Model Short Report

October 20, 2020

Data Cleaning

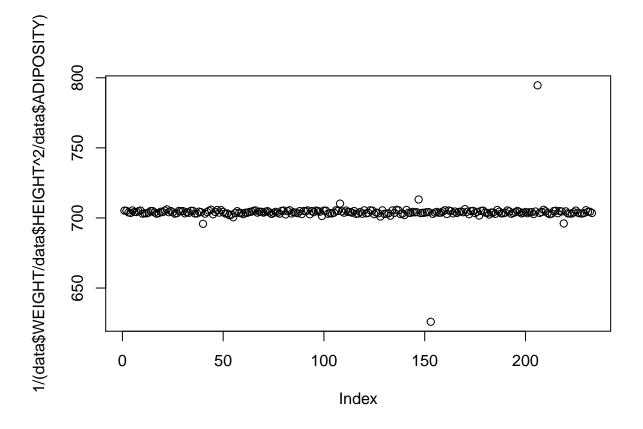
We first clean the data by boxplot.

```
data = read.csv("BodyFat.csv")
index = c()
for(i in 1:length(data))
   {
   index = c(index,which(is.element(data[,i], boxplot(data[,i],plot=FALSE)$out)==1))
   }
index = sort(unique(index))

data = data[-index,]
```

Now, we clean the data by the relaionship among height weight and Adiposity.

```
plot(1/(data$WEIGHT/data$HEIGHT^2/data$ADIPOSITY))
```



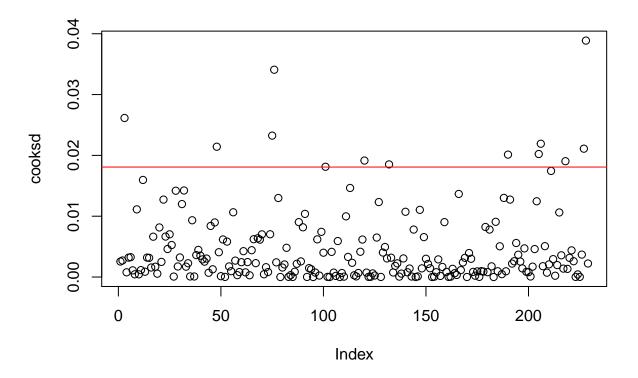
```
index = which(abs(1/(data$WEIGHT/data$HEIGHT^2/data$ADIPOSITY)-700)>50)
data = data[-index,]
```

Then, we clean the data manually.

```
selected_WEIGHT = data[,c('WEIGHT')] <300
selected_BODYFAT = data[,c('BODYFAT')]> 2 & data[,c('BODYFAT')]< 45
selected_HEIGHT = data[,c('HEIGHT')] > 30
selected_item = which(selected_WEIGHT&selected_HEIGHT&selected_BODYFAT)
data = data[selected_item,]
```

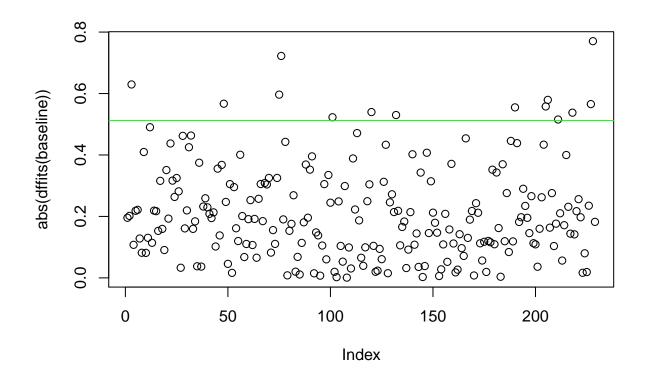
Now, we clean the data by detecting the influtial points of the baseline model $\lim(BODYFAT \sim .)$.

```
data = data[,-c(1,3)]
baseline = lm(BODYFAT~.,data = data)
cooksd = cooks.distance(baseline)
plot(cooksd)
abline(h = 4*mean(cooksd, na.rm=T), col="red")
```



```
index = which(cooksd>=4*mean(cooksd, na.rm=T))
#index = which(cooksd>=0.03)

n=dim(model.matrix(baseline))[1]
p=dim(model.matrix(baseline))[2]
plot(abs(dffits(baseline)))
abline(h=1,col='red')
abline(h=2*sqrt(p/n),col='green')
```



```
index = c(index,which(abs(dffits(baseline))>1))
index = sort(unique(index))
data = data[-index,]
```

