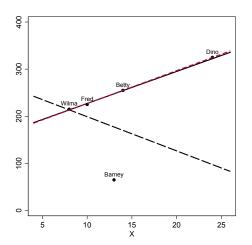
GSERM 2017

Regression III
Outliers / Influence and
Robust Inference

June 21, 2017 (morning session)

Discrepancy, Leverage, and Influence



Note: Solid line is the regression fit for Wilma, Fred, and Betty only. Long-dashed line is the regression for Wilma, Fred, Betty, and Barney. Short-dashed (red) line is the regression for Wilma, Fred, Betty and Dino.

Discrepancy, Leverage, and Influence

 $Influence = Leverage \times Discrepancy$

Leverage

$$\hat{\mathbf{Y}} = \mathbf{X}\hat{\boldsymbol{\beta}} \\
= \mathbf{X}[(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{Y}] \\
= \mathbf{H}\mathbf{Y}$$

where

$$\mathbf{H} = \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'.$$

$$h_i = \mathbf{X}_i(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}_i'$$

Residuals

Variation:

$$\widehat{\mathsf{Var}(\hat{u}_i)} = \hat{\sigma}^2 [1 - \mathsf{X}_i(\mathsf{X}'\mathsf{X})^{-1}\mathsf{X}_i'] \tag{1}$$

$$\widehat{\mathsf{s.e.}(\hat{u}_i)} = \hat{\sigma}\sqrt{[1-\mathsf{X}_i(\mathsf{X}'\mathsf{X})^{-1}\mathsf{X}_i']}$$

$$= \hat{\sigma}\sqrt{1-h_i}$$
(2)

"Standardized":

$$\tilde{u}_i = \frac{\hat{u}_i}{\hat{\sigma}\sqrt{1 - h_i}} \tag{3}$$

Residuals

"Studentized": define

$$\hat{\sigma}_{-i}^{2} = \text{Variance for the } N-1 \text{ observations } \neq i$$

$$= \frac{\hat{\sigma}^{2}(N-K)}{N-K-1} - \frac{\hat{u}_{i}^{2}}{(N-K-1)(1-h_{i})}. \tag{4}$$

Then:

$$\hat{u}_i' = \frac{\hat{u}_i}{\hat{\sigma}_{-i}\sqrt{1 - h_i}} \tag{5}$$

Influence

"DFBETA":

$$D_{ki} = \hat{\beta}_k - \hat{\beta}_{k(-i)} \tag{6}$$

"DFBETAS" (the "S" is for "standardized):

$$D_{ki}^* = \frac{D_{ki}}{\widehat{\mathsf{s.e.}}(\widehat{\beta}_{k(-i)})} \tag{7}$$

Cook's D:

$$D_{i} = \frac{\tilde{u}_{i}^{2}}{K} \times \frac{h_{i}}{1 - h_{i}}$$

$$= \frac{h_{i}\hat{u}_{i}^{2}}{K\hat{\sigma}^{2}(1 - h_{i})^{2}}$$
(8)

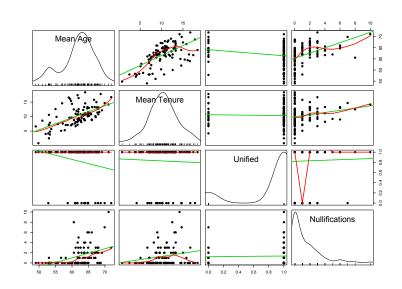
```
> # No Barney OR Dino...
> summary(lm(Y~X,data=subset(flintstones,name!="Dino" & name!="Barney")))
Residuals:
    2 4 5
0.714 -2.143 1.429
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 159.286 6.776 23.5 0.027 *
Х
              6.786 0.619 11.0 0.058 .
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
Residual standard error: 2.67 on 1 degrees of freedom
Multiple R-squared: 0.992, Adjusted R-squared: 0.984
F-statistic: 120 on 1 and 1 DF, p-value: 0.0579
```

```
> # No Barney (Dino included...)
> summary(lm(Y~X,data=subset(flintstones,name!="Barney")))
Residuals:
       2
-8.88e-16 2.63e-01 -2.11e+00 1.84e+00
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 157.368 2.465 63.8 0.00025 ***
Х
              6.974
                        0.161 43.3 0.00053 ***
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
Residual standard error: 1.99 on 2 degrees of freedom
Multiple R-squared: 0.999, Adjusted R-squared: 0.998
F-statistic: 1.87e+03 on 1 and 2 DF, p-value: 0.000534
```

