# Lab_8

February 26, 2021

## 1 Lab 8

Author: Yunting Chiu

Mail: yc6705a@american.edu

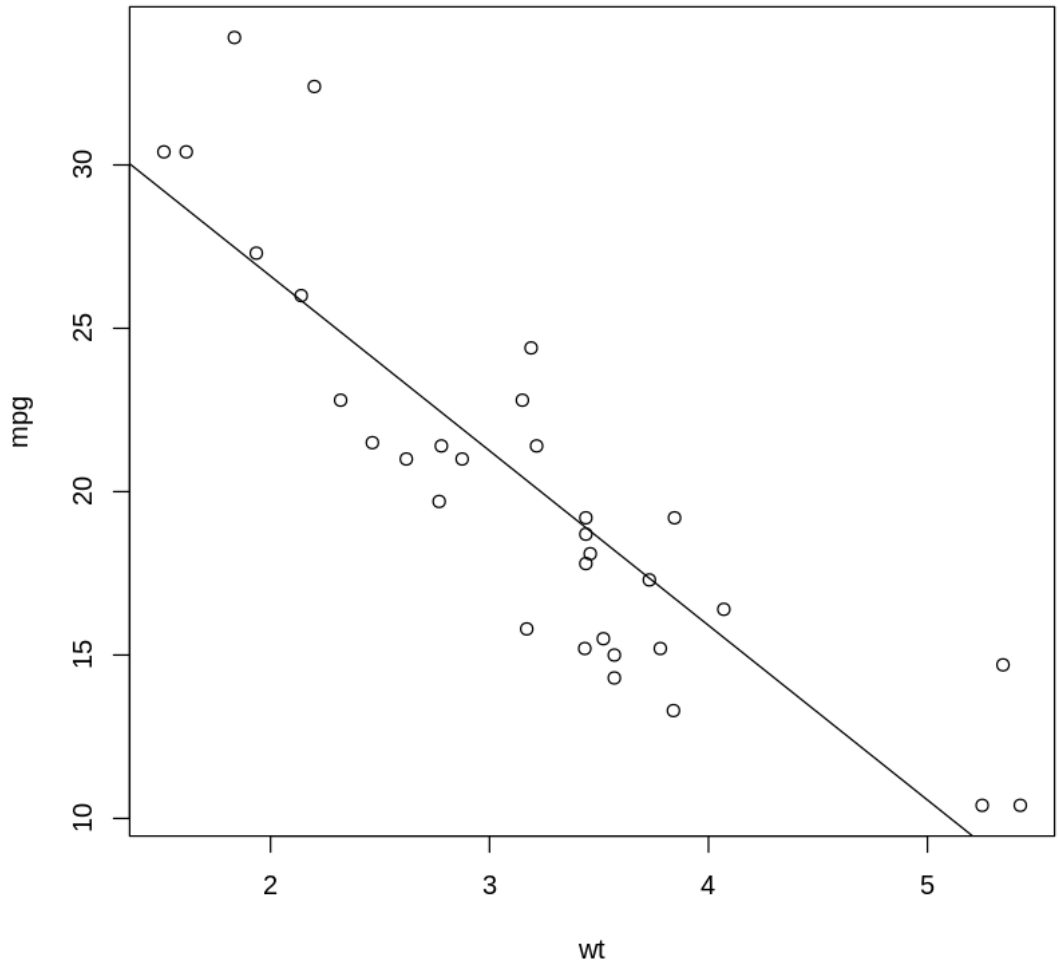
[9]:
```
# install the library
library(tidyverse)
```

```
Warning message in system("timedatectl", intern = TRUE):
"running command 'timedatectl' had status 1"
  Attaching packages                      tidyverse
1.3.0

 ggplot2 3.3.3      purrr   0.3.4
 tibble  3.1.0      dplyr   1.0.4
 tidyr   1.1.2      stringr 1.4.0
 readr   1.4.0      forcats 0.5.1

  Conflicts
tidyverse_conflicts()
 dplyr::filter() masks stats::filter()
 dplyr::lag()    masks stats::lag()
```

