Regression Models: Assignment 1

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Importing libraries

```
library(dplyr)
library(MuMIn)
library(MASS)
```

Exercise 1

Simulation

```
sim = list()
for (j in 1:1000) {
    vals = c()
    for (i in 1:100) {
        run = 3 + 3*cos(i/10 + 50) + rnorm(1, mean=0, sd=1)
        vals = c(vals, run)
    }
    sim[[j]] = vals
}
sim
```

Exercise 2

Importing the data

```
d <- data.frame(read.table('../data/index.txt', header=TRUE))
```

```
X = d$PovPct
Y = d$Brth15to17
beta1 = cov(X, Y)/var(X)
beta0 = mean(Y) - beta1*mean(X)
```

```
beta1
#> [1] 1.373345
beta0
#> [1] 4.267293
```

Exercise 3

First we have the log-likelihood function for β and σ^2

$l(\sigma^2|X) = \sum_{i=1}^{n} log(\frac{1}{\sqrt{2\pi\sigma^2}} - \frac{(Y_i-(\beta_0+\beta_1 x_{ik}+\cdots+\beta_k x_{ik}))^2}{2\sigma^2})$

$\propto -\frac{n}{2}log(\sigma^2) - \frac{(Y-X\beta)\prime(Y-X\beta)}{2\sigma^2}$

Differentiating the second expression:

$\frac{\partial l}{\partial \sigma}(-\frac{n}{2}log(\sigma^2) - \frac{(Y-X\beta)\prime(Y-X\beta)}{2\sigma^2}) = 0$

We get:

$-\frac{n}{2}(\frac{1}{\sigma^2})(2\sigma) - (Y - X\beta)\prime(Y - X\beta) * (-2)(2\sigma^{-3}) = 0$

We reduce the expression further:

$-\frac{n}{\sigma} + \frac{(Y-X\beta)\prime(Y-X\beta)}{\sigma^3} = 0$

We multiply both sides by σ^3 and we get:

$-n\sigma^2 + (Y - X\beta)\prime(Y - X\beta) = 0$

And solving for σ^2 we get:

$\hat{\sigma^2} = \frac{(Y-X\beta)\prime(Y-X\beta)}{n}$

Which is our maximum likelihood estimator for σ^2

Exercise 4

Exercise 5

```
bodyfat <- data.frame(read.table('../data/bodyfat.txt', header=TRUE))
modall <- lm(hwfat ~., data = bodyfat)
summary(modall)
#>
#> Call:
#> lm(formula = hwfat ~ ., data = bodyfat)
#>
#> Residuals:
#>    Min     1Q Median     3Q    Max
#> -6.162 -1.858 -0.464  2.502  8.177
#>
#> Coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept) 13.29370    9.63027   1.380   0.1718
#> age         -0.32893    0.32158  -1.023   0.3098
#> ht          -0.06731    0.16051  -0.419   0.6762
#> wt          -0.01365    0.02591  -0.527   0.5999
#> abs          0.37142    0.08837   4.203 7.55e-05 ***
#> triceps      0.38743    0.13761   2.815   0.0063 **
#> subscap      0.11405    0.14193   0.804   0.4243
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Residual standard error: 3.028 on 71 degrees of freedom
#> Multiple R-squared:  0.8918, Adjusted R-squared:  0.8827
#> F-statistic: 97.54 on 6 and 71 DF,  p-value: < 2.2e-16
```

The sum of residuals is zero:

```
residuals <- sum(resid(modall))
```

The sum of the observed data is equal to the sum of the fitted values

```
Y_hat <- predict(modall, bodyfat[1:length(names(bodyfat))-1])
sum(bodyfat$hwfat) - sum(Y_hat)
#> [1] 4.547474e-13
```

The residuals are orthogonal to the predictors

```
sum(residuals*bodyfat[1:length(names(bodyfat))-1])
#> [1] -3.077268e-10
```

The residuals are orthogonal to the fitted values

```
sum(residuals*Y_hat)
#> [1] -1.568657e-11
```

Exercise 6

```
options(na.action = "na.fail")
modall <- lm(hwfat ~., data = bodyfat)
combs <- dredge(modall, extra = "R^2")
#> Fixed term is "(Intercept)"
print("best model")
#> [1] "best model"
combs[combs$"R^2" == max(combs$"R^2")]
#> Global model call: lm(formula = hwfat ~ ., data = bodyfat)
#> ---
#> Model selection table
#>    (Intrc)    abs     age       ht  sbscp  trcps       wt    R^2 df  logLik
#> 64   13.29 0.3714 -0.3289 -0.06731 0.1141 0.3874 -0.01365 0.8918  8 -193.43
#>     AICc delta weight
#> 64 404.9  5.58      1
#> Models ranked by AICc(x)
```