"COVRATIO":

$$\mathsf{COVRATIO}_i = \left[(1 - h_i) \left(\frac{N - K - 1 + \hat{u}_i'^2}{N - K} \right)^K \right]^{-1} \tag{9}$$

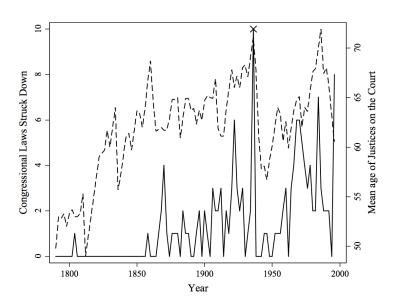
Example: Federal Judicial Review, 1789-1996



```
> Fit<-lm(nulls~age+tenure+unified)
> summarv(Fit)
Residuals:
   Min
          1Q Median 3Q
                             Max
-2.7857 -1.0773 -0.3634 0.4238 6.9694
Coefficients:
          Estimate Std. Error t value Pr(>|t|)
(Intercept) -12.10340 2.54324 -4.759 6.57e-06 ***
           age
tenure
         -0.06692 0.06427 -1.041 0.300
unified 0.71760 0.45844 1.565 0.121
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
```

Residual standard error: 1.715 on 100 degrees of freedom Multiple R-squared: 0.2324, Adjusted R-squared: 0.2093 F-statistic: 10.09 on 3 and 100 DF, p-value: 7.241e-06

Federal Judicial Review and Mean SCOTUS Age



Residuals, etc.

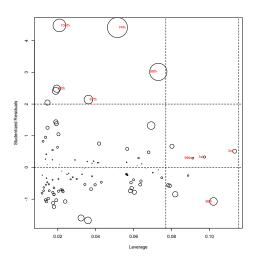
- > FitResid<-(nulls predict(Fit)) # residuals
- > FitStandard<-rstandard(Fit) # standardized residuals
- > FitStudent<-rstudent(Fit) # studentized residuals
- > FitCooksD<-cooks.distance(Fit) # Cook's D
- > FitDFBeta<-dfbeta(Fit) # DFBeta
- > FitDFBetaS<-dfbetas(Fit) # DFBetaS
- > FitCOVRATIO<-covratio(Fit) # COVRATIOs

Studentized Residuals

```
> FitStudent[74]
     74
4.415151
> Congress74<-rep(0,length=104)</pre>
> Congress74[74]<-1
> summary(lm(nulls~age+tenure+unified+Congress74))
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -10.17290 2.37692 -4.280 4.33e-05 ***
             0.18820 0.04177 4.505 1.82e-05 ***
age
tenure
          -0.06356 0.05905 -1.076 0.284
unified 0.55159 0.42282 1.305 0.195
Congress74 7.14278 1.61779 4.415 2.58e-05 ***
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
Residual standard error: 1.576 on 99 degrees of freedom
Multiple R-squared: 0.3586, Adjusted R-squared: 0.3327
F-statistic: 13.84 on 4 and 99 DF, p-value: 5.304e-09
```

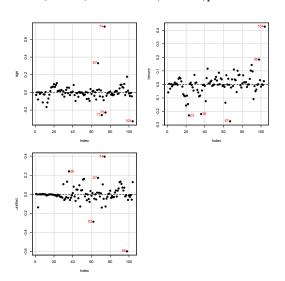
"Bubble Plot"

> influencePlot(Fit,id.n=4,labels=Congress,id.cex=0.8, id.col="red",xlab="Leverage")



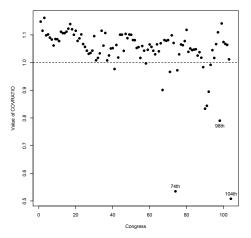
DFBETAS

> dfbetasPlots(Fit,id.n=5,id.col="red",main="",pch=19)



COVRATIO Plot

- > plot(FitCOVRATIO~congress,pch=19,xlab="Congress",ylab="Value of COVRATIO")
- > abline(h=1,lty=2)



Sensitivity Analyses: Omitting Outliers

```
> Outlier<-rep(0,104)
> Outlier[74]<-1
> Outlier[98]<-1
> Outlier[104]<-1
> DahlSmall<-Dahl[which (Outlier==0).]
> summary(lm(nulls~age+tenure+unified,data=DahlSmall))
Call:
lm(formula = nulls ~ age + tenure + unified, data = DahlSmall)
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) -10.38536    1.99470   -5.206   1.08e-06 ***
          age
tenure -0.10069 0.04974 -2.024 0.0457 *
unified 0.76645 0.36069 2.125 0.0361 *
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
Residual standard error: 1.319 on 97 degrees of freedom
Multiple R-squared: 0.2578, Adjusted R-squared: 0.2349
F-statistic: 11.23 on 3 and 97 DF, p-value: 2.167e-06
```

Thinking About Diagnostics



Observational Data Complex Data Structure Informative Missingness Complex / Uncertain Causality Experimental Data Simple Data Structure No / Uninformative Missingness Simple / Clear Causality

One Approach

Pena, E.A. and E.H. Slate. 2006. "Global Validation of Linear Model Assumptions." *J. American Statistical Association* 101(473):341-354.

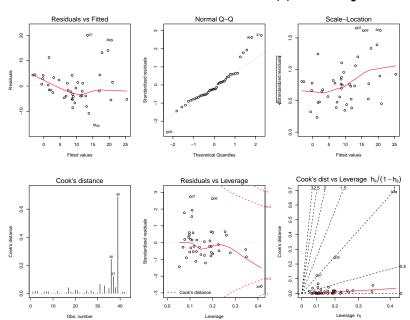
Tests for:

- Normality in ûs (via skewness & kurtosis tests)
- "Link function" (linearity / additivity)
- Constant variance and uncorrelatedness in ûs ("heteroskedasticity" test)

In Action

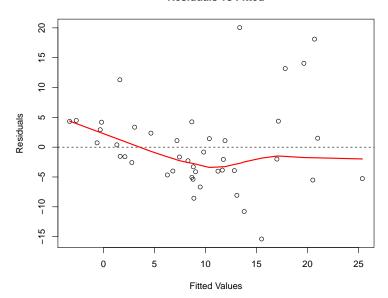
```
> Fit <- with(Africa, lm(adrate~gdppppd+muslperc+subsaharan+healthexp+
                 literacv+internalwar))
> library(gvlma)
> Nope <- gvlma(Fit)
> display.gvlmatests(Nope)
ASSESSMENT OF THE LINEAR MODEL ASSUMPTIONS
USING THE GLOBAL TEST ON 4 DEGREES-OF-FREEDOM:
Level of Significance = 0.05
Call:
 gvlma(x = Fit)
                    Value
                           p-value
                                                      Decision
Global Stat
                   21.442 0.0002587 Assumptions NOT satisfied!
                    5.720 0.0167698 Assumptions NOT satisfied!
Skewness
Kurtosis
                    2.345 0.1256876
                                       Assumptions acceptable.
Link Function
                    5.892 0.0152059 Assumptions NOT satisfied!
Heteroscedasticity 7.485 0.0062227 Assumptions NOT satisfied!
```

Another Approach: plot(fit)

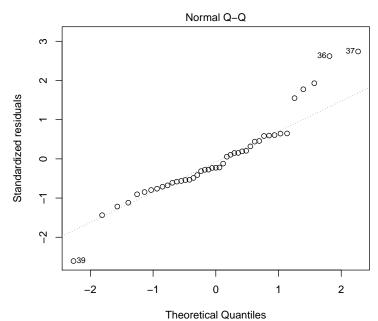


#1: Residuals vs. Fitted Values

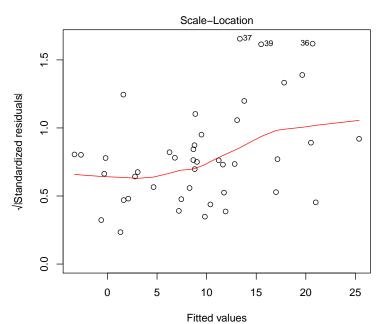
Residuals vs Fitted



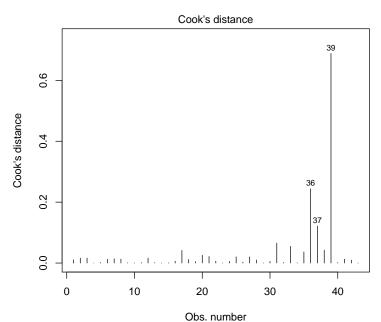
#2: Q-Q Plot of \hat{u} s



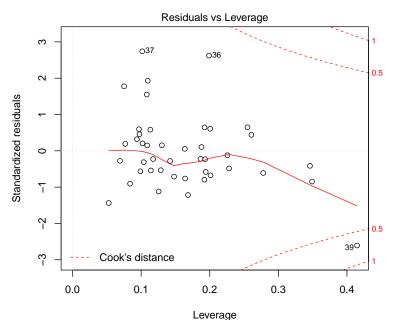
"Scale-Location" Plot



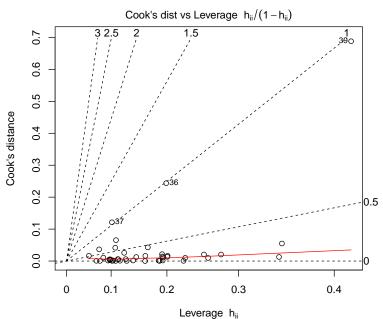
Cook's D



Residuals vs. Leverage



Cook's D vs. Leverage



BREAK

"Robust" Inference

Many of the assumptions of the classical linear regression model are necessary for accurate variance estimation, but not necessarily for unbiasedness. These are also commonly violated in practice. Under such circumstances, we often turn to "robust" methods for variance estimation.

- "Robust" (Huber / White) variance-covariance estimators
- Permutation / exact tests
- Jacknife
- Bootstrap
- Cross-Validation

Bootstrapping...

The population is to the sample as the sample is to the bootstrap sample.

Practical (Nonparametric) Bootstrapping

- Draw one bootstrap sample of size *N* with replacement from the original data,
- Estimate the parameter(s) $\tilde{\theta}_{k \times 1}$,
- Repeat steps 1 and 2 R times, to get $\tilde{\theta}_r$, $r \in \{1, 2, ...R\}$, comprising elements $\tilde{\theta}_{rk}$,
- Examine the empirical characteristics of the resulting distribution(s) of $\tilde{\theta}_{rk}$.

Why Bootstrap?

- It's intuitive.
- It's simple.
- It's robust.

Bootstrap Example

```
> Justices<-read.csv("Justices.csv")</pre>
> attach(Justices)
> summary(Justices)
                                          civrts
    name
                        score
                                                          econs
                           :-1.0000
                                             :19.80
 Length:31
                    Min.
                                      Min.
                                                      Min.
                                                             :34.60
 Class :character
                   1st Qu.:-0.4700
                                      1st Qu.:35.90
                                                      1st Qu.:43.85
 Mode :character
                    Median: 0.3300
                                      Median: 43.70
                                                      Median: 50.20
                    Mean
                           : 0.1210
                                      Mean
                                             :51.42
                                                      Mean
                                                             :55.75
                    3rd Qu.: 0.6250
                                      3rd Qu.:75.55
                                                      3rd Qu.:66.65
                    Max. : 1.0000
                                             :88.90
                                      Max.
                                                      Max.
                                                             :81.70
  Neditorials
                      eratio
                                                        InNedit
                                       scoresa
 Min.
        : 2,000
                  Min.
                         : 0.5000
                                    Min.
                                           :0.0000
                                                     Min.
                                                            :0.6931
                                                     1st Qu.:1.3863
 1st Qu.: 4.000
                  1st Qu.: 0.7083
                                    1st Qu.:0.1936
 Median : 6.000
                  Median : 1.0000
                                    Median : 0.2500
                                                     Median :1.7918
 Mean : 8.742
                  Mean : 2.0242
                                    Mean :0.4599
                                                     Mean
                                                            :1.8442
 3rd Qu.:11.500
                  3rd Qu.: 2.5000
                                    3rd Qu.:0.8281
                                                     3rd Qu.:2.4414
```

Max.

:1.0000

Max.

:3.8501

:11.7500

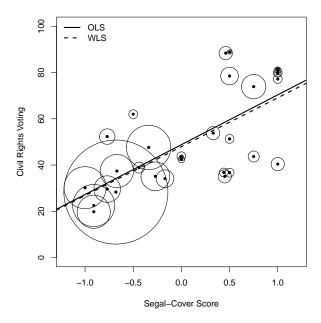
Max.

:47.000

Max.

Bootstrap Example

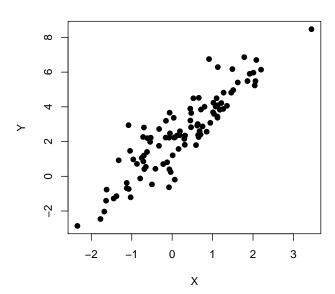
Figure 1: Plot of civrts Against score, Weighted by Neditorials



Bootstrapping: "By Hand"

```
N<-100
reps<-999
set.seed(1337)
X<-rnorm(N)
Y < -2 + 2 * X + rnorm(N)
data<-data.frame(Y,X)
fitOLS<-lm(Y~X)
CI<-confint(fitOLS)
BO<-numeric(reps)
B1<-numeric(reps)
for (i in 1:reps) {
  temp<-data[sample(1:N,N,replace=TRUE),]
  temp.lm<-lm(Y~X,data=temp)
  B0[i]<-temp.lm$coefficients[1]
  B1[i]<-temp.lm$coefficients[2]
BvHandB0<-median(B0)
ByHandB1<-median(B1)
ByHandCI.BO<-quantile(B0,probs=c(0.025,0.975)) # <-- 95% c.i.s
ByHandCI.B1<-quantile(B1,probs=c(0.025,0.975))
```

Bootstrapping "By Hand"

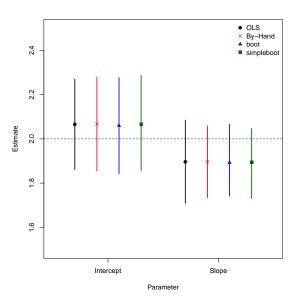


Bootstrapping Via boot

Bootstrapping Via simpleboot

```
library(simpleboot)
Simple<-lm.boot(fitOLS,reps)
SimpleB0<-perc(Simple,.50)[1]
SimpleB1<-perc(Simple,.50)[2]
Simple.CIs<-perc(Simple,perc(0.025,0.975))</pre>
```

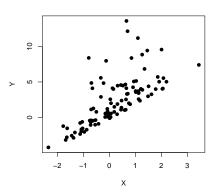
Bootstrapping Results



Bootstrapping: Skewed Residuals

```
N<-100
reps<-999
```

set.seed(1337)
X<-rnorm(N)
ustar<-rchisq(N,2) # <- skewed u.s
Y<-2+2*X*(ustar-mean(ustar))
data<-data.frame(Y,X)
fitULS<-lm(Y*X)
CI<-confinit(fitOLS)</pre>



Skewed Residuals: Results