### 1.1 Stuntized Residuals and Outliers

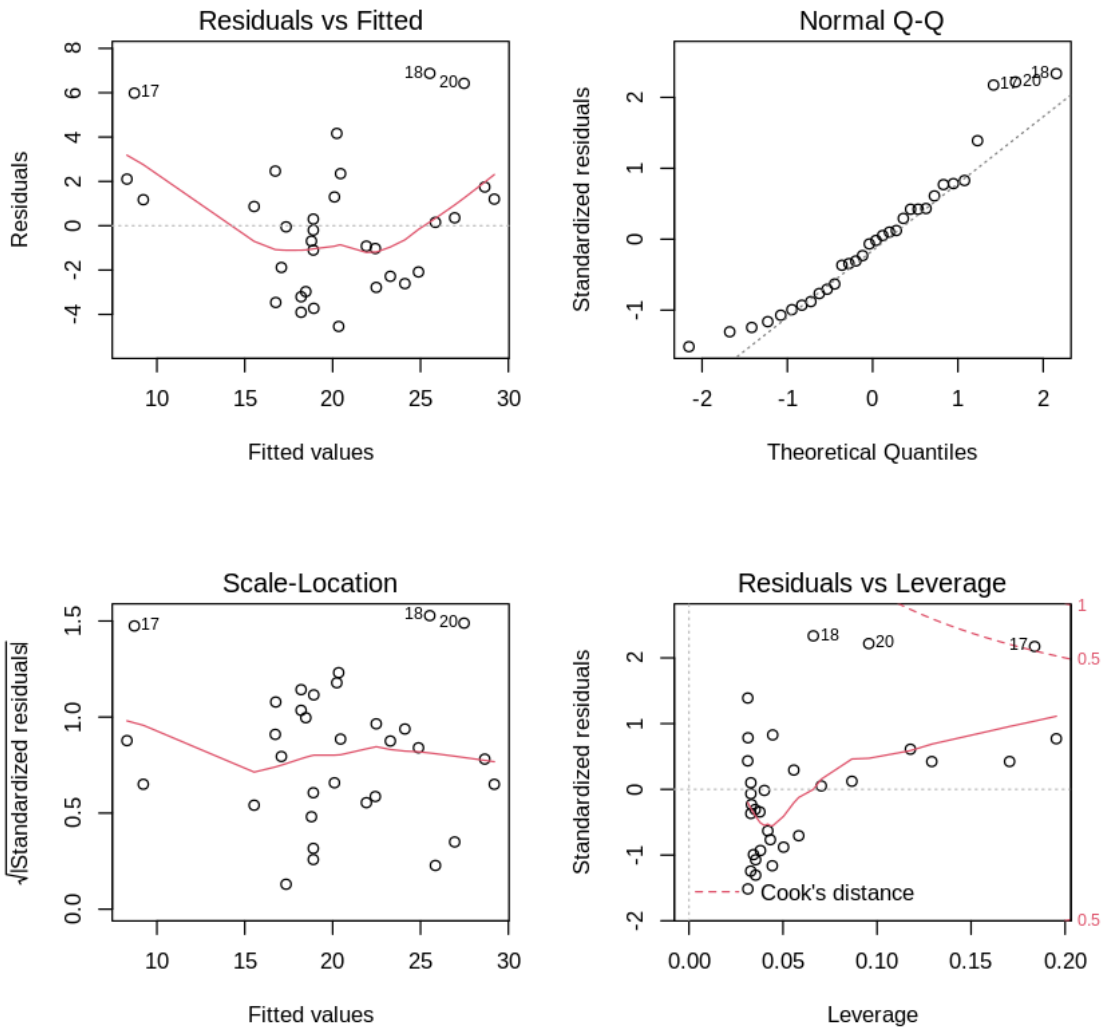
[10]:
```
attach(mtcars)
reg = lm( mpg ~ wt )
plot(wt, mpg)
abline(reg)
```

```
The following object is masked from package:ggplot2:

    mpg
```




We will focus on **residual plots**. - Residuals vs Fitted: see the yhat vs ei. A strong pattern indicates non-linearity in the data. - Normal QQ: drawing up the data to check whether or not they follow a normal distribution. - Scale-Location: testing the variance is constant or not. The ideal case is the data points along with the horizontal line. - Residual vs Leverage: finding the influantial observations on this plot. The data point is above the dust line, which means that it would probably be an influential point.

