RepositoryCodes-Final1

October 7, 2019

1 Introduction

Body fat percentage is total mass of fat divided by total body mass, it is a important factor to show a person's health level, too high or too low will caused diseases. There are some body fat calculators online, however, there are too many variables. In this project, we try to find a simple, accurate and robust model to predict boday fat Percentage which obeys the 'Rule of Thumb'.

[1]:

```
library(car)
library(leaps)
library(faraway)
library(glmnet)
```

```
Loading required package: carData
Registered S3 methods overwritten by 'lme4':
  method                          from
  cooks.distance.influence.merMod car
  influence.merMod                car
  dfbeta.influence.merMod         car
  dfbetas.influence.merMod        car

Attaching package: 'faraway'

The following objects are masked from 'package:car':

    logit, vif

Loading required package: Matrix
Loading required package: foreach
Loaded glmnet 2.0-18
```

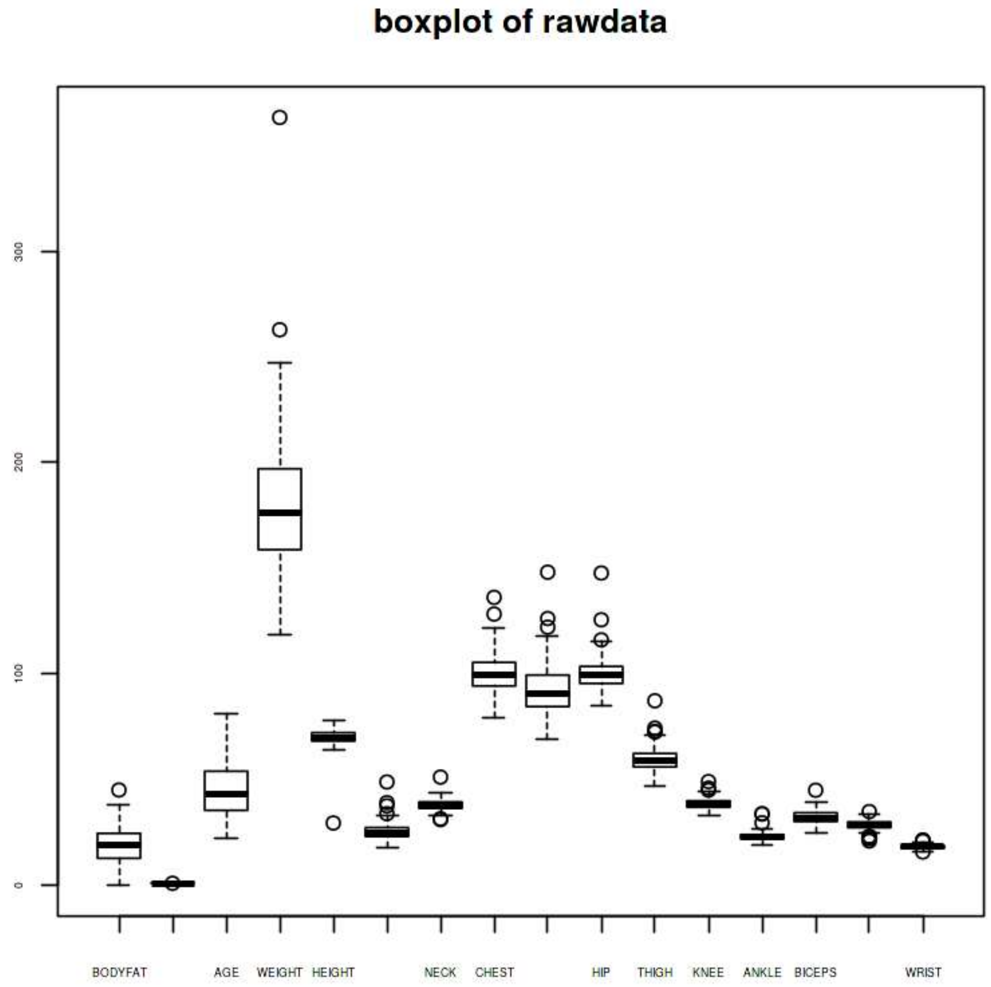
2 Part 1: Dealing with raw data

Read in the raw data and do data cleaning (detect and delete the points which bodyfat does not have a linear relationship of 1 / density)

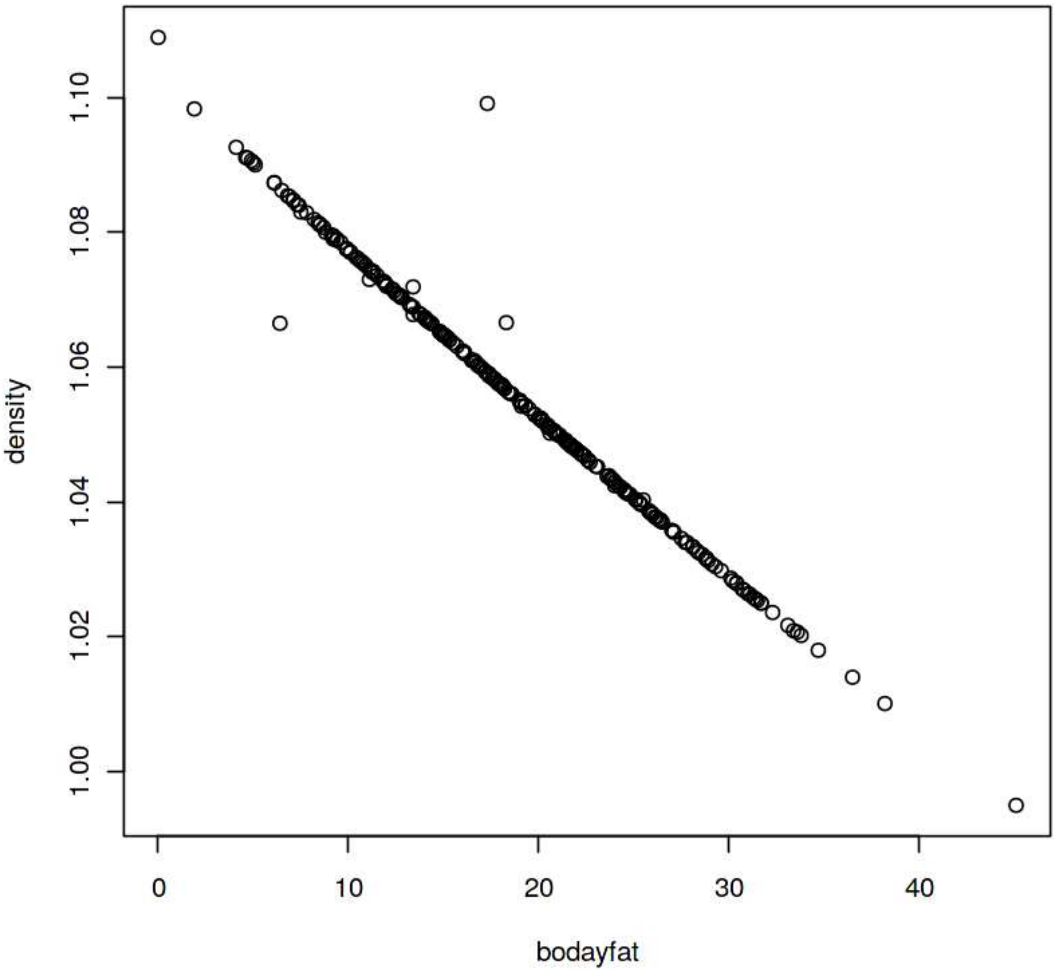
[2]:

```
data = read.csv("BodyFat.csv", row.names = 1)
boxplot(data,main="boxplot of rawdata",cex.axis=0.4)

plot(data$BODYFAT,data$DENSITY,xlab="bodayfat",ylab="density")
text(1:length(data[,1]), data$BODYFAT, 1:length(data[,1]),cex=0.5)
B = 495*(1/data$DENSITY)-450
plot(B-data$BODYFAT,xlab = 'Observations', ylab = 'B-Bodyfat(%)', main =␣
 ↪"siri's equation")
text(c(48,76,96,182,216),␣
 ↪B[c(48,76,96,182,216)]-data$BODYFAT[c(48,76,96,182,216)],␣
 ↪c(48,76,96,182,216),cex=0.8,pos=4)
```

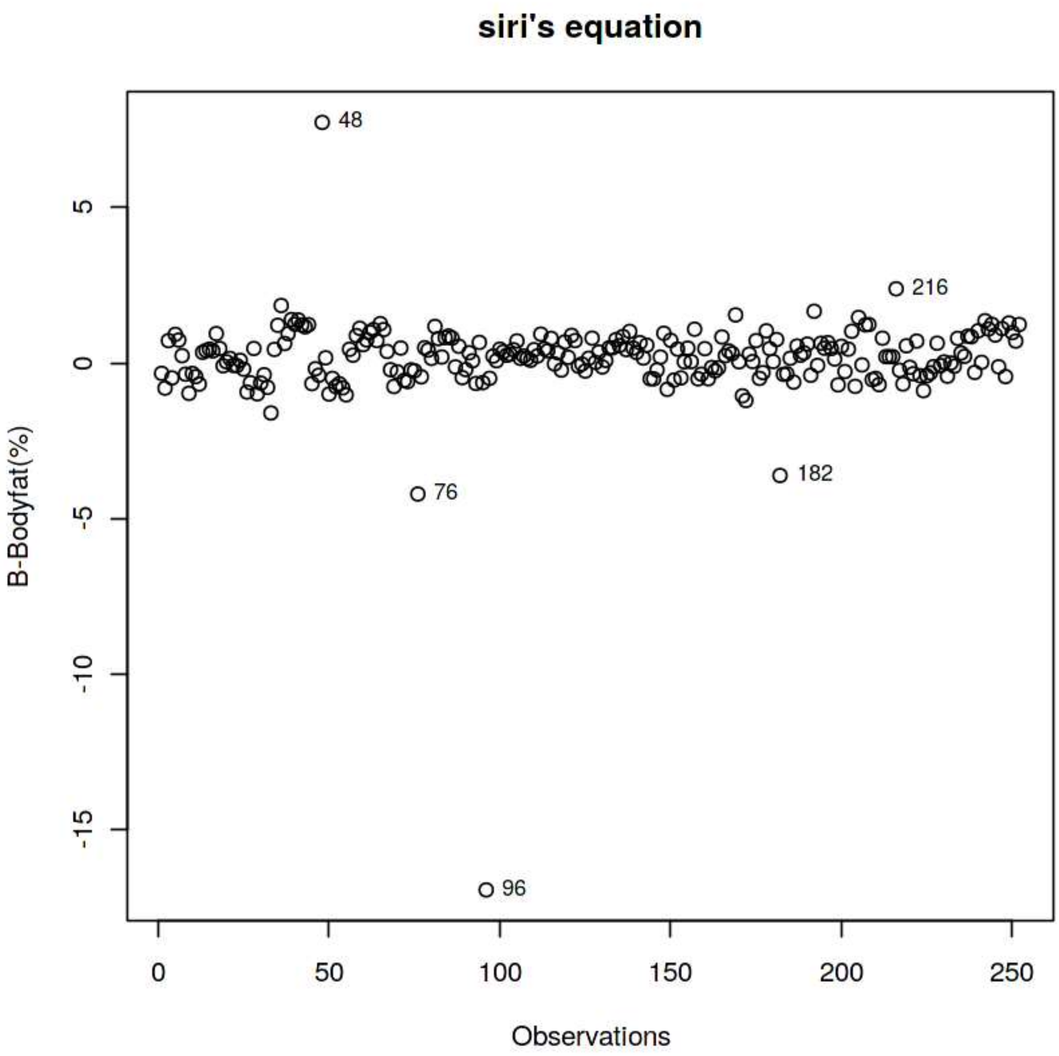
[2]:



[2]:



[2]:

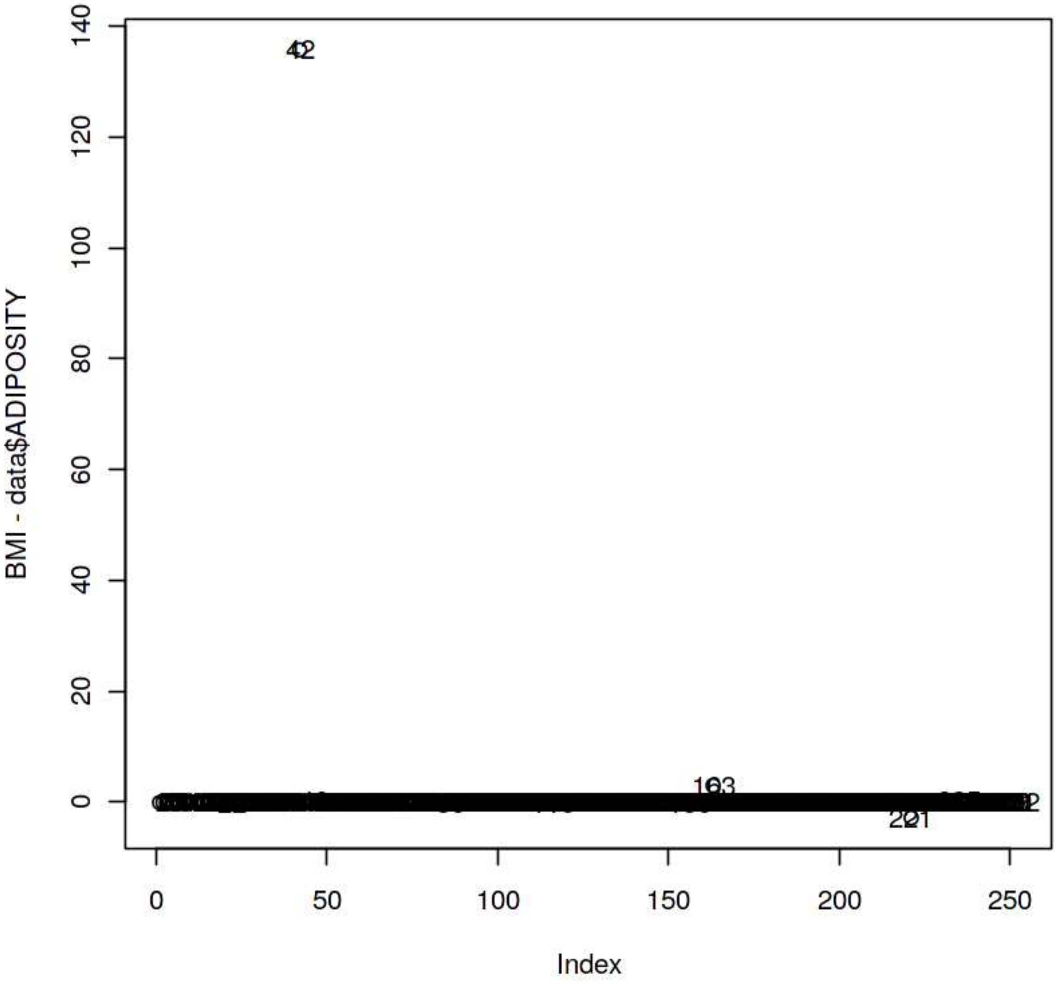


Continue data cleaning (detect and delete the points having wrong relationship of ADIPOSITY, WEIGHT and HEIGHT), then get rid of DENSITY

