

Regression Assumptions & Diagnostics

Fundamental Techniques in Data Science with R



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Outline

Assumptions & Diagnostics

Regression Diagnostics

Influential Observations

Treating Influential Observations



ASSUMPTIONS & DIAGNOSTICS



Why Assume?

Consider the following equation:

$$5 = x + y$$

What are the values of x and y ?



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$$y = 5 - x$$



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What if we assume that $y = x$?



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$$y = 5 - x$$

What if we assume that $y = x$?

$$5 = x + y$$

$$0 = x - y$$



Why Assume?

Consider the following equation:

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What are the values of x and y ?

$$y = 5 - x$$

What if we assume that $y = x$?

$$5 = x + y$$

$$0 = x - y$$

Now we have enough information:

$$5 = x + x = 2x \Rightarrow x = y = 2.5$$



Assumptions of MLR

If you google assumptions, many will show up and there are many ways to frame the question. For the course, only the ones highlighted in this lecture will be considered for exam.

The assumptions of the linear model can be stated as follows:

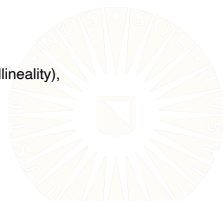
1. The model is linear in the parameters.

- This is OK: $Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \beta_4 X^2 + \beta_5 X^3 + \varepsilon$
- This is not: $Y = \beta_0 X^{\beta_1} + \varepsilon$

2. The predictor matrix is *full rank*.

- $N > P$
- No X_p can be a linear combination of other predictors.

X_3 can't be the sum of X_1 and X_2 . For example: BMI with height and weight (high collineality), model would still predict but high errors.



Assumptions of MLR

3. The predictors are strictly exogenous.

- The predictors do not correlated with the errors.

The predictors cannot correlate with the errors terms.

- $\text{Cov}(\hat{Y}, \varepsilon) = 0$

Expectation of the errors is zero.

Problematic, because we cant really test.

- $E[\varepsilon_n] = 0$

4. The errors have constant, finite variance.

- $\text{Var}(\varepsilon_n) = \sigma^2 < \infty$

Homogeneity of variance. Professor does not know anything with infinite error.

Linear reg models for mean and not variance.

5. The errors are uncorrelated.

- $\text{Cov}(\varepsilon_i, \varepsilon_j) = 0, i \neq j$

6. The errors are normally distributed.

- $\varepsilon \sim N(0, \sigma^2)$

Least important, in practice.



Assumptions of MLR

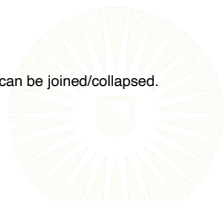
The assumption of *spherical errors* combines Assumptions 4 and 5.

$$\text{Var}(\varepsilon) = \begin{bmatrix} \sigma^2 & 0 & \cdots & 0 \\ 0 & \sigma^2 & \cdots & 0 \\ 0 & 0 & \ddots & 0 \\ 0 & 0 & \cdots & \sigma^2 \end{bmatrix} = \sigma^2 \mathbf{I}_N$$

We can combine Assumptions 3, 4, 5, and 6 by assuming independent and identically distributed normal errors:

- $\varepsilon \stackrel{iid}{\sim} \mathbf{N}(\mathbf{0}, \sigma^2)$

Confusing theme because assumptions can be joined/collapsed.



Consequences of Violating Assumptions

1. If the model is not linear in the parameters, then we're not even working with linear regression.
 - We need to move to entirely different modeling paradigm.
2. If the predictor matrix is not full rank, the model is not estimable.
 - The parameter estimates cannot be uniquely determined from the data.
3. If the predictors are not exogenous, the estimated regression coefficients will be biased. Worst consequence!
4. If the errors are not spherical, the standard errors will be biased. Combines assum 4 and 5
 - The estimated regression coefficients will be unbiased, though.
5. If errors are non-normal, small-sample inferences may be biased.
 - The justification for some tests and procedures used in regression analysis may not hold.

Regression Diagnostics

Checking assumptions, always done after estimating the model.

If some of the assumptions are (grossly) violated, the inferences we make using the model may be wrong.

- We need to check the tenability of our assumptions before leaning too heavily on the model estimates.

