Regression Models: Assignment 1

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Installing libraries used

```
packages = c("dplyr","MuMIn","MASS","leaps","glmnet","car")
for (package in packages) {
    install.packages(package)
}
```

Importing libraries

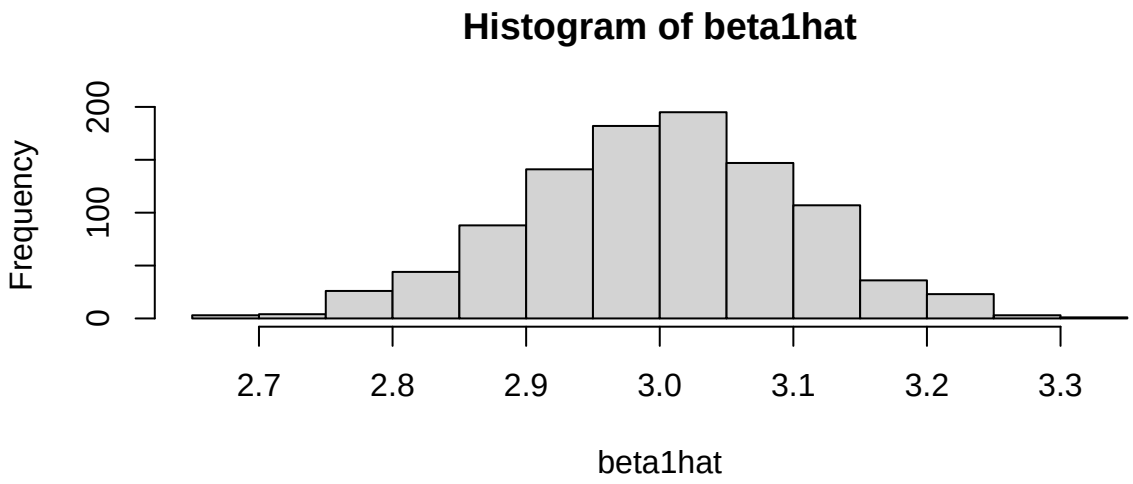
```
library(dplyr)
library(MuMIn)
library(MASS)
library(leaps)
library(glmnet)
library(car)
```

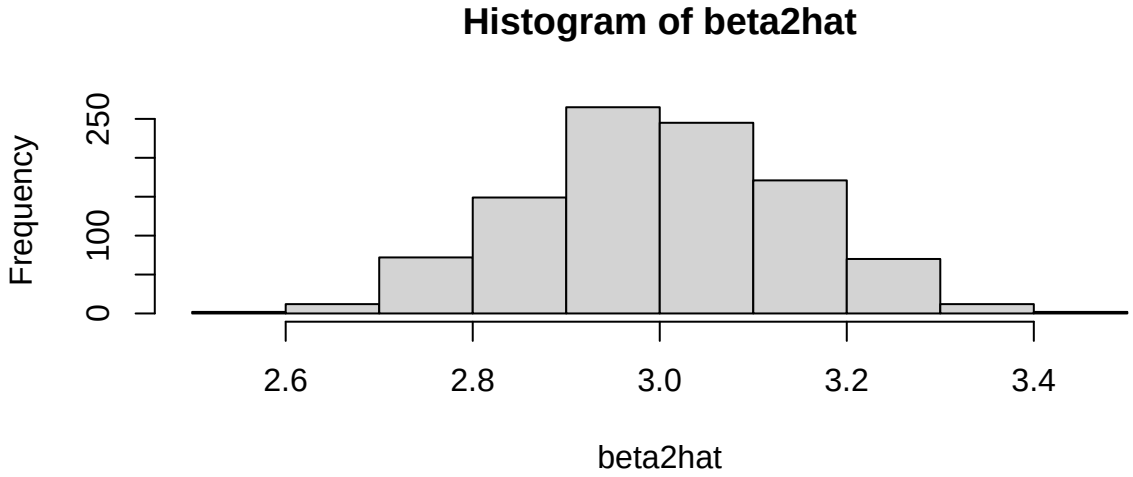
Exercise 1

Simulation

```
# terms
s = list()
X = list()

# betas estimation
beta_est = list()
beta1hat = c()
beta2hat = c()

# variables
phi = 50
beta1 = 3
beta2 = 3
x1 = matrix(rep(1,100),nrow=100,byrow=T)

# simulation
simulation <- function(mean,sd,phi,beta1,beta2,iters,size) {
    for (j in 1:iters) {
        loop_s = matrix(rep(0,size),nrow=size,byrow=T)
        loop_x2 = matrix(rep(0,size),nrow=size,byrow=T)
        for (i in 1:size) {
            e = rnorm(1, mean=mean, sd=sd)
            loop_x2[i] = cos(i/10 + phi)
            loop_s[i] = beta1 + beta2*loop_x2[i] + e
        }
        X[[j]] = cbind(x1,loop_x2)
        s[[j]] = loop_s
        beta_est[[j]] = ginv(t(X[[j]])%*%X[[j]])%*%t(X[[j]])%*%loop_s
        beta1hat = c(beta1hat, beta_est[[j]][1])
        beta2hat = c(beta2hat, beta_est[[j]][2])
    }
    # plotting beta1hat and beta2hat
    par(mfrow=c(2,1))
    hist(beta1hat)
    hist(beta2hat)
    return(c(mean(beta1hat),mean(beta2hat)))
}
```

```r
means <- simulation(mean=0, sd=1, phi=phi, beta1=beta1, beta2=beta2, iters=1000, size=100)
```





We know that the estimate is unbiased if its expected value of our estimators is equal to the real value of our estimators (in this case $E[\hat{\beta}_1]) = \beta_1$ and $E[\hat{\beta}_2]) = \beta_2$ as the sample size $n \to$ inf.

