LungCapData

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```
LungCapData <- read.delim(file.choose(),header = TRUE)
attach(LungCapData)
```

check names

```
names(LungCapData)
```

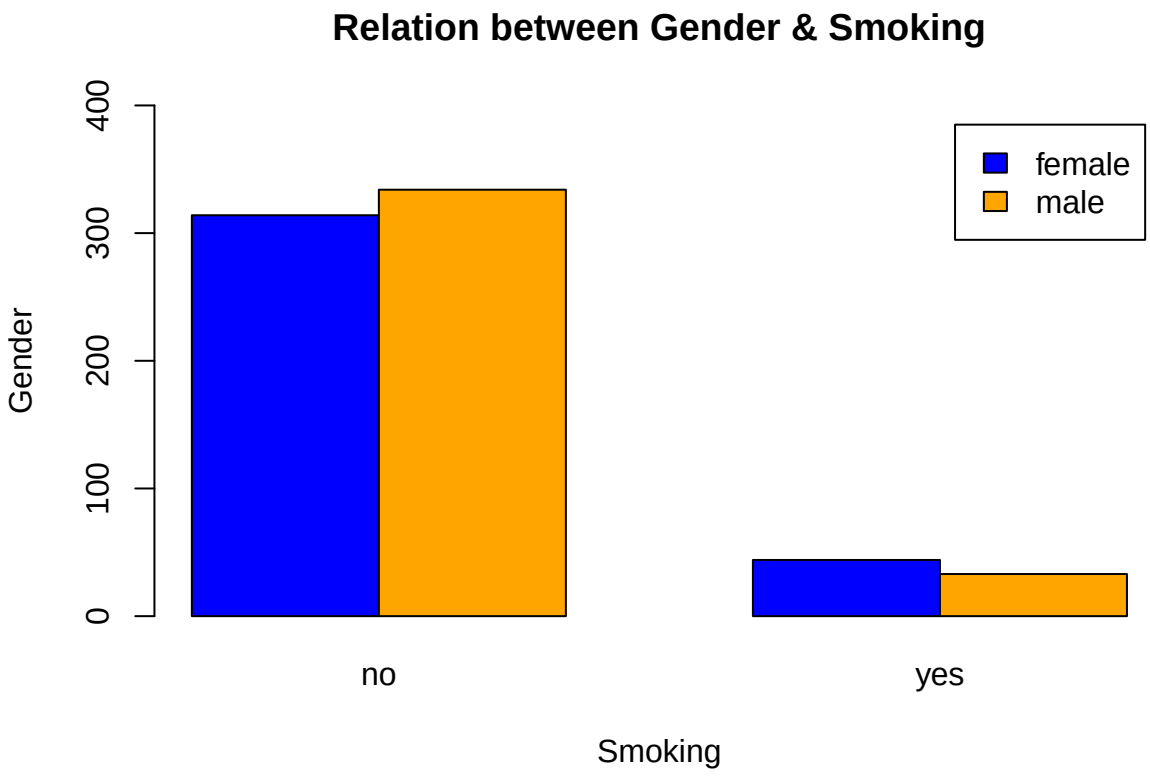
```
## [1] "LungCap"   "Age"       "Height"    "Smoke"     "Gender"    "Caesarean"
```

relation between Gender and Smoke :

```
Table1 <- table(Gender ,Smoke)
Table1
```

```
##         Smoke
## Gender    no yes
##   female 314  44
##   male   334  33
```

```
barplot(Table1 , beside = TRUE , legend=TRUE ,xlab = "Smoking" , ylab = "Gender" ,
        main = "Relation between Gender & Smoking" ,ylim = c(0,400),col = c("blue" , "orange") )
```



categorical variables by chisq test :

H0 : No relation between smoking frequency and gender

```
chisq.test(Table1 , correct = TRUE)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  Table1
## X-squared = 1.7443, df = 1, p-value = 0.1866
```

p-value > 0.05 , Fail to reject H0

calculate OR , RR :