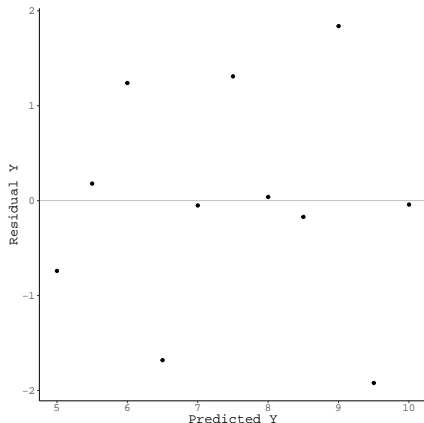
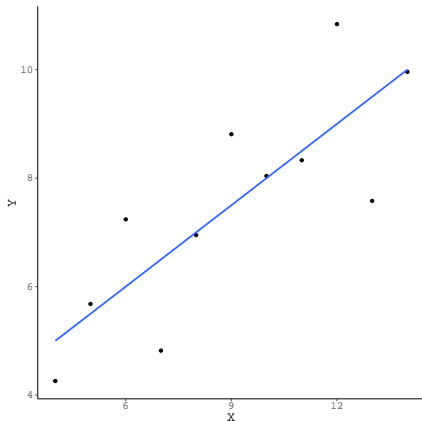
These checks are called *regression diagnostics*.

- Graphical visualizations Focus on graphical viz in the course.
Tests are significance tests, and have their own assumptions, so it is harder to deal with.
- Quantitative indices/measures
- Formal statistical tests



Residual Plots

One of the most useful diagnostic graphics is the plot of residuals vs. predicted values.



Residual Plots

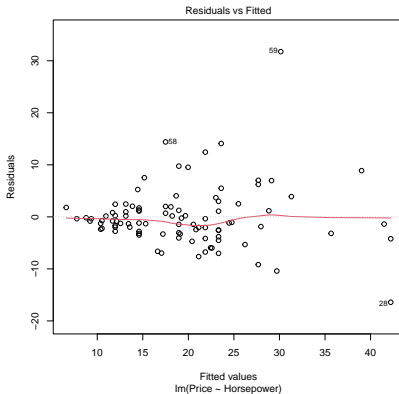
We can easily generate a simple plot of residuals vs. fitted values by plotting the fitted `lm()` object in R.

```
out1 <- lm(Price ~ Horsepower,  
           data = Cars93)
```

```
plot(out1, 1)
```

the `plot()` fitted model returns a set of plots. 1 is for the first.

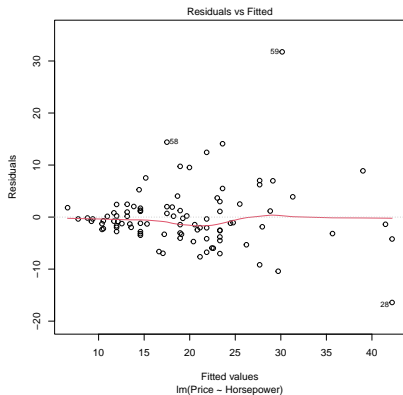
small residual variance in small values,
residual variance larger with larger x.



Heteroscedasticity

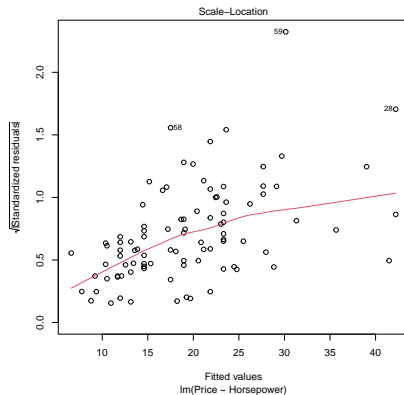
Non-constant error variance (*heteroscedasticity*) violates Assumption 4.

```
plot(out1, 1)
```



```
plot(out1, 3)
```

y axis: function of residuals. make residuals positive. if line is not flat, there is a problem.



Consequences of Heteroscedasticity

Non-constant error variance will not bias the parameter estimates.

- The best fit line is still correct.
- Our measure of uncertainty around that best fit line is wrong.

Heteroscedasticity will bias standard errors (usually downward).

