

1 Diagnostic Plots for Linear Models with R

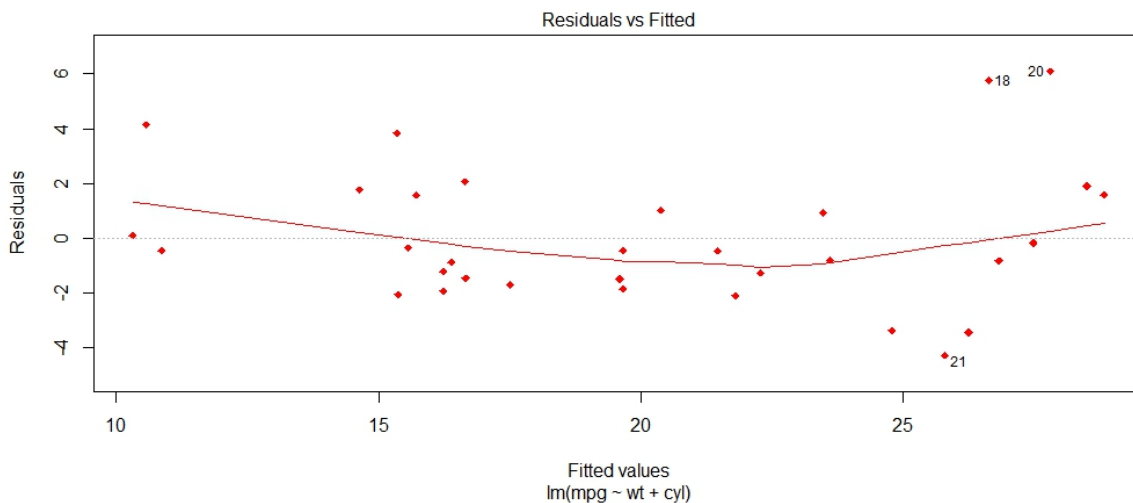
There are six plots (selectable by `which`) are currently available:

1. a plot of residuals against fitted values,
2. a Scale-Location plot of $\sqrt{| residuals |}$ against fitted values,
3. a Normal Q-Q plot,
4. a plot of Cook's distances versus row labels,
5. a plot of residuals against leverages,
6. a plot of Cook's distances against $leverage/(1-leverage)$.

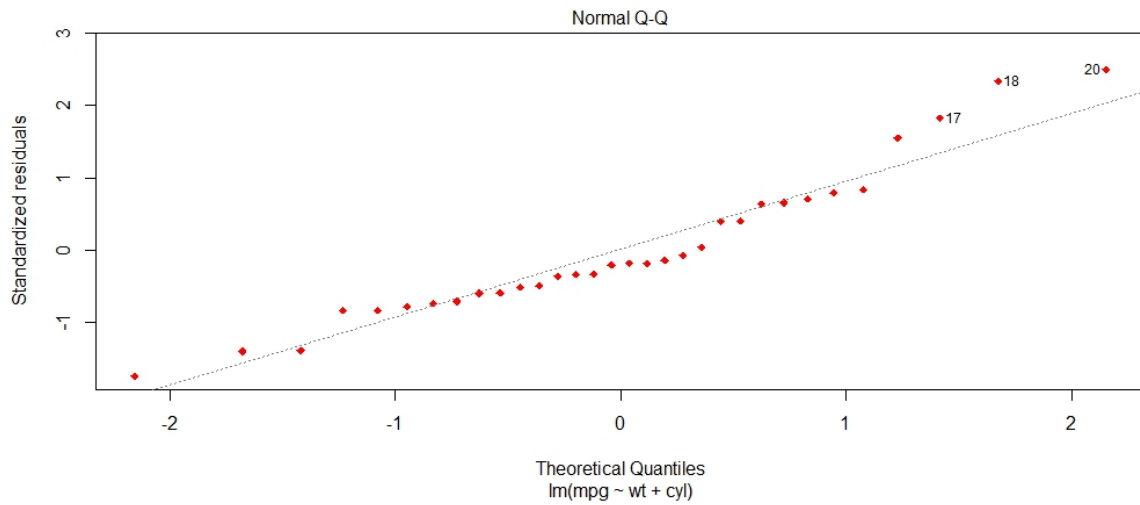
By default, the first three and 5 are provided, if you just type something like `plot(fit)`.

```
plot(lm(mpg~wt+cyl),which=c(1),pch=18,col="red")
plot(lm(mpg~wt+cyl),which=c(2),pch=18,col="red")
plot(lm(mpg~wt+cyl),which=c(3),pch=18,col="red")
plot(lm(mpg~wt+cyl),which=c(4),pch=18,col="red")
plot(lm(mpg~wt+cyl),which=c(5),pch=18,col="red")
plot(lm(mpg~wt+cyl),which=c(6),pch=18,col="red")
```