Exercise 7

Exercise 8

We define a list with all the models excluding, in each one, a single variable.

```
models <- list()
vars <- c("age","ht","wt","abs","triceps","subscap")
models[[1]] <- update(modall,.~.-age)
models[[2]] <- update(modall,.~.-ht)
models[[3]] <- update(modall,.~.-wt)
models[[4]] <- update(modall,.~.-abs)
models[[5]] <- update(modall,.~.-triceps)
models[[6]] <- update(modall,.~.-subscap)
```

We run ANOVA with both the models without each variable and the main model including all the other variables.

We can see the pvalues for the ANOVA where each specific variable was excluded:

```
anovas <- list()
pvalues <- c()
amount_of_vars <- length(names(bodyfat))-1
for (i in 1:amount_of_vars) {
    anovas[[i]] <- anova(models[[i]],modall)
    pvalues <- c(pvalues, sum(anovas[[i]][2,"Pr(>F)"]))
}
for (i in 1:length(vars)) {
    print(paste("excluding: ", vars[i], ": ", pvalues[i] , sep=""))
}
#> [1] "excluding: age: 0.30983932449522"
#> [1] "excluding: ht: 0.67622546378066"
#> [1] "excluding: wt: 0.599878887504826"
#> [1] "excluding: abs: 7.54898491342447e-05"
#> [1] "excluding: triceps: 0.006301112532879 72"
#> [1] "excluding: subscap: 0.424314507846979"
```

Then we compare with summary:

```
summary(modall)[4]
#> $coefficients
#>                Estimate Std. Error    t value     Pr(>|t|)
#> (Intercept) 13.29369860 9.63026704  1.3804081 1.717917e-01
#> age         -0.32893403 0.32157778 -1.0228755 3.098393e-01
#> ht          -0.06730905 0.16050751 -0.4193514 6.762255e-01
#> wt          -0.01365183 0.02590783 -0.5269385 5.998789e-01
#> abs          0.37141976 0.08836595  4.2032001 7.548985e-05
#> triceps      0.38742647 0.13761017  2.8153912 6.301113e-03
#> subscap      0.11405213 0.14192779  0.8035927 4.243145e-01
```

And we can see we get the same pvalues in the summary. Therefore viewing the summary can be a much faster version of performing such testing.

as a result we get that the least meaningful variable (the variable that explains the lowest variance of the model) is the variable ht (height) followed by the variable wt (weight).

Exercise 9

Given that $E[\hat{Y}|X_h] = \hat{Y_h} \sim N(X_h\beta, \sigma^2 X_h(X'X)X_h')$

$\Rightarrow \hat{y_h} \pm t_{n-(k+1),\frac{\alpha}{2}} * \hat{\sigma}\sqrt{h_{ii}}$

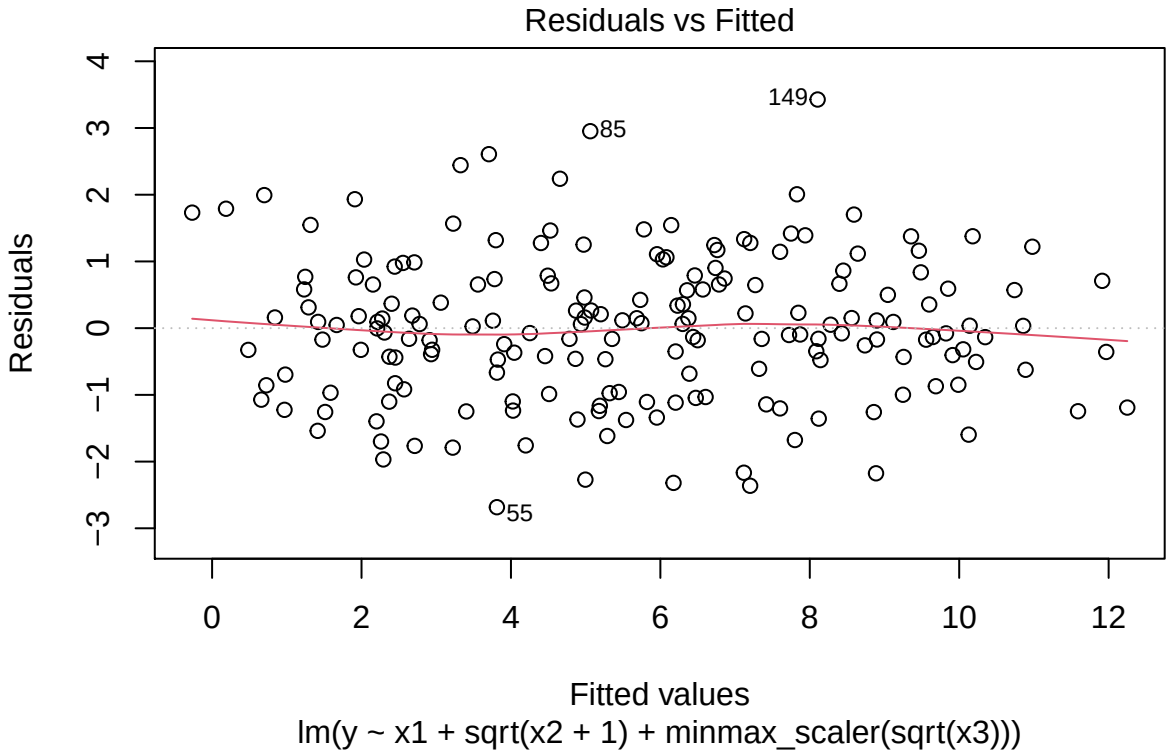
where h_{ii} is the diagonal of our H matrix.