- Test statistics will be too large.
- CIs will be too narrow.
- We will have inflated Type I error rates.

To get valid inference, we need to address (severe) heteroscedasticity.



Treating Heteroscedasticity

1. Transform your outcome using a concave function (e.g., $\ln(Y)$, \sqrt{Y}).
 - These transformations will shrink extreme values more than small/moderate ones.
 - It's usually a good idea to first shift the variable's scale by setting the minimum value to 1.
2. Refit the model using *weighted least squares*.
 - Create inverse weights using functions of the residual variances or quantities highly correlated therewith.
3. Use a *Heteroscedasticity Consistent* (HC) estimate of the asymptotic covariance matrix. Best solution.
 - Robust standard errors, Huber-White standard errors, Sandwich estimators
 - HC estimators correct the standard errors for non-constant error variance.

Example

```
## The 'sandwich' package provides several HC estimators:
library(sandwich)

## the 'lmtest' package provides fancy testing tools for linear models:
library(lmtest)

## Use sandwich estimator to compute ACOV matrix:
hcCov <- vcovHC(out1)      robust asymptotic covar matrix: hipotetical covar matrix of intercept and slopes.

## Test coefficients with robust SEs:
robTest <- coeftest(out1, vcov = hcCov)

## Test coefficients with default SEs:
defTest <- summary(out1)$coefficients
```

Example

```
## Compare robust and default approaches:
```

```
robTest
```

Parameter estimates are identical. robust standard errors are a bit larger.

```
t test of coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.398769	2.078200	-0.6731	0.5026
Horsepower	0.145371	0.017164	8.4696	4.051e-13 ***

```
---
```

```
Signif. codes:
```

```
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
defTest
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.3987691	1.8200164	-0.7685475	4.441519e-01
Horsepower	0.1453712	0.0118978	12.2183251	6.837464e-21

Correlated Errors

One extra way: omitted variables.

Errors can become correlated in two basic ways:

1. Serial dependence

- When modeling longitudinal data, the errors for a given observational unit are correlated over time.
- We can detect temporal dependence by examining the *autocorrelation* of the residuals.

2. Clustering

- Your data have some important, unmodeled, grouping structure.
 - Children nested within classrooms
 - Romantic couples
 - Departments within a company
- We can detect problematic levels of clustering with the *intraclass correlation coefficient* (ICC).
 - We need to know the clustering variable to apply the ICC.



Treating Correlated Errors

Serially dependent errors in a longitudinal model usually indicate an inadequate model.

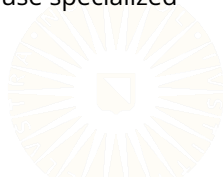
- Your model is ignoring some important aspect of the temporal variation that is being absorbed by the error terms.
- Hopefully, you can add the missing component to your model.



Treating Correlated Errors

Clustering can be viewed as theoretically meaningful or as a nuisance factor that just needs to be controlled.

- If the clustering is meaningful, you should model the data using *multilevel modeling*.
 - Hierarchical linear regression
 - Mixed models
 - Random effects models
- If the clustering is an uninteresting nuisance, you can use specialized HC variance estimators that deal with clustering.



Example

```
## Read in some data:
```

```
LeeBryk <- readRDS(paste0(dataDir, "lee_bryk.rds"))
```

```
## Check the data:
```

```
str(LeeBryk, vec.len = 3)
```

```
'data.frame': 7185 obs. of 5 variables:
```

```
$ schoolid: int  1 1 1 1 1 1 1 1 ...
```

```
$ math     : num  5.88 19.71 20.35 8.78 ...
```

```
$ ses      : num  -1.53 -0.59 -0.53 -0.67 -0.16 0.02 -0.62 -1 ...
```

```
$ msas     : num  -0.43 -0.43 -0.43 -0.43 -0.43 -0.43 -0.43 -0.43 ...
```

```
$ sector   : Factor w/ 2 levels "public","private": 1 1 1 1 1 1 1 1 ...
```

```
## Estimate a linear regression model:
```

```
fit <- lm(math ~ ses + sector, data = LeeBryk)
```

```
## Calculate the residual ICC:
```

```
ICC::ICCbare(x = LeeBryk$schoolid, y = resid(fit))
```

```
[1] 0.07487712
```

Expect school clustering having an effect: check the ICC of the residuals.