[3]:

```
BMI=703*(data$WEIGHT/(data$HEIGHT)^2)
plot(BMI-data$ADIPOSITY)
text(1:length(data[,1]), BMI-data$ADIPOSITY, 1:length(data[,1]),cex=1)

# get rid of density and get a new dataset
data_new = data[, -2]
```

[3]:



Then delete possible outliers:

[4]:

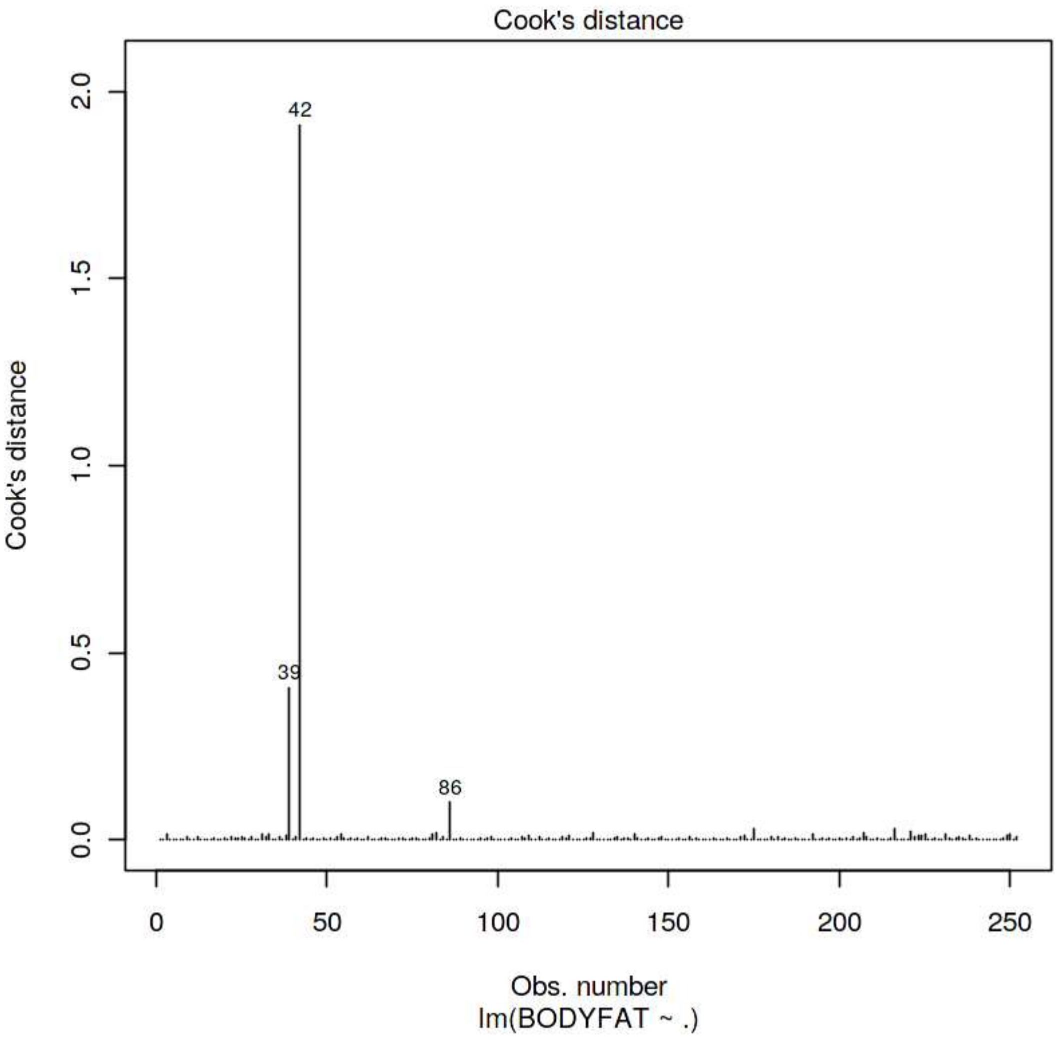
```
#check the cook's distance one by one
model1<- lm(BODYFAT ~ ., data = data_new)
plot(model1, which = 4)
#check the possible outliers
data[c(39, 42, 48, 96,86, 76, 163,182,221),]
```

[4]:

A data.frame: 9 × 16

	BODYFAT <dbl>	DENSITY <dbl>	AGE <int>	WEIGHT <dbl>	HEIGHT <dbl>	ADIPOSITY <dbl>	NECK <dbl>	CHEST <dbl>
39	33.8	1.0202	46	363.15	72.25	48.9	51.2	136.2
42	31.7	1.0250	44	205.00	29.50	29.9	36.6	106.0
48	6.4	1.0665	39	148.50	71.25	20.6	34.6	89.8
96	17.3	1.0991	53	224.50	77.75	26.1	41.1	113.2
86	25.8	1.0386	67	167.00	67.50	26.0	36.5	98.9
76	18.3	1.0666	61	148.25	67.50	22.9	36.0	91.6
163	13.3	1.0690	33	184.25	68.75	24.4	40.7	98.9
182	0.0	1.1089	40	118.50	68.00	18.1	33.8	79.3
221	12.7	1.0706	54	153.25	70.50	24.5	38.5	99.0

[4]:



No.39 has too large weight; No.42 is way too short.

No.48,No.76,No.96 does not match the relationship between bodyfat and density.

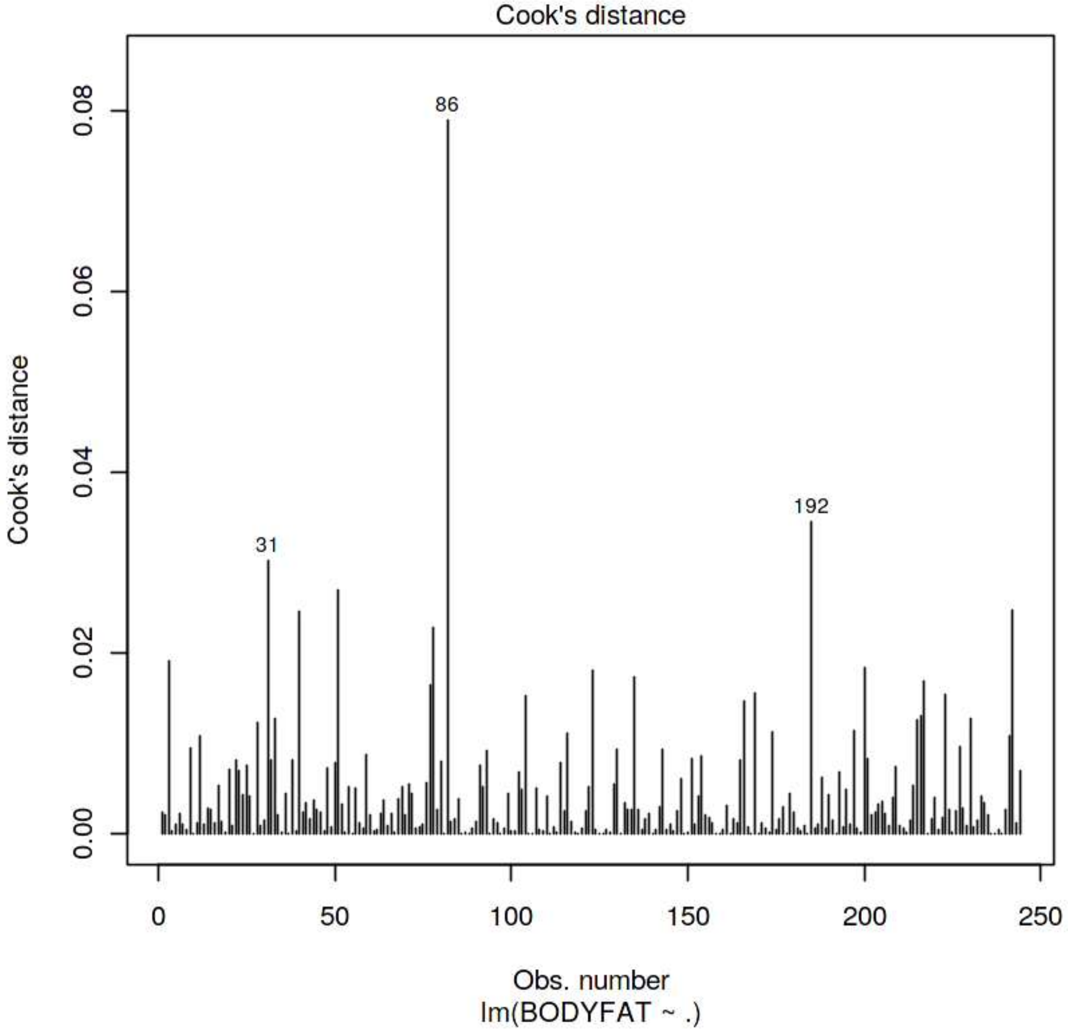
No.182 has bodyfat 0, it is a mistake.

No.221,No.163 don't obey the BMI equation (also No.42).

We remove them and scale the data to get a new dataset. Then check the Cook's distance again.

[5]:
```r
data_clean = data_new[c(-39,-42, -48, -96, -76, -163, -182, -221), ]
data_clean<-data.frame(scale(data_clean))#scale the data
write.csv(data_clean,"bodyfat_clean.csv",row.names = F)

#check the cook's distance again
model = lm(BODYFAT ~ ., data = data_clean)
plot(model, which = 4)
```

[5]:



We check new data's Cook's distance again and find nothing weird.

3 Part 2: Model selection

The methods we use are: AIC, BIC, Mallow's Cp, Adjusted-R^2 and lasso.

[6]:
```
full = lm(BODYFAT ~ ., data = data_clean)
base = lm(BODYFAT ~ 1, data = data_clean)
```

1. AIC (Backward, forward and both sides)

[7]:

```
model_AIC_b = step(full, direction = "backward", trace = 0)
print(model_AIC_b)
summary(model_AIC_b)

model_AIC_f = step(base, direction = "forward", trace = 0,scope = list(lower =␣
 ↪base, upper = full))
print(model_AIC_f)

model_AIC_t = step(base, direction = "both", trace = 0, scope = list(lower =␣
 ↪base, upper = full))
print(model_AIC_t)
```

```
Call:
lm(formula = BODYFAT ~ AGE + WEIGHT + HEIGHT + ADIPOSITY + NECK +
    ABDOMEN + HIP + THIGH + FOREARM + WRIST, data = data_clean)

Coefficients:
(Intercept)          AGE       WEIGHT       HEIGHT    ADIPOSITY         NECK
  1.413e-15    9.644e-02   -1.021e+00    3.811e-01    7.602e-01   -9.918e-02
    ABDOMEN          HIP        THIGH      FOREARM        WRIST
  1.076e+00   -1.642e-01    1.701e-01    8.393e-02   -1.678e-01
```

[7]:

```
Call:
lm(formula = BODYFAT ~ AGE + WEIGHT + HEIGHT + ADIPOSITY + NECK +
    ABDOMEN + HIP + THIGH + FOREARM + WRIST, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-1.25248 -0.35972 -0.03786  0.36854  1.20348

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.413e-15  3.276e-02   0.000  1.00000
AGE          9.644e-02  4.809e-02   2.005  0.04608 *
WEIGHT      -1.021e+00  4.902e-01  -2.083  0.03831 *
HEIGHT       3.811e-01  2.435e-01   1.565  0.11896
ADIPOSITY    7.602e-01  4.288e-01   1.773  0.07755 .
NECK        -9.918e-02  6.358e-02  -1.560  0.12017
ABDOMEN      1.076e+00  1.111e-01   9.684  < 2e-16 ***
HIP         -1.642e-01  1.133e-01  -1.449  0.14879
THIGH        1.701e-01  7.905e-02   2.152  0.03241 *
FOREARM      8.393e-02  4.880e-02   1.720  0.08680 .
WRIST       -1.678e-01  5.704e-02  -2.942  0.00359 **
---
```

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5117 on 233 degrees of freedom
Multiple R-squared:  0.7489,	Adjusted R-squared:  0.7381
F-statistic: 69.49 on 10 and 233 DF,  p-value: < 2.2e-16
```

```
Call:
lm(formula = BODYFAT ~ ABDOMEN + WEIGHT + WRIST + BICEPS, data = data_clean)

Coefficients:
(Intercept)      ABDOMEN       WEIGHT        WRIST       BICEPS
  2.369e-16    1.204e+00   -4.139e-01   -1.477e-01    1.077e-01
```

```
Call:
lm(formula = BODYFAT ~ ABDOMEN + WEIGHT + WRIST + BICEPS, data = data_clean)

Coefficients:
(Intercept)      ABDOMEN       WEIGHT        WRIST       BICEPS
  2.369e-16    1.204e+00   -4.139e-01   -1.477e-01    1.077e-01
```

2. BIC (Backward, forward and both sides)

[8]:

```r
n = dim(data_clean)[1]
model_BIC_b = step(full, direction = "backward", trace = 0, k = log(n))
print(model_BIC_b)
summary(model_BIC_b)

model_BIC_f = step(base, direction = "forward", trace = 0, scope = list(lower = base, upper = full), k = log(n))
print(model_BIC_f )

model_BIC_t = step(full, direction = "both", trace = 0, k = log(n))
print(model_BIC_t)
summary(model_BIC_t)
```

```
Call:
lm(formula = BODYFAT ~ WEIGHT + ABDOMEN + WRIST, data = data_clean)

Coefficients:
(Intercept)       WEIGHT      ABDOMEN        WRIST
  1.574e-16   -3.238e-01    1.189e+00   -1.376e-01
```

[8]:

```
Call:
lm(formula = BODYFAT ~ WEIGHT + ABDOMEN + WRIST, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-1.18875 -0.37533 -0.03202  0.38206  1.20597

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.574e-16  3.329e-02   0.000  1.00000
WEIGHT      -3.238e-01  7.969e-02  -4.063 6.58e-05 ***
ABDOMEN      1.189e+00  6.861e-02  17.329  < 2e-16 ***
WRIST       -1.376e-01  4.878e-02  -2.821  0.00519 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5199 on 240 degrees of freedom
Multiple R-squared:  0.733,     Adjusted R-squared:  0.7297
F-statistic: 219.6 on 3 and 240 DF,  p-value: < 2.2e-16
```

```
Call:
lm(formula = BODYFAT ~ ABDOMEN + WEIGHT + WRIST, data = data_clean)