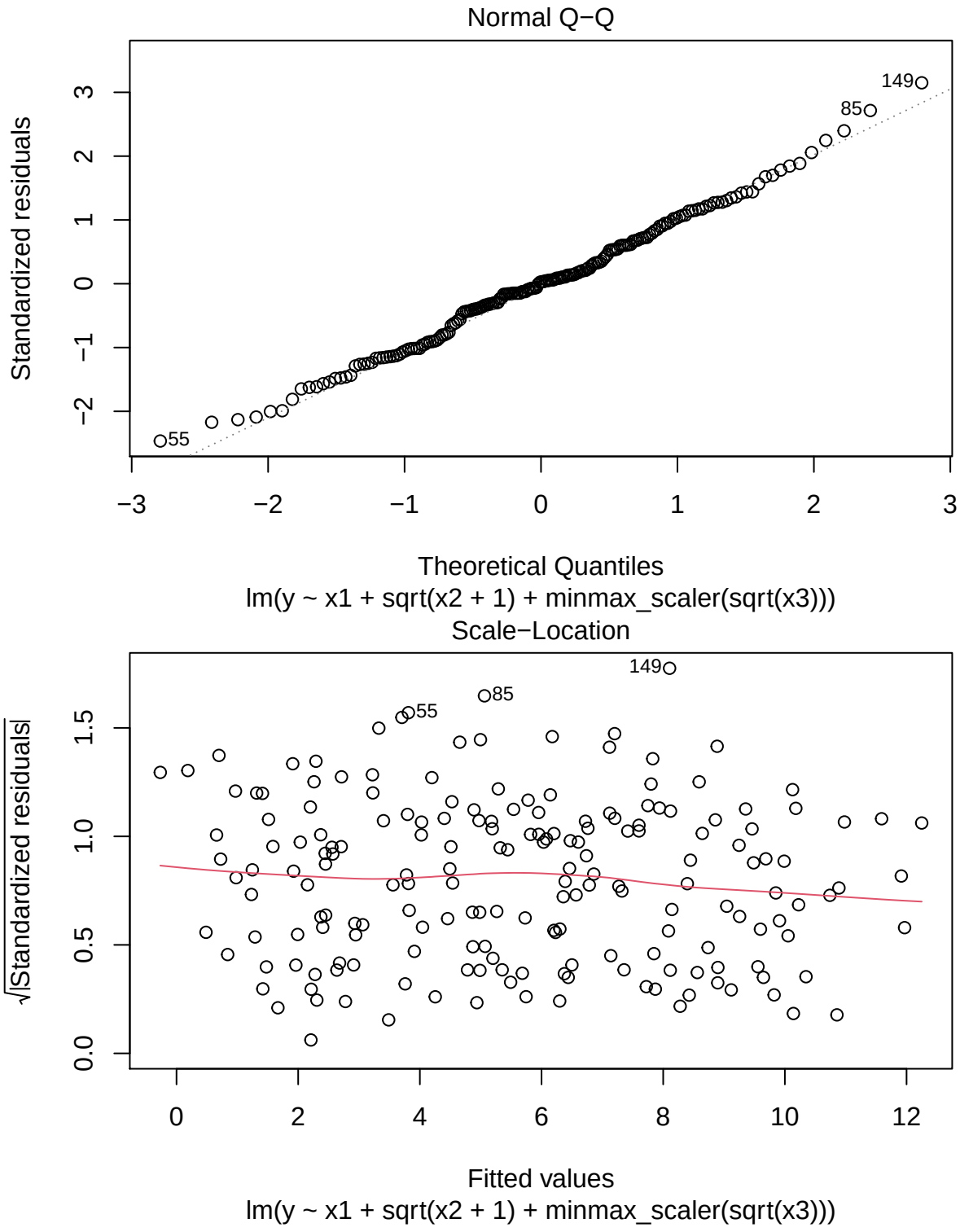
is our expression for the $(1-\alpha)\%$ confidence interval for $\hat{Y_h}$ when σ^2 is unknown.