[11]:
```
par(mfrow = c(2, 2)) # Return to the 2x2 plot window
plot(reg)
```




## 1.2 Studentized residuals and testing for outliers

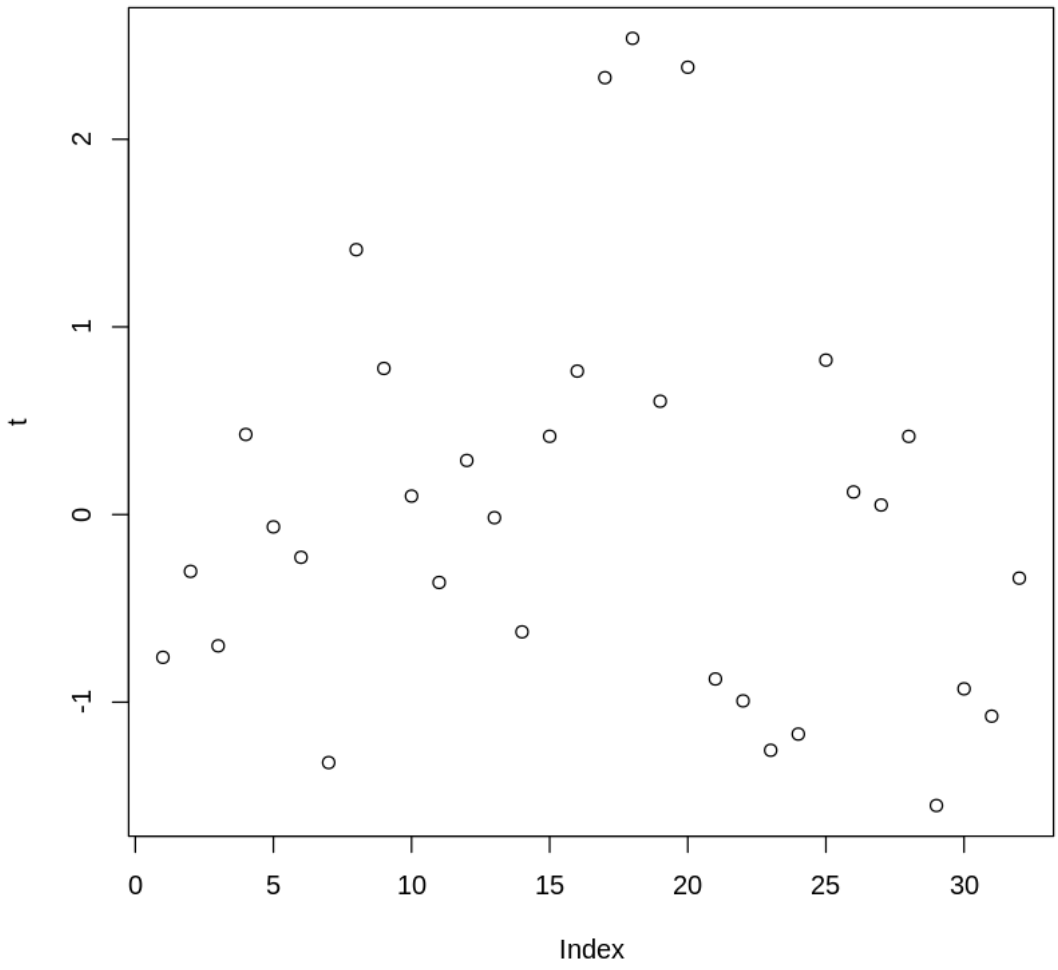
Based on the Residuals vs Leverage plot above, we should focus on the influential outliers. That is, $|\text{rstudent(reg)}| > 2$.

[12]:
```
t = rstudent(reg) # Studentized residuals
t
par(mfrow=c(1,1)) # Return to the 1x1 plot window
plot(t) # See if there are any nonlinear trends
t[abs(t)>2]
```

**1** -0.760769767767308 **2** -0.30274049912238 **3** -0.699723286066695 **4** 0.42681175832875 **5** -0.0657005929406649 **6** -0.227795873402642 **7** -1.32167204102416 **8** 1.41169344019973 **9**

0.778768380543418 **10** 0.0984418674688788 **11** -0.361928384450121 **12** 0.288376284812941 **13**
-0.0165549609096952 **14** -0.625154142137688 **15** 0.417097093510937 **16** 0.764447736215124 **17**
2.32816206125152 **18** 2.53780105948126 **19** 0.603859107559708 **20** 2.38384375526598 **21**
-0.876228974964037 **22** -0.992902171214059 **23** -1.25610442750003 **24** -1.1699145098449 **25**
0.823262284033516 **26** 0.120416134706099 **27** 0.050903962936754 **28** 0.416682410673085 **29**
-1.55056009946433 **30** -0.928734335844879 **31** -1.0742670322719 **32** -0.338770556771007

**17** 2.32816206125152 **18** 2.53780105948126 **20** 2.38384375526598




### 1.3 Compare with the Bonferroni-adjusted quantile from t-distribution.

The test revealed no outliers.

[13]:
```
n = length(wt) # 32 observations
n
qt( 0.025/n, n-2 ) # degrees of freedom is n-2
t[ abs(t) > abs(qt( 0.025/n, n-2 )) ]
```

32

-3.47873553679339

### 1.4 Testing Normality using Shapiro-Wilk normality test

- Normal QQ-plot and Shapiro-Wilk normality test is both a good method to check the normality.
- With the small p-value 0.03711, we have evidence to reject the null (H0: data is normal distrnuted), meaning that the data tested are not normality.
- W measures how close the graph is to a straight line.