X (grouping variable) Y variable grouped.

intra class correl coeff: amount of variability explained by grouping factor. Super tiny values are ok.

Example

```
## Robust tests:
```

```
coeftest(fit, vcov = vcovCL(fit, ~ schoolid))
```

Use robust test to fix clustering influence.
Corrects standard error issues.

t test of coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	11.79965	0.20318	58.0746	< 2.2e-16 ***
ses	2.94860	0.12794	23.0475	< 2.2e-16 ***
sectorprivate	1.93495	0.31717	6.1006	1.111e-09 ***

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
## Raw tests:
```

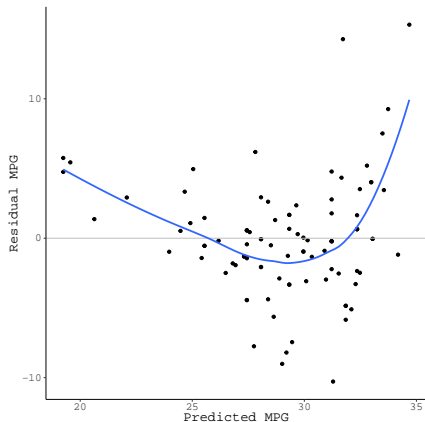
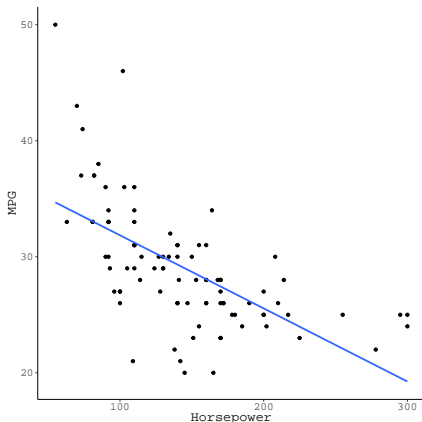
```
summary(fit)$coefficients
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	11.799654	0.10612759	111.18366	0.000000e+00
ses	2.948605	0.09782968	30.14019	5.002687e-188
sectorprivate	1.934953	0.15249200	12.68888	1.676478e-36

Linearity

Each modeled X must exhibit a linear relation with Y .

- We can define X via nonlinear transformations of the original data.



Treating Residual Nonlinearity

Nonlinearity in the residual plots is usually a sign of either:

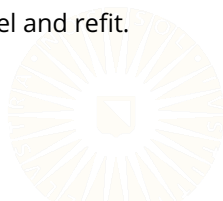
1. Model misspecification
2. Influential observations

This type of model misspecification usually implies omitted functions of modeled variables.

- Polynomial terms
- Interactions

The solution is to include the omitted term into the model and refit.

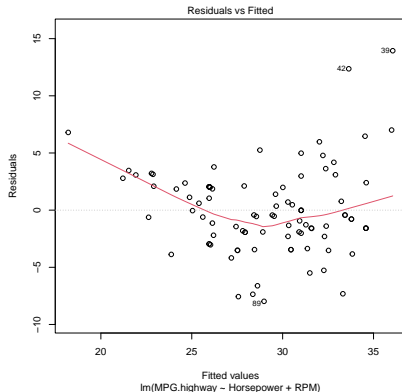
- This is very much easier said than done.



Limitations of Residual Plots

In multiple regression models, basic residual plots won't tell us which predictors exhibit nonlinear associations.

```
out3 <-  
  lm(MPG.highway ~ Horsepower + RPM,  
     data = Cars93)
```

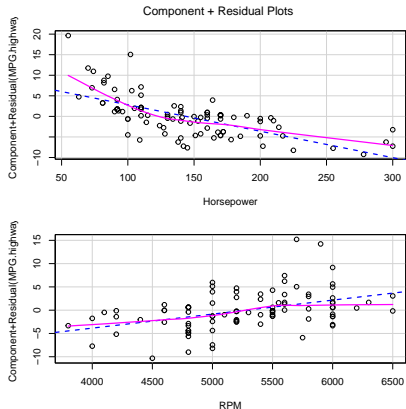


Component + Residual Plots

Partial residual plot

We can use *Component + Residual Plots* (AKA, partial residual plots) to visualize the unique effects of each *X* variable.

```
library(car)  
crPlots(out3)
```



Omitted Variables

The most common cause of endogeneity (i.e., violating Assumption 3) is *omitted variable bias*.

