Lec 04: Linear Regression Analysis

Last Updated 2017-10-15 20:24:10

Contents

Assigned Reading

PMA5: Chapters 6-7

Simple Regression and Correlation (*PMA5 Ch 6*)

Aims

- Describe the relationship between an independent variable X and a continuous dependent variable Y as a straight line. The textbook discusses two cases:
  - Fixed-X: values of X are preselected by investigator
  - Variable-X: have random sample of (X, Y) values
  - Calculations are the same,
- Draw inferences regarding this relationship
- Predict value of Y for a given value of X

Mathmatical Model

- The mean of Y values at any given X is $\beta_0 + \beta_1 X$
- The variance of Y values at any X is σ^2 (same for all X)
- Y values are normally distributed at any given X (need for inference)

Parameter Estimates

- Estimate the slope β_1 and intercept β_0 using least-squares methods.
- The residual mean squared error (RMSE) is an estimate of the variance s^2
- Typically interested in inference on β_1
  - Assume no relationship between X and Y $(H_0 : \beta_1 = 0)$ until there is reason to believe there is one $(H_0 : \beta_1 \neq 0)$

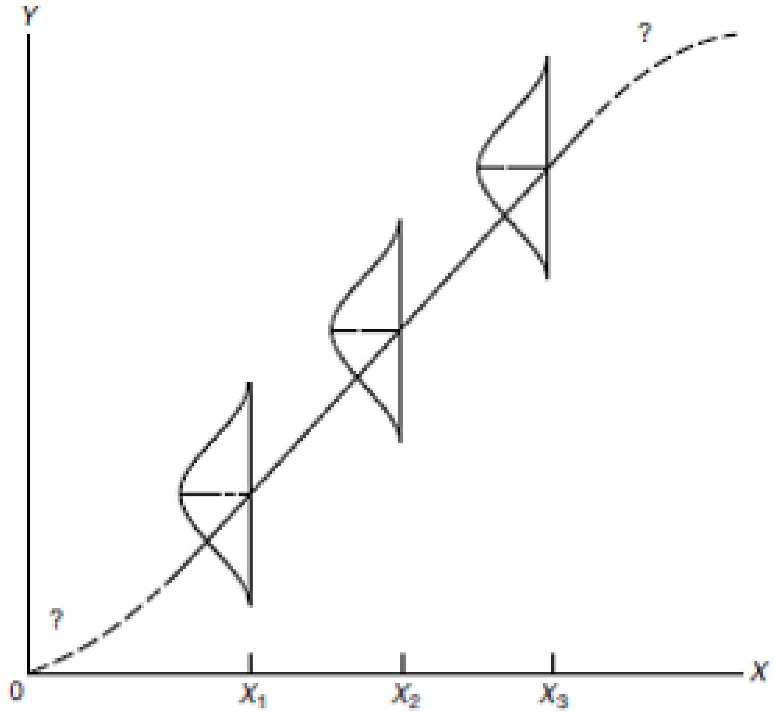


Figure 6.2: *Simple Linear Regression Model for Fixed X's*

Figure 1: Figure 6.2

Interval estimation

- Everything is estimated with some degree of error
- Confidence intervals for the mean of Y
- Prediction intervals for an individual Y

Which one is wider? Why?

Corelation Coefficient

- The correlation coefficient ρ measures the strength of association between X and Y in the *population*.
- $\sigma^2 = VAR(Y|X)$ is the variance of Y for a specific X.
- $\sigma_y^2 = VAR(Y)$ is the variance of Y for all X's.

$$\sigma^2 = \sigma_y^2(1-\rho^2)$$

$$\rho^2 = \frac{\sigma_y^2 - \sigma^2}{\sigma_y^2}$$

- ρ^2 = reduction in variance of Y associated with knowledge of X/original variance of Y
- **Coefficient of Determiniation**: $100\rho^2$ = % of variance of Y associated with X or explained by X
- Caution: association vs. causation.