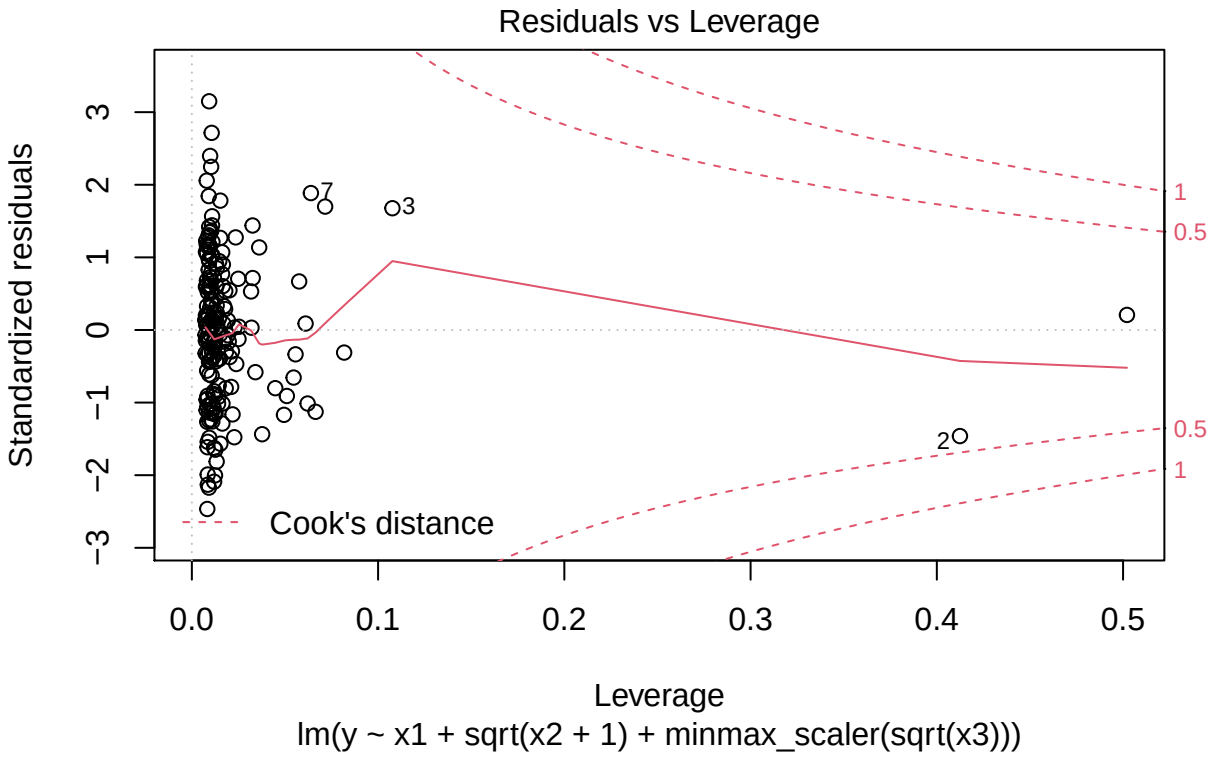
Exercise 10

```
minmax_scaler <- function(x) {
    return((x-min(x))/(max(x)-min(x)))
}


transform <- data.frame(read.table('../data/Transform_V2.txt', header=TRUE))
trm1 <- lm(y ~ x1 + sqrt(x2+1) + minmax_scaler(sqrt(x3)), data=transform)
plot(trm1)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(y ~ x1 + sqrt(x2 + 1) + minmax_scaler(sqrt(x3)))
Scale−Location
√|Standardized residuals|
Fitted values
lm(y ~ x1 + sqrt(x2 + 1) + minmax_scaler(sqrt(x3)))
149
85
55


Residuals vs Leverage
Standardized residuals
3
2
1
0
−1
−2
−3
7
3
2
1
0.5
0.5
1
Cook's distance
0.0
0.1
0.2
0.3
0.4
0.5
Leverage
lm(y ~ x1 + sqrt(x2 + 1) + minmax_scaler(sqrt(x3)))