[14]:
```
shapiro.test(t)
```

```
        Shapiro-Wilk normality test

data:  t
W = 0.92916, p-value = 0.03711
```

## 2 Testing HOMOSCEDASTICITY (constant variance)

Look at the residual plots including a plot of t^2 vs fitted values
Below is the Breausch-Pagan test, and it is included in R package called "car".

- ncvTest: Computes a score test of the hypothesis of constant error variance against the alternative that the error variance changes with the level of the response (fitted values), or with a linear combination of predictors.

Reference: https://cran.r-project.org/web/packages/car/index.html

[15]:
```
#------------------------------------------------------------------------------
# Revision history:
# 2009-09-28 by J. Fox (renamed)
# 2012-07-01 Rewritten by S. Weisberg.  The 'data' argument is now gone
# 2013-07-09 Works correctly if data arg is not set in the model
#            works correctly if the formula in 'lm' is an argument
# 2014-11-06 Fixed conflicts with objects in base package. J. Fox
# 2018-06-07 format p-value. J. Fox
#------------------------------------------------------------------------------

# score test of nonconstant variance (J. Fox)
```

```
ncvTest <- function(model, ...){
    UseMethod("ncvTest")
}

ncvTest.lm <- function(model, var.formula, ...) {
    data <- getCall(model)$data
    model <- if (!is.null(data)){
        data <- eval(data, envir=environment(formula(model)))
        update(model, formula(model), na.action="na.exclude", data=data)
    }
    else update(model, formula(model), na.action="na.exclude")
    sumry <- summary(model)
    residuals <- residuals(model, type="pearson")
    S.sq <- df.residual(model)*(sumry$sigma)^2/sum(!is.na(residuals))
    .U <- (residuals^2)/S.sq
    if (missing(var.formula)) {
        mod <- lm(.U ~ fitted.values(model))
        varnames <- "fitted.values"
        var.formula <- ~ fitted.values
        df <- 1
    }
    else {
        form <- as.formula(paste(".U ~ ", as.character(var.formula)[[2]],␣
 ↪sep=""))
        mod <- if(!is.null(data)){
            data$.U <- .U
            lm(form, data=data)
        }
        else lm(form)
        df <- sum(!is.na(coefficients(mod))) - 1
    }
    SS <- anova(mod)$"Sum Sq"
    RegSS <- sum(SS) - SS[length(SS)]
    Chisq <- RegSS/2
    result <- list(formula=var.formula, formula.name="Variance",␣
 ↪ChiSquare=Chisq, Df=df,
        p=pchisq(Chisq, df, lower.tail=FALSE), test="Non-constant Variance␣
 ↪Score Test")
    class(result) <- "chisqTest"
    result
}

ncvTest.glm <- function(model, ...){
    stop("requires lm object")
}
```

```
print.chisqTest <- function(x, digits=getOption("digits"), ...){
    title <- if (!is.null(x$test)) x$test else "Chisquare Test"
    cat(title,"\n")
    if (!is.null(x$formula)) cat(x$formula.name,
        "formula:", as.character(x$formula), "\n")
    cat(paste0("Chisquare = ", format(x$ChiSquare, digits=digits), ", Df = ",␣
 ↪x$Df,
        ", p = ", format.pval(x$p, digits=max(1, digits - 2)), "\n"))
    invisible(x)
}
```

- If p-value <= $\alpha$, which means Homo. is rejected in favor of Heter. is assumed.
- p = 0.84556 indicates we fail to reject the null, meaning that data tested the constant variance.

[17]:
```
ncvTest(reg)
```

```
Non-constant Variance Score Test
Variance formula: ~ fitted.values
Chisquare = 0.03794177, Df = 1, p = 0.84556
```