Coefficients:
(Intercept)      ABDOMEN       WEIGHT        WRIST
  1.574e-16    1.189e+00   -3.238e-01   -1.376e-01


Call:
lm(formula = BODYFAT ~ WEIGHT + ABDOMEN + WRIST, data = data_clean)

Coefficients:
(Intercept)       WEIGHT      ABDOMEN        WRIST
  1.574e-16   -3.238e-01    1.189e+00   -1.376e-01
```

[8]:

```
Call:
lm(formula = BODYFAT ~ WEIGHT + ABDOMEN + WRIST, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-1.18875 -0.37533 -0.03202  0.38206  1.20597
```

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.574e-16  3.329e-02   0.000  1.00000
WEIGHT      -3.238e-01  7.969e-02  -4.063 6.58e-05 ***
ABDOMEN      1.189e+00  6.861e-02  17.329  < 2e-16 ***
WRIST       -1.376e-01  4.878e-02  -2.821  0.00519 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5199 on 240 degrees of freedom
Multiple R-squared:  0.733,	Adjusted R-squared:  0.7297
F-statistic: 219.6 on 3 and 240 DF,  p-value: < 2.2e-16
```

3. Mallow’s cp

[9]:

```r
X = data_clean[, -1]
Y = data_clean$BODYFAT
g = leaps(X, Y, nbest = 1)
Cpplot(g)
print(colnames(data_clean)[c(1, 2, 3, 4, 5, 7,8,9,13,14) + 1])
cp_model = BODYFAT ~ AGE +WEIGHT+ HEIGHT +ADIPOSITY+NECK+ ABDOMEN +HIP+ THIGH +FOREARM + WRIST
cp_lm = lm(cp_model, data=data_clean)
summary(cp_lm)
```

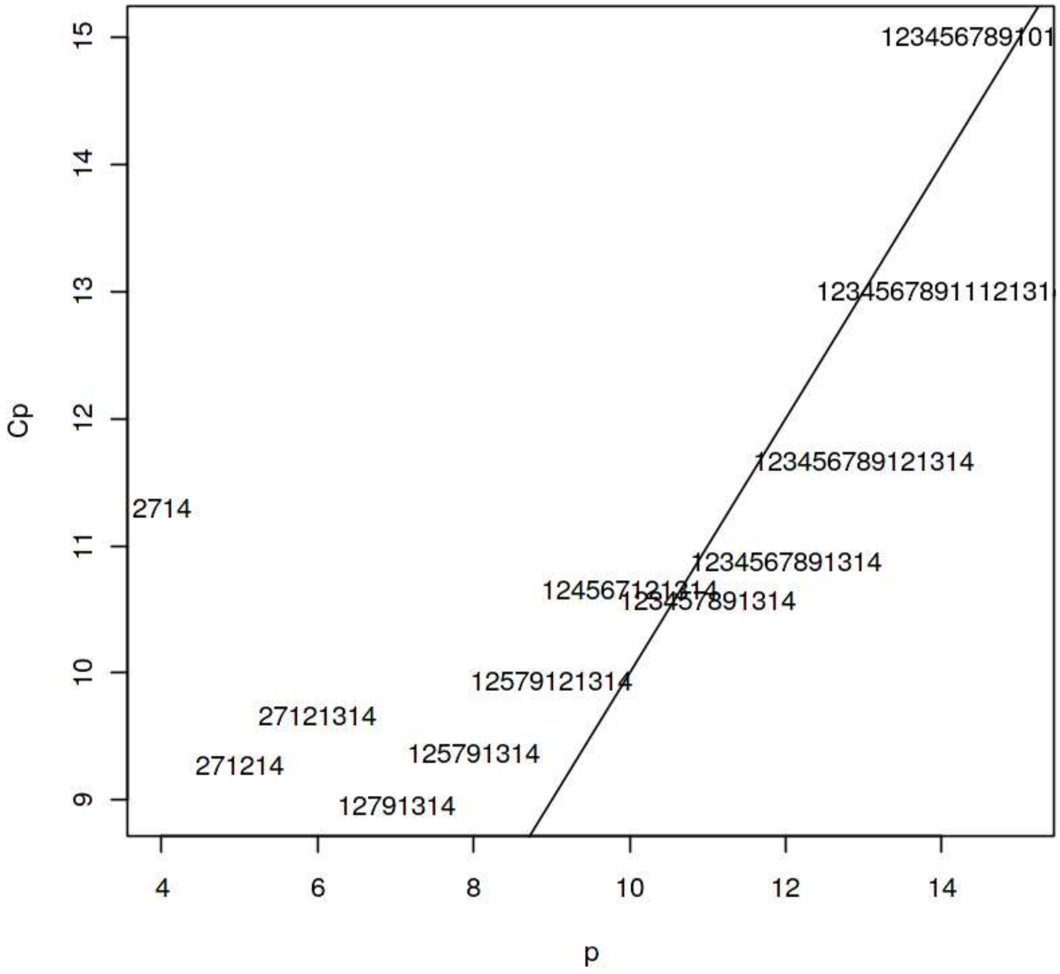
```
 [1] "AGE"       "WEIGHT"    "HEIGHT"    "ADIPOSITY" "NECK"      "ABDOMEN"
 [7] "HIP"       "THIGH"     "FOREARM"   "WRIST"
```

[9]:

```
Call:
lm(formula = cp_model, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-1.25248 -0.35972 -0.03786  0.36854  1.20348

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.413e-15  3.276e-02   0.000  1.00000
AGE          9.644e-02  4.809e-02   2.005  0.04608 *
WEIGHT      -1.021e+00  4.902e-01  -2.083  0.03831 *
HEIGHT       3.811e-01  2.435e-01   1.565  0.11896
ADIPOSITY    7.602e-01  4.288e-01   1.773  0.07755 .
NECK        -9.918e-02  6.358e-02  -1.560  0.12017
ABDOMEN      1.076e+00  1.111e-01   9.684  < 2e-16 ***
HIP         -1.642e-01  1.133e-01  -1.449  0.14879
```

```
THIGH        1.701e-01  7.905e-02   2.152  0.03241 *
FOREARM      8.393e-02  4.880e-02   1.720  0.08680 .
WRIST       -1.678e-01  5.704e-02  -2.942  0.00359 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5117 on 233 degrees of freedom
Multiple R-squared:  0.7489,    Adjusted R-squared:  0.7381
F-statistic: 69.49 on 10 and 233 DF,  p-value: < 2.2e-16
```

[9]:



4. Adjusted R square

[10]:

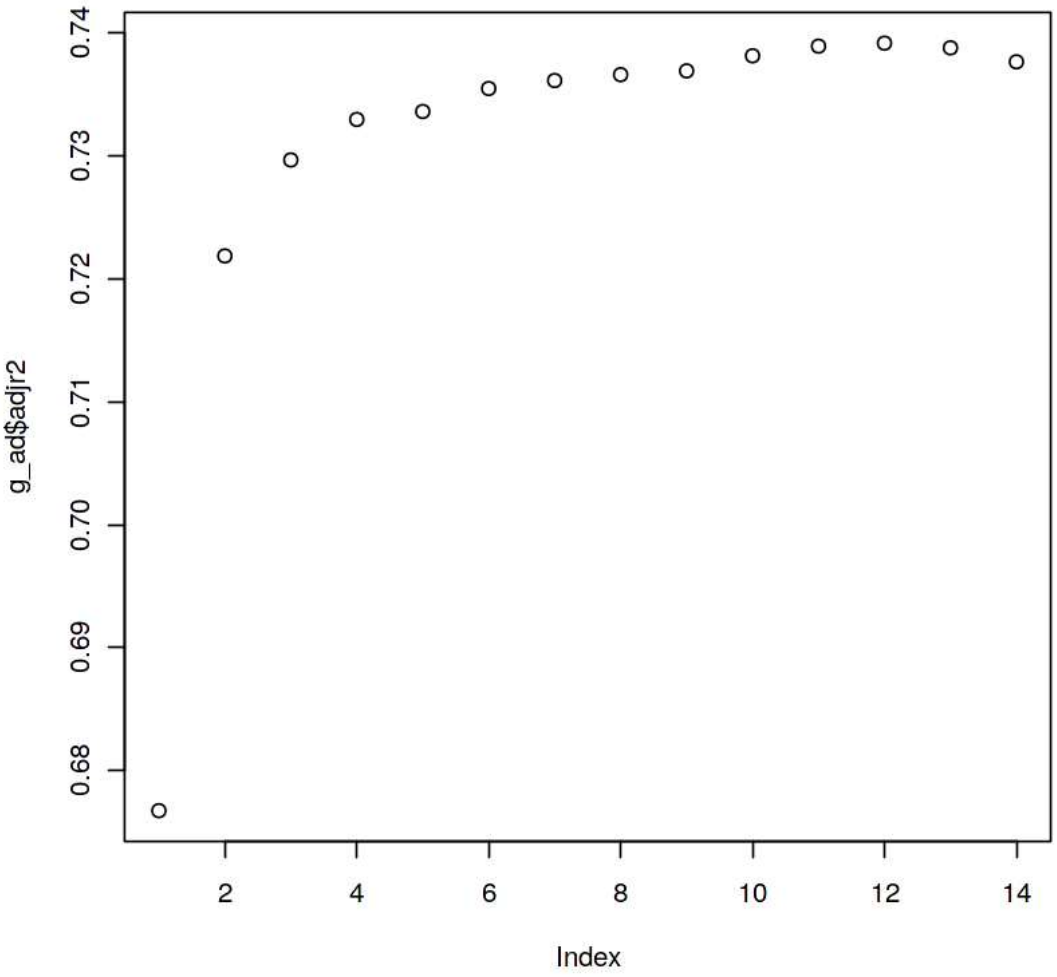
```
g_ad = leaps(X, Y, nbest = 1,method="adjr2")
plot(g_ad$adjr2)
(g_ad$which)[which(g_ad$adjr2==max(g_ad$adjr2)),]
print(colnames(data_clean)[c(1:9, 12:14) + 1])
Ad_r=BODYFAT~AGE +WEIGHT+ HEIGHT +ADIPOSITY+NECK+CHEST+ ABDOMEN +HIP+ THIGH␣
 ↪+BICEPS+FOREARM + WRIST
adr_model<-lm(Ad_r,data=data_clean)
print(adr_model)
```

[10]:

```
1 TRUE 2 TRUE 3 TRUE 4 TRUE 5 TRUE 6 TRUE 7 TRUE 8 TRUE 9 TRUE A FALSE B FALSE
C                 TRUE D                    TRUE E                    TRUE
```

```
 [1] "AGE"       "WEIGHT"    "HEIGHT"    "ADIPOSITY" "NECK"      "CHEST"
 [7] "ABDOMEN"   "HIP"       "THIGH"     "BICEPS"    "FOREARM"   "WRIST"

Call:
lm(formula = Ad_r, data = data_clean)

Coefficients:
(Intercept)          AGE       WEIGHT       HEIGHT    ADIPOSITY         NECK
  1.451e-15    9.742e-02   -9.867e-01    3.979e-01    8.468e-01   -1.014e-01
      CHEST      ABDOMEN          HIP        THIGH       BICEPS      FOREARM
 -1.483e-01    1.123e+00   -1.831e-01    1.208e-01    6.640e-02    6.720e-02
      WRIST
 -1.780e-01
```

[10]:



5. Lasso

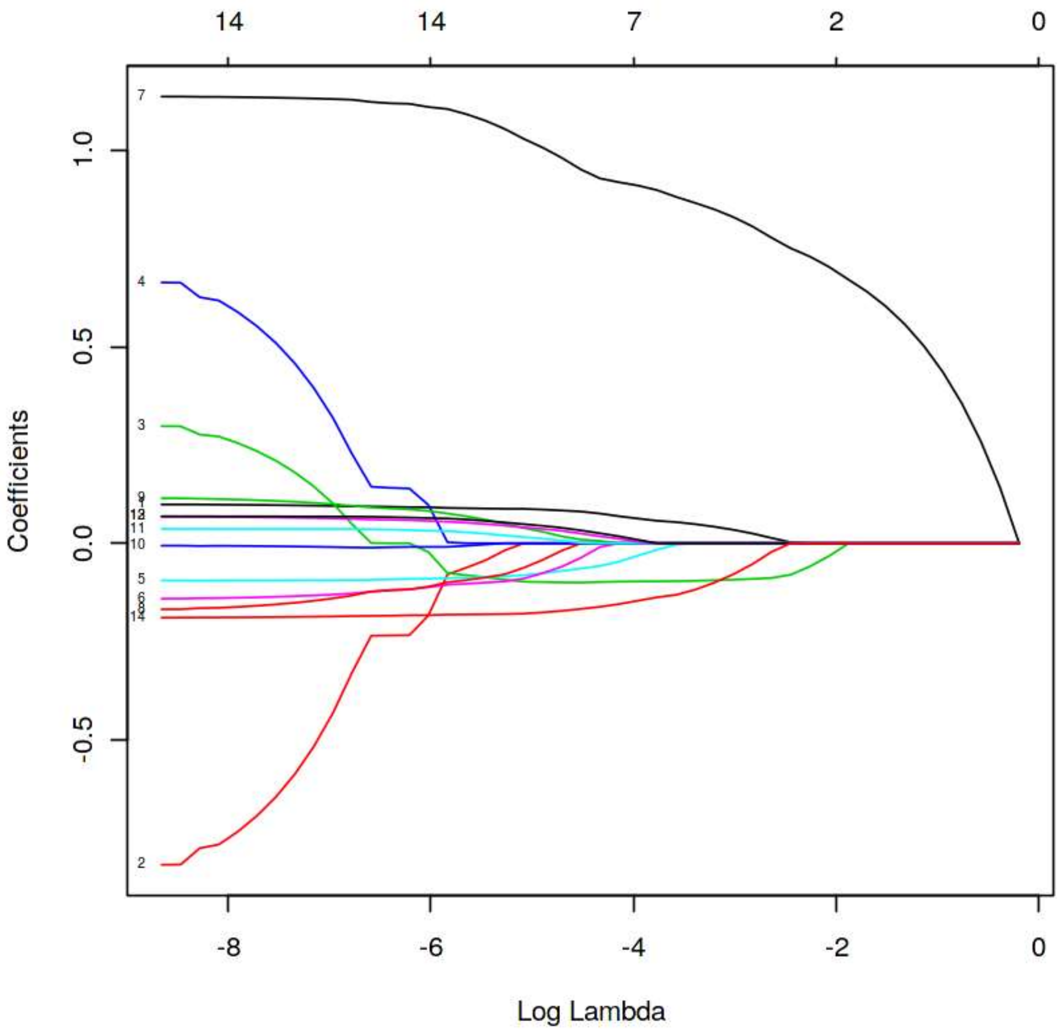
[11]:

```
model_l <- glmnet(as.matrix(data_clean[,2:15]), data_clean$BODYFAT, family =␣
 ↪"gaussian", nlambda = 50, alpha = 1,standardize = T)
print(model_l)
plot(model_l, xvar = "lambda", label = T)
cvfit <- cv.glmnet(as.matrix(data_clean[,2:15]), data_clean$BODYFAT, family =␣
 ↪"gaussian", type.measure = "mse", nfolds = 10,alpha = 1)
plot(cvfit)
print(coef(cvfit, s = "lambda.1se" ))
model_lasso<- BODYFAT ~ AGE + HEIGHT  + ABDOMEN +  WRIST
model_l<-lm(BODYFAT ~ AGE + HEIGHT  + ABDOMEN +  WRIST,data=data_clean)
print(model_l)
```

```
Call:  glmnet(x = as.matrix(data_clean[, 2:15]), y = data_clean$BODYFAT,
family = "gaussian", alpha = 1, nlambda = 50, standardize = T)

      Df   %Dev    Lambda
 [1,]  0 0.0000 0.8218000
 [2,]  1 0.2125 0.6809000
 [3,]  1 0.3584 0.5643000
 [4,]  1 0.4586 0.4676000
 [5,]  1 0.5273 0.3875000
 [6,]  1 0.5746 0.3211000
 [7,]  1 0.6070 0.2660000
 [8,]  1 0.6293 0.2205000
 [9,]  1 0.6446 0.1827000
[10,]  2 0.6557 0.1514000
[11,]  2 0.6732 0.1254000
[12,]  2 0.6852 0.1039000
[13,]  3 0.6936 0.0861300
[14,]  4 0.7041 0.0713700
[15,]  4 0.7137 0.0591400
[16,]  4 0.7203 0.0490100
[17,]  4 0.7249 0.0406100
[18,]  4 0.7280 0.0336500
[19,]  5 0.7303 0.0278800
[20,]  5 0.7324 0.0231100
[21,]  7 0.7346 0.0191500
[22,]  7 0.7366 0.0158700
[23,]  9 0.7384 0.0131500
[24,] 10 0.7405 0.0108900
[25,] 11 0.7427 0.0090270
[26,] 11 0.7445 0.0074810
[27,] 11 0.7457 0.0061990
[28,] 12 0.7467 0.0051360
[29,] 13 0.7474 0.0042560
[30,] 13 0.7479 0.0035270
[31,] 14 0.7483 0.0029230
[32,] 14 0.7493 0.0024220
[33,] 13 0.7498 0.0020070
[34,] 13 0.7499 0.0016630
[35,] 14 0.7500 0.0013780
[36,] 14 0.7506 0.0011420
[37,] 14 0.7512 0.0009462
[38,] 14 0.7517 0.0007840
[39,] 14 0.7520 0.0006497
[40,] 14 0.7522 0.0005384
[41,] 14 0.7523 0.0004461
[42,] 14 0.7524 0.0003697
[43,] 14 0.7525 0.0003063
```

```
[44,] 14 0.7525 0.0002538
[45,] 14 0.7526 0.0002103
[46,] 14 0.7526 0.0001743
```