We can test for this with our 1000 simulation sample:

```r
print(means)
#> [1] 3.000306 3.000889
```

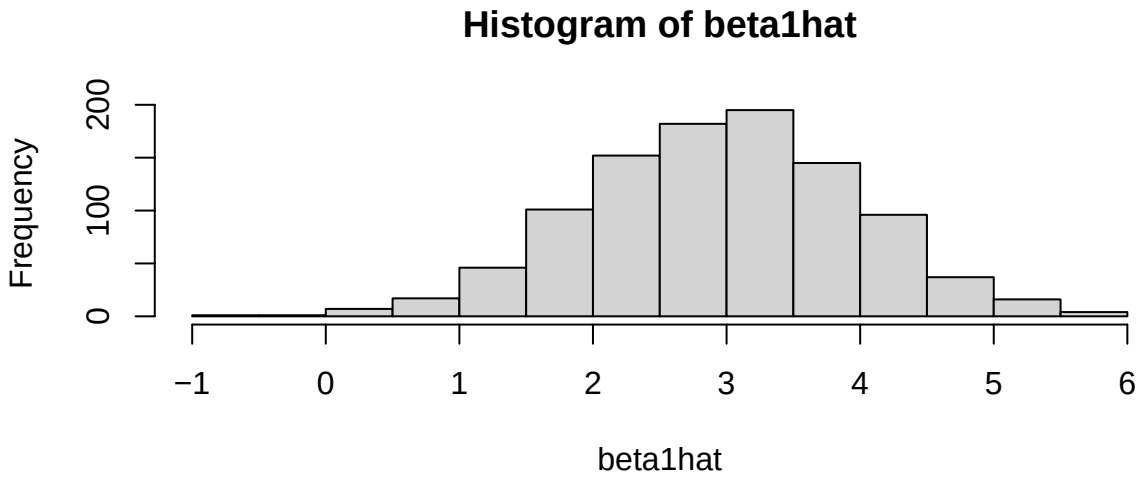
Calculating a relative error for each one of these values:

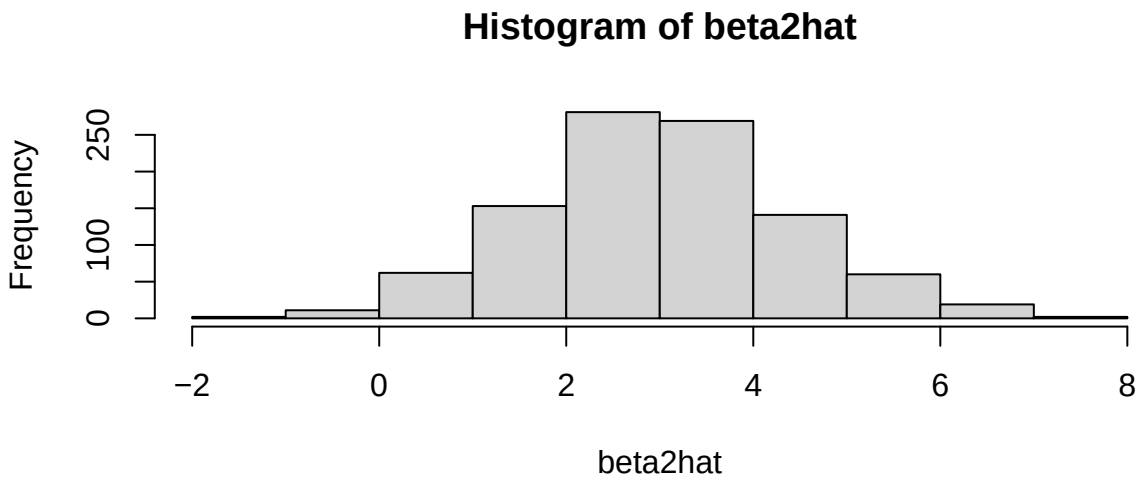
```r
betas = c(beta1,beta2)
for (i in 1:length(means)) {
    print(paste("beta ",i, " hat has a relative error of: ", abs(means[i]-betas[i])/betas[i]))
}
#> [1] "beta  1  hat has a relative error of:  0.00010193240505 42267"
#> [1] "beta  2  hat has a relative error of:  0.00029642405936 7251"
```

Which are <1% incorrect versus the real betas, therefore, these estimators are unbiased.