### 2.1 This package also has a built-in outlier test

[18]:
```
#-------------------------------------------------------------------------------
# Revision history:
# 2009-09-28 by J. Fox (renamed)
# 2010-04-14 by J. Fox fixed error in reporting largest abs rstudent
# 2012-12-12 by J. Fox fixed handling of labels argument
# 2019-01-02 by J. Fox added lmerMod method
# 2019-05-12 by J. Fox fixed spelling of "Bonferroni"
#-------------------------------------------------------------------------------

# Bonferroni test for an outlier (J. Fox)

outlierTest <- function(model, ...){
        UseMethod("outlierTest")
}

outlierTest.lm <- function(model, cutoff=0.05, n.max=10, order=TRUE,␣
 ↪labels=names(rstudent), ...){
        rstudent <- rstudent(model)
        if (length(rstudent) != length(labels))
                stop("Number of labels does not correspond to number of␣
 ↪residuals.")
    else names(rstudent) <- labels
        df <- df.residual(model) - 1
        rstudent <- rstudent[!is.na(rstudent)]
        n <- length(rstudent)
```

```
        p <- if (class(model)[1] == "glm")
                        2*(pnorm(abs(rstudent), lower.tail=FALSE))
                else 2*(pt(abs(rstudent), df, lower.tail=FALSE))
        bp <- n*p
        ord <- if (order) order(bp) else 1:n
        ord <- ord[bp[ord] <= cutoff]
        result <- if (length(ord) == 0){
                        which <- which.max(abs(rstudent))
                        list(rstudent=rstudent[which], p=p[which], bonf.
 ↪p=bp[which], signif=FALSE, cutoff=cutoff)
                }
                else {
                        if (length(ord) > n.max) ord <- ord[1:n.max]
                        result <- list(rstudent=rstudent[ord], p=p[ord], bonf.
 ↪p=bp[ord], signif=TRUE, cutoff=cutoff)
                }
        class(result)<-"outlierTest"
        result
}

outlierTest.lmerMod <- function(model, ...){
  outlierTest.lm(model, ...)
}

print.outlierTest<-function(x, digits=5, ...){
        if (!x$signif){
                cat("No Studentized residuals with Bonferroni p <", x$cutoff)
                cat("\nLargest |rstudent|:\n")
        }
        bp <- x$bonf
        bp[bp > 1] <- NA
        table <- data.frame(rstudent=x$rstudent,
                "unadjusted p-value"=signif(x$p, digits), "Bonferroni␣
 ↪p"=signif(bp, digits),
                check.names=FALSE)
        rownames(table) <- names(x$rstudent)
        print(table)
        invisible(x)
}
```

The p-value 0.016788 indicates no outliers.

[20]:
```
outlierTest(reg)
```

```
No Studentized residuals with Bonferroni p < 0.05
Largest |rstudent|:
```

```
   rstudent unadjusted p-value Bonferroni p
18 2.537801           0.016788       0.5372
```

# 3 LACK OF FIT TEST

## 3.1 The ToothGrowth dataset has only 3 different values of X = dose

- The response is the length of odontoblasts (cells responsible for tooth growth) in 60 guinea pigs. Each animal received one of three dose levels of vitamin C (0.5, 1, and 2 mg/day) by one of two delivery methods, orange juice or ascorbic acid (a form of vitamin C and coded as VC).
- A data frame with 60 observations on 3 variables.

[29]:
```
attach(ToothGrowth)
names(ToothGrowth)
head(ToothGrowth)
table(dose) # the only values that dose takes
```

```
The following objects are masked from ToothGrowth (pos = 3):

    dose, len, supp


The following objects are masked from ToothGrowth (pos = 4):

    dose, len, supp


The following objects are masked from ToothGrowth (pos = 5):

    dose, len, supp


The following objects are masked from ToothGrowth (pos = 6):

    dose, len, supp


The following objects are masked from ToothGrowth (pos = 7):

    dose, len, supp


The following objects are masked from ToothGrowth (pos = 8):

    dose, len, supp
```

1. 'len' 2. 'supp' 3. 'dose'

A data.frame: 6 × 3

| | len <dbl> | supp <fct> | dose <dbl> |
|---|---|---|---|
| 1 | 4.2 | VC | 0.5 |
| 2 | 11.5 | VC | 0.5 |
| 3 | 7.3 | VC | 0.5 |
| 4 | 5.8 | VC | 0.5 |
| 5 | 6.4 | VC | 0.5 |
| 6 | 10.0 | VC | 0.5 |