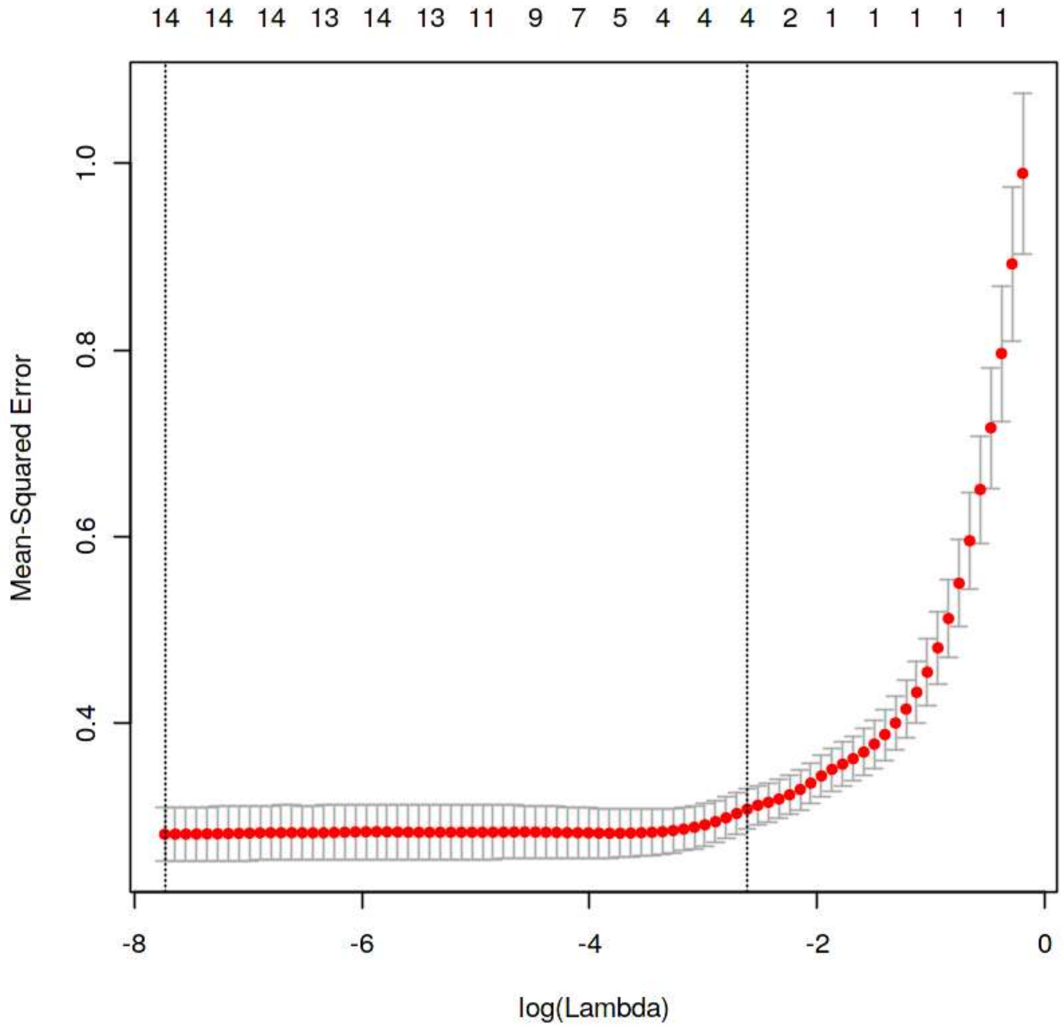
[11]:



```
15 x 1 sparse Matrix of class "dgCMatrix"
                         1
(Intercept) -1.056100e-16
AGE          1.174299e-02
WEIGHT       .
HEIGHT      -8.806614e-02
ADIPOSITY    .
NECK         .
CHEST        .
ABDOMEN      7.732062e-01
```

```
HIP           .
THIGH         .
KNEE          .
ANKLE         .
BICEPS        .
FOREARM       .
WRIST        -1.752753e-02

Call:
lm(formula = BODYFAT ~ AGE + HEIGHT + ABDOMEN + WRIST, data = data_clean)

Coefficients:
(Intercept)          AGE       HEIGHT      ABDOMEN        WRIST
 -3.209e-16    7.994e-02   -1.020e-01    9.444e-01   -2.036e-01
```

[11]:



4 Part3: Other analysis

We compare the models above by their summary table and plots.

[12]:

```
summary(model_AIC_b)
summary(model_AIC_f)
summary(model_AIC_t)



summary(model_BIC_b)
summary(model_BIC_f)
summary(model_BIC_t)

summary(cp_lm)
summary(adr_model)
summary(model_l)
```

[12]:

```
Call:
lm(formula = BODYFAT ~ AGE + WEIGHT + HEIGHT + ADIPOSITY + NECK +
    ABDOMEN + HIP + THIGH + FOREARM + WRIST, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-1.25248 -0.35972 -0.03786  0.36854  1.20348

Coefficients:
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NECK        -9.918e-02  6.358e-02  -1.560  0.12017
ABDOMEN      1.076e+00  1.111e-01   9.684  < 2e-16 ***
HIP         -1.642e-01  1.133e-01  -1.449  0.14879
THIGH        1.701e-01  7.905e-02   2.152  0.03241 *
FOREARM      8.393e-02  4.880e-02   1.720  0.08680 .
WRIST       -1.678e-01  5.704e-02  -2.942  0.00359 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5117 on 233 degrees of freedom
Multiple R-squared:  0.7489,    Adjusted R-squared:  0.7381
```

```
F-statistic: 69.49 on 10 and 233 DF,  p-value: < 2.2e-16
```

[12]:

```
Call:
lm(formula = BODYFAT ~ ABDOMEN + WEIGHT + WRIST + BICEPS, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.23562 -0.36528 -0.01922  0.39216  1.12071 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  2.369e-16  3.308e-02   0.000  1.00000    
ABDOMEN      1.204e+00  6.860e-02  17.549  < 2e-16 ***
WEIGHT      -4.139e-01  9.123e-02  -4.536 9.07e-06 ***
WRIST       -1.477e-01  4.875e-02  -3.029  0.00272 ** 
BICEPS       1.077e-01  5.412e-02   1.990  0.04774 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5168 on 239 degrees of freedom
Multiple R-squared:  0.7373,	Adjusted R-squared:  0.7329 
F-statistic: 167.7 on 4 and 239 DF,  p-value: < 2.2e-16
```

[12]:

```
Call:
lm(formula = BODYFAT ~ ABDOMEN + WEIGHT + WRIST + BICEPS, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.23562 -0.36528 -0.01922  0.39216  1.12071 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  2.369e-16  3.308e-02   0.000  1.00000    
ABDOMEN      1.204e+00  6.860e-02  17.549  < 2e-16 ***
WEIGHT      -4.139e-01  9.123e-02  -4.536 9.07e-06 ***
WRIST       -1.477e-01  4.875e-02  -3.029  0.00272 ** 
BICEPS       1.077e-01  5.412e-02   1.990  0.04774 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5168 on 239 degrees of freedom
Multiple R-squared:  0.7373,	Adjusted R-squared:  0.7329 
F-statistic: 167.7 on 4 and 239 DF,  p-value: < 2.2e-16
```

[12]:

```
Call:
lm(formula = BODYFAT ~ WEIGHT + ABDOMEN + WRIST, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-1.18875 -0.37533 -0.03202  0.38206  1.20597

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.574e-16  3.329e-02   0.000  1.00000
WEIGHT      -3.238e-01  7.969e-02  -4.063 6.58e-05 ***
ABDOMEN      1.189e+00  6.861e-02  17.329  < 2e-16 ***
WRIST       -1.376e-01  4.878e-02  -2.821  0.00519 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5199 on 240 degrees of freedom
Multiple R-squared:  0.733,	Adjusted R-squared:  0.7297
F-statistic: 219.6 on 3 and 240 DF,  p-value: < 2.2e-16
```

[12]:

```
Call:
lm(formula = BODYFAT ~ ABDOMEN + WEIGHT + WRIST, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-1.18875 -0.37533 -0.03202  0.38206  1.20597

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.574e-16  3.329e-02   0.000  1.00000
ABDOMEN      1.189e+00  6.861e-02  17.329  < 2e-16 ***
WEIGHT      -3.238e-01  7.969e-02  -4.063 6.58e-05 ***
WRIST       -1.376e-01  4.878e-02  -2.821  0.00519 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5199 on 240 degrees of freedom
Multiple R-squared:  0.733,	Adjusted R-squared:  0.7297
F-statistic: 219.6 on 3 and 240 DF,  p-value: < 2.2e-16
```

[12]:

```
Call:
lm(formula = BODYFAT ~ WEIGHT + ABDOMEN + WRIST, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.18875 -0.37533 -0.03202  0.38206  1.20597 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  1.574e-16  3.329e-02   0.000  1.00000    
WEIGHT      -3.238e-01  7.969e-02  -4.063 6.58e-05 ***
ABDOMEN      1.189e+00  6.861e-02  17.329  < 2e-16 ***
WRIST       -1.376e-01  4.878e-02  -2.821  0.00519 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5199 on 240 degrees of freedom
Multiple R-squared:  0.733,	Adjusted R-squared:  0.7297 
F-statistic: 219.6 on 3 and 240 DF,  p-value: < 2.2e-16
```

[12]:

```
Call:
lm(formula = cp_model, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.25248 -0.35972 -0.03786  0.36854  1.20348 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  1.413e-15  3.276e-02   0.000  1.00000    
AGE          9.644e-02  4.809e-02   2.005  0.04608 *  
WEIGHT      -1.021e+00  4.902e-01  -2.083  0.03831 *  
HEIGHT       3.811e-01  2.435e-01   1.565  0.11896    
ADIPOSITY    7.602e-01  4.288e-01   1.773  0.07755 .  
NECK        -9.918e-02  6.358e-02  -1.560  0.12017    
ABDOMEN      1.076e+00  1.111e-01   9.684  < 2e-16 ***
HIP         -1.642e-01  1.133e-01  -1.449  0.14879    
THIGH        1.701e-01  7.905e-02   2.152  0.03241 *  
FOREARM      8.393e-02  4.880e-02   1.720  0.08680 .  
WRIST       -1.678e-01  5.704e-02  -2.942  0.00359 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5117 on 233 degrees of freedom
```

```
Multiple R-squared:  0.7489,	Adjusted R-squared:  0.7381 
F-statistic: 69.49 on 10 and 233 DF,  p-value: < 2.2e-16
```

[12]:

```
Call:
lm(formula = Ad_r, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.24761 -0.34427 -0.02745  0.37215  1.16835 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  1.451e-15  3.270e-02   0.000  1.00000    
AGE          9.742e-02  4.824e-02   2.019  0.04460 *  
WEIGHT      -9.867e-01  4.954e-01  -1.992  0.04757 *  
HEIGHT       3.979e-01  2.433e-01   1.635  0.10338    
ADIPOSITY    8.468e-01  4.323e-01   1.959  0.05134 .  
NECK        -1.014e-01  6.367e-02  -1.592  0.11273    
CHEST       -1.483e-01  1.086e-01  -1.365  0.17357    
ABDOMEN      1.123e+00  1.143e-01   9.825  < 2e-16 ***
HIP         -1.831e-01  1.155e-01  -1.585  0.11440    
THIGH        1.208e-01  8.401e-02   1.438  0.15169    
BICEPS       6.640e-02  6.020e-02   1.103  0.27115    
FOREARM      6.720e-02  5.070e-02   1.326  0.18631    
WRIST       -1.780e-01  5.731e-02  -3.107  0.00213 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5107 on 231 degrees of freedom
Multiple R-squared:  0.752,	Adjusted R-squared:  0.7391 
F-statistic: 58.38 on 12 and 231 DF,  p-value: < 2.2e-16
```

