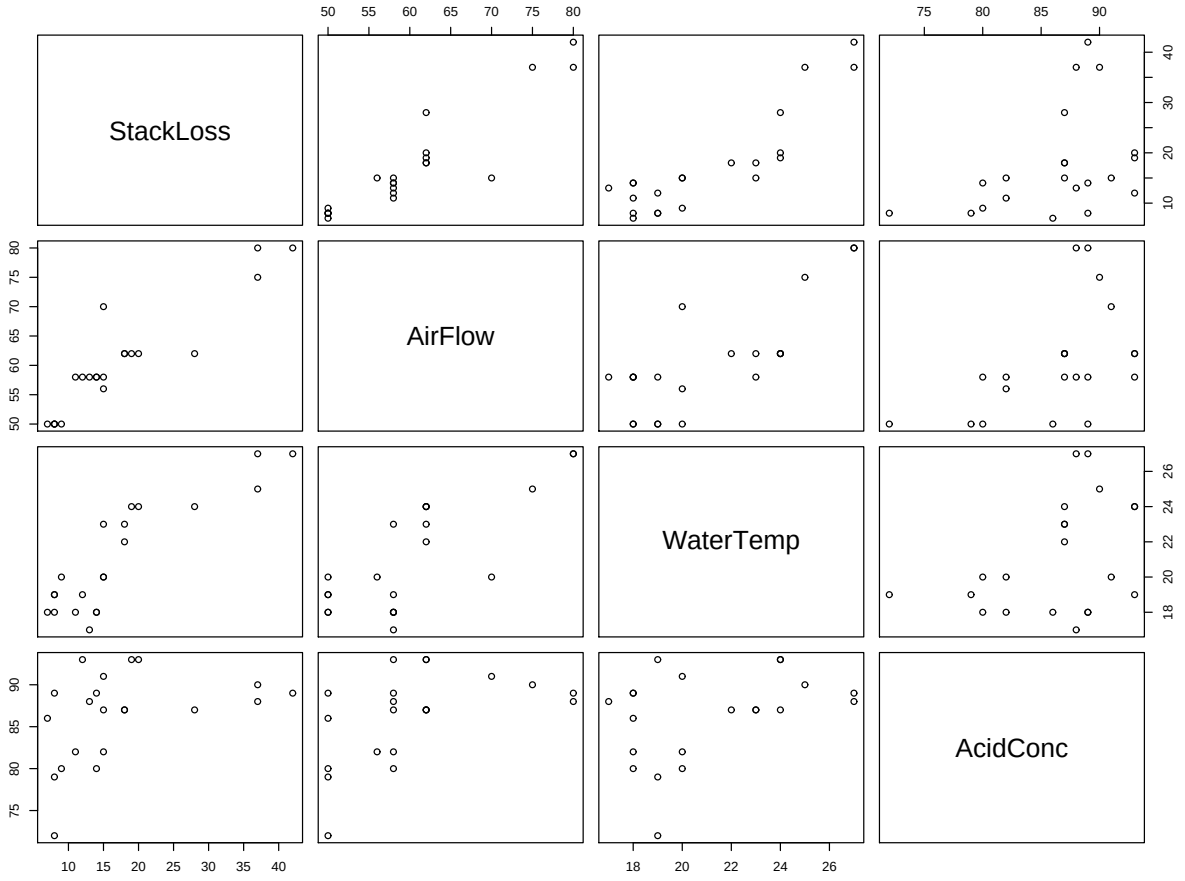
Regression Diagnostics in R/S-Plus

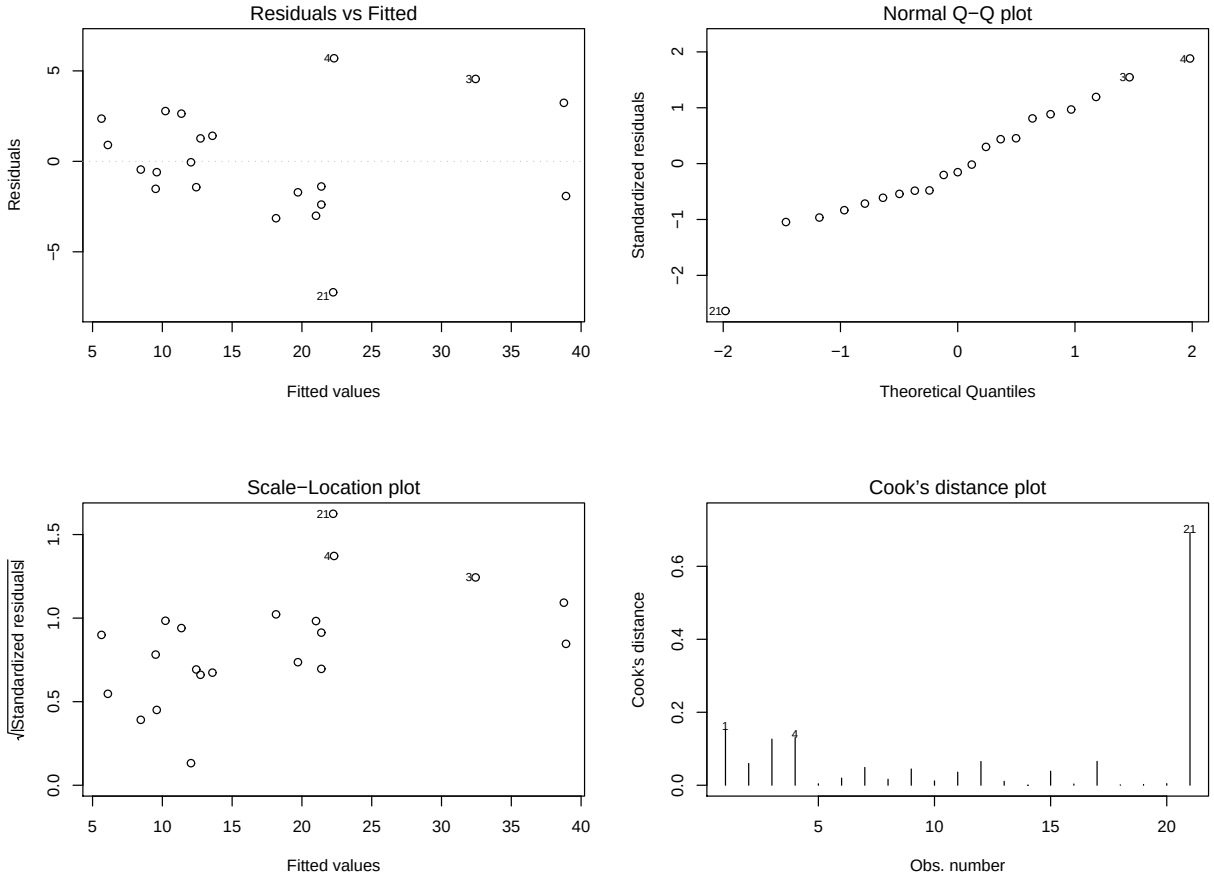
Example: Stack Loss Data

```
> stackloss <- read.table("http://www.stat.duke.edu/courses/Spring03/sta244/Data/stackloss",
              header=T)

# Always plot the data!!!
> postscript("stackloss-pair.ps")
> pairs(stackloss)
> dev.off()
```




```
#  Fit the linear model with all variables, no transformations

> lm1 <- lm(StackLoss ~ ., qr=T, data=stackloss)

# use qr = T  as an option in order to obtain additional diagnostics later.

> par(mfrow=c(2,2))
> plot(lm1)
> postscript("stackloss-residuals.ps")
> dev.off()
```

Anything alarming?




```
> summary(lm1)
Call:
lm(formula = StackLoss ~ ., data = stackloss, qr = T)

Residuals:
    Min      1Q  Median      3Q     Max
-7.2377 -1.7117 -0.4551  2.3614  5.6978