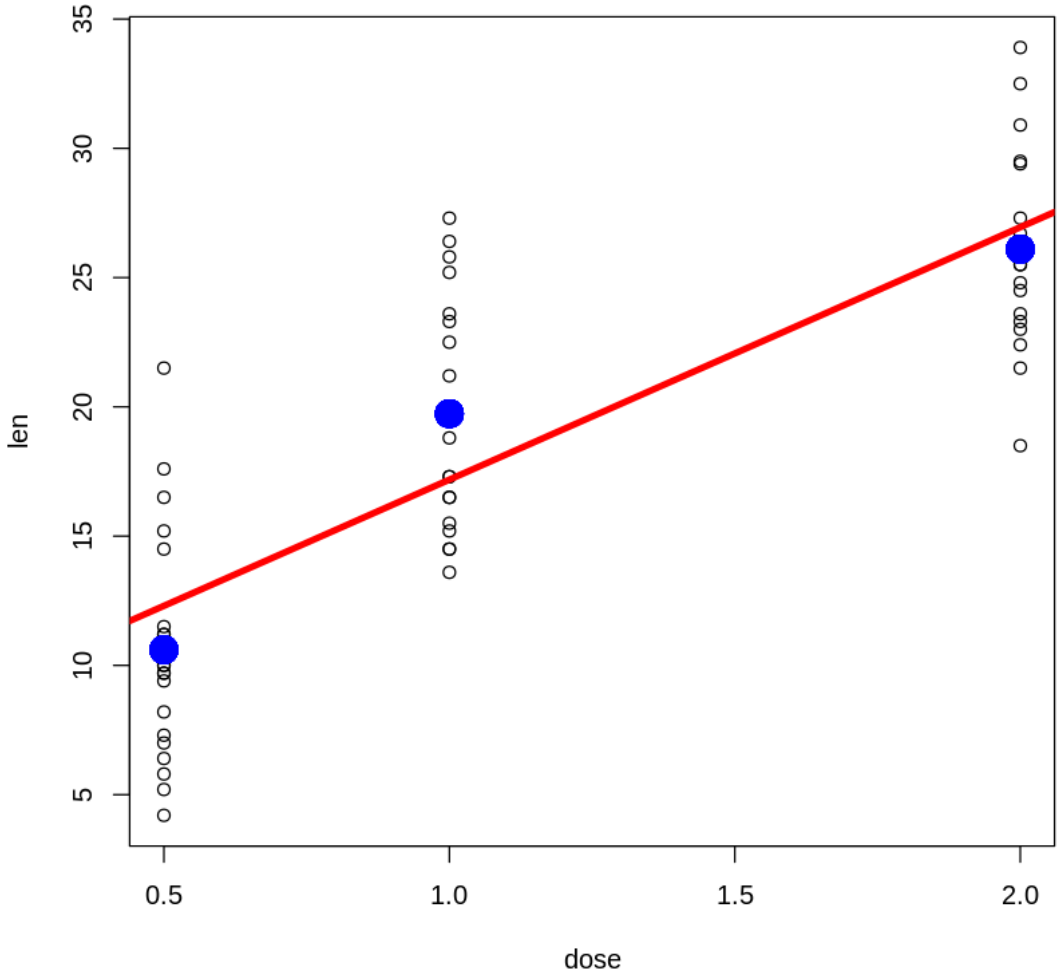
```
dose
0.5   1   2
 20  20  20
```

- Fit two regression models:
- reduced = simple linear regression predicting Y = length in terms of X = dose
- full = using group means to predict Y for each value of X, thus treating X as a categorical variable

[33]:
```
reduced = lm(len ~ dose) # assume linearity,
full = lm(len ~ as.factor(dose)) # the model does NOT assume linearity
summary(reduced)
summary(full)
plot(dose, len)
abline(reduced,col="red",lwd=4)
points(dose, predict(full), col="blue", lwd=10) # predicted the values using␣
 ↪the full model
```

```
Call:
lm(formula = len ~ dose)

Residuals:
    Min      1Q  Median      3Q     Max
-8.4496 -2.7406 -0.7452  2.8344 10.1139

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   7.4225     1.2601    5.89 2.06e-07 ***
dose          9.7636     0.9525   10.25 1.23e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.601 on 58 degrees of freedom
Multiple R-squared:  0.6443,        Adjusted R-squared:  0.6382
F-statistic: 105.1 on 1 and 58 DF,  p-value: 1.233e-14
```

```
Call:
lm(formula = len ~ as.factor(dose))

Residuals:
    Min      1Q  Median      3Q     Max
-7.6000 -3.2350 -0.6025  3.3250 10.8950

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       10.6050     0.9486  11.180 5.39e-16 ***
as.factor(dose)1   9.1300     1.3415   6.806 6.70e-09 ***
as.factor(dose)2  15.4950     1.3415  11.551  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.242 on 57 degrees of freedom
Multiple R-squared:  0.7029,        Adjusted R-squared:  0.6924
F-statistic: 67.42 on 2 and 57 DF,  p-value: 9.533e-16
```




### 3.2 Here is the rigorous F-test for the lack of fit

- RSS is SSR
- Model 1 is linear, and Model 2 is non-linear model
- If the p-value is less than critical value, meaning that the relation between x and y is not linear.
- The non-linear (full) model therefore is better since the p-value is small. Conversely, there is a lack of fit in the linear regression model.