[12]:

```
Call:
lm(formula = BODYFAT ~ AGE + HEIGHT + ABDOMEN + WRIST, data = data_clean)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.25508 -0.37499 -0.03633  0.39655  1.14166 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept) -3.209e-16  3.324e-02   0.000  1.00000    
AGE          7.994e-02  3.722e-02   2.148  0.03272 *  
```

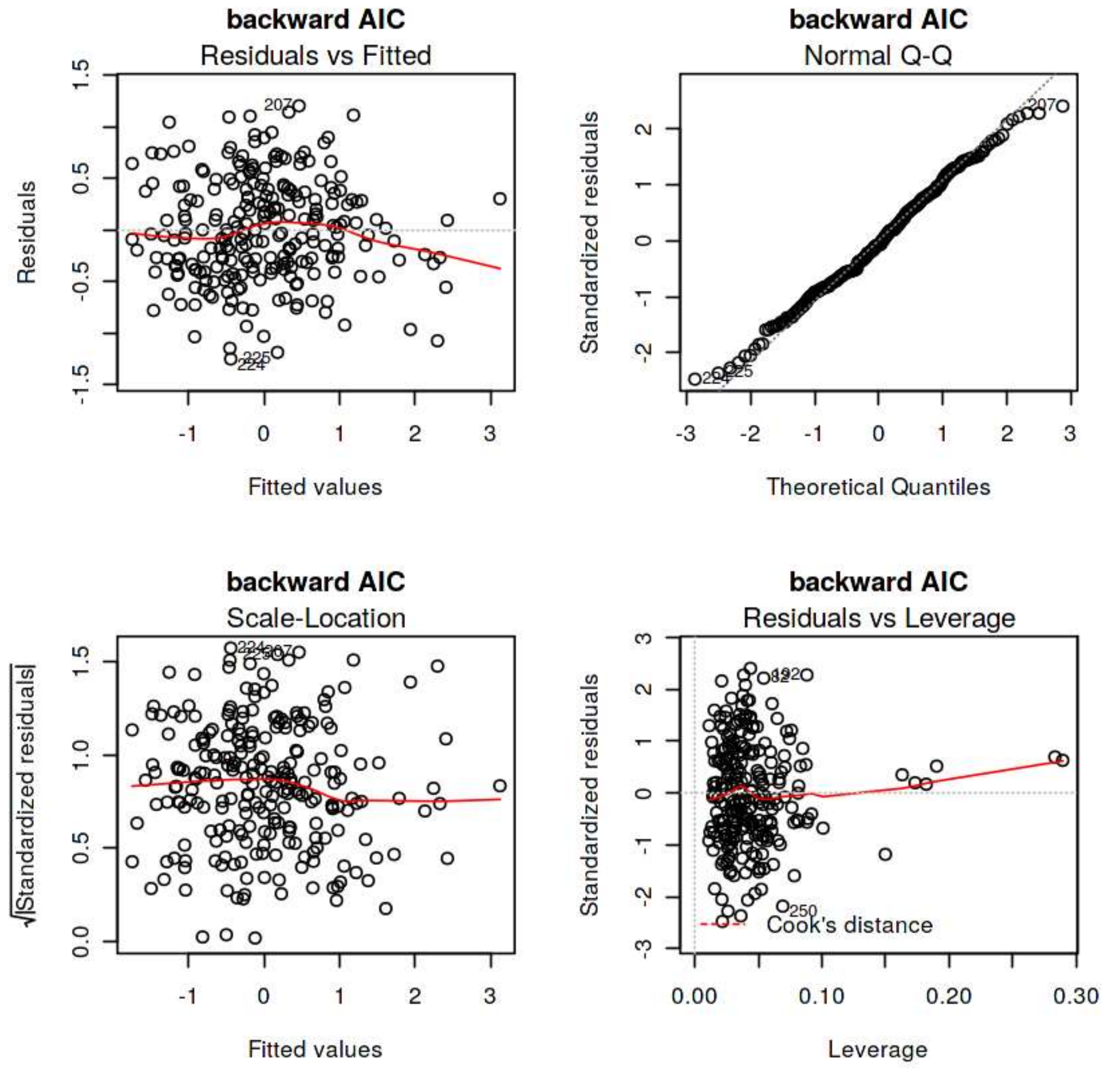
```
HEIGHT      -1.020e-01  3.905e-02  -2.612  0.00958 **
ABDOMEN      9.444e-01  4.223e-02  22.361  < 2e-16 ***
WRIST       -2.036e-01  4.591e-02  -4.434 1.41e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5193 on 239 degrees of freedom
Multiple R-squared:  0.7348,    Adjusted R-squared:  0.7304
F-statistic: 165.5 on 4 and 239 DF,  p-value: < 2.2e-16
```

4.1 Diagnostic plot

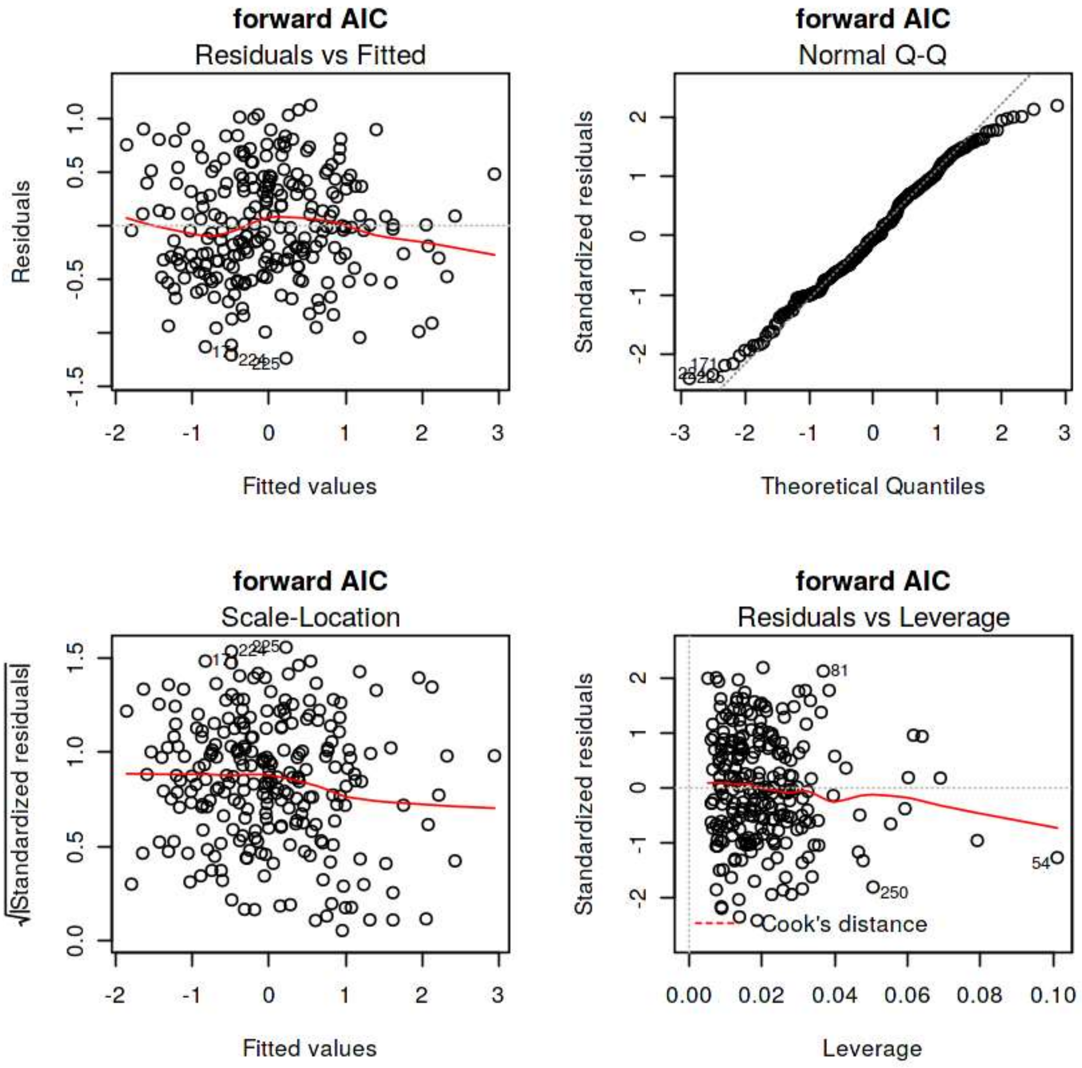
[13]:

```
layout(matrix(1:4, byrow = TRUE, nrow = 2))
plot(model_AIC_b,main="backward AIC")
plot(model_AIC_f,main="forward AIC")
plot(model_AIC_t,main="both sided AIC")
plot(model_BIC_b,main="backward BIC")
plot(model_BIC_f,main="forward BIC")
plot(model_BIC_t,main="both sided BIC")
plot(model_l,main="lasso model")
plot(cp_lm,main="Mallow's cp model")
plot(adr_model,main="adjusted Rsq model")
```

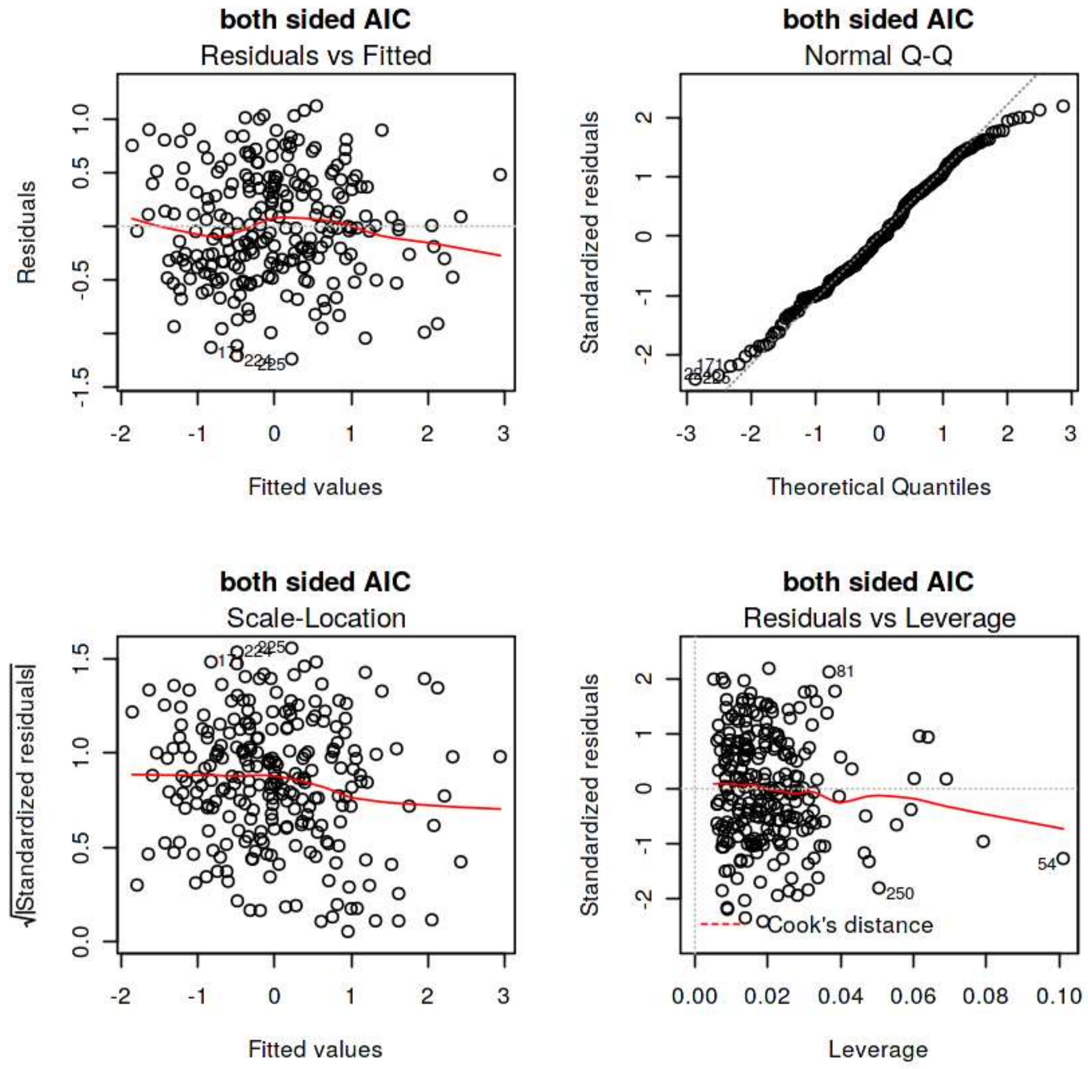
[13]:


backward AIC
Residuals vs Fitted
Residuals
Fitted values
-1.5
-0.5
0.5
1.5
-1
0
1
2
3
207
225
224
backward AIC
Normal Q-Q
Standardized residuals
Theoretical Quantiles
-2
-1
0
1
2
-3
-2
-1
0
1
2
3
207
224
225
backward AIC
Scale-Location
√|Standardized residuals|
Fitted values
0.0
0.5
1.0
1.5
-1
0
1
2
3
224
225
207
backward AIC
Residuals vs Leverage
Standardized residuals
Leverage
-3
-2
-1
0
1
2
3
0.00
0.10
0.20
0.30
82
192
250
Cook's distance

