

Regression Diagnostics

Merlise Clyde

September 6, 2017

Outline

- ▶ Leverage

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- ▶ Standardized Residuals

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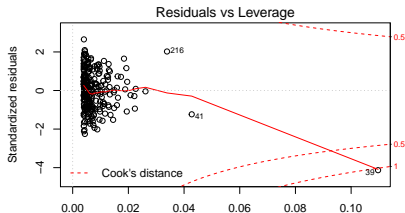
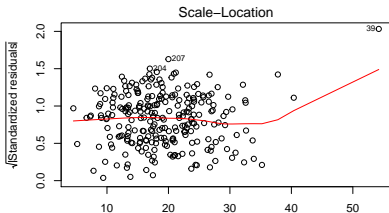
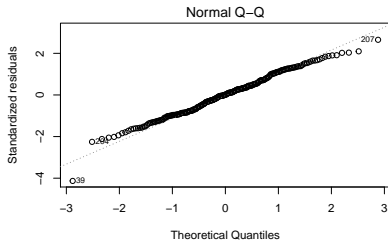
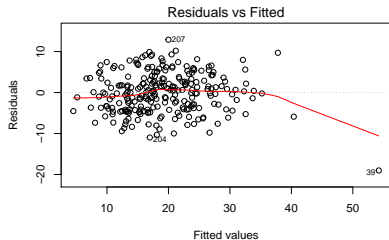
- ▶ Leverage
- ▶ Standardized Residuals
- ▶ Outlier Test

Outline

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- ▶ Standardized Residuals
- ▶ Outlier Test
- ▶ Cook's Distance

Residual Plots

```
bodyfat.lm = lm(Bodyfat ~ Abdomen, data=bodyfat)
par(mfrow=c(2,2))
plot(bodyfat.lm, ask=F)
```



Features of Plots

- ▶ Residuals versus fitted values

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- ▶ standardized residuals versus leverage with contours of Cook's distance: shows influential points where points greater than 1 or $4/n$ are considered influential
- ▶ Case 39 appears to be influential and have a large standardized residual!

Hat Matrix

- predictions

$$\hat{\mathbf{Y}} = \mathbf{X}\hat{\boldsymbol{\beta}} = \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{Y}$$

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 - ▶ potentially influential
- ▶ Leverage: measure of how far x_i is from center of data

$$h_{ii} = 1/n + (\mathbf{x}_i - \bar{\mathbf{x}})^T \left((\mathbf{X} - \mathbf{1}\bar{\mathbf{x}}^T)^T (\mathbf{X} - \mathbf{1}\bar{\mathbf{x}}^T) \right)^{-1} (\mathbf{x}_i - \bar{\mathbf{x}})$$

Residual Analysis

- residuals

$$\mathbf{e} = \mathbf{Y} - \hat{\mathbf{Y}} = (\mathbf{I} - \mathbf{H})\mathbf{Y}$$

$$\text{var}(e_i) = \hat{\sigma}^2(1 - h_{ii})$$

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- ▶ if leverage is near 1 then residual is near 0 and variance is near 0 and r_i is approximately 0 (may not be helpful)

Predicted Residual

- ▶ Estimates without Case (i):

$$\begin{aligned}\hat{\beta}_{(i)} &= (\mathbf{X}_{(i)}^T \mathbf{X}_{(i)})^{-1} \mathbf{X}_{(i)}^T \mathbf{Y}_{(i)} \\ &= \hat{\beta} - \frac{(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{x}_i e_i}{1 - h_{ii}}\end{aligned}$$

*Standardized predicted residual is

$$\frac{e_{(i)}}{\sqrt{\text{var}(e_{(i)})}} = \frac{e_i / (1 - h_{ii})}{\hat{\sigma} / \sqrt{1 - h_{ii}}} = \frac{e_i}{\hat{\sigma} \sqrt{1 - h_{ii}}}$$

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$$e_{(i)} = y_i - \mathbf{x}_i^T \hat{\beta}_{(i)} = \frac{e_i}{1 - h_{ii}}$$

