## Studentized Residuals

### Definition

Studentized residuals are the standardized "jackknifed" residuals. "Jackknifing" is the process of leave one out such that the studentized residual is the residual where  $y_i$  is compared to the fitted model point  $\hat{y}_i$  where  $y_i$  is not included (equation 1). In equation 1, the denominator is no longer the Mean Square Error, but the Predicted Sum of Squares, or PRESS statistics. NOTE:  $h_{ii}$  is called "leverage" in that it measures the ability of a point to change the regression coefficient (slope) of the model. The greater the effect of moving  $y_i$  on the regression slope, the greater its "leverage."

### **Equations**

$$t_i = \frac{\hat{e_i}}{\hat{\sigma}\sqrt{1 - h_{ii}}}$$
$$h_{ii} = \frac{d\hat{y_i}}{dy_i}$$

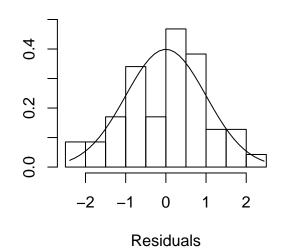
Density

## **Example Plots**

# Studentized Residuals for swiss Model Fertility ~.

## 

# Distribution of Studentized Residuals



## Interpretation and Use

Studentized residuals allow for evaluating how much of an outlier or leverage point that each  $y_i$  is in the data. It serves two purposes in diagnositics. First, the values of  $t_i$  indicate if any points are particularly influential in the model if their values lie outside +-2. Second, the

distribution of the studentized residuals can indicate if the data are non-normal when the distribution does not follow a normal distribution.

#### Further Avenues

QQ Plots - Studentized residuals provide a good method to identify if the residuals are non-normal. A QQ plot will better indicate if this is true for determining model goodness-of-fit.

#### R Code

```
library(MASS)
library(car)
data(swiss)
model <- lm(Fertility ~ ., data=swiss)</pre>
studentResids <- studres(model)</pre>
#plot(studentResids, ylab="Studentized Residuals",
         main="Studentized Residuals for \n swiss Model Fertility ~ .")
#abline(0,0)
\#abline(h=2, lty = 3)
\#abline(h=-2, lty = 3)
#hist(studentResids, freq=FALSE,
         main="Distribution of \nStudentized Residuals",
         xlab = "Residuals", ylim = c(0, 0.5))
\#xfit < -seq(min(studentResids), max(studentResids), length=40)
#yfit<-dnorm(xfit)</pre>
#lines(xfit, yfit)
```