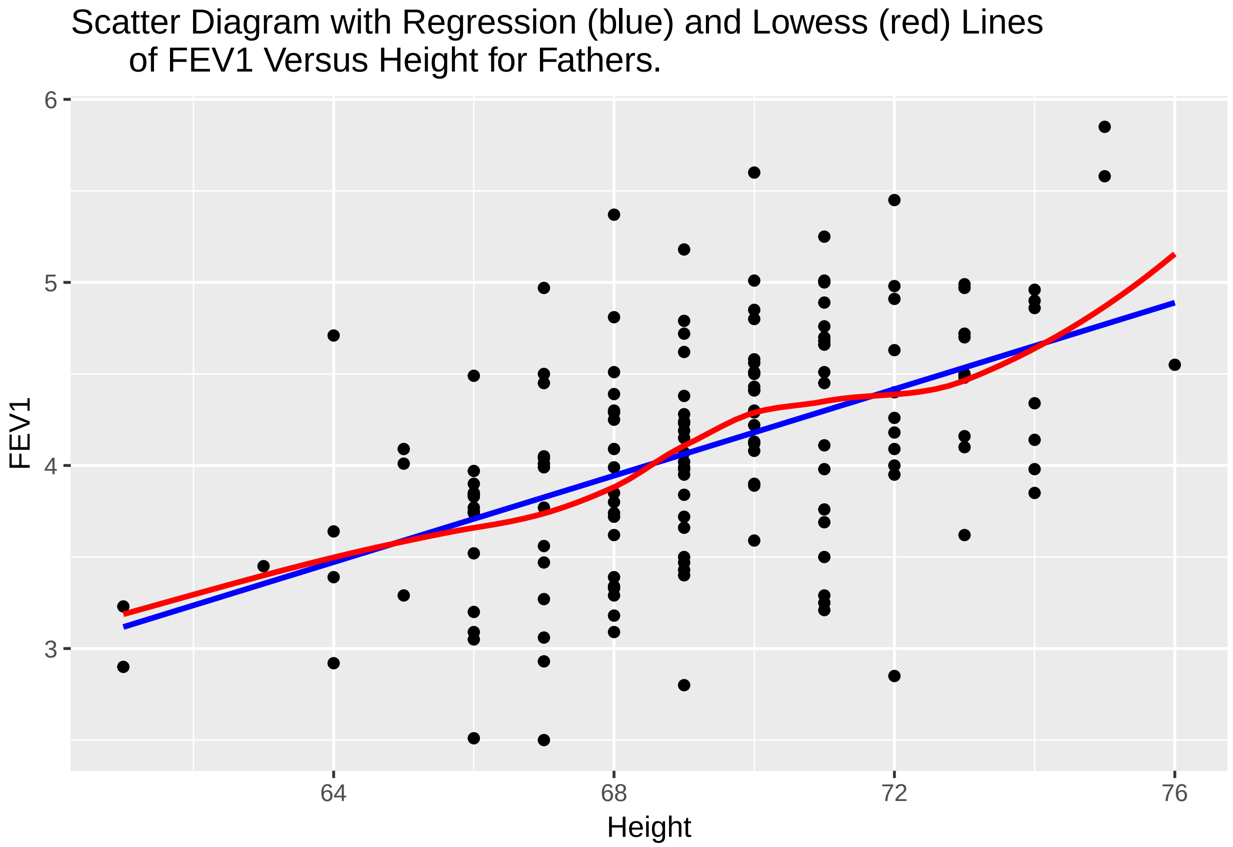
Example: Lung Function

Section 6.3 1. Read in the analysis data set for the lung function.

```
fev <- read.delim("https://norcalbiostat.netlify.com/data/Lung_081217.txt", sep="\t", header=TRUE)
```

2. Create a scatterplot of FEV versus height for fathers. Add a blue linear regression line and red lowess line. Add appropriate plot titles and axes labels. R Cookbook reference

```
library(ggplot2)
qplot(y=FFEV1, x=FHEIGHT, geom="point", data=fev, xlab="Height", ylab="FEV1",
      main="Scatter Diagram with Regression (blue) and Lowess (red) Lines
      of FEV1 Versus Height for Fathers.") +
      geom_smooth(method="lm", se=FALSE, col="blue") +
      geom_smooth(se=FALSE, col="red")
```



There does appear to be a tendency for taller men to have higher FEV1.