```
library(epiR)
```

```
## Loading required package: survival
## Warning: package 'survival' was built under R version 3.6.1
## Package epiR 1.0-2 is loaded
## Type help(epi.about) for summary information
```

```
##
```

```
epi.2by2(Table1 , method = "cohort.count" , conf.level = 0.95)
```

```
##              Outcome +    Outcome -      Total        Inc risk *
## Exposed +          314           44        358              87.7
## Exposed -          334           33        367              91.0
## Total              648           77        725              89.4
##                   Odds
## Exposed +         7.14
## Exposed -        10.12
## Total             8.42
##
## Point estimates and 95% CIs:
## -------------------------------------------------------------------
## Inc risk ratio                                 0.96 (0.92, 1.01)
## Odds ratio                                     0.71 (0.44, 1.14)
## Attrib risk *                                  -3.30 (-7.79, 1.19)
## Attrib risk in population *                    -1.63 (-5.32, 2.06)
## Attrib fraction in exposed (%)                 -3.76 (-9.12, 1.34)
## Attrib fraction in population (%)              -1.82 (-4.34, 0.64)
## -------------------------------------------------------------------
##  Test that odds ratio = 1: chi2(1) = 2.077 Pr>chi2 = 0.15
##  Wald confidence limits
##  CI: confidence interval
##  * Outcomes per 100 population units
```

Odds of Females not smoking are 0.71 times odds of males not smoking

```
1/0.71
```

```
## [1] 1.408451
```

Odds of males not smoking are 1.4 times odds of Females not smoking

check normality

```
library(moments)
skewness(LungCap)
```

```
## [1] -0.2274017
```

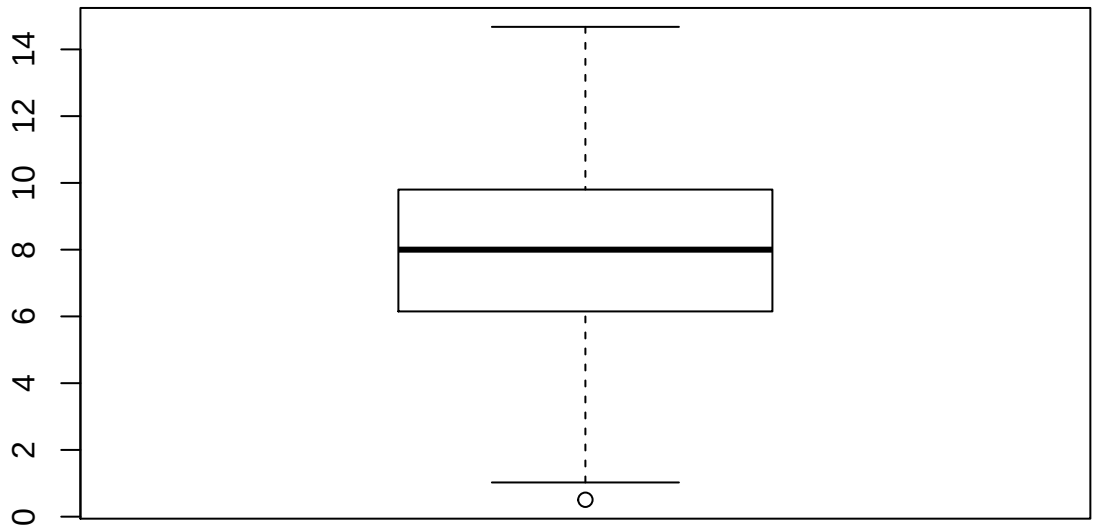
accepted level from -1 to +1

```
kurtosis(LungCap)
```

```
## [1] 2.68148
```

accepted level from -2 to +2 may to +3

```r
boxplot(LungCap)
```



visually ,data is normally distributed

One-sample t-test for lung Capacity :

Test H0 =8 , conf.interval = 0.95 :