If we increase the value of sigma by ~10x the original value ($\sigma = 1$):

```
means <- simulation(mean=0, sd=10, phi=phi, beta1=beta1, beta2=beta2, iters=1000, size=100)
```





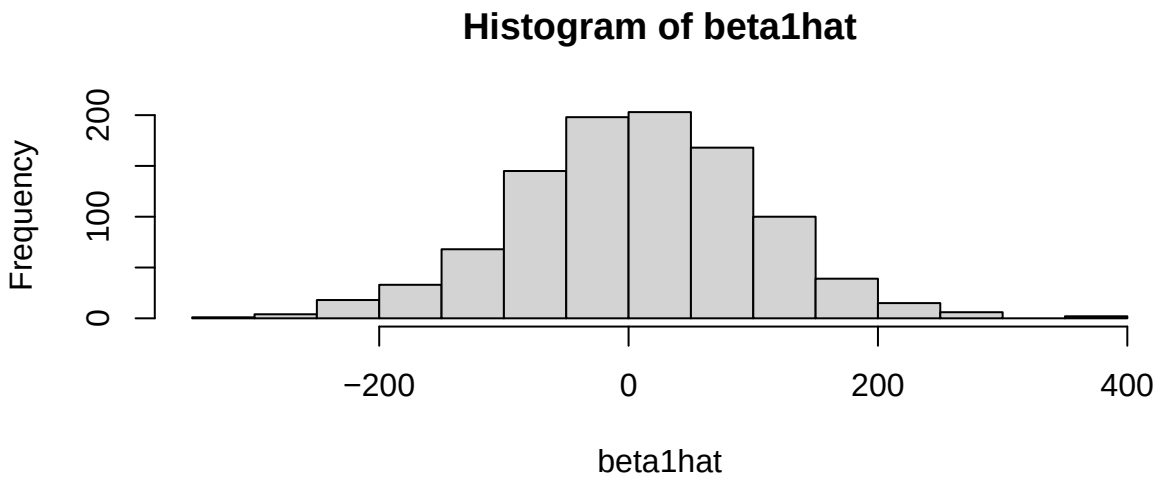

```
print(means)
#> [1] 2.959975 2.999230
```

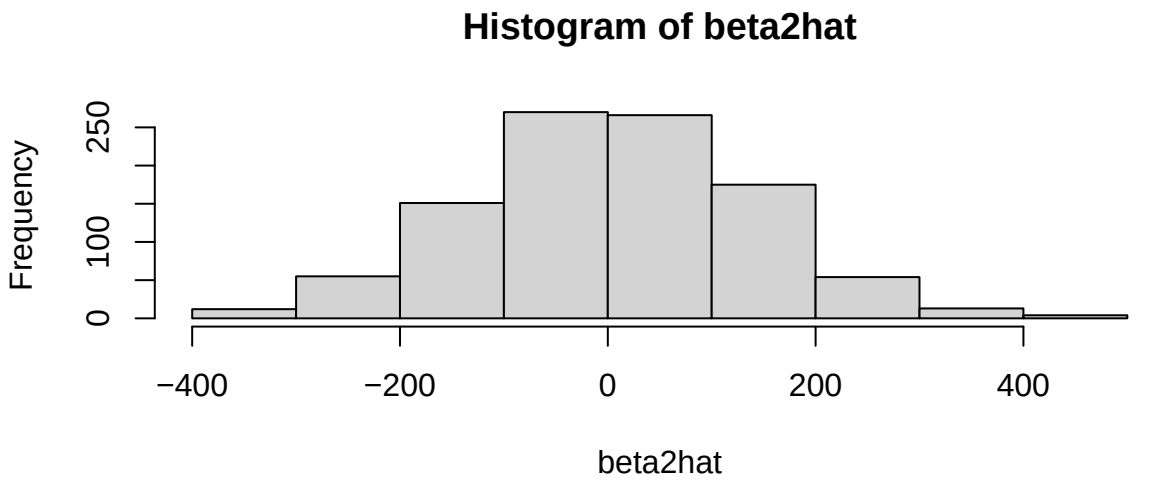
```
betas = c(beta1,beta2)
for (i in 1:length(means)) {
    print(paste("beta ",i, " hat has a relative error of: ", abs(means[i]-betas[i])/betas[i]))
}
#> [1] "beta  1  hat has a relative error of:  0.0133415513964946"
#> [1] "beta  2  hat has a relative error of:  0.00025666396938184"
```

We can see that our relative error increases, therefore our estimation would either require a significantly larger amount of iterations to reach a the same estimation accuracy. So then we could say that our residuals being a lot more disperse can measurably affect the accuracy of our prediction.

If we increase the value of sigma by ~1000x the original value ($\sigma = 1$):

```
means <- simulation(mean=0, sd=1000, phi=phi, beta1=beta1, beta2=beta2, iters=1000, size=100)
```






```
print(means)
#> [1] 7.199174 5.353528
```

```
betas = c(beta1,beta2)
for (i in 1:length(means)) {
    print(paste("beta ",i, " hat has a relative error of: ", abs(means[i]-betas[i])/betas[i]))
}
#> [1] "beta  1  hat has a relative error of:  1.399724706427 71"
#> [1] "beta  2  hat has a relative error of:  0.78450940243512"
```

In an attempt to show a waaaaay worse scenario, here we can see our relative error is not only large but, having tried running this a few times, the relative error can reach massive amounts, being, at times, even way higher than 100% wrong.