- If we leave an important predictor variable out of our equation, some modeled predictors will become endogenous and their estimated regression slopes will be biased.
- The omitted variable must be correlated with Y and at least one of the modeled X_p , to be a problem.



Omitted Variables

Assume the following is the true regression model.

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \varepsilon$$

Now, suppose we omit Z from the model:

$$Y = \beta_0 + \beta_1 X + \omega$$

$$\omega = \varepsilon + \beta_2 Z$$

Our new error, ω , is a combination of the true error, ε , and the omitted term, $\beta_2 Z$.

- Consequently, if X and Z are correlated, omitting Z induces a correlation between X and ω (i.e., endogeneity).



Treating Omitted Variable Bias

Omitted variable bias can have severe consequences, but you can't really test for it.

- The *errors* are correlated with the predictors, but our model is estimated under the assumption of exogeneity, so the *residuals* from our model will generally be uncorrelated with the predictors.
- We mostly have to pro-actively work to include all relevant variables in our model.

Can't omit "important" variables, some will always be in the residuals but not important ones.

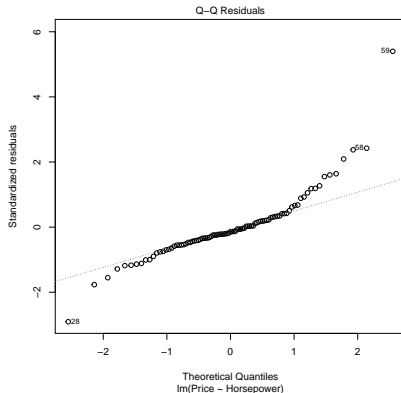


Normality Assumption

```
plot(out1, 2)
```

One of the best ways to evaluate the normality of the error distribution with a Q-Q Plot.

- Plot the quantiles of the residual distribution against the theoretically ideal quantiles.
- We can actually use a Q-Q Plot to compare any two distributions.



Consequences of Violating Normality

In small samples, with fixed predictors, normally distributed errors imply normal sampling distributions for the regression coefficients.

- In large samples, the central limit theorem implies normal sampling distributions for the coefficients, regardless of the error distribution.

Probably not that severe consequences, won't affect coefficients.



Consequences of Violating Normality

In small samples, with *fixed* predictors, normally distributed errors imply normal sampling distributions for the regression coefficients.

- In large samples, the central limit theorem implies normal sampling distributions for the coefficients, regardless of the error distribution.

Prediction intervals require normally distributed errors.

- Confidence intervals for predictions share the same normality requirements as the coefficients' sampling distributions.

Probably bias in prediction interval if normality violated.



Consequences of Violating Normality

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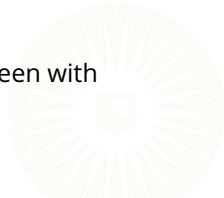
- In large samples, the central limit theorem implies normal sampling distributions for the coefficients, regardless of the error distribution.

Prediction intervals require normally distributed errors.

- Confidence intervals for predictions share the same normality requirements as the coefficients' sampling distributions.

Parameter estimates will not be fully efficient.

- Standard errors will be larger than they would have been with normally distributed errors.



Treating Violations of Normality

We usually don't need to do anything about non-normal errors.

- The CLT will protect our inferences.



Treating Violations of Normality

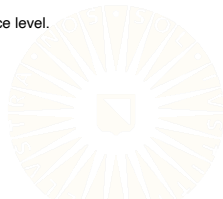
We usually don't need to do anything about non-normal errors.

- The CLT will protect our inferences.

We can use *bootstrapping* to get around the need for normality.

1. Treat your sample as a synthetic population from which you draw many new samples (with replacement).
2. Estimate your model in each new sample.
3. The replicates of your estimated parameters generate an empirical sampling distribution that you can use for inference.

Hist of sampling of the slope and estimates. Chop the tails and form lower and upper confidence level.
Only assumption is that the data is representative of the pop.
(Done at credpago)



Treating Violations of Normality

We usually don't need to do anything about non-normal errors.