```r
t.test(LungCap , mu=8 , alternative = "two.sided" , conf.level = 0.95)
```

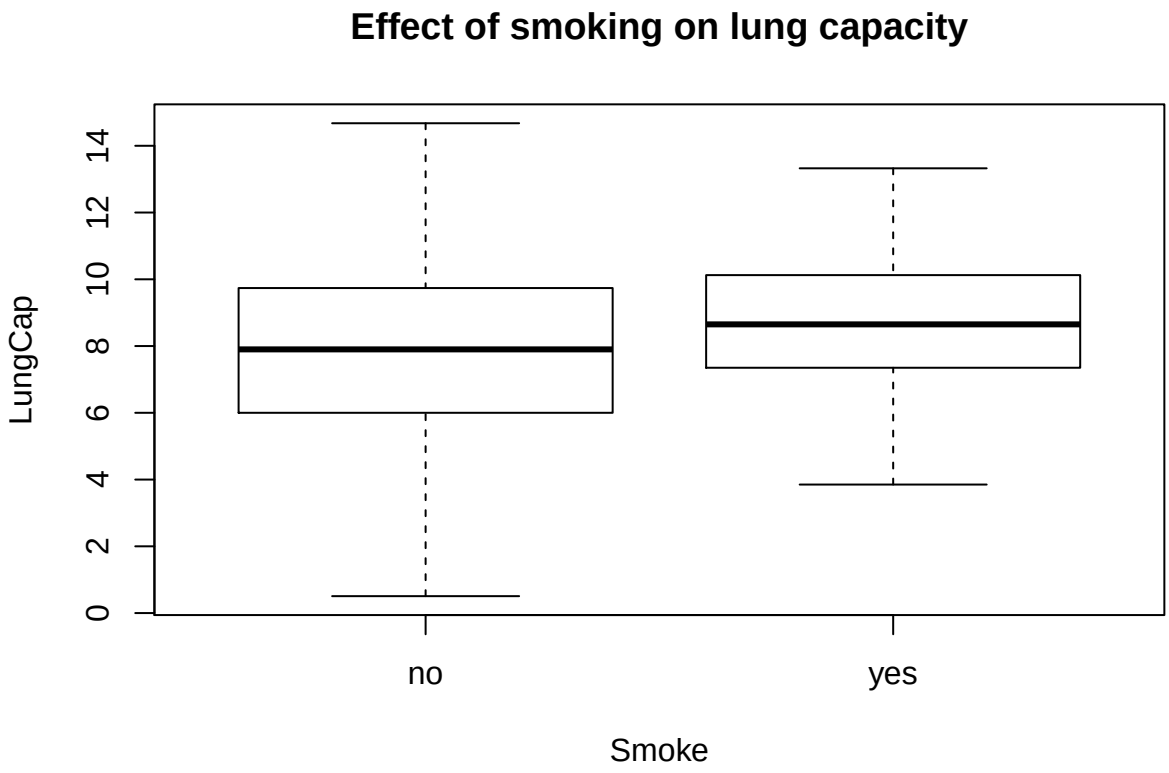
```
##
##  One Sample t-test
##
## data:  LungCap
## t = -1.3842, df = 724, p-value = 0.1667
## alternative hypothesis: true mean is not equal to 8
## 95 percent confidence interval:
##  7.669052 8.057243
## sample estimates:
## mean of x
##  7.863148
```

p-value >0.05 , fail to reject H0

Relation between Smoke & lung Capacity :

H0 : mean of smokers = mean of non smokers :

```
boxplot(LungCap~Smoke , main = "Effect of smoking on lung capacity")
```



check variance :

```
var(LungCap[Smoke == "yes"])
```

```
## [1] 3.545292
```

```
var(LungCap[Smoke == "no"])
```

```
## [1] 7.431694
```

so variance not equal

```
t.test(LungCap~Smoke , mu=0 , alternative = "two.sided" , var.eq = F, conf.level =  0.95)
```

```
##
##  Welch Two Sample t-test
##
## data:  LungCap by Smoke
## t = -3.6498, df = 117.72, p-value = 0.0003927
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
```