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

1- $\sum_{i=1}^{n} \hat{\epsilon_i}$

$\hat{\epsilon} = Y - \hat{Y} = (I - H)Y$

$\sum_{i=0}^{n} \hat{\epsilon_i} = I'\hat{\epsilon} = I'(I - H)'Y$

Given that the matrix $(I - H)$ is eigenpotent:

$\Rightarrow ((I - H)(I))'Y = 0'Y = 0$

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

We use regsubsets to find the best model combinations by adjusted R^2

```
options(na.action = "na.fail")
modall <- lm(hwfat ~., data = bodyfat)
combs <- leaps::regsubsets(bodyfat[,1:6],bodyfat[,7])
summary(combs)
#> Subset selection object
#> 6 Variables  (and intercept)
#>         Forced in Forced out
#> age         FALSE      FALSE
#> ht          FALSE      FALSE
#> wt          FALSE      FALSE
#> abs         FALSE      FALSE
#> triceps     FALSE      FALSE
#> subscap     FALSE      FALSE
#> 1 subsets of each size up to 6
#> Selection Algorithm: exhaustive
#>          age ht  wt  abs triceps subscap
#> 1  ( 1 ) " " " " " " "*" " "     " "
#> 2  ( 1 ) " " " " " " "*" "*"     " "
#> 3  ( 1 ) "*" " " " " "*" "*"     " "
#> 4  ( 1 ) "*" "*" " " "*" "*"     " "
#> 5  ( 1 ) "*" " " "*" "*" "*"     "*"
#> 6  ( 1 ) "*" "*" "*" "*" "*"     "*"
```

And their corresponding $R^{2} values:

```
summary(combs)$adjr2
#> [1] 0.8409068 0.8801014 0.8849817 0.8846381 0.8840129 0.8826699
```

We can see the best model is the one with the following R^2

```
max(summary(combs$adjr2))
#> [1] "NULL"
```

Which corresponds to the model which uses the variables **age**, **ht**, **abs** and **triceps**.