[34]:
```
anova(reduced, full) # two anova tables
```

A anova: 2 × 6

| | Res.Df <dbl> | RSS <dbl> | Df <dbl> | Sum of Sq <dbl> | F <dbl> | Pr(>F) <dbl> |
|---|---|---|---|---|---|---|
| 1 | 58 | 1227.905 | NA | NA | NA | NA |
| 2 | 57 | 1025.775 | 1 | 202.13 | 11.23191 | 0.001432177 |

# 4 Box-Cox Transformation

- Find the best power transformation of responses that fixes non-normality.
- Make the data following a normal distribution.
- Before we run the regression model, we need to check the data are following a normal distribution. However, with p-value = 0.03711, which means the data tested are not normality.

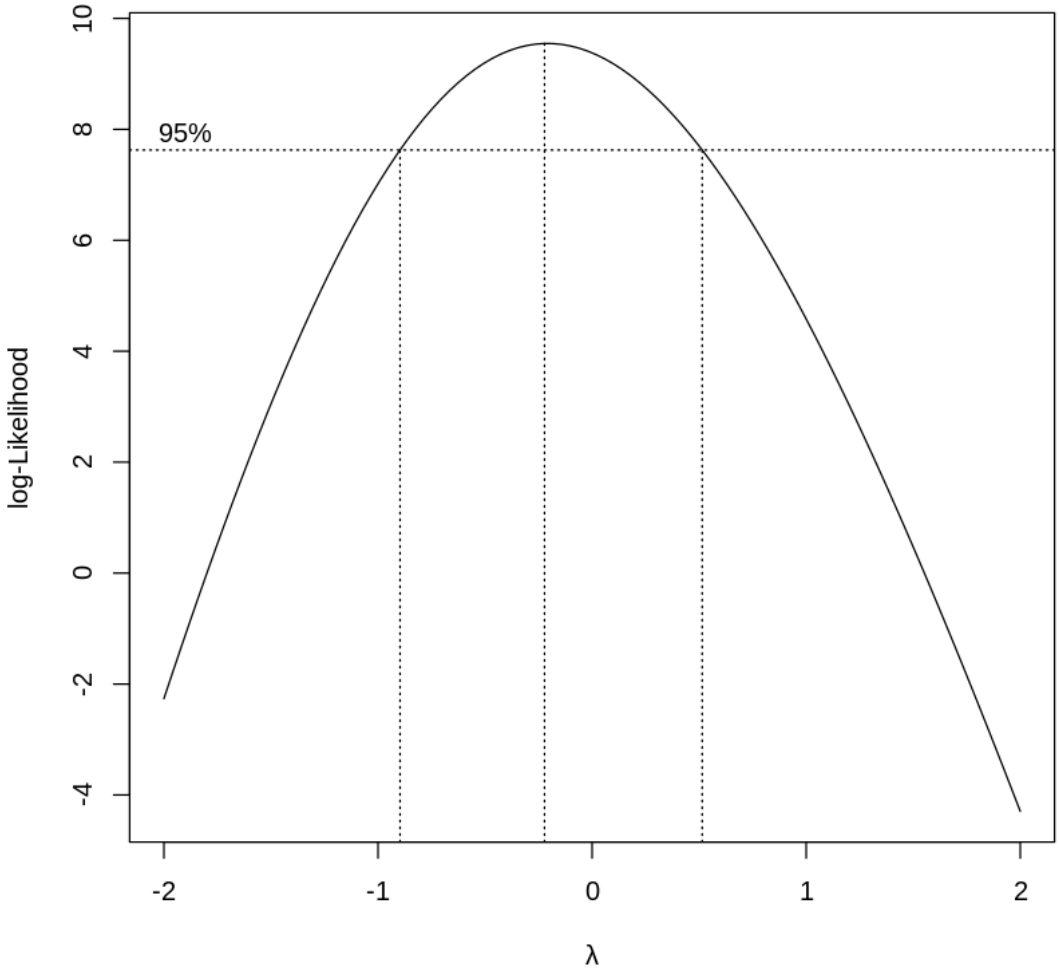
[2]:
```
attach(mtcars)
# Fit a linear regression model, save studentized residuals, and test their␣
 ↪Normal distribution
reg = lm( mpg ~ wt )
t = rstudent(reg)
shapiro.test(t)
```

