Nonlinear regression and Cross-validation Statistical Learning

Carranza-Alarcón Yonatan-Carlos¹

¹Université de technologie de Compiègne

Outline

Cook's Distance

- 2 A"perfect" linear regression versus a Non-linear regression
- Nested Cross-validation

Overview

Cook's Distance

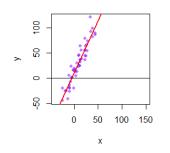
- A"perfect" linear regression versus a Non-linear regression

Cook's Distance

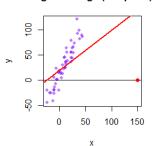
Data points with large residuals (outliers) and/or high leverage may distort the outcome and accuracy of a regression.

$$D_i = \frac{\sum_{j=1}^n \left(\widehat{y}_j - \widehat{y}_{j(i)}\right)^2}{ps^2}, \quad \text{where} \quad s^2 = \frac{\mathbf{e}^\top \mathbf{e}}{n-p}$$

No oulier regressor



High leverage (red point)



If Cook's distance of the observation i is bigger, so this one influences in the estimation of β .

Linear regression - Outlier

Given the following simulated data set $\mathcal{D} = \{(x_i, y_i)\}$, with 2 outlier points:

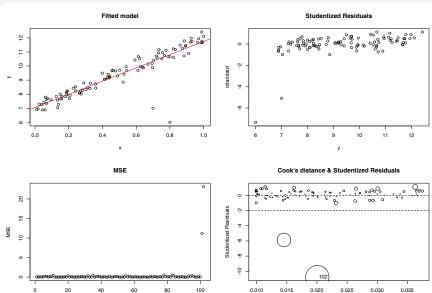
$$y_i = 5x_i + 7 + \epsilon, \quad x_i \sim \mathcal{U}(0, 1), \quad \epsilon \sim \mathcal{N}(0, \sigma = 0.3)$$

$$\mathcal{D} = \mathcal{D} \cup \{(0.7, 7), (0.8, 6)\}$$

```
2 \times - runif(100)
3 \text{ y} \leftarrow 5*x + 7 + \text{rnorm}(100, \text{ sd} = 0.3)
4 # outlier points
5 \times < -c(x, 0.7, 0.8)
6 y < -c(y, 7, 6)
7 plot(x, y, main="Fitted model")
8 fit.linear <- lm(y~x)</pre>
9 summary(fit.linear)
10 abline(fit.linear$coefficients[1], fit.linear$coefficients[2], col="red")
11 plot(y,rstandard(fit.linear),ylab='rstandard',main="Studentized Residuals")
13 influencePlot(fit.linear, main="Cook's distance & Studentized Residuals")
```

1 # linear simulation + outlier

Exploring training data set





Hat-Values

Overview

2 A"perfect" linear regression versus a Non-linear regression

Linear regression

Theoretical linear model

Let us consider the two following theoretical linear model:

$$\mathcal{D}_1: \ y_i = 4 + 5\sin(x_i) + \epsilon_i, \ x_i \sim \mathcal{U}(0, 10), \epsilon \sim \mathcal{N}(0, \sigma = 1) \quad \text{(Nonlinear)}$$

$$\mathcal{D}_2: \ y_i = 4 + 5 * x_i + \epsilon_i, \ x_i \sim \mathcal{U}(0, 10), \epsilon \sim \mathcal{N}(0, \sigma = 3) \quad \text{(Linear)}$$

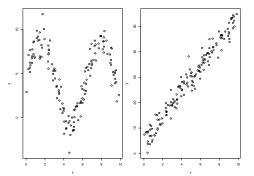
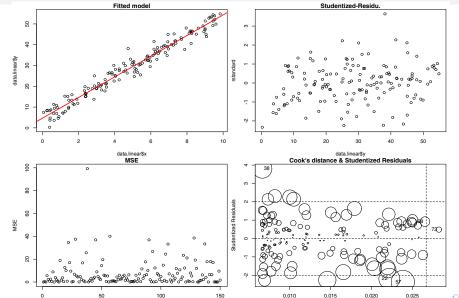
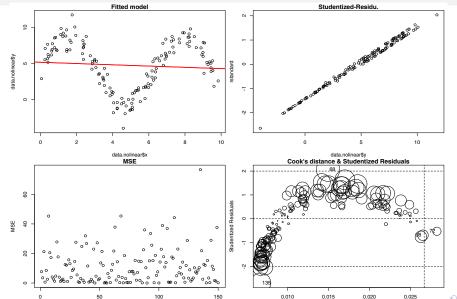


Figure: Nonlinear (left: \mathcal{D}_1) and linear (right: \mathcal{D}_2) data generated.

