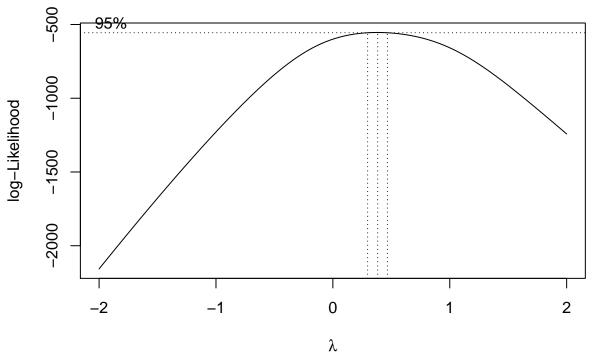
```
## Effect of individual observations

## Python data revisited
python <- read.csv("csv/FLpython.csv")
python$male <- ifelse(python$sex == 'M', 1, 0) # 1 = M, 0 =F

mpf2 <- lm(fat ~ male + mass + svl, data = python)

# Last time we used a Box-Cox transformation
library(MASS)
bc <- boxcox(mpf2)</pre>
```

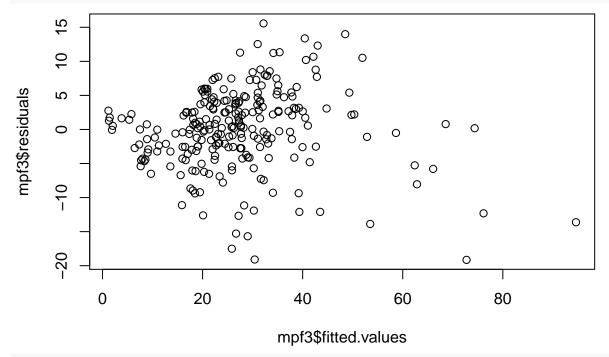


```
lambda <- bc$x[which.max(bc$y)]
mpf3 <- lm((fat ^ lambda - 1) / lambda ~ male + mass + svl, data = python)
summary(mpf3)</pre>
```

```
##
## Call:
## lm(formula = (fat^lambda - 1)/lambda ~ male + mass + svl, data = python)
## Residuals:
      Min
              1Q Median
                            3Q
## -19.146 -2.910
                  0.297
                         3.688 15.568
##
## Coefficients:
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -8.0558134 2.1813183 -3.693 0.000273 ***
             -1.7849310 0.7776166 -2.295 0.022560 *
## male
              0.0004461 0.0000864
                                  5.164 5.03e-07 ***
## mass
              ## svl
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
```

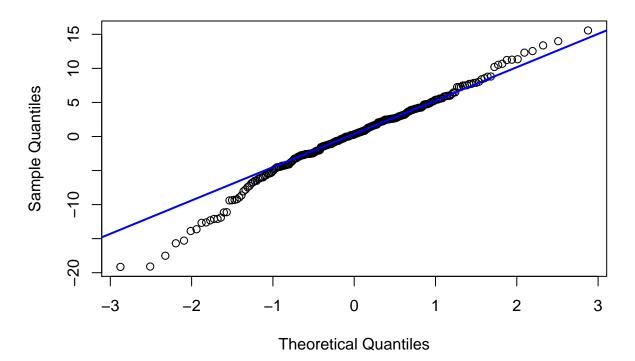
```
## Residual standard error: 5.939 on 244 degrees of freedom
## Multiple R-squared: 0.8356, Adjusted R-squared: 0.8336
## F-statistic: 413.5 on 3 and 244 DF, p-value: < 2.2e-16</pre>
```

plot(mpf3\$fitted.values, mpf3\$residuals)



qqnorm(mpf3\$residuals)
qqline(mpf3\$residuals, col = "blue", lwd = 2)

Normal Q-Q Plot

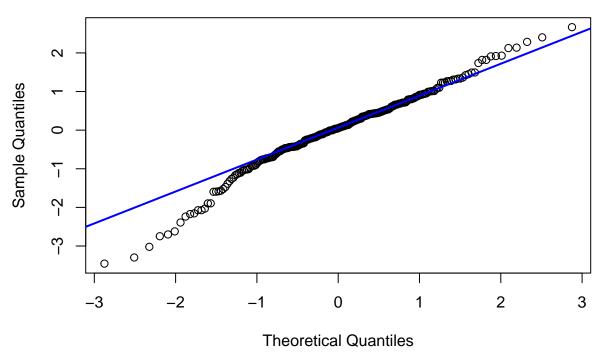


```
# Quantities for individual observations
studres(mpf3) # studentized residuals
hatvalues(mpf3) # leverage
cooks.distance(mpf3) # Cook's distance
# Residual plots with studentized residuals
plot(mpf3$fitted.values,
     studres(mpf3),
     xlab = "Fitted values",
     ylab = "Studentized residuals")
abline(h = c(3, -3), col = "red", lty = 2)
                                     0
                                                  0
      \sim
                                                    0
Studentized residuals
                                                  0
                                                   0
      0
                                                     0
      7
                                                             0
                                           0
      -2
                                           0 0
                                                                       0
                                                      0
                                 00
                                                                                     0
      က
                                    0
                                                                    0
             0
                           20
                                           40
                                                                         80
                                                          60
                                           Fitted values
which(abs(studres(mpf3)) > 3)
## 122 181 245
## 122 181 245
```