We can also do this same calculation using the function dredge (albeit less efficiently):

```
combs <- dredge(modall, extra = "R^2")
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

We know that:

$SST = \sum_{i=1}^{n}(y_i - \bar{y})^2$
$= \sum_{i=1}^{n}(y_i - \hat{y}_i + \hat{y}_i - \bar{y})^2$
$= \sum_{i=1}^{n}(y_i - \hat{y}_i)^2 + 2\sum_{i=1}^{n}(y_i - \hat{y}_i)(\hat{y}_i - \bar{y}) + \sum_{i=1}^{n}(\hat{y}_i - \bar{y})^2$
$= SSE + SSR + 2\sum_{i=1}^{n}(y_i - \hat{y}_i)(\hat{y}_i - \bar{y})$

No we must prove that:

$2\sum_{i=1}^{n}(y_i - \hat{y}_i)(\hat{y}_i - \bar{y}) = 0$

So then we have:

$\sum_{i=1}^{n}(y_i - \hat{y}_i)(\hat{y}_i - \bar{y}) = \sum_{i=1}^{n}(y_i - \hat{y}_i)\hat{y}_i - \sum_{i=1}^{n}(y_i - \hat{y}_i)\bar{y} = 0$

Because we know that:

$\sum_{i=1}^{n}(y_i - \hat{y}_i)\hat{y}_i = 0$

Given that the residuals must be orthogonal to the fitted values.

And:

$\sum_{i=1}^{n}(y_i - \hat{y}_i)\bar{y} = 0$

Because the sum of the observed data is equal to the sum of the fitted values:

$\sum_{i=1}^{n} y_i = \sum_{i=1}^{n} \hat{y}_i$

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

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

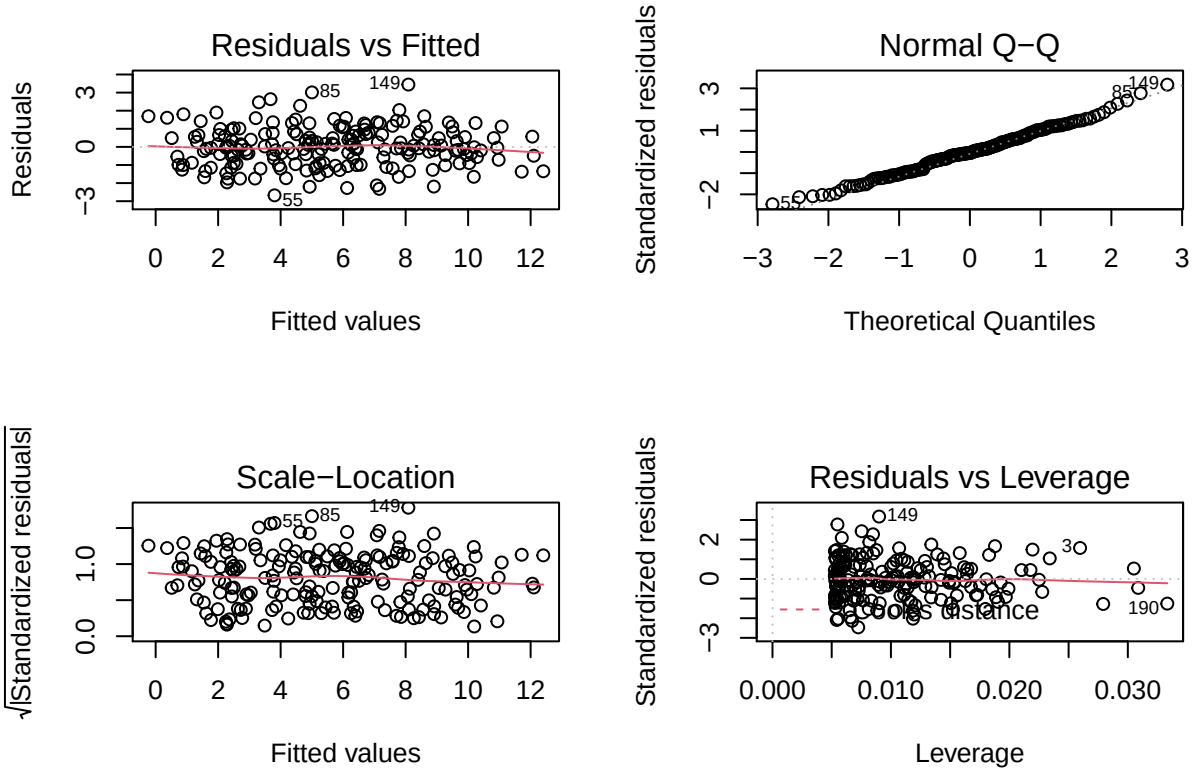
where h_{ii} is the diagonal of our H matrix.

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

Exercise 10

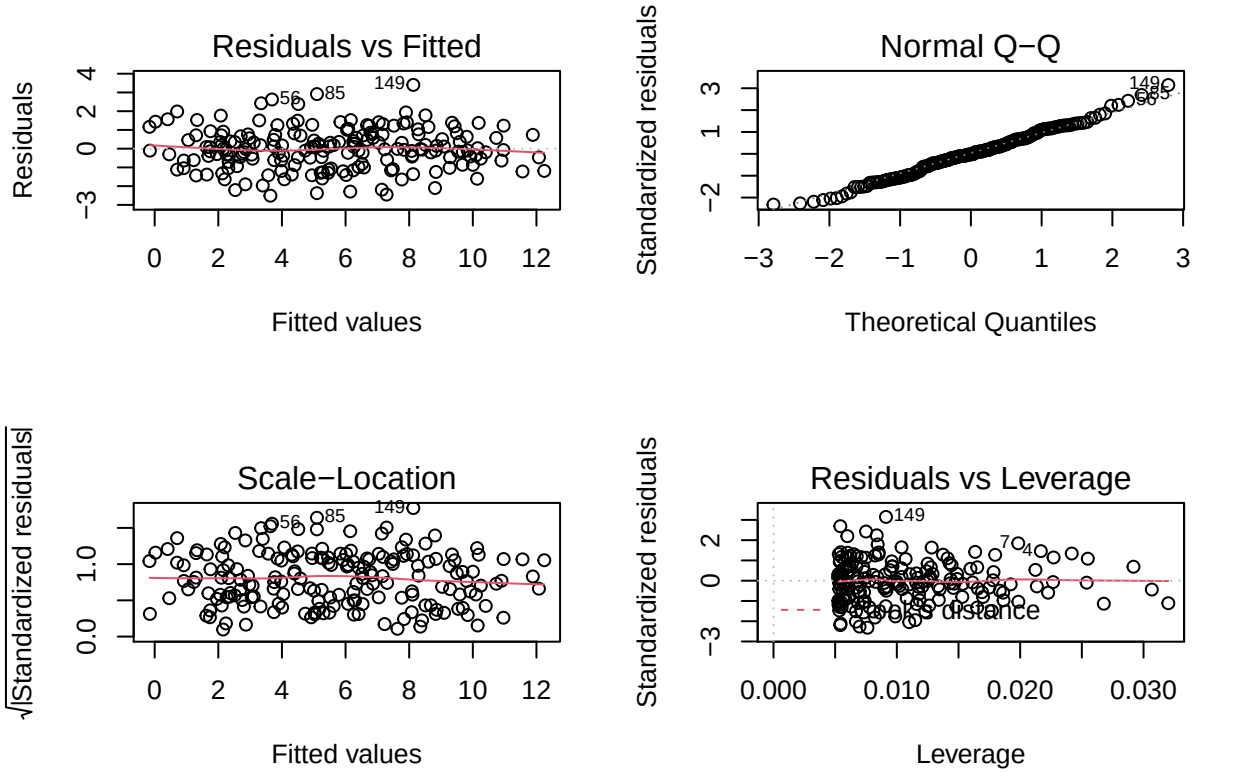
```
minmax_scaler <- function(x) {
    return((x-min(x))/(max(x)-min(x)))
}
```