3. Fit a linear model and report the regression parameter estimates.

```
model <- lm(FFEV1 ~ FHEIGHT, data=fev)
summary(model)
```

```
##
## Call:
## lm(formula = FFEV1 ~ FHEIGHT, data = fev)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.56688 -0.35290  0.04365  0.34149  1.42555
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -4.08670    1.15198  -3.548 0.000521 ***
## FHEIGHT      0.11811    0.01662   7.106 4.68e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5638 on 148 degrees of freedom
## Multiple R-squared:  0.2544, Adjusted R-squared:  0.2494
## F-statistic:  50.5 on 1 and 148 DF,  p-value: 4.677e-11
```

The least squares equation is $Y = -4.087 + 0.118X$.

4. Test for a significant relationship between height and FEV. Include a p-value and a confidence interval for the parameter estimate in your conclusion.

```r
confint(model)
```

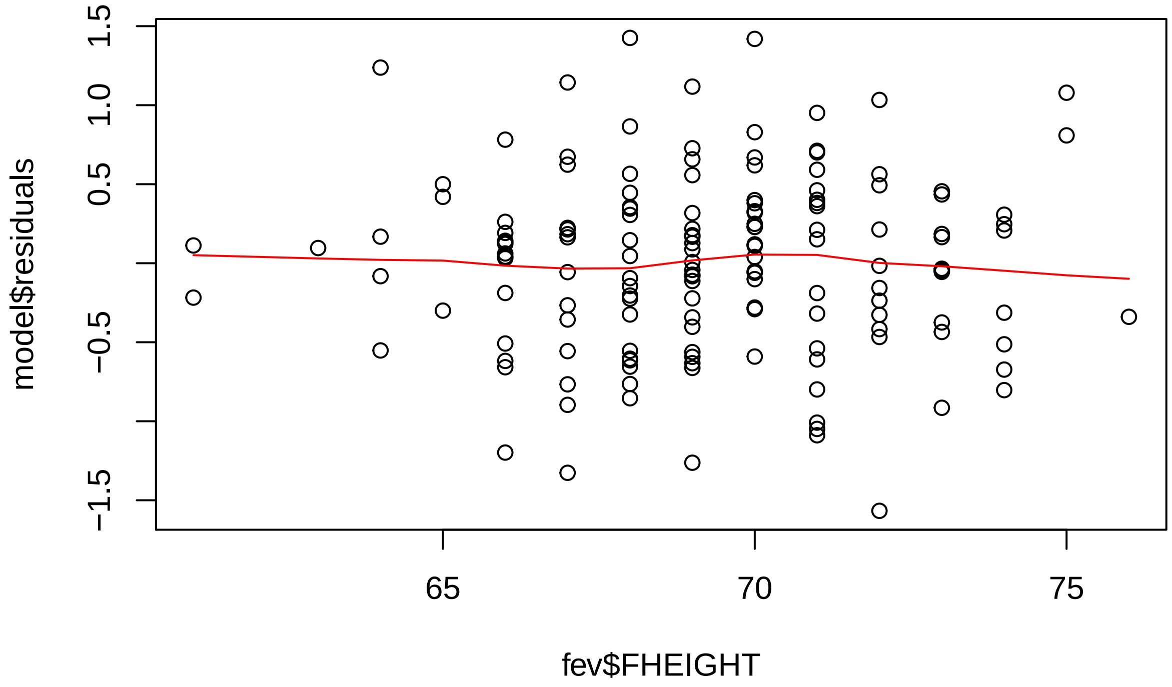
```
##                   2.5 %     97.5 %
## (Intercept) -6.36315502 -1.8102499
## FHEIGHT      0.08526328  0.1509472
```

For ever inch taller a father is, his FEV1 measurement significantly increases by .12 (95%CI: .09, .15, p<.0001). The correlation between FEV1 and height is $\sqrt{.2544} = 0.5$.