- ▶ variance

$$\text{var}(e_{(i)}) = \frac{\sigma^2}{1 - h_{ii}}$$

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$$\text{SSE}_{(i)} = \text{SSE} - \frac{e_i^2}{1 - h_{ii}}$$
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- ▶ Externally Standardized residuals

$$t_i = \frac{e_{(i)}}{\sqrt{\hat{\sigma}_{(i)}^2/(1 - h_{ii})}} = \frac{y_i - \mathbf{x}_i^T \hat{\boldsymbol{\beta}}_{(i)}}{\sqrt{\hat{\sigma}_{(i)}^2/(1 - h_{ii})}} = r_i \left(\frac{n - p - 1}{n - p - r_i^2} \right)^{1/2}$$

Distribution of Externally Standardized Residuals

$$t_i = \frac{e_{(i)}}{\sqrt{\hat{\sigma}_{(i)}^2/(1 - h_{ii})}} = \frac{y_i - \mathbf{x}_i^T \hat{\boldsymbol{\beta}}_{(i)}}{\sqrt{\hat{\sigma}_{(i)}^2/(1 - h_{ii})}} \sim \text{St}(n - p - 1)$$

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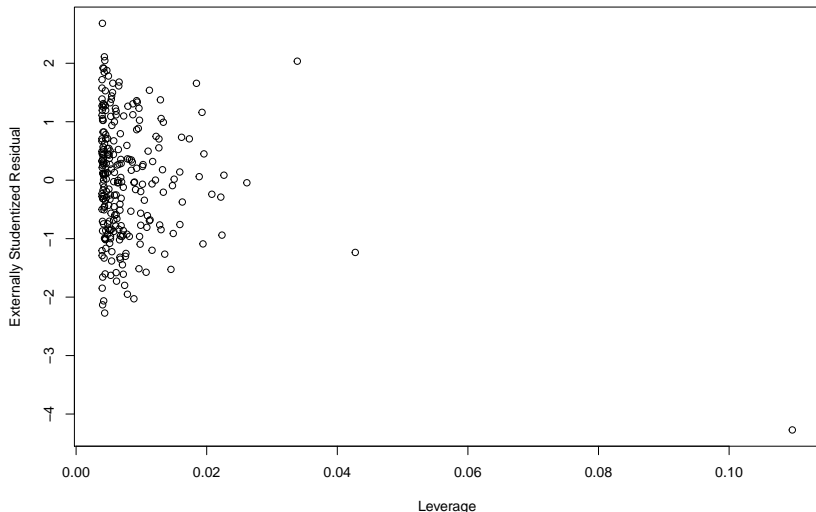
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- ▶ Can extend to include multiple δ_i and δ_j to test that case i and j are both outliers
- ▶ Extreme case $\boldsymbol{\mu} = \mathbf{X}\boldsymbol{\beta} + \mathbf{I}_n \boldsymbol{\alpha}$ all points have their own mean!

R Code

```
plot(rstudent(bodyfat.lm) ~ hatvalues(bodyfat.lm),  
     ylab="Externally Studentized Residual",  
     xlab="Leverage")
```