```
##  -1.3501778 -0.4003548
## sample estimates:
##  mean in group no mean in group yes
##          7.770188          8.645455
```

p-value < 0.05 , reject H0 , Smoking has a significant effect on lung capacity

H0 : Median of lung capacity of smokers = Median of lung capacity of non smokers

```
wilcox.test(LungCap~Smoke , mu=0 , alternative = "two.sided" ,
            conf.int=T,  conf.level =  0.95 , paired=F , exact=F,correct=F)
```

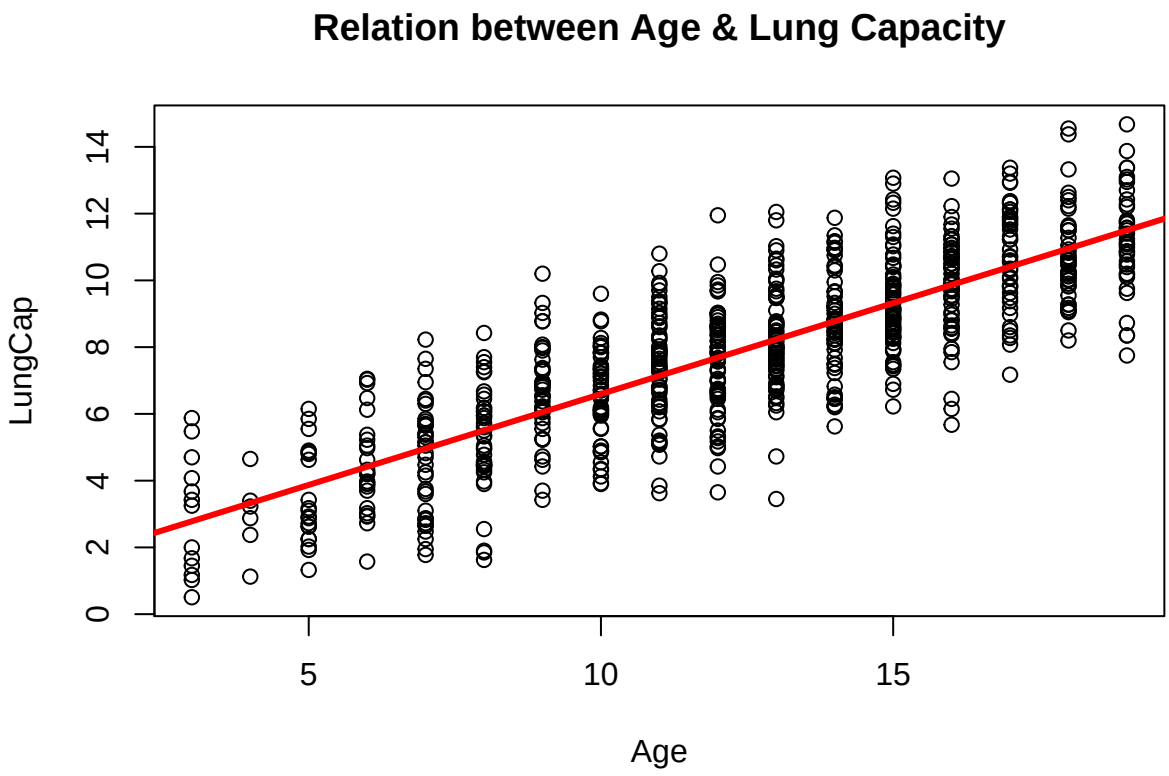
```
##
##  Wilcoxon rank sum test
##
## data:  LungCap by Smoke
## W = 20128, p-value = 0.005533
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -1.399989 -0.249989
## sample estimates:
## difference in location
##             -0.8000564
```

p-value < 0.05 , reject H0 , Smoking has a significant effect on lung capacity

model the relation between Age , LungCap :

use simple linear regression

```
model1 <- lm(LungCap~Age)
plot(Age,LungCap,main = "Relation between Age & Lung Capacity")
abline(model1 ,col=2 , lwd=3)
```