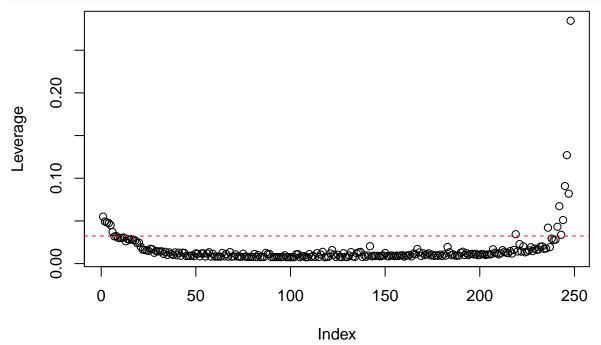
qqnorm(studres(mpf3))

qqline(studres(mpf3), col = "blue", lwd = 2)

Normal Q-Q Plot



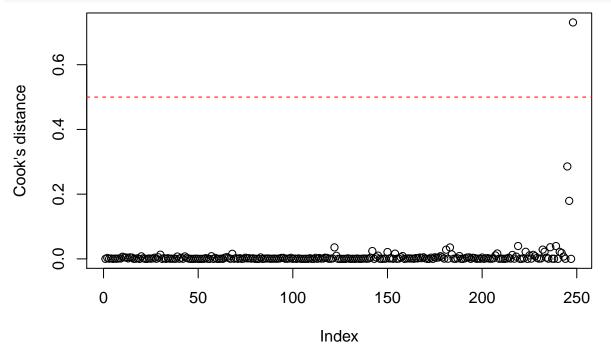




which(hatvalues(mpf3) > 2 * mean(hatvalues(mpf3)))

1 2 3 4 5 6 8 219 236 241 242 243 244 245 246 247 248

```
##
                  mass length
       sex
             svl
                                     fat male
## 1
         F
            70.0
                    186
                          77.5
                                   6.000
## 2
         М
            76.0
                    310
                          83.8
                                 11.000
                                            1
## 3
         М
            77.0
                    260
                          86.1
                                   6.000
                                            1
## 4
         Μ
            78.0
                    262
                          87.1
                                   8.000
                                            1
## 5
         M 81.0
                    306
                          91.1
                                   4.000
                                            1
## 6
         M 93.5
                    605
                         104.6
                                 18.959
                                            1
## 8
         F 105.0
                    800
                         117.5
                                 17.000
                                            0
## 219
         M 285.0 27000
                         316.2 3230.000
## 236
         M 330.0 32600
                         370.9 4374.000
                                            1
## 241
                         424.2 3156.000
         F 376.0 38280
                                            0
         F 381.0 43910
## 242
                         424.9 4002.000
                                            0
## 243
         F 384.5 34540
                         432.4 3500.000
## 244
         F 405.5 41660
                         455.3 5688.000
                                            0
## 245
         F 409.0 49900
                         460.2 2988.000
                                            0
## 246
         F 416.0 55260
                         469.1 4618.000
                                            0
## 247
         F 422.0 49350
                         473.4 6818.000
                                            0
         F 482.0 75500
                         545.0 8406.000
## 248
                                            0
# Cook's distance
plot(cooks.distance(mpf3), ylab = "Cook's distance")
```



```
which(cooks.distance(mpf3) > 0.5)
```

abline(h = 0.5, col = "red", lty = 2)

248 ## 248

Let's look at actual changes in beta estimates
mpf3\$coefficients # with all the data

```
## (Intercept) male mass
## -8.0558134354 -1.7849310101 0.0004461197 0.1431491887
# e.g., fit without obs 248
mpf4 <-
 lm((fat ^ lambda - 1) / lambda ~ male + mass + svl, data = python[-248, ])
mpf4$coefficients
## (Intercept)
                        male
                                     mass
## -6.6475616056 -1.6605858218 0.0005743312 0.1313793189
# e.g., fit without obs 50
mpf5 <-
 lm((fat ^ lambda - 1) / lambda ~ male + mass + svl, data = python[-50, ])
mpf5$coefficients
## (Intercept)
                        male
                                     mass
## -8.0628754675 -1.7805093651 0.0004462354 0.1431573753
```