- The CLT will protect our inferences.

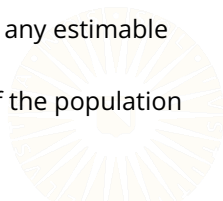
We can use *bootstrapping* to get around the need for normality.

1. Treat your sample as a synthetic population from which you draw many new samples (with replacement).
2. Estimate your model in each new sample.
3. The replicates of your estimated parameters generate an empirical sampling distribution that you can use for inference.

Bootstrapping can be used for inference on pretty much any estimable parameter, but it won't work with small samples.

- Need to assume that your sample is representative of the population

Tends to normality, but not necessarily.



INFLUENTIAL OBSERVATIONS



Influential Observations

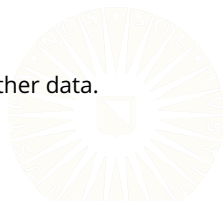
How outliers may affect the results? Not only identifying them.

Influential observations contaminate analyses in two ways:

1. Exert too much influence on the fitted regression model
2. Invalidate estimates/inferences by violating assumptions

There are two distinct types of influential observations:

1. Outliers
 - Observations with extreme outcome values, relative to the other data.
 - Observations with outcome values that fit the model very badly.
2. High-leverage observations Extreme cases, but in respect to the x.
 - Observation with extreme predictor values, relative to other data.



Outliers

Outliers can be identified by scrutinizing the residuals.

- Observations with residuals of large magnitude may be outliers.
- The difficulty arises in quantifying what constitutes a “large” residual.

If the residuals do not have constant variance, then we cannot directly compare them.

- We need to standardize the residuals in some way.



Detecting Outliers

Standardization uses the variation of all data, including the effect of the outlier, contaminating the technique. That is why another sort of standardization is used here.

We are specifically interested in *externally studentized residuals*.

- We can't simply standardize the ordinary residuals.
 - *Internally studentized residuals*
 - Outliers can pull the regression line towards themselves.
 - The internally studentized residuals for outliers will be too small.

Begin by defining the concept of a *deleted residual*:

$$\hat{\varepsilon}_{(n)} = Y_n - \hat{Y}_{(n)}$$

- $\hat{\varepsilon}_{(n)}$ quantifies the distance of Y_n from the regression line estimated after excluding the n th observation.



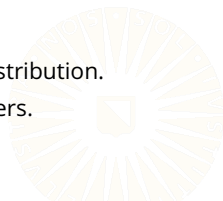
Studentized Residuals

If we standardize the deleted residual, $\hat{\varepsilon}_{(n)}$, we get the externally studentized residual:

$$t_{(n)} = \frac{\hat{\varepsilon}_{(n)}}{SE_{\hat{\varepsilon}_{(n)}}}$$

The externally studentized residuals have two very useful properties:

1. Each $t_{(n)}$ is scaled equivalently.
 - We can directly compare different $t_{(n)}$.
2. The $t_{(n)}$ are *Student's t* distributed.
 - We can quantify outliers in terms of quantiles of the t distribution.
 - $|t_{(n)}| > 3.0$ is a common rule of thumb for flagging outliers.



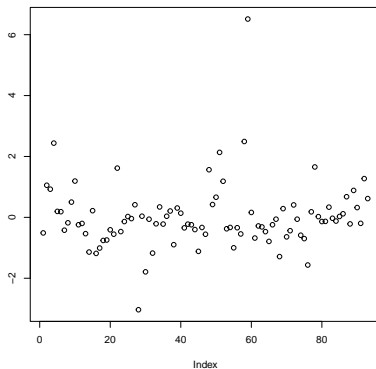
Studentized Residual Plots

```
rstudent(out1) %>% plot()
```

1 point larger than 6

Index plots of the externally studentized residuals can help spotlight potential outliers.

- Look for observations that clearly “stand out from the crowd.”



High-Leverage Points

leverage values: quantifies how much each row of data influences the fit of data

We identify high-leverage observations through their *leverage* values.

- An observation's leverage, h_n , quantifies the extent to which its predictors affect the fitted regression model.
- Observations with X values very far from the mean, \bar{X} , affect the fitted model disproportionately.