Assumptions of Linear Regression

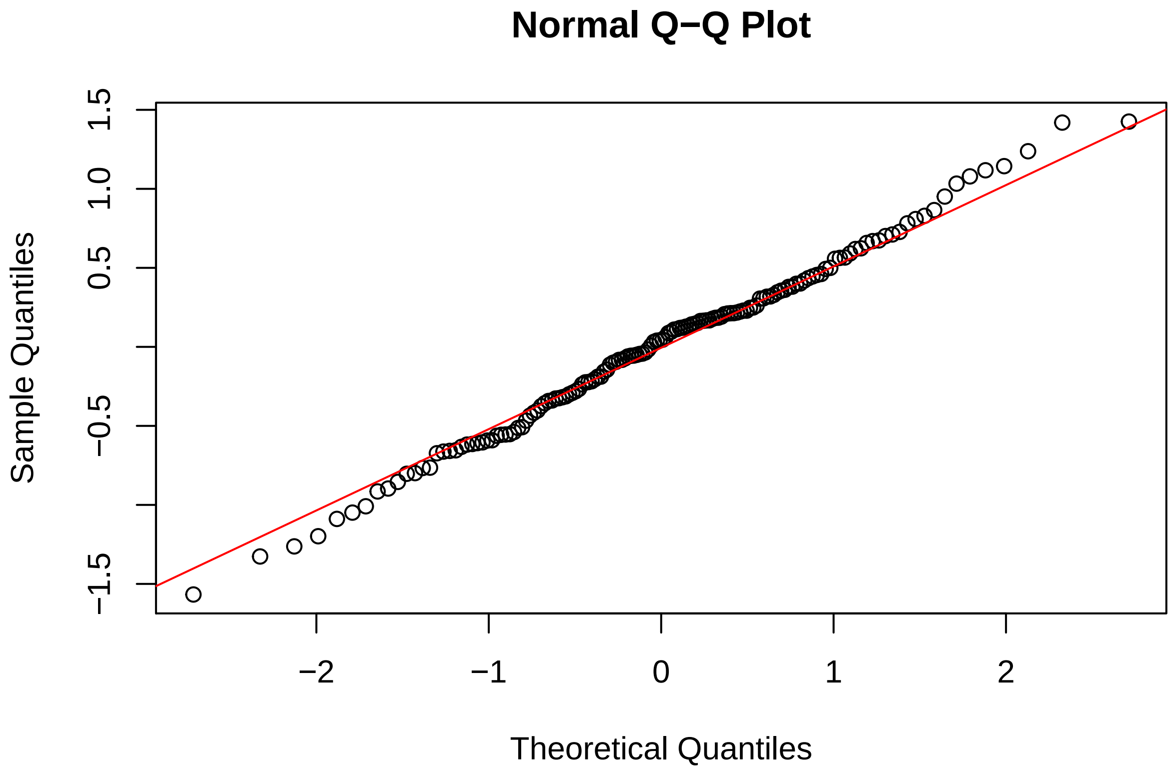
- Homogeneity of variance (same σ^2)
  - Not extremely serious
  - Can use transformations to achieve it
  - Graphical assessment: Plot the residuals against the x variable, add a lowess line. This assumption is upheld if there is no relationship/trend between the residuals and the predictor.

```r
plot(model$residuals ~ fev$FHEIGHT)
lines(lowess(model$residuals ~ fev$FHEIGHT), col="red")
```