Modeling

Residuals:

```
#SLRmodel = lm(BODYFAT~AGE+WEIGHT+HEIGHT+ADIPOSITY+NECK+CHEST+ABDOMEN+HIP+THIGH+KNEE+ANKLE+BICEPS+FOREA
model0 = lm(BODYFAT~1,data = data)
model2 = lm(BODYFAT~.*.*.,data = data)
model1 = lm(BODYFAT~.*.,data = data)

modelAIC = step(model0, scope=list(upper = model1,lower = model0), direction="both",trace = 0)

#modelBIC = step(model0, scope=list(upper = model1,lower = model0), direction="both",trace = 0,k=log(le
summary(modelAIC)

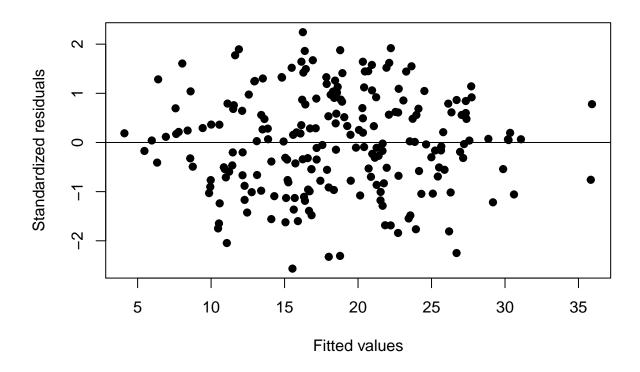
##
## Call:
## lm(formula = BODYFAT ~ ABDOMEN + WEIGHT + WRIST + FOREARM + NECK +
## AGE + THIGH + KNEE + HIP + CHEST + WEIGHT:THIGH + ABDOMEN:NECK +
## FOREARM:CHEST, data = data)
##
```

```
10 Median
                             3Q
## -8.7369 -2.3932 0.0852 2.5596 7.5548
##
## Coefficients:
                Estimate Std. Error t value Pr(>|t|)
                7.598992 58.555399
                                    0.130 0.896874
## (Intercept)
## ABDOMEN
               -1.355830 0.747080 -1.815 0.071032 .
                0.369880 0.155162
## WEIGHT
                                    2.384 0.018060 *
## WRIST
               ## FOREARM
                          2.980447
                                   1.642 0.102066
                4.895043
## NECK
               -6.026065 1.842921 -3.270 0.001265 **
## AGE
                0.074661 0.027505
                                    2.714 0.007212 **
## THIGH
                                    3.507 0.000558 ***
                1.621559 0.462329
## KNEE
               -0.371934 0.228121 -1.630 0.104570
## HIP
               -0.198447
                          0.132480 -1.498 0.135711
                1.074049
## CHEST
                          0.844073
                                    1.272 0.204672
## WEIGHT:THIGH -0.006896
                          0.002456 -2.808 0.005480 **
## ABDOMEN: NECK
                0.060035
                          0.019884
                                    3.019 0.002861 **
## FOREARM: CHEST -0.042138 0.029255 -1.440 0.151314
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 3.446 on 202 degrees of freedom
## Multiple R-squared: 0.7701, Adjusted R-squared: 0.7553
## F-statistic: 52.04 on 13 and 202 DF, p-value: < 2.2e-16
#summary(modelBIC)
```

Model Diagnostics

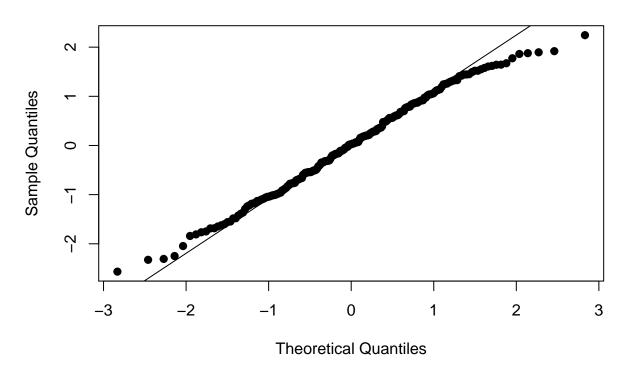
```
plot(predict(modelAIC),rstandard(modelAIC),type="p",pch=19,main = "Standardized Residuals vs Fitted Val
abline(a=0,b=0)
```

Standardized Residuals vs Fitted Values



qqnorm(rstandard(modelAIC),pch=19,main = "Q-Q plot of standardized residuals")
qqline(rstandard(modelAIC))

Q-Q plot of standardized residuals



```
cooksd = cooks.distance(modelAIC)
par(mfrow = c(1,2))
plot(cooksd,type="p",pch=19,ylab="Cooks Distance",main = "Cooks Distance")

n=dim(model.matrix(baseline))[1]
p=dim(model.matrix(baseline))[2]
plot(abs(dffits(modelAIC)),ylab = "DFFITS",type = "p",pch=19,ylim = c(0,1.05),main = "DFFITS")
abline(h=1,col='red')
```