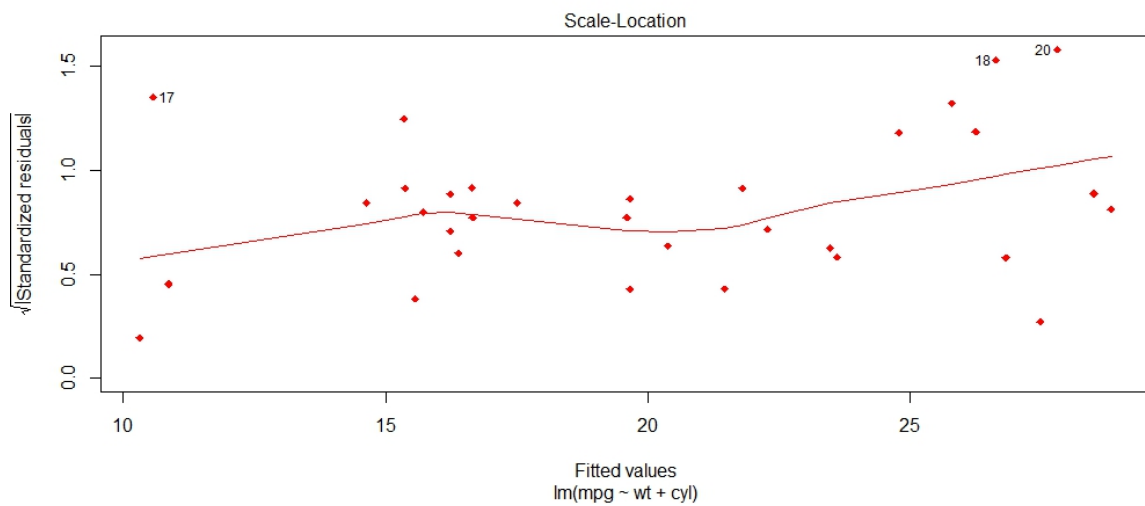
- The **Scale-Location** plot, also called Spread-Location (or S-L plot), takes the square root of the absolute residuals in order to diminish skewness ($\sqrt{|E|}$) is much less skewed than $|E|$ for Gaussian zero-mean E).
- **Plot 5** - The **Residual-Leverage** plot shows contours of equal Cook's distance, for values of `cook.levels` (by default 0.5 and 1) and omits cases with leverage one with a warning. If the leverages are constant (as is typically the case in a balanced aov situation) the plot uses factor level combinations instead of the leverages for the x-axis.
(*The factor levels are ordered by mean fitted value.*)