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -39.9197    11.8960  -3.356  0.00375 **
AirFlow       0.7156     0.1349   5.307  5.8e-05 ***
WaterTemp     1.2953     0.3680   3.520  0.00263 **
AcidConc     -0.1521     0.1563  -0.973  0.34405
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.243 on 17 degrees of freedom
Multiple R-Squared: 0.9136,     Adjusted R-squared: 0.8983
F-statistic:  59.9 on 3 and 17 DF,  p-value: 3.016e-09
```

Diagnostics

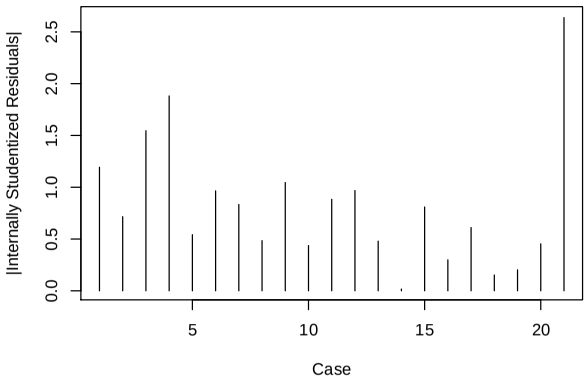
The function `ls.diag` is used to obtain many standard regression diagnostics. It was originally used with an argument that was the output of the function lsfit, but if you use `qr=T` in the `lm` command, you can use ls.diag() with lm's output too. The output is a list with the following numeric components:

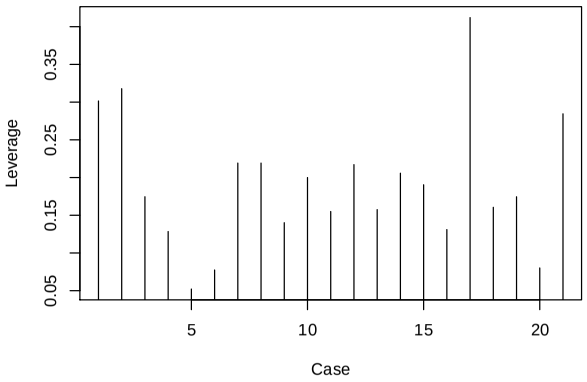
- std.dev: The standard deviation of the errors, an estimate of sigma.
- hat: diagonal entries h_{ii} of the hat matrix H
- std.res: standardized residuals
- stud.res: studentized residuals
- cooks: Cook's distances
- dfits: DFITS statistics
- correlation: correlation matrix
- std.err: standard errors of the regression coefficients
- cov.scaled: Scaled covariance matrix of the coefficients
- cov.unscaled: Unscaled covariance matrix of the coefficients

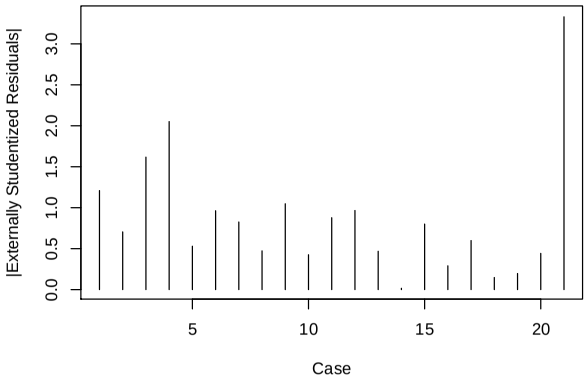
Back to the example:

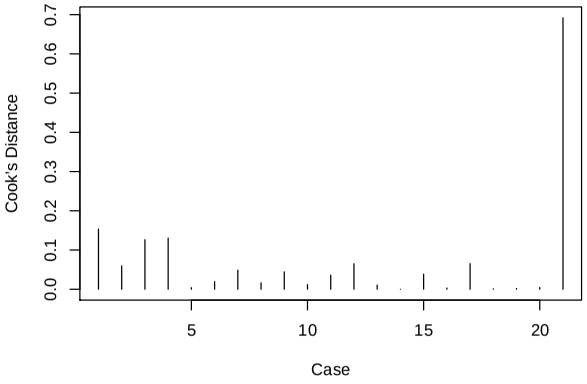
```
> stack.diag <- ls.diag(lm1)
> names(stack.diag)
 [1] "std.dev"      "hat"          "std.res"      "stud.res"     "cooks"
 [6] "dfits"        "correlation"  "std.err"      "cov.scaled"   "cov.unscaled"

> par(mfrow=c(2,2))
> plot(abs(stack.diag$std.res), ylab="|Internally Studentized Residuals|", xlab="Case", type="h")
> plot(stack.diag$hat, ylab="Leverage", xlab="Case",  type="h")
> plot(abs(stack.diag$stud.res), ylab="|Externally Studentized Residuals|", xlab="Case", type="h")
> plot(stack.diag$cooks, ylab="Cook's Distance", ,type="h",xlab="Case")


> 2*(1- pt(max(abs(stack.diag$stud.res)), 16)) #p-value for largest stud residual
[1] 0.00423804
> .05/21  # Bonferonni adjustment for alpha
[1] 0.002380952
> max(abs(stack.diag$stud.res))
[1] 3.330493
> qt(1 - .025/21, 16)  # critical value for rejection region with
Bonferonni adjustment
[1] 3.603616
```

What do we conclude from this?


|Internally Studentized Residuals|
0.0
0.5
1.0
1.5
2.0
2.5
5
10
15
20
Case


Leverage
0.05
0.15
0.25
0.35
5
10
15
20
Case


|Externally Studentized Residuals|
0.0
0.5
1.0
1.5
2.0
2.5
3.0
5
10
15
20
Case


Cook's Distance
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
5
10
15
20
Case