

#### Author: Nicholas G Reich, Jeff Goldsmith

#### This material is part of the statsTeachR project

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## Today's Lecture

- Model selection vs. model checking
- Continue with model checking (regression diagnostics)

Model selection vs. model checking

 $\beta_{z} + \beta_{z} \chi_{z} + \beta_{z} \chi_{z} \dots$ Assume  $y | \mathbf{x} = f(\mathbf{x}) + \epsilon$ 

model selection focuses on how you construct f(·);
 model checking asks whether the 
 *e* match the assumed form.

# Model checking: possible challenges

#### Two major areas of concern

- Global lack of fit, or general breakdown of model assumptions
  - Linearity
  - Unbiased, uncorrelated errors  $E(\epsilon|x) = E(\epsilon) = 0$
  - Constant variance  $Var(y|x) = Var(\epsilon|x) = \sigma^2$
  - Independent errors
  - Normality of errors
- Effect of influential points and outliers

Model checking: possible solutions + Stutegies

Global lack of fit, or general breakdown of model assumptions

- Residual analysis QQ plots, residual plots against fitted values and predictors
- Adjusted variable plots
- Effect of influential points and outliers
  - Measure of leverage, influence, outlying-ness

#### Residual plots: verifying assumptions - (arre lated errors - Construct von ability - Normality assumption



Which assumptions are these plots evaluating?



# QQ-plots for checking Normality of residuals

#### QQ plot defined

QQ-plot stands for quantile-quantile plot, and is used to compare two distributions. If the two distributions are the same, then each point (which represents a quantile from each distribution) should lie along the transformer. For a single (x, y) point

- x = a specific quantile for the N(0,1) distribution
- y = the same quantile from the (standardized, if meeded) sample of data

#### example: Gaussian or Normal(0,1) distribution

```
d1 <- rnorm(1000)
layout(matrix(1:2, nrow = 1))
hist(d1, breaks = 50, xlim = c(-6, 6))
qqnorm(d1, pch = 19)
qqline(d1)</pre>
```





d1

Normal Q-Q Plot



example: Student's T-distribution with 6 d.f.

```
d1 <- rt(1000, df = 5)
layout(matrix(1:2, nrow = 1))
hist(d1, breaks = 50, xlim = c(-6, 6))
qqnorm(d1, pch = 19)
qqline(d1)</pre>
```



### example: Truncated Gaussian

```
d1 <- rnorm(1000)
d1 <- subset(d1, abs(d1) < 2)
layout(matrix(1:2, nrow = 1))
hist(d1, breaks = 50, xlim = c(-6, 6))
qqnorm(d1, pch = 19)
qqline(d1)</pre>
```



#### QQ-plots for our three fits from earlier



### Model checking: possible solutions

Global lack of fit, or general breakdown of model assumptions
 Residual analysis - QQ plots, residual plots against fitted values and predictors
 Adjusted variable plots - checking line mity in MLR
 Effect of influential points and outliers

Measure of leverage, influence, outlying-ness

#### Points can be isolated in three ways

- Leverage point outlier in x, measured by hat matrix
- Outlier outlier in y, measured by residual
- Influential point a point that largely affects  $\beta$ 
  - Deletion influence;  $|\hat{m{eta}} \hat{m{eta}}_{(-i)}|$
  - Basically, a high-leverage outlier

We measure leverage (the "distance" of  $\mathbf{x}_i$  from the distribution of  $\mathbf{x}$ ) using

$$h_{ii} = \mathbf{x}_i^{\mathsf{T}} (\mathbf{X}^{\mathsf{T}} \mathbf{X})^{-1} \mathbf{x}_i$$

where  $h_{ii}$  is the  $(i, i)^{th}$  entry of the hat matrix. Where, recall



# Quantifying Leverage via the Hat Matrix $\gamma_{1} = \beta_{0} + \beta_{1} \chi_{1} + \beta_{2} \chi_{2} + \xi_{2}$ g = 3

Note that

$$\sum_{i} h_{ii} \stackrel{def}{=} tr(\mathbf{H}) = p$$

where p is the total number of independent predictors (i.e.  $\beta$ s) in your model (including a  $\beta_0$  if you have one).

What counts as "big" leverage?

- Average leverage is p/n
- Typical rules of thumb are 2p/n or 3p/n
- Leverage plots can be useful as well

### Example Leverage plot with lung data





#### Outliers

- When we refer to "outliers" we typically mean "points that don't have the same mean structure as the rest of the data"
- Residuals give an idea of "outlying-ness", but we need to standardize somehow

• We can use the fact that 
$$Var(\hat{\epsilon}_i) = \sigma^2(1 - h_{ii}) \dots$$

## Outliers

 $\left(-\frac{i}{L}\right)$ 

The standardized residual is given by

$$\hat{\epsilon}^*_i = rac{\hat{\epsilon}_i}{\sqrt{Var(\hat{\epsilon}_i)}} = rac{\hat{\epsilon}_i}{\hat{\sigma}\sqrt{(1-h_{ii})}}$$

The Studentized residual is given by

$$t_{i} = \frac{\hat{\epsilon}_{(-i)}}{\hat{\sigma}_{(-i)}\sqrt{(1-h_{ii})}} = \hat{\epsilon}_{i}^{*} \left(\frac{n-p}{n-p-\hat{\epsilon}_{i}^{*2}}\right)^{1/2}$$

Studentized residuals follow a  $t_{n-p-1}$  distribution.

#### Influence

Intuitively, "influence" is a combination of outlying-ness and leverage. More specifically, we can measure the "deletion influence" of each observation: quantify how much  $\hat{\beta}$  changes if an observation is left out.

- $|\hat{\boldsymbol{\beta}} \hat{\boldsymbol{\beta}}_{(-i)}|$
- Cook's distance is

$$D_{i} = \frac{(\hat{\boldsymbol{\beta}} - \hat{\boldsymbol{\beta}}_{(i)})^{T} (\mathbf{X}^{T} \mathbf{X}) (\hat{\boldsymbol{\beta}} - \hat{\boldsymbol{\beta}}_{(i)})}{p \hat{\sigma}^{2}}$$

$$= \frac{(\hat{\mathbf{y}} - \hat{\mathbf{y}}_{(-i)})^{T} (\hat{\mathbf{y}} - \hat{\mathbf{y}}_{(-i)})}{p \hat{\sigma}^{2}}$$

$$= \underbrace{\frac{1}{p} \hat{\epsilon}_{i}^{2} \underbrace{\frac{h_{ii}}{1 - h_{ii}}}_{0 \text{ trypes}} \text{ trengl}$$

Suppose you fit a linear model in R;

- hatvalues gives the diagonal elements of the hat matrix h<sub>ii</sub> (leverages)
- rstandard gives the standardized residuals
- rstudent gives the studentized residuals
- cooks.distance gives the Cook's distances

hatvalues (mlr 1)

#### Built-in R plots for 1m objects

You can also use the plot.lm() function to look at leverage, outlying-ness, and influence all together. Recall that

$$D_i = \frac{1}{p} \hat{\epsilon}_i^2 \frac{h_{ii}}{1 - h_{ii}}$$





## Today's big ideas