High-Leverage Points

We identify high-leverage observations through their *leverage* values.

- An observation's leverage, h_n , quantifies the extent to which its predictors affect the fitted regression model.
- Observations with X values very far from the mean, \bar{X} , affect the fitted model disproportionately.

In simple linear regression, the n th leverage is given by:

$$h_n = \frac{1}{N} + \frac{(X_n - \bar{X})^2}{\sum_{m=1}^N (X_m - \bar{X})^2}$$

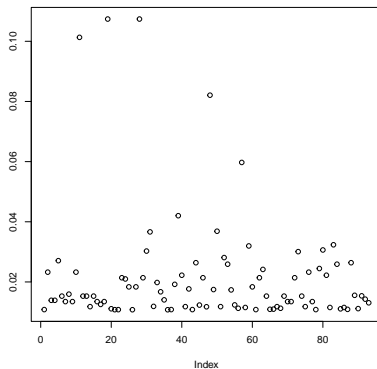


Leverage Plots

```
hatvalues(out1) %>% plot()
```

Index plots of the leverage values can help spotlight high-leverage points.

- Again, look for observations that clearly “stand out from the crowd.”



Outliers & Leverages → Influential Points

Observations with high leverage or large (externally) studentized residuals are not necessarily influential.

- High-leverage observations tend to be more influential than outliers.
- The worst problems arise from observations that are both outliers and have high leverage.

Measures of influence simultaneously consider extremity in both X and Y dimensions.

- Observations with high measures of influence are very likely to cause problems.



Measures of Influence

All measures of influence use the same logic as the deleted residual.

- Compare models estimated from the whole sample to models estimated from samples excluding individual observations.

One of the most common measures of influence is *Cook's Distance*.

$$\begin{aligned}\text{Cook's } D_n &= \frac{\sum_{n=1}^N \left(\hat{Y}_n - \hat{Y}_{(n)} \right)^2}{(P+1) \hat{\sigma}^2} \\ &= (P+1)^{-1} t_n^2 \frac{h_n}{1-h_n}\end{aligned}$$

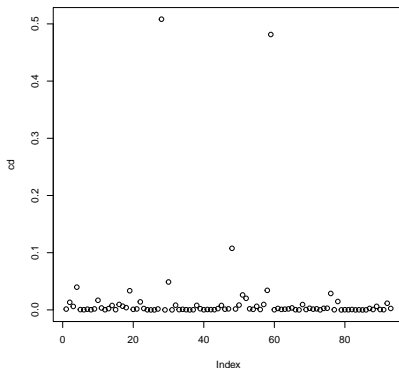


Plots of Cook's Distance

```
cd <- cooks.distance(out1)  
plot(cd)
```

Index plots of Cook's distances can help spotlight the influential points.

- Look for observations that clearly “stand out from the crowd.”



Removing Influential Observations

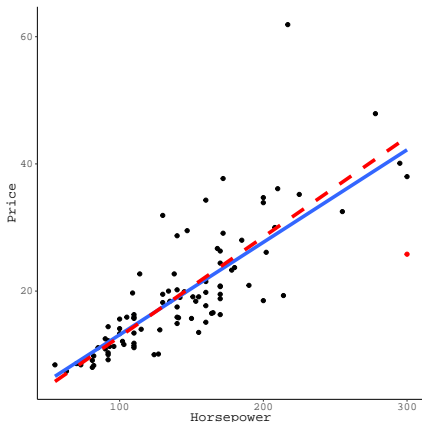
```
(maxD <- which.max(cd))
```

28

28

Observation number 28 was the most influential according to Cook's Distance.

- Removing that observation has a small impact on the fitted regression line.
- Influential observations don't only affect the regression line, though.



Removing Influential Observations

```
## Exclude the influential case:
```

```
Cars93.2 <- Cars93[-maxD, ]
```

```
## Fit model with reduced sample:
```

```
out2 <- lm(Price ~ Horsepower, data = Cars93.2)
```

```
round(summary(out1)$coefficients, 6)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.398769	1.820016	-0.768548	0.444152
Horsepower	0.145371	0.011898	12.218325	0.000000

```
round(summary(out2)$coefficients, 6)
```

Intercept seems to have changed, but the scale is large. The t values didnt change much.

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-2.837646	1.806418	-1.570868	0.119722
Horsepower	0.156750	0.011996	13.066942	0.000000

Removing Influential Observations

What about residuals?