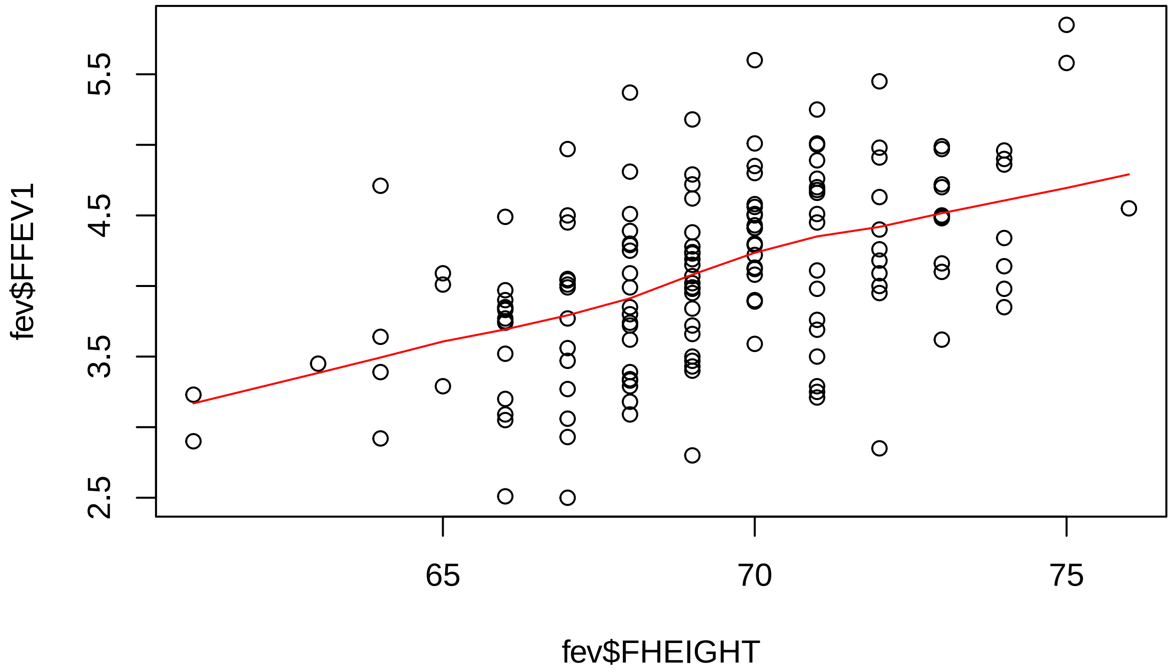
- Normal residuals
  - Slight departures OK
  - Can use transformations to achieve it
  - Graphical assessment: normal qqplot of the model residuals.

```r
qqnorm(model$residuals)
qqline(model$residuals, col="red")
```