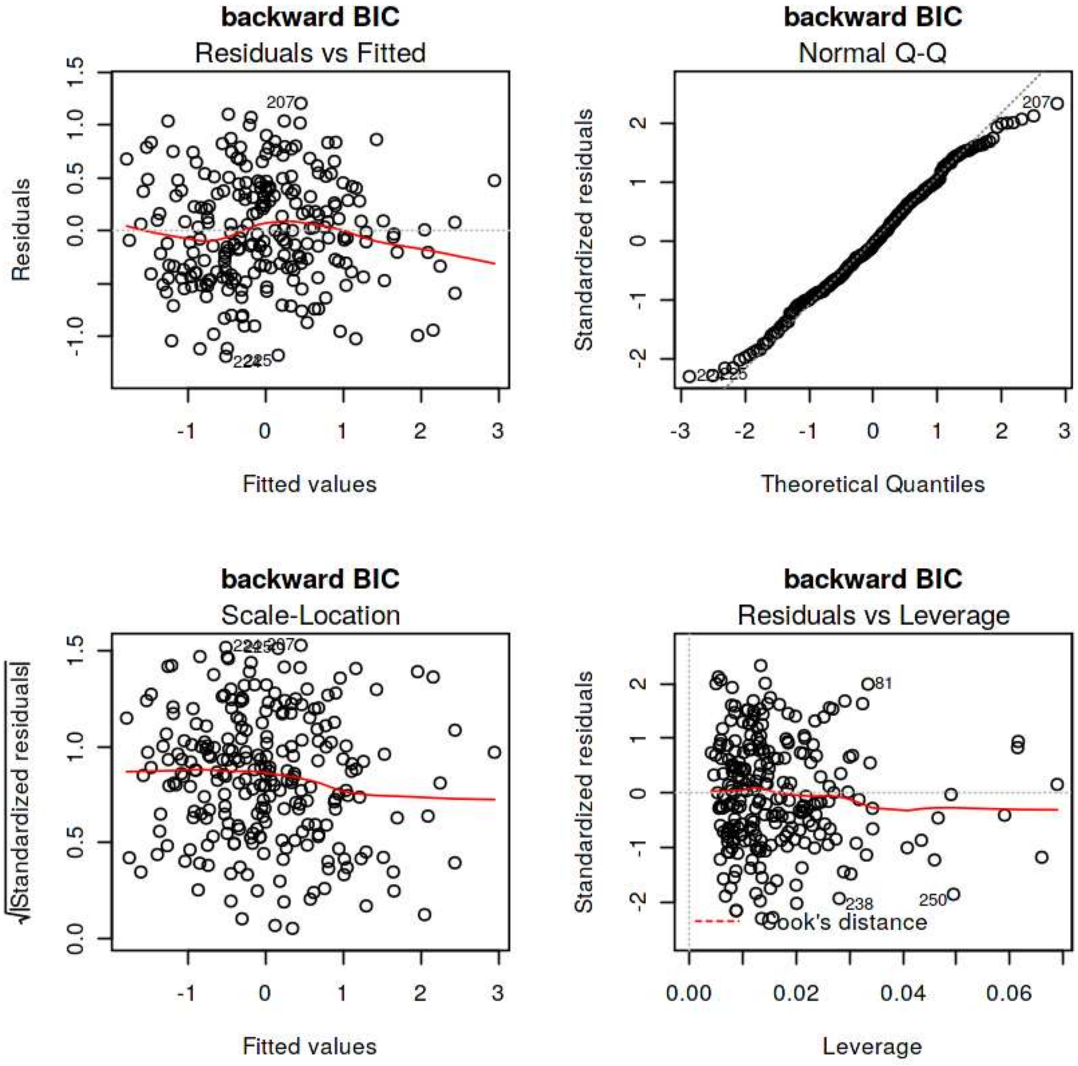
[13]:


forward AIC
Residuals vs Fitted
Residuals
-1.5
-0.5
0.5
1.0
-2
-1
0
1
2
3
Fitted values
171
224
225
forward AIC
Normal Q-Q
Standardized residuals
-2
-1
0
1
2
-3
-2
-1
0
1
2
3
Theoretical Quantiles
224
171
225
forward AIC
Scale-Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
-2
-1
0
1
2
3
Fitted values
171
224
225
forward AIC
Residuals vs Leverage
Standardized residuals
-2
-1
0
1
2
0.00
0.02
0.04
0.06
0.08
0.10
Leverage
81
250
54
Cook's distance

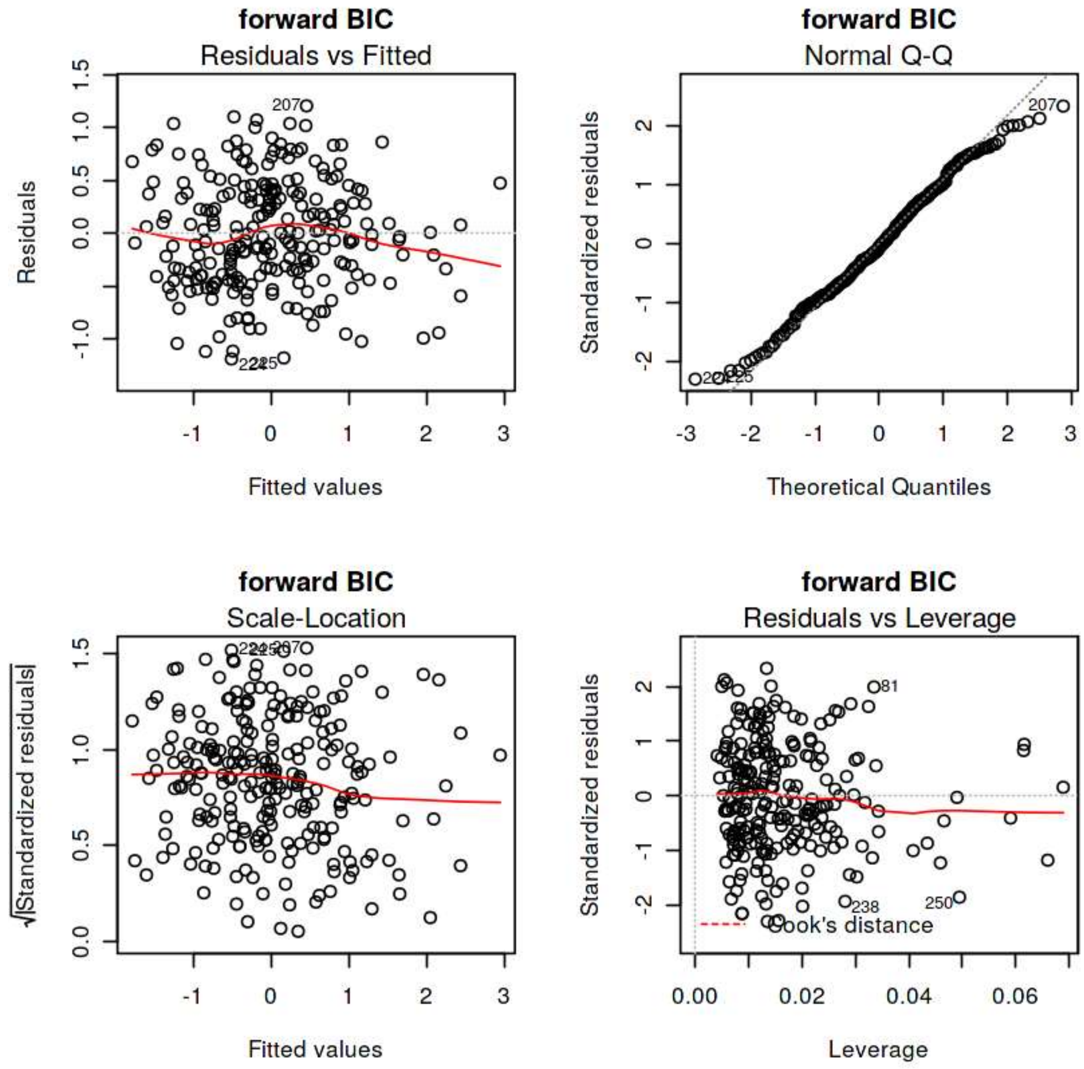
[13]:


both sided AIC
Residuals vs Fitted
Residuals
-1.5
-0.5
0.5
1.0
Fitted values
-2
-1
0
1
2
3
171
224
225
both sided AIC
Normal Q-Q
Standardized residuals
-2
-1
0
1
2
Theoretical Quantiles
-3
-2
-1
0
1
2
3
171
224
225
both sided AIC
Scale-Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
Fitted values
-2
-1
0
1
2
3
171
224
225
both sided AIC
Residuals vs Leverage
Standardized residuals
-2
-1
0
1
2
Leverage
0.00
0.02
0.04
0.06
0.08
0.10
81
250
54
Cook's distance

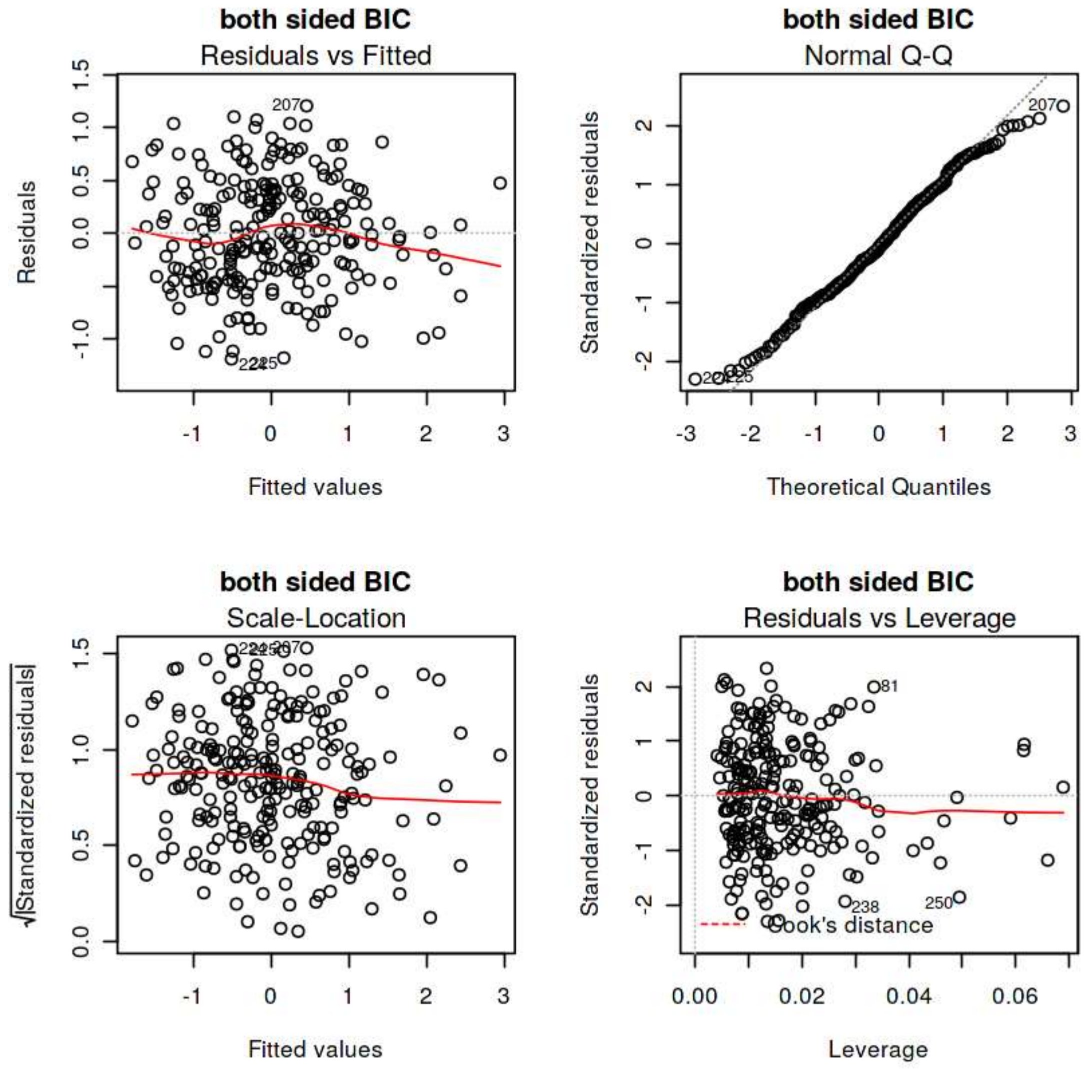
[13]:


backward BIC
Residuals vs Fitted
Residuals
Fitted values
-1.0
0.0
0.5
1.0
1.5
-1
0
1
2
3
207
224
225
backward BIC
Normal Q-Q
Standardized residuals
Theoretical Quantiles
-2
-1
0
1
2
-3
-2
-1
0
1
2
3
207
224
225
backward BIC
Scale-Location
√|Standardized residuals|
Fitted values
0.0
0.5
1.0
1.5
-1
0
1
2
3
224
225
207
backward BIC
Residuals vs Leverage
Standardized residuals
Leverage
-2
-1
0
1
2
0.00
0.02
0.04
0.06
81
238
250
Cook's distance

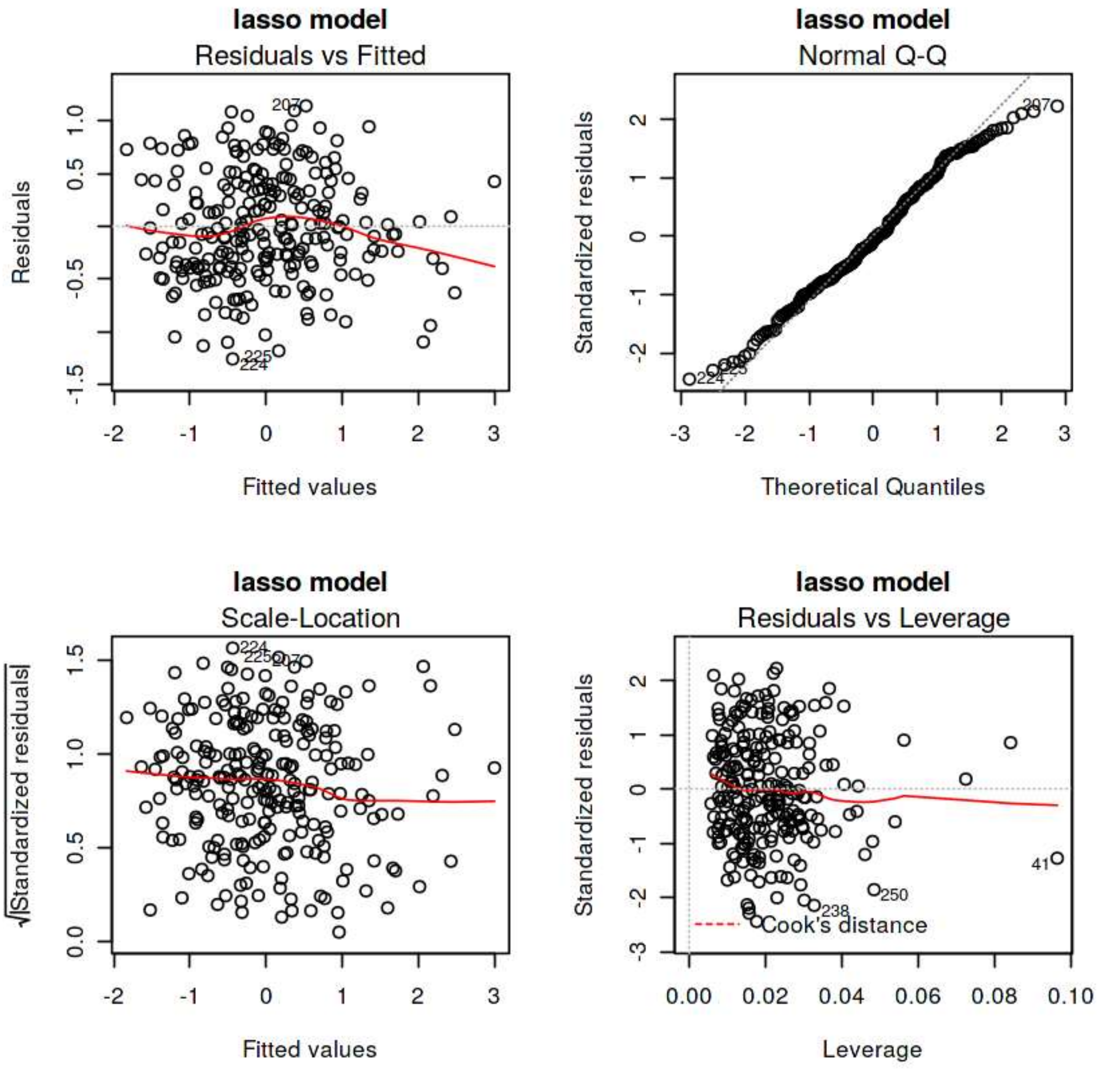
[13]:


forward BIC
Residuals vs Fitted
Residuals
Fitted values
-1.0
0.0
0.5
1.0
1.5
-1
0
1
2
3
207
224
225
forward BIC
Normal Q-Q
Standardized residuals
Theoretical Quantiles
-2
-1
0
1
2
-3
-2
-1
0
1
2
3
207
224
225
forward BIC
Scale-Location
√|Standardized residuals|
Fitted values
0.0
0.5
1.0
1.5
-1
0
1
2
3
224
225
207
forward BIC
Residuals vs Leverage
Standardized residuals
Leverage
-2
-1
0
1
2
0.00
0.02
0.04
0.06
81
238
250
Cook's distance