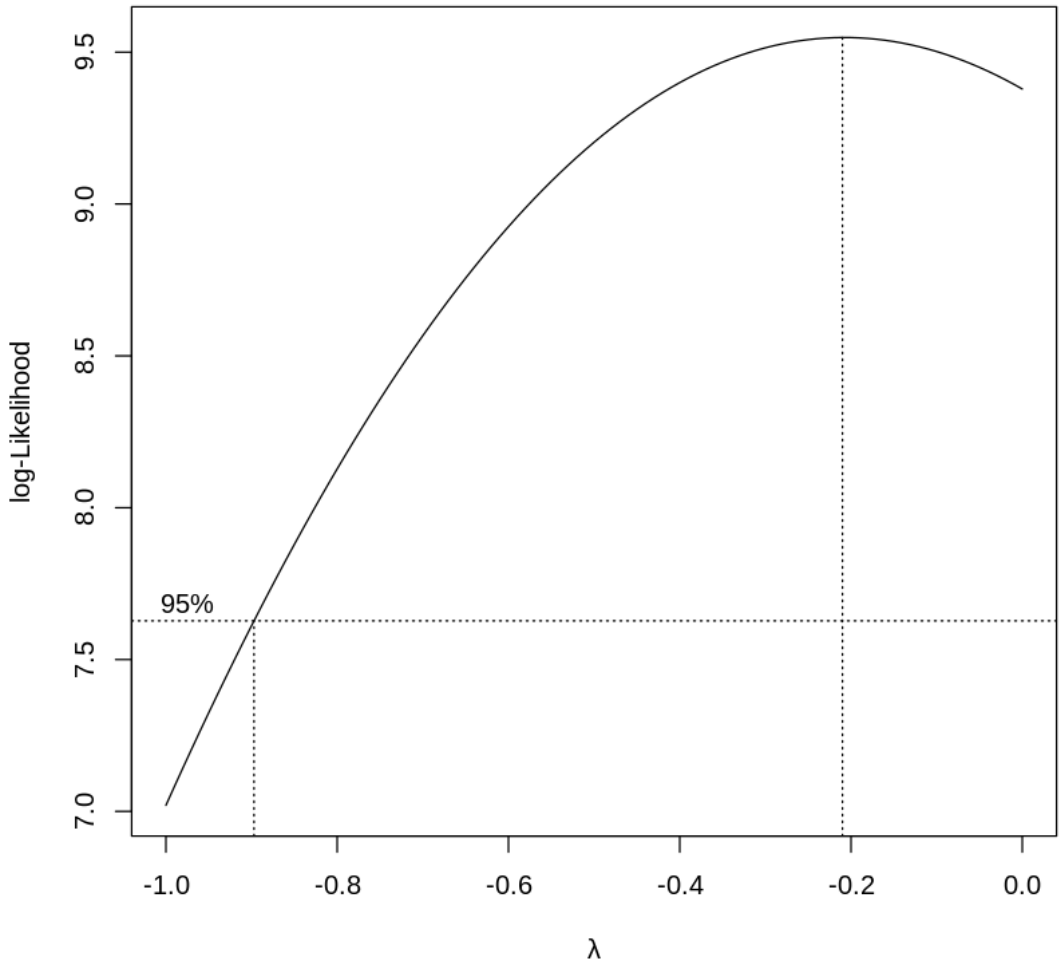
```
The following objects are masked from mtcars (pos = 3):

    am, carb, cyl, disp, drat, gear, hp, mpg, qsec, vs, wt



        Shapiro-Wilk normality test

data:  t
W = 0.92916, p-value = 0.03711
```

We need to focus on "the largest Y-value" mapping to the X position. Thus, the optimal lambda is somewhere between -1 to 0. Then, we zoom in the -1:0 domain.

[4]:
```
# Results are marginal, so let's look for the best transformation. Box-Cox is␣
 ↪available in package "MASS"
install.packages("MASS")
library(MASS)
boxcox(reg)
boxcox(reg,lambda=seq(-1,0,0.01))
```

```
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)
```


95%
log-Likelihood
10
8
6
4
2
0
-2
-4
-2
-1
0
1
2
λ




We can see that the best lambda is very close to -0.2 on x-axis (the peak spot). The next step is we check residuals for normality.

- consider changing lm(y~x) to lm(y^lambda ~ x) to met the normality.

[8]:
```
Z = mpg^(-2)
newreg = lm(Z ~ wt)
t = rstudent(newreg)
shapiro.test(t)

# optimal lambda
Z = mpg^(-0.2)
newreg = lm(Z ~ wt)
t = rstudent(newreg)
```

```
shapiro.test(t)
```

```
        Shapiro-Wilk normality test

data:  t
W = 0.97259, p-value = 0.5736
```

```
        Shapiro-Wilk normality test

data:  t
W = 0.95892, p-value = 0.2566
```

According to the second table (Z = mpg^(-0.2)), the p-value is greater than $\alpha$ on new response variable z, meaning that the model passed the "challenge of normality".