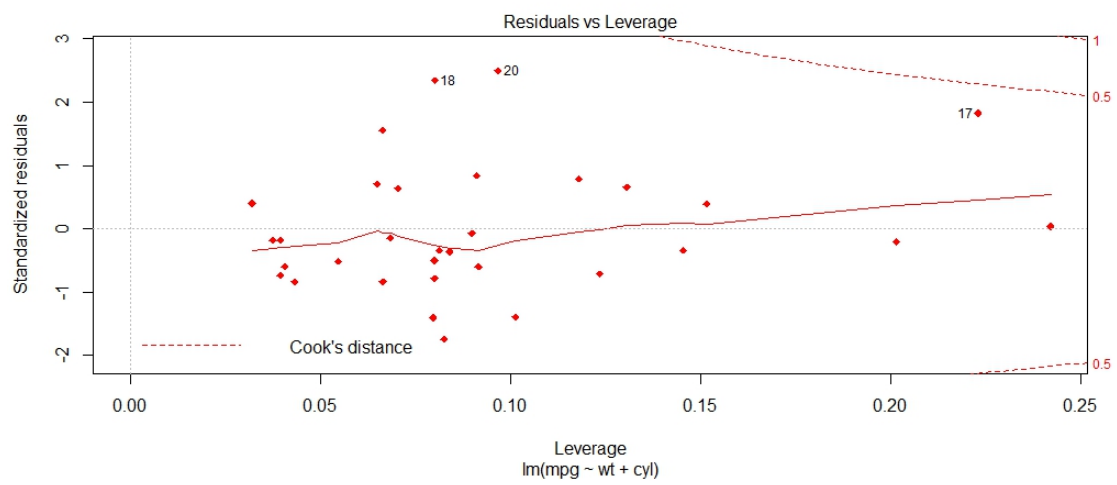
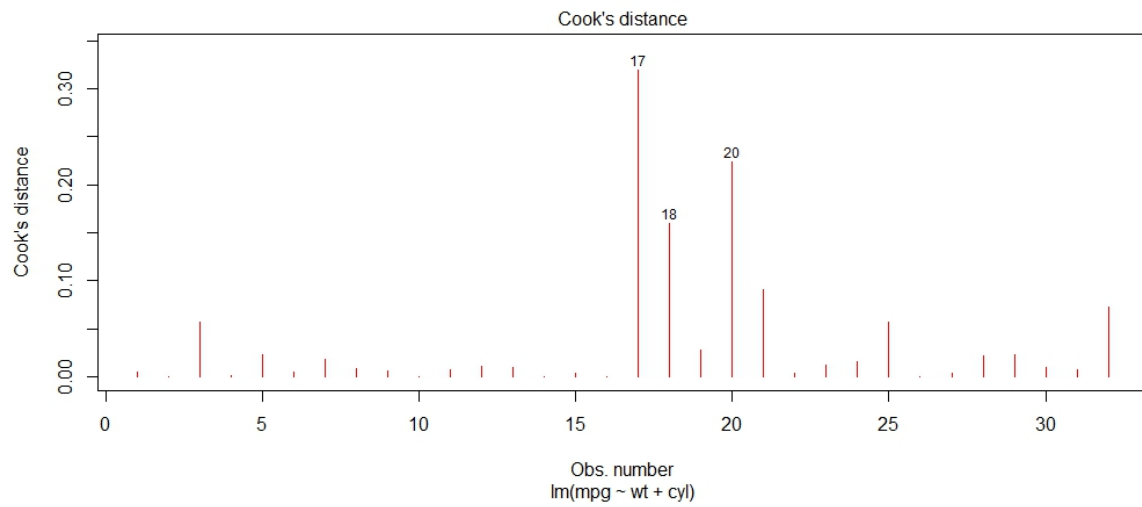
Plot 2 : Normal Probability Plot



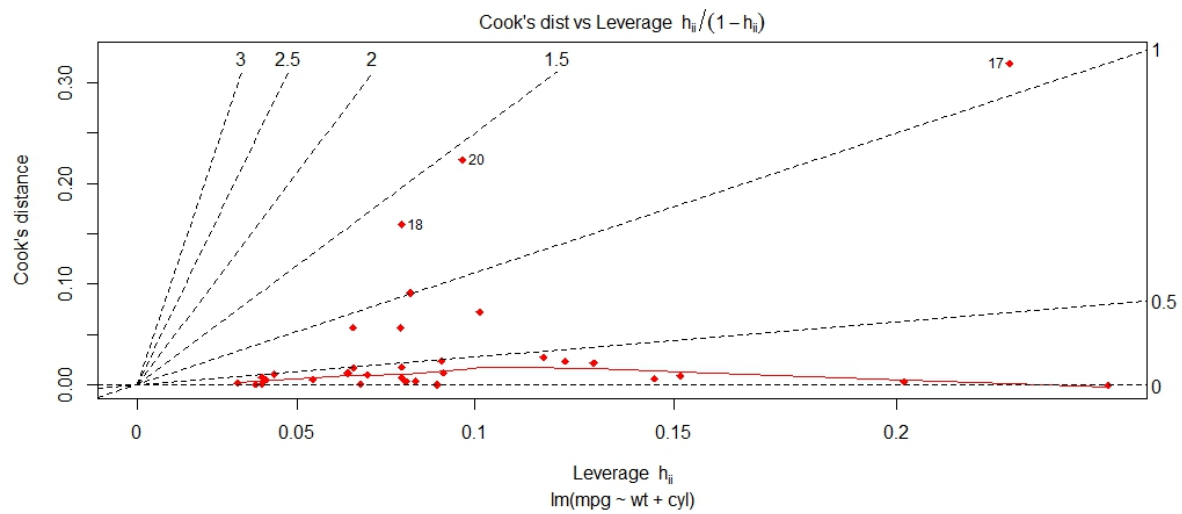
This plot is used to assess the validity of the normality of the residuals.



Plot 5 : Cook's Distance



Plot 6 : Cook's Distance vs Leverage



Plot the four default plots together:

```
par(mfrow=c(4,1))
plot(fittedmodel)
par(opar)
```