```
cor(Age,LungCap ,method="pearson")
```

```
## [1] 0.8196749
```

there is positive strong correlation

Denisty plots : check if the response variable is close to normal :

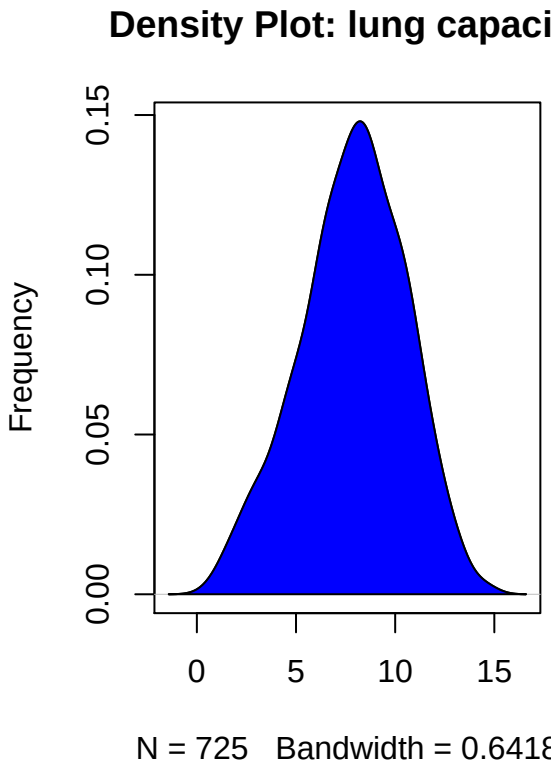
```
library(e1071)
```

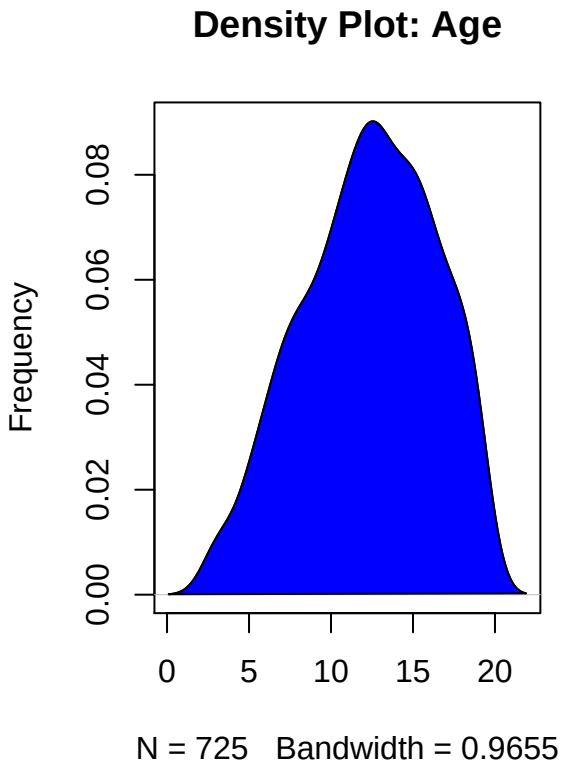
```
## Warning: package 'e1071' was built under R version 3.6.1
```

```
##
## Attaching package: 'e1071'
```

```
## The following objects are masked from 'package:moments':
##
##     kurtosis, moment, skewness
```

```
par(mfrow=c(1, 2))  # divide graph area in 2 columns
plot(density(LungCap), main="Density Plot: lung capacity", ylab="Frequency")
# density plot for 'lung capacity'
polygon(density(LungCap), col="blue")
plot(density(Age), main="Density Plot: Age", ylab="Frequency")  # density plot for 'dist'
polygon(density(Age), col="blue")
```





built linear model equation :

```
model1 <- lm(LungCap~Age)
model1
```

```
##
## Call:
## lm(formula = LungCap ~ Age)
##
## Coefficients:
## (Intercept)          Age
##      1.1469       0.5448
```

lungCap = intercept + slopeAge $lungCap = 1.1469 + 0.5448$ Age

check the residuals and significance

H0 : slope = 0