```
transform <- data.frame(read.table('../data/Transform_V2.txt', header=TRUE))
trm1 <- lm(y ~ sqrt(x2+1), data=transform)
trm2 <- lm(y ~ I(x3^(2)), data=transform)
par(mfrow=c(2,2))
plot(trm1)
```



We can see that the square root transformation is appropriate for the X_2 variable

```
par(mfrow=c(2,2))
plot(trm2)
```

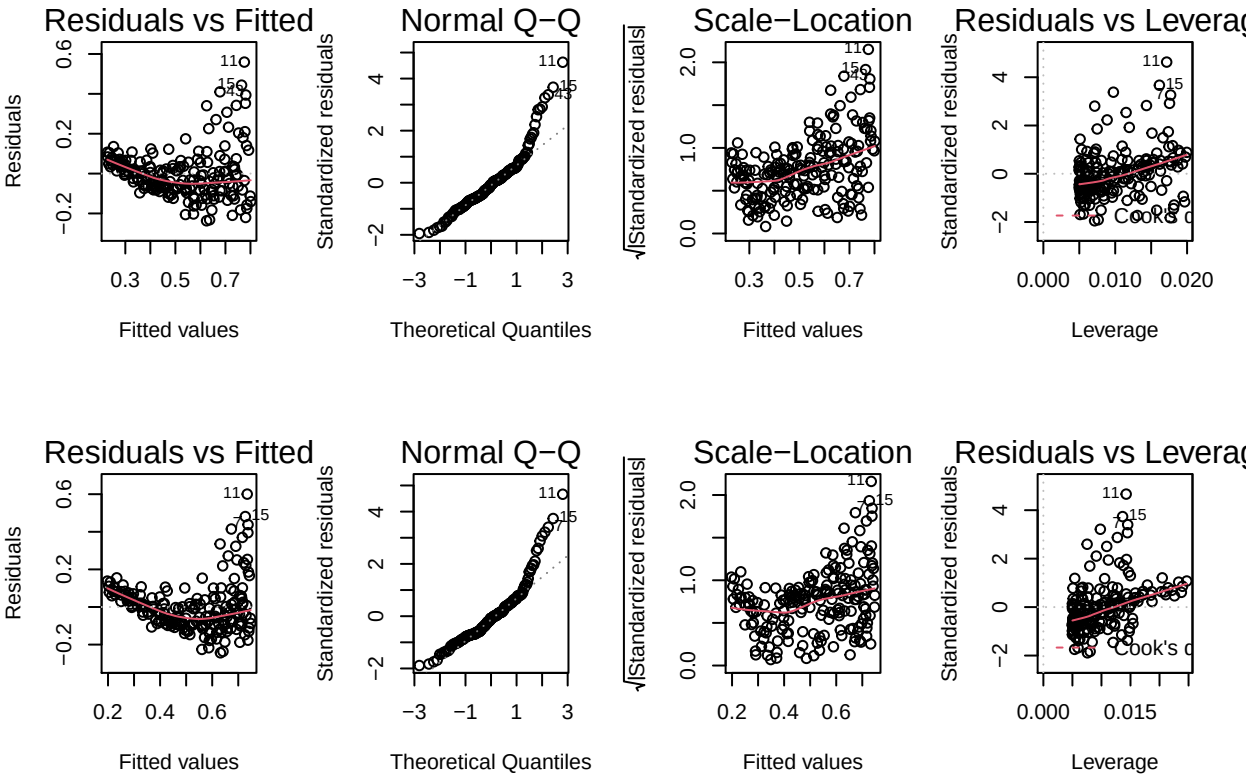


We can see that the X^2 transformation is appropriate for the X_3 variable

Exercise 11

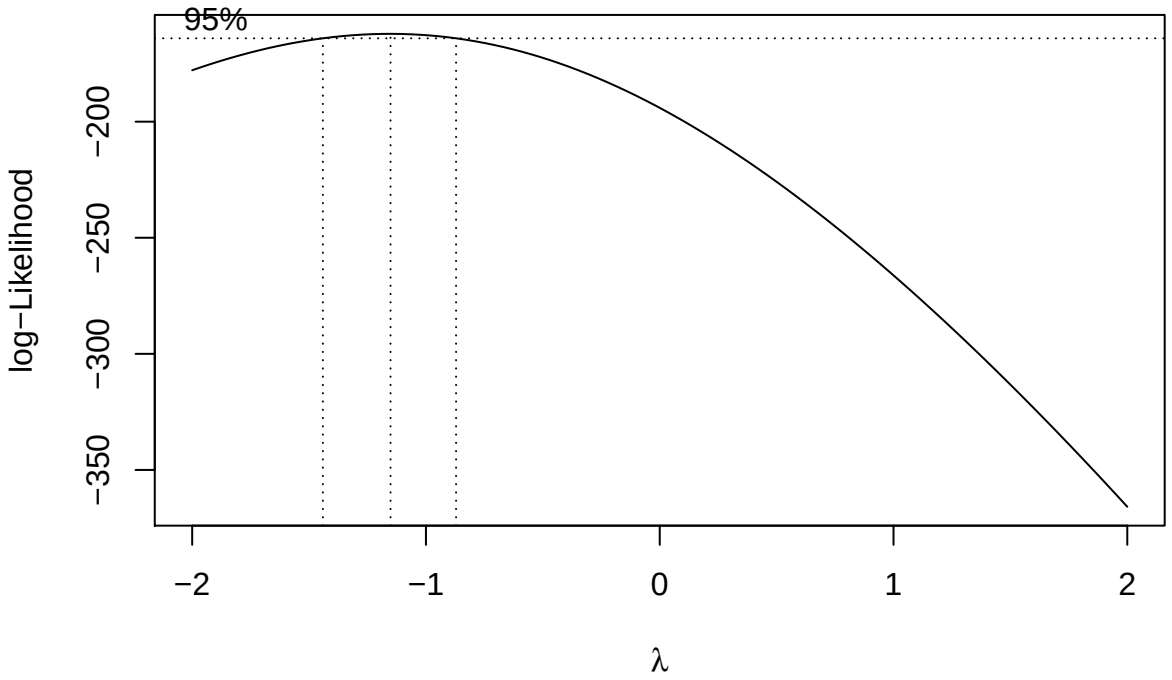
```
bxcx_transf <- function(x, lambda) {
    if (lambda == 0) {
        return(log(x))
    } else {
        return((x^(lambda)-1)/lambda)
    }
}
```