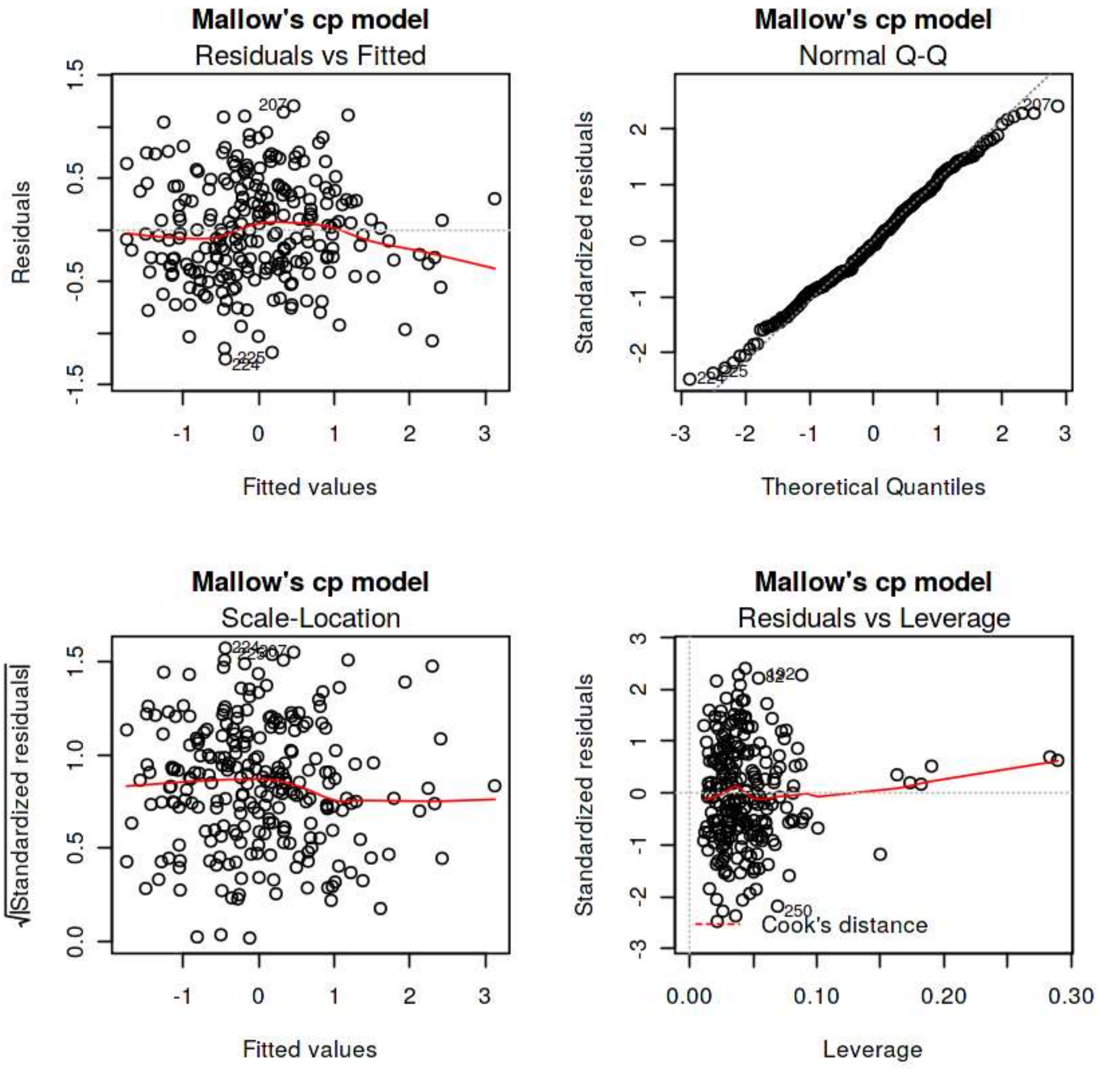
[13]:


both sided BIC
Residuals vs Fitted
Residuals
Fitted values
207
225
-1.0
0.0
0.5
1.0
1.5
-1
0
1
2
3
both sided BIC
Normal Q-Q
Standardized residuals
Theoretical Quantiles
207
225
-2
-1
0
1
2
-3
-2
-1
0
1
2
3
both sided BIC
Scale-Location
√|Standardized residuals|
Fitted values
225
207
0.0
0.5
1.0
1.5
-1
0
1
2
3
both sided BIC
Residuals vs Leverage
Standardized residuals
Leverage
81
238
250
Cook's distance
-2
-1
0
1
2
0.00
0.02
0.04
0.06

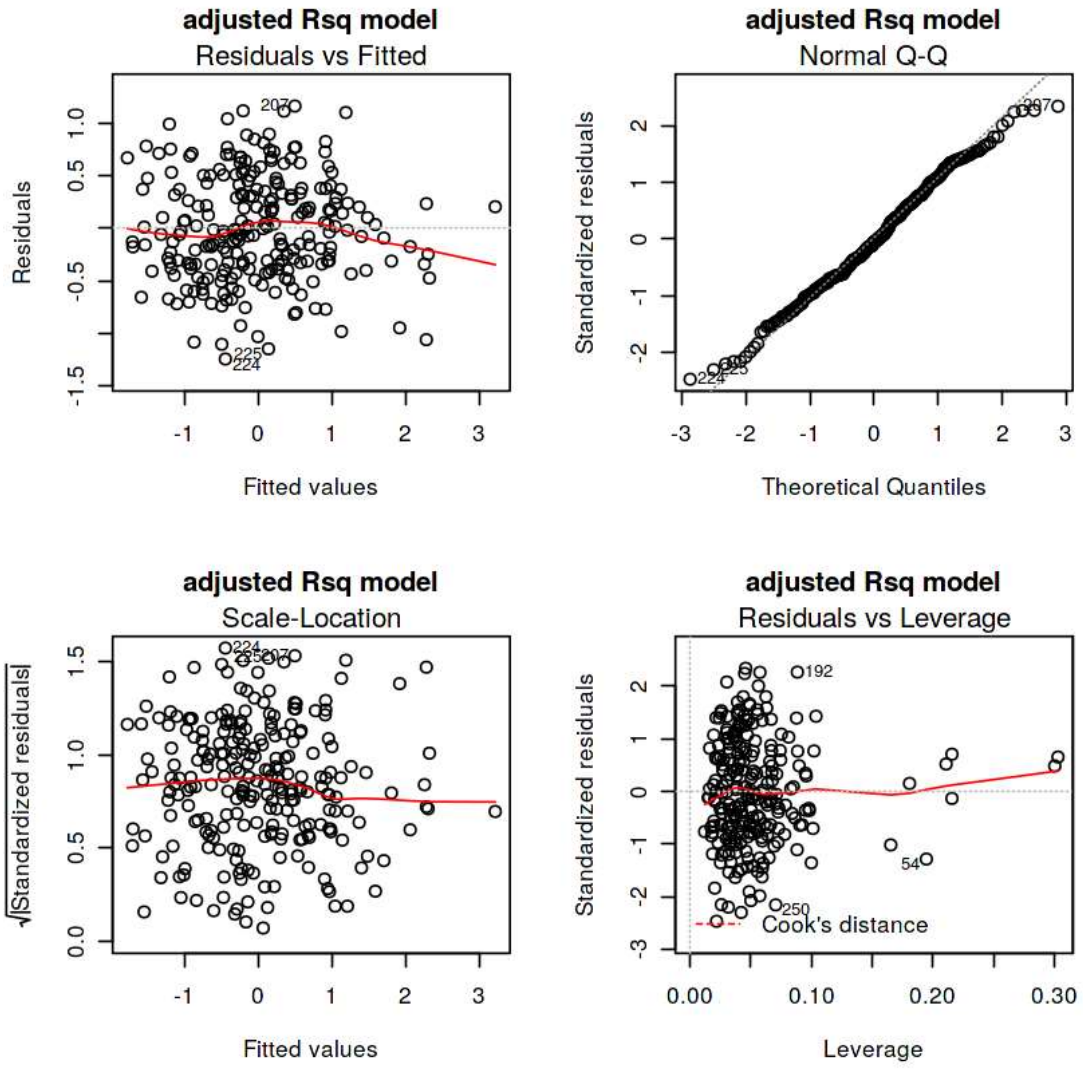
[13]:


lasso model
Residuals vs Fitted
Residuals
Fitted values
-1.5
-0.5
0.5
1.0
-2
-1
0
1
2
3
207
225
224
lasso model
Normal Q-Q
Standardized residuals
Theoretical Quantiles
-2
-1
0
1
2
-3
-2
-1
0
1
2
3
207
224
225
lasso model
Scale-Location
√|Standardized residuals|
Fitted values
0.0
0.5
1.0
1.5
-2
-1
0
1
2
3
224
225
207
lasso model
Residuals vs Leverage
Standardized residuals
Leverage
-3
-2
-1
0
1
2
0.00
0.02
0.04
0.06
0.08
0.10
41
250
238
Cook's distance

[13]:


Mallow's cp model
Residuals vs Fitted
Residuals
Fitted values
207
225
224
1.5
0.5
-0.5
-1.5
-1
0
1
2
3
Mallow's cp model
Normal Q-Q
Standardized residuals
Theoretical Quantiles
207
224
225
2
1
0
-1
-2
-3
-2
-1
0
1
2
3
Mallow's cp model
Scale-Location
√|Standardized residuals|
Fitted values
224
225
207
1.5
1.0
0.5
0.0
-1
0
1
2
3
Mallow's cp model
Residuals vs Leverage
Standardized residuals
Leverage
192
82
250
Cook's distance
3
2
1
0
-1
-2
-3
0.00
0.10
0.20
0.30

[13]:



Also do ANOVA table among them, model BIC forward is the best considering the F statistics and adjusted R square.

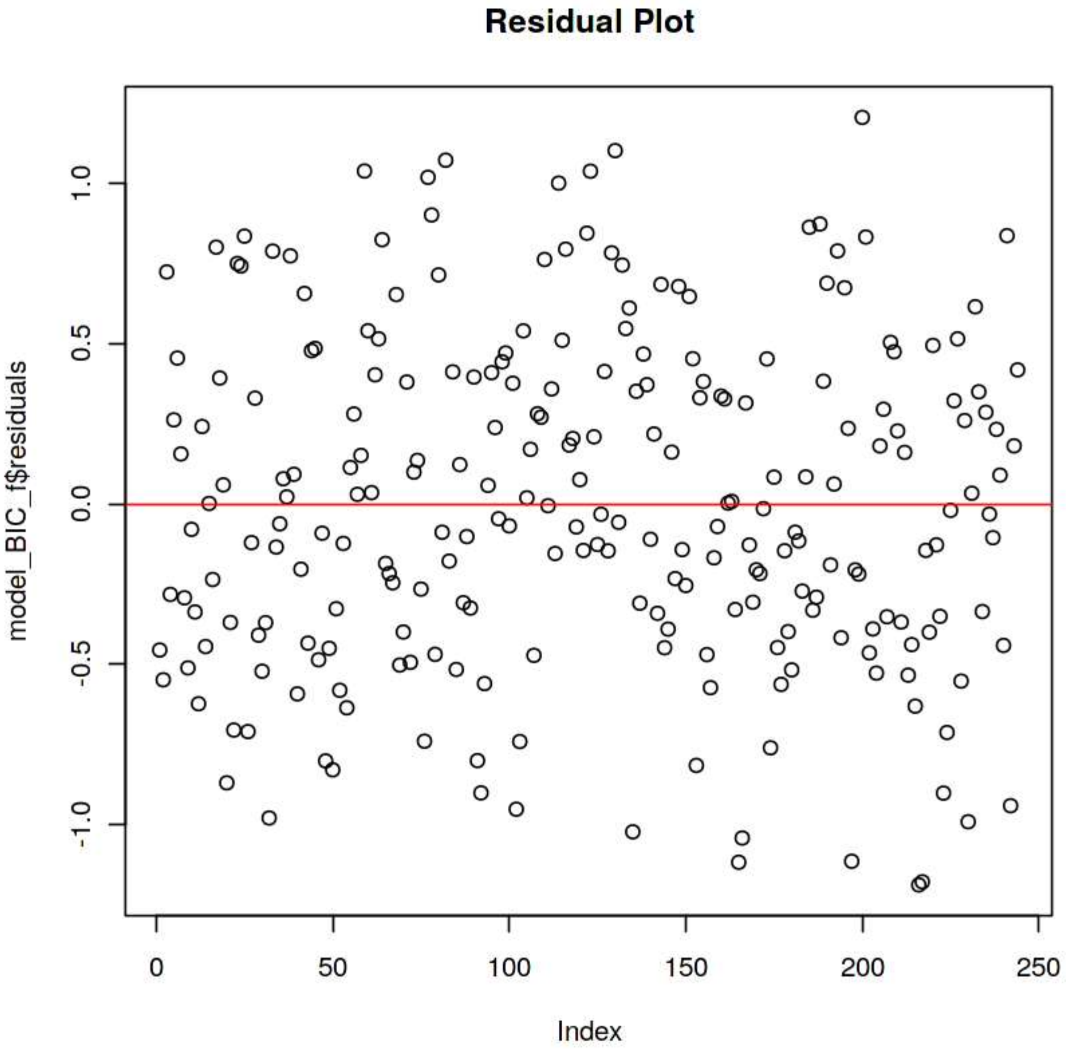
[0]:

```
```

[14]:

```
plot(model_BIC_f$residuals,main="Residual Plot")
abline(h=0,col="red")
```

[14]:



4.1.1 According to the model selection steps above, it seems that *abdomen, weight and wrist* are three most important predictors. By "rule of thumb" we can choose our predictors among them. Now check the possible multicolinearity betweeen abdomen, wrist and weight. We create cleaned data that are not scaled again

[15]:

```
new_data_clean = data_new[c(-39, -42, -48, -96, -76, -163, -182, -221), ]
```

[16]:

```
cor(new_data_clean$WRIST,new_data_clean$ABDOMEN)
cor(new_data_clean$WEIGHT,new_data_clean$ABDOMEN)
cor(new_data_clean$WRIST,new_data_clean$WEIGHT)
```

```
vif(lm(BODYFAT ~ ABDOMEN + WEIGHT + WRIST, data = new_data_clean))
vif(lm(BODYFAT ~ ABDOMEN + WEIGHT, data = new_data_clean))
vif(lm(BODYFAT ~ ABDOMEN + WRIST, data = new_data_clean))
```

[16]:

```
0.603049909542607
```

[16]:

```
0.872690169082953
```

[16]:

```
0.726881563271104
```

[16]:

```
ABDOMEN          4.23126966566092 WEIGHT          5.70873762070487 WRIST
 2.13887303654502
```

[16]:

```
ABDOMEN          4.19442205244338 WEIGHT          4.19442205244298
```

[16]:

```
ABDOMEN           1.57150964502599 WRIST          1.57150964502593
```

It seems that these predictors are correlated but can not be considered as multicollinearity. We consider using only two variables and see the model's performence.