```
summary(model1)
```

```
##
## Call:
## lm(formula = LungCap ~ Age)
##
## Residuals:
```

```
##     Min      1Q  Median      3Q     Max
## -4.7799 -1.0203 -0.0005  0.9789  4.2650
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.14686    0.18353   6.249 7.06e-10 ***
## Age          0.54485    0.01416  38.476  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.526 on 723 degrees of freedom
## Multiple R-squared:  0.6719, Adjusted R-squared:  0.6714
## F-statistic:  1480 on 1 and 723 DF,  p-value: < 2.2e-16
```

p-value <0.05 , reject H0 67% of the variation in Lung Capicity is explained by Age

test H0: variation mean squared regression = variation mean squared errors

```
anova(model1)
```

```
## Analysis of Variance Table
##
## Response: LungCap
##            Df Sum Sq Mean Sq F value    Pr(>F)
## Age         1 3447.0  3447.0  1480.4 < 2.2e-16 ***
## Residuals 723 1683.5     2.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sqrt(2.3)
```

```
## [1] 1.516575
```

p-value < 0.05 , reject H0

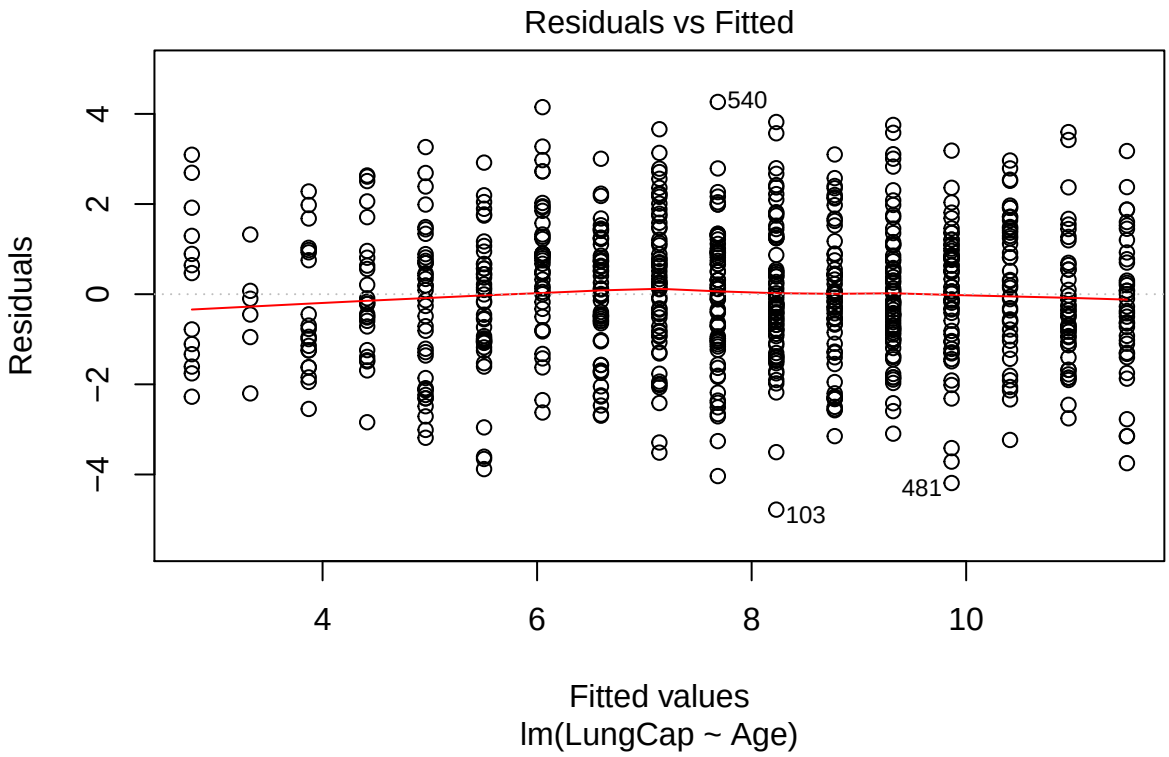
Getting the coeffecient confedience interval :