```
transform2 <- data.frame(read.table('../data/Transform2_V2.txt', header=TRUE))
trm1 <- lm(y2 ~ x1, data=transform2)
trm2 <- lm(y2 ~ x2, data=transform2)
par(mfrow=c(2,4))
plot(trm1)
plot(trm2)
```

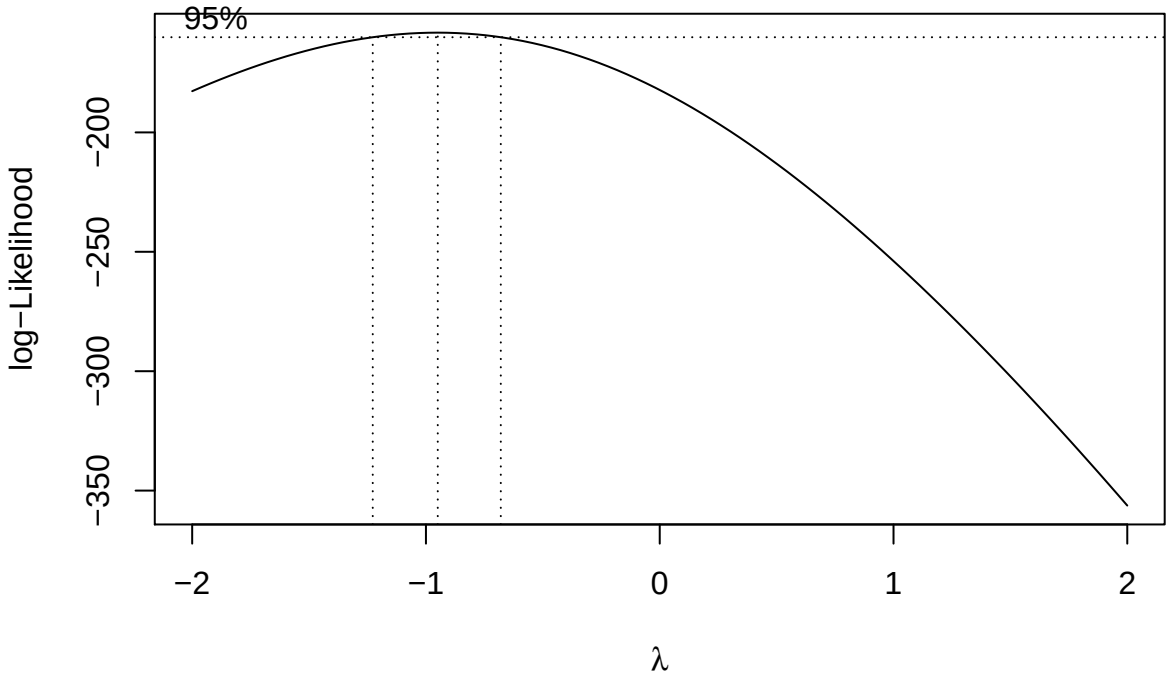


Neither variable has constant variance, therefore we apply a boxcox transformation to both X_2 and X_3.