We consider using only two variables or even only one to see the model's performence-try to use only two x and check the model results

[17]:

```
summary(lm(BODYFAT ~ ABDOMEN + WRIST, data = new_data_clean))
summary(lm(BODYFAT ~ ABDOMEN + WEIGHT, data = new_data_clean))
```

[17]:

```
Call:
lm(formula = BODYFAT ~ ABDOMEN + WRIST, data = new_data_clean)

Residuals:
    Min      1Q  Median      3Q     Max 
-9.3973 -2.9225 -0.2025  2.9356 10.3555 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) -11.19959    5.39785  -2.075   0.0391 *  
ABDOMEN       0.72574    0.03234  22.440  < 2e-16 ***
WRIST        -2.02533    0.36453  -5.556 7.29e-08 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.087 on 241 degrees of freedom
Multiple R-squared:  0.7146,	Adjusted R-squared:  0.7123 
F-statistic: 301.8 on 2 and 241 DF,  p-value: < 2.2e-16
```

[17]:

```
Call:
```

```
lm(formula = BODYFAT ~ ABDOMEN + WEIGHT, data = new_data_clean)

Residuals:
    Min      1Q  Median      3Q     Max 
-10.129  -2.897  -0.116   2.880   9.816 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) -42.30901    2.45220 -17.253  < 2e-16 ***
ABDOMEN       0.90497    0.05195  17.420  < 2e-16 ***
WEIGHT       -0.12520    0.01974  -6.344  1.1e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.018 on 241 degrees of freedom
Multiple R-squared:  0.7241,    Adjusted R-squared:  0.7218 
F-statistic: 316.3 on 2 and 241 DF,  p-value: < 2.2e-16
```

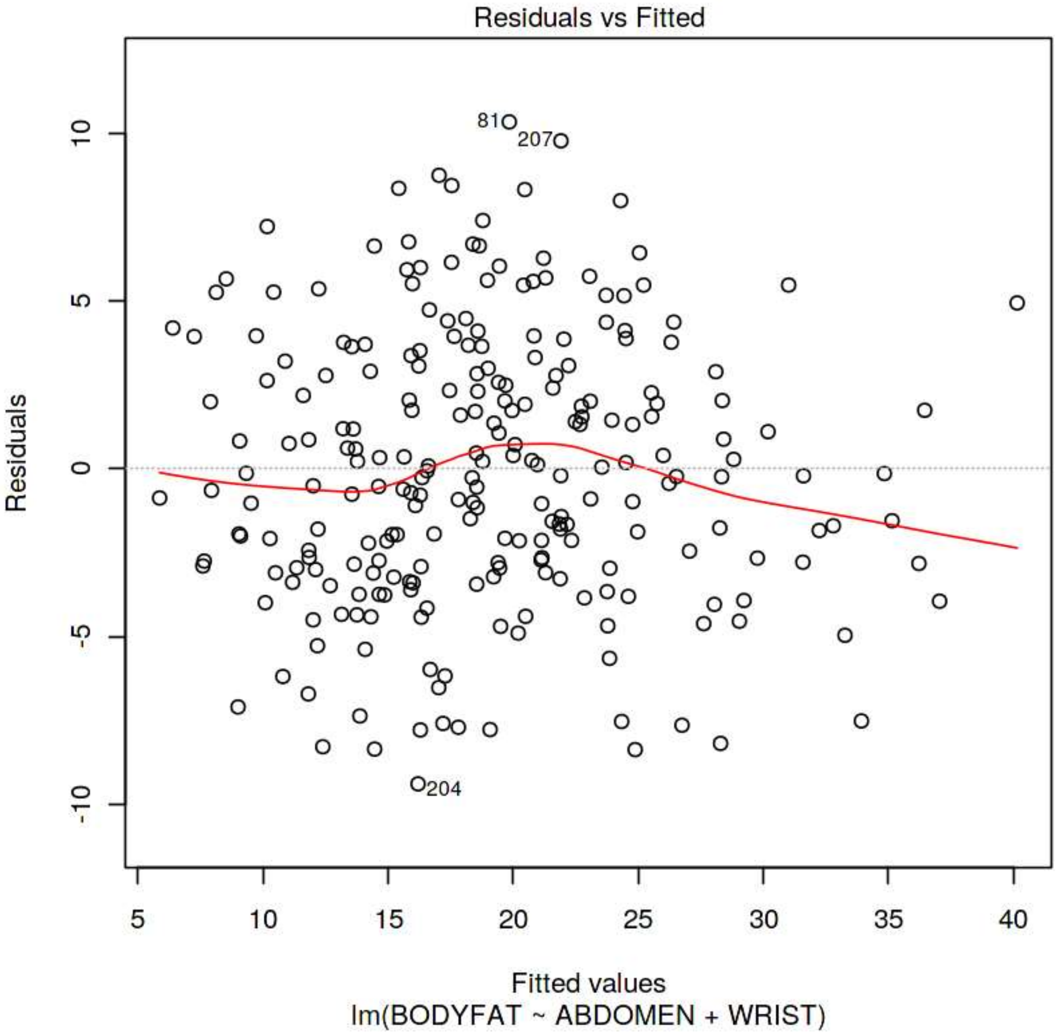
By summary table, we can see the R-square value of “ABDOMEN and WRIST” model and ABDOMEN and WEIGHT are almost the same. Also, by VIF analysis we find the VIF of “ABDOMEN and WEIGHT” model is larger than “ABDOMEN and WRIST” model.

So our final model should be BODYFAT ~ ABDOMEN + WRIST because it is they are two most important predictors and it can be easily measured. Then we do model diagnostics.

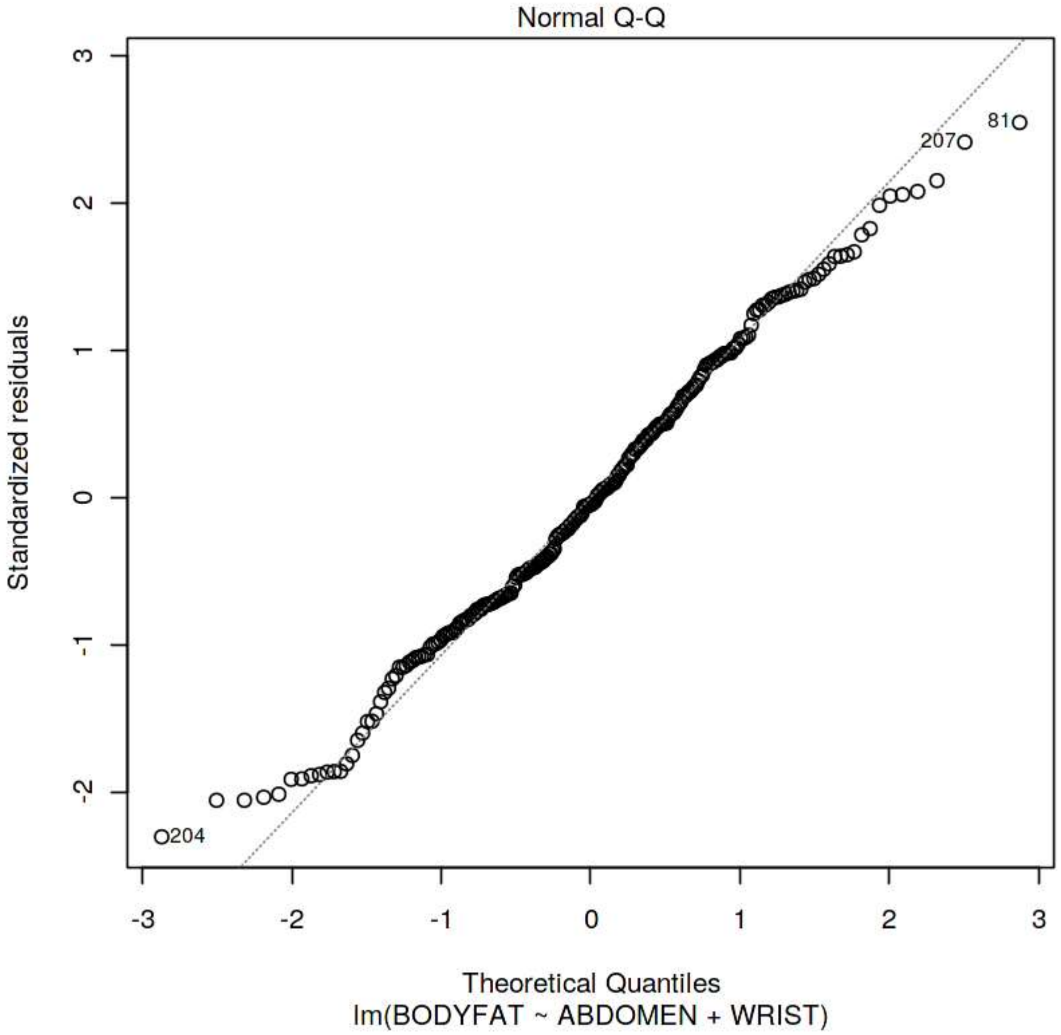
[18]:

```
final_model<-lm(BODYFAT ~ ABDOMEN + WRIST, data = new_data_clean)
plot(final_model,which=1)
plot(final_model,which=2)
plot(final_model,which=4)
```

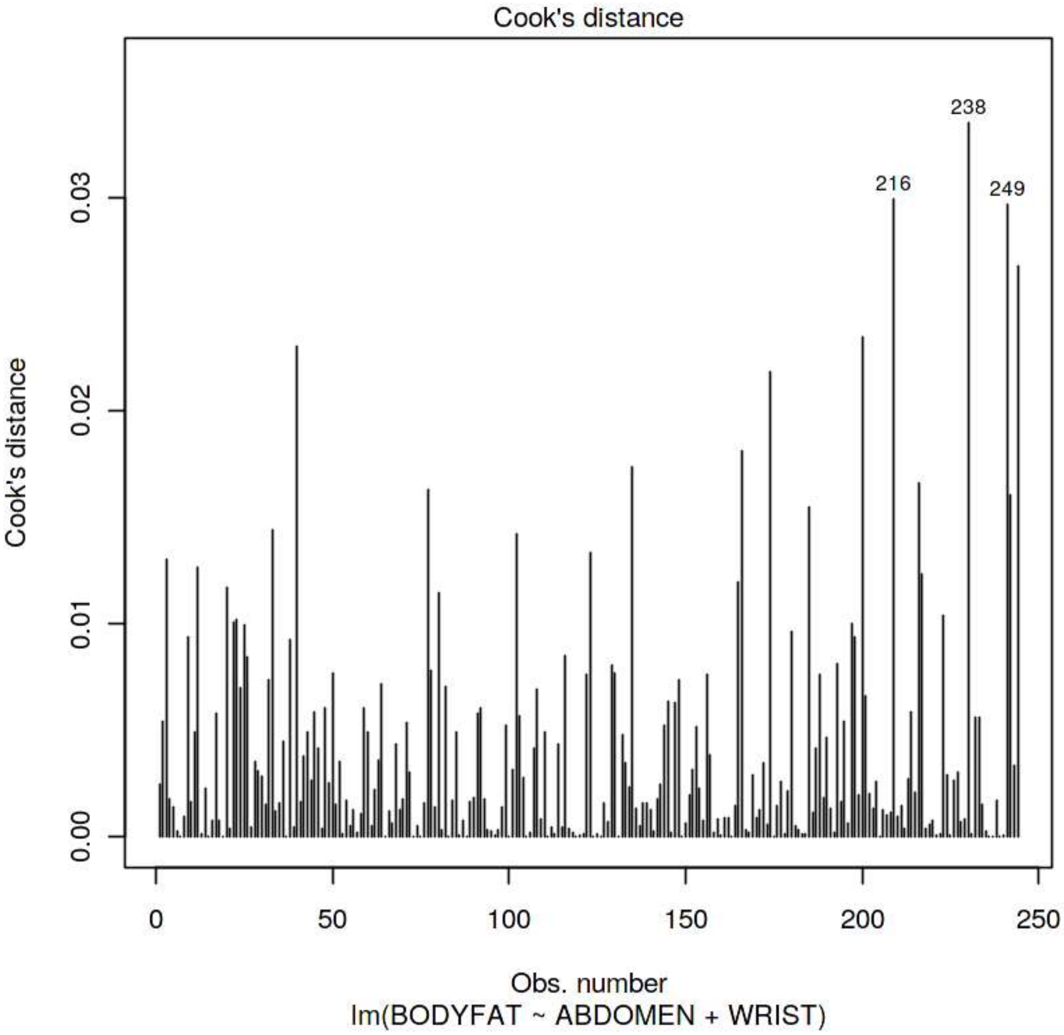
[18]:


Residuals vs Fitted
Residuals
10
5
0
-5
-10
5
10
15
20
25
30
35
40
Fitted values
lm(BODYFAT ~ ABDOMEN + WRIST)
81
207
204

[18]:


Normal Q-Q
Standardized residuals
3
2
1
0
-1
-2
-3
-2
-1
0
1
2
3
81
207
204
Theoretical Quantiles
lm(BODYFAT ~ ABDOMEN + WRIST)

[18]:



Advantages of Our Model

1.Our final model is simple and straightforward. The variables included for prediction is easy to get.

2.The model is robust.

3.The model is accurate as the adjusted R-squared is greater than 0.6.