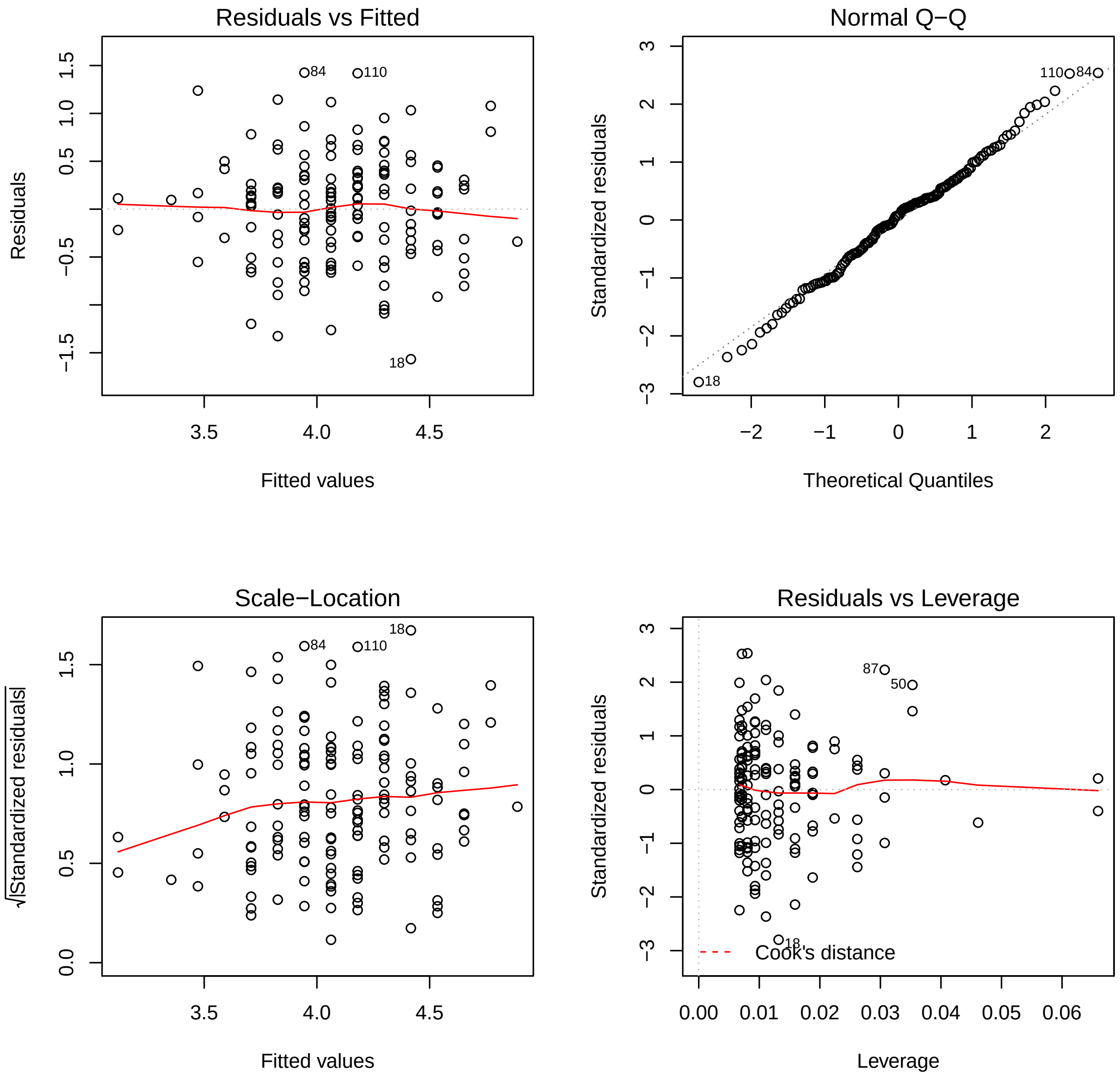
- Randomness / Independence
  - Very serious
  - Can use hierarchical models for clustered samples
  - No real good way to “test” for independence. Need to know how the sample was obtained.
- Linear relationship
  - Slight departures OK
  - Can use transformations to achieve it
  - Graphical assessment: Simple scatterplot of y vs x. Looking for linearity in the relationship. Should be done prior to any analysis.

```r
plot(fev$FFEV1 ~ fev$FHEIGHT)
lines(lowess(fev$FFEV1 ~ fev$FHEIGH), col="red")
```



Some of these plots can be displayed by simply plotting the model output. The advantage of this is that the observations that are potential outliers are labeled with their row number.

```
par(mfrow=c(2,2))
plot(model)
```



What to watch out for

- Representative sample
- Range of prediction should match observed range of X in sample
- Use of nominal or ordinal, rather than interval or ratio data
- Errors-in-variables
- Correlation does not imply causation
- Violation of assumptions
- Influential points
- Appropriate model

The book goes into more detail about influential points, and how outliers can have different affects on the model results depending on if they are an outlier in Y vs an outlier in X (or both).