```
boxcox(trm2)
```

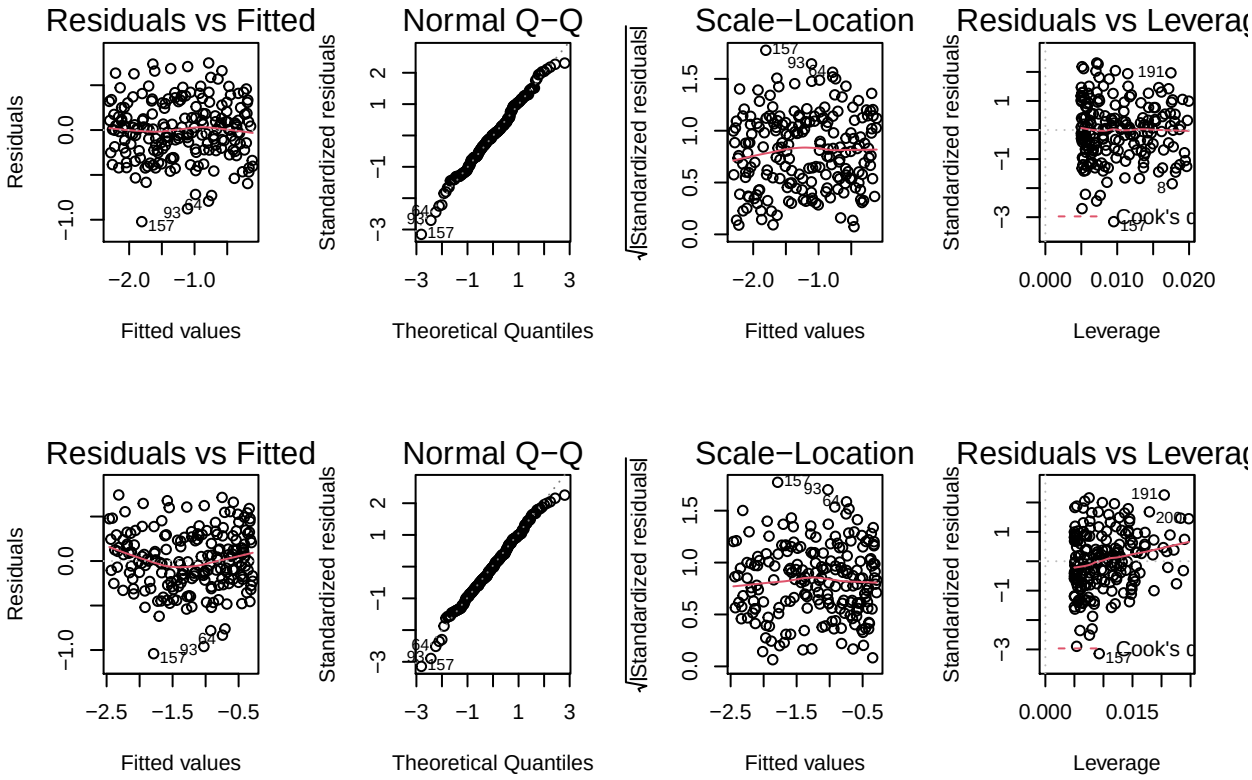



```
boxcox(trm1)
```



As -1 is in the confidence interval for both models, we will apply a boxcox transformation using $\lambda = -1$.

```
transform2 <- data.frame(read.table('../data/Transform2_V2.txt', header=TRUE))
trm1 <- lm(bxcx_transf(y2,-1) ~ x1, data=transform2)
trm2 <- lm(bxcx_transf(y2,-1) ~ x2, data=transform2)
par(mfrow=c(2,4))
plot(trm1)
plot(trm2)
```



Here we see the situation has improved significantly and we now have constant variance.

Exercise 12

Exercise 13

Using R's function to calculate VIF for our model:

```
vif(modall)
#>       age        ht        wt       abs   triceps   subscap
#>  1.553994  2.582940 10.194274 10.799321 10.951090 14.114459
```

We can see that the VIF score for **triceps**, **abs**, **wt** and **subscap** are all above 10 and therefore very high.

Programming my own VIF function:

The approach here is to set up a linear model using the variable who's VIF score we want to calculate in each loop using its predictors as its predictors (basically passing through the function the section of our dataframe that corresponds to predictor variables).

Essentially doing the following:

$X_1 = k_1 + k_2X_2 + k_3X_3 + \cdots + k_nX_n$

Where each k_i is a constant, and each X_i is a predictor.

Then we calculate the VIF score for each one of them using the coefficient of determination of the fitted values of the model and the real values of the predictor that we set as dependent variable in the model corresponding to that loop and adding these elements to a list.

```
vif_mc <- function(X) {
    result <- c()
    for (i in 1:(length(names(X)))) {
        variables <- names(X)
        preds <- 1:length(names(X))
        preds <- preds[preds != i]
        other_vars <- ""
        for (j in 1:(length(names(X))-1)) {
            ov = variables[variables != variables[i]]
            if (j > 1) {
                other_vars = paste(other_vars, "+" ,ov[j])
            } else {
                other_vars = ov[j]
            }

        }
        model <- lm(paste(variables[i], "~", other_vars), data=X)
        result <- c(result, 1/(1-((cor(X[i],fitted(model)))^2)))
    }
    names(result) <- names(X)
    result
}
```

Returning its values:

```
vif_mc(bodyfat[1:6])
#>       age        ht        wt       abs   triceps   subscap
#>  1.553994  2.582940 10.194274 10.799321 10.951090 14.114459
```

We can see that we get the same values as with the original VIF function from the *car* library.

Exercise 14