Exploring linear regression



Exploring non-linear regression



Polynomial regression model

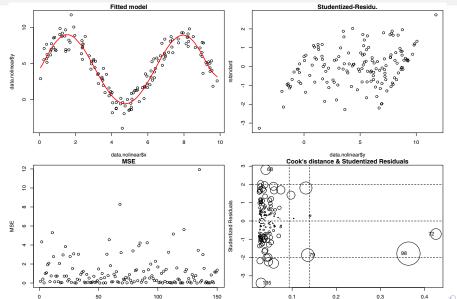
Given $y_i, x_i, \beta_0 \in \mathbb{R}$ and $\beta_* \in \mathbb{R}$, we may consider the following models:

$$\mathbf{y} = \beta_0 + \mathbf{x_i}\beta_1 + \mathbf{x_i}^2\beta_2$$
 (Quadratic model)
 $\mathbf{y} = \beta_0 + \mathbf{x_i}\beta_1 + \dots + \mathbf{x_i}^6\beta_k$ (Polynomial model of degree 6)
 $\mathbf{y} = \beta_0 + \mathbf{x_i}\beta_1 + \ln(\mathbf{x_i})\beta_2$ (Logarithm model)
 $\mathbf{y} = \beta_0 + \mathbf{x_i}\beta_1 + \exp(\mathbf{x_i})\beta_2$ (Exponential model)
... (Infinity Combinations)

I would like to use the polynomial model of degree 6, i.e. (in R):

```
1 fit.nonlinear \leftarrow Im(y\sim 1 + poly(x, 6, raw=T), data=data)
```

Polynomial regression model



Overview

Cook's Distance

A"perfect" linear regression versus a Non-linear regression

Nested Cross-validation

Nested and non-nested Cross-validation

Hyper-parameter

Tuning a hyper-parameter of the statistical model.

Estimation

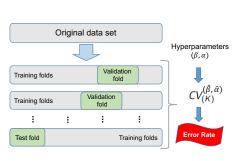
Estimation of the parameters of the statistical model.

Comparing

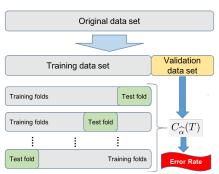
Comparing performance of different statistical models.

Nested and non-nested Cross-validation

Non-nested cross-validation

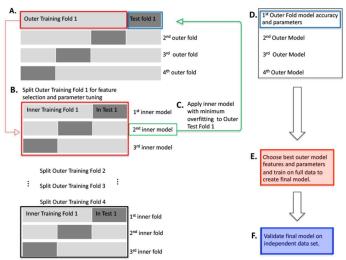


NESTED CROSS-VALIDATION

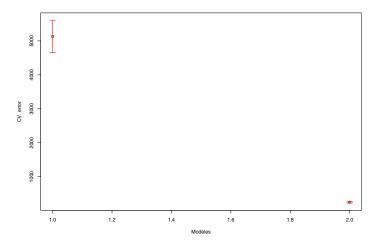


Nested Cross-validation[1]

Standard Nested Cross Validation (nCV)



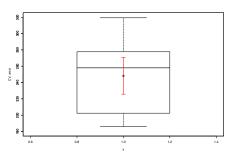
Regularized regression vs K-nearest-neighbor



KNN(left) and Regression elastic-net(right)

Conclusion

- We always choose the statistical model that has the lowest mean error and and the lowest variability.
- Boxplot \neq Interval confidence of the error of cross-validation.



References



Saeid Parvandeh et al. "Consensus features nested cross-validation". In: Bioinformatics 36.10 (2020), pp. 3093-3098.