P-Value

- P-value for test that observation with largest studentized residual is an outlier

```
abs.ti = abs(rstudent(bodyfat.lm))  
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- ▶ Issues with multiple comparisons if we compare each p-value to $\alpha = 0.05$
- ▶ Bonferroni compares p-values to α/n

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- ▶ The **familywise error rate** (FWER) is the probability of rejecting at least one true H_i (making at least one type I error).

$$\begin{aligned}\text{FWER} &= P \left\{ \bigcup_{i=1}^{n_0} \left(p_i \leq \frac{\alpha}{n} \right) \right\} \leq \sum_{i=1}^{n_0} \left\{ P \left(p_i \leq \frac{\alpha}{n} \right) \right\} \leq n_0 \frac{\alpha}{n} \leq n \frac{\alpha}{n} \\ &= \alpha\end{aligned}$$

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- ▶ Link https://en.wikipedia.org/wiki/Bonferroni_correction

Bonferroni Correction

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abs.ti = abs(rstudent(bodyfat.lm))  
pval= 2*(1- pt(abs.ti, bodyfat.lm$df - 1))  
min(pval) < .05/nrow(bodyfat)
```

```
## [1] TRUE
```

```
sum(pval < .05/nrow(bodyfat))
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```
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- ▶ Bonferroni multiplicity adjustment compare each p-value to α/n and reject null (point is not an outlier) if the p-value is less than α/n

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- ▶ Bonferroni multiplicity adjustment compare each p-value to α/n and reject null (point is not an outlier) if the p-value is less than α/n
- ▶ Start with max absolute value of t_i (or min p-value)
- ▶ Case 39 would be considered an outlier based on Bonferroni or other multiplicity adjustments. no other outliers

Cook's Distance

- ▶ Measure of influence of case i on predictions

$$D_i = \frac{\|\mathbf{Y} - \hat{\mathbf{Y}}_{(i)}\|^2}{\hat{\sigma}^2 p}$$

after removing the i th case

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$$D_i = \frac{\|\mathbf{Y} - \hat{\mathbf{Y}}_{(i)}\|^2}{\hat{\sigma}^2 p}$$

after removing the i th case

- ▶ Easier way to calculate

$$D_i = \frac{e_i^2}{\hat{\sigma}^2 p} \left[\frac{h_{ii}}{(1 - h_{ii})^2} \right],$$

$$D_i = \frac{r_{ii}}{p} \frac{h_{ii}}{1 - h_{ii}}$$

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- ▶ Case 39 looks an influential outlier!
- ▶ Impact on predictions?

Predictions with Case 39

```
predict(bodyfat.lm, newdata=bodyfat[39,],  
        se=T, interval="prediction")
```

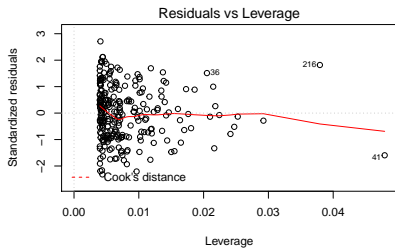
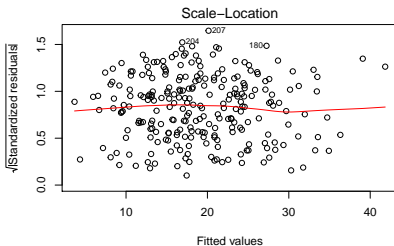
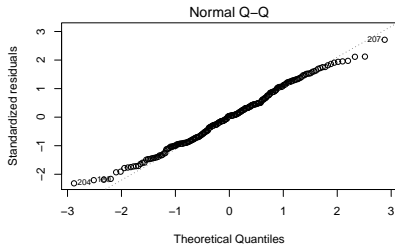
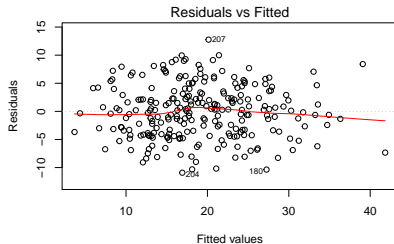
```
## $fit  
##           fit           lwr           upr  
## 39 54.21599 44.0967 64.33528  
##  
## $se.fit  
## [1] 1.615311  
##  
## $df  
## [1] 250  
##  
## $residual.scale  
## [1] 4.877484
```

Predictions without Case 39

```
bodyfatsub.lm = lm(Bodyfat ~ Abdomen, data=bodyfat,  
                  subset=c(-39))  
predict(bodyfatsub.lm, newdata=bodyfat[39,],  
        se=T, interval="prediction")
```

```
## $fit  
##           fit           lwr           upr  
## 39 56.55856 46.71172 66.40541  
##  
## $se.fit  
## [1] 1.655744  
##  
## $df  
## [1] 249  
##  
## $residual.scale  
## [1] 4.717441
```

Residual Checks without Case 39



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- ▶ Next: Transformations