```
partSummary(out1, 2)
```

Residuals:

Min	1Q	Median	3Q	Max
-16.413	-2.792	-0.821	1.803	31.753

```
partSummary(out2, 2)
```

Residuals:

Min	1Q	Median	3Q	Max
-11.4069	-3.0349	-0.5912	1.8530	30.7229

Removing Influential Observations

Reduced range of residuals also reduced variability. And R increases (explains more variability)

```
summary(out1)[c("sigma", "r.squared", "fstatistic")] %>%  
  unlist() %>%  
  head(3)
```

sigma	r.squared	fstatistic.value
5.976953	0.621287	149.287468

```
summary(out2)[c("sigma", "r.squared", "fstatistic")] %>%  
  unlist() %>%  
  head(3)
```

sigma	r.squared	fstatistic.value
5.7243112	0.6548351	170.7449721

Removing Influential Observations

```
(maxDs <- sort(cd) %>% names() %>% tail(2) %>% as.numeric())
```

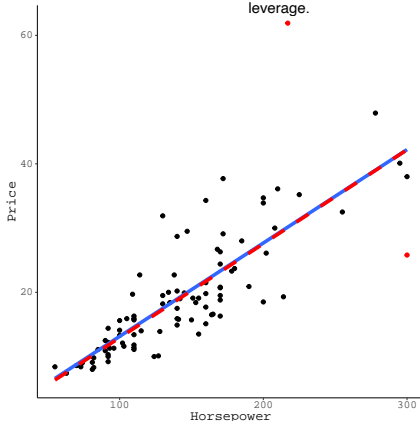
```
[1] 59 28
```

If we remove the two most influential observations, 59 and 28, the fitted regression line barely changes at all.

- The influences of these two observations were counteracting one another.
- We're probably still better off, though.

leverage values are more influential: x variables are fixed. Y variable is a random variable. A problem with Y can be absorbed by the error term.

This dot does not have the biggest cd because it has a more normal leverage.



Removing Influential Observations

```
## Exclude influential cases:
```

```
Cars93.2 <- Cars93[-maxDs, ]
```

```
## Fit model with reduced sample:
```

```
out2.2 <- lm(Price ~ Horsepower, data = Cars93.2)
```

```
round(summary(out1)$coefficients, 6)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.398769	1.820016	-0.768548	0.444152
Horsepower	0.145371	0.011898	12.218325	0.000000

```
round(summary(out2.2)$coefficients, 6)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.695315	1.494767	-1.134166	0.25977
Horsepower	0.146277	0.009986	14.648807	0.00000

Removing Influential Observations

```
partSummary(out1, 2)
```

Residuals:

Min	1Q	Median	3Q	Max
-16.413	-2.792	-0.821	1.803	31.753

```
partSummary(out2.2, 2)
```

Range dramatically decreases

Residuals:

Min	1Q	Median	3Q	Max
-10.3079	-2.5786	-0.6084	1.9775	14.5793

Removing Influential Observations

```
summary(out1)[c("sigma", "r.squared", "fstatistic")] %>%  
  unlist() %>%  
  head(3)
```

sigma	r.squared	fstatistic.value
5.976953	0.621287	149.287468

Getting rid of noise the effect was 8% more explaining of variability. Even if influential cases don't change slope so much, it is nice to treat due to influence on residuals.

```
summary(out2.2)[c("sigma", "r.squared", "fstatistic")] %>%  
  unlist() %>%  
  head(3)
```

sigma	r.squared	fstatistic.value
4.7053314	0.7068391	214.5875491

Treating Influential Points

The most common way to address influential observations is simply to delete them and refit the model.

- This approach is often effective—and always simple—but it is not fool-proof.
- Although an observation is influential, we may not be able to justify excluding it from the analysis.

Robust regression procedures can estimate the model directly in the presence of influential observations.

- Observations in the tails of the distribution are weighted less in the estimation process, so outliers and high-leverage points cannot exert substantial influence on the fit.
- We can do robust regression with the `r1m()` function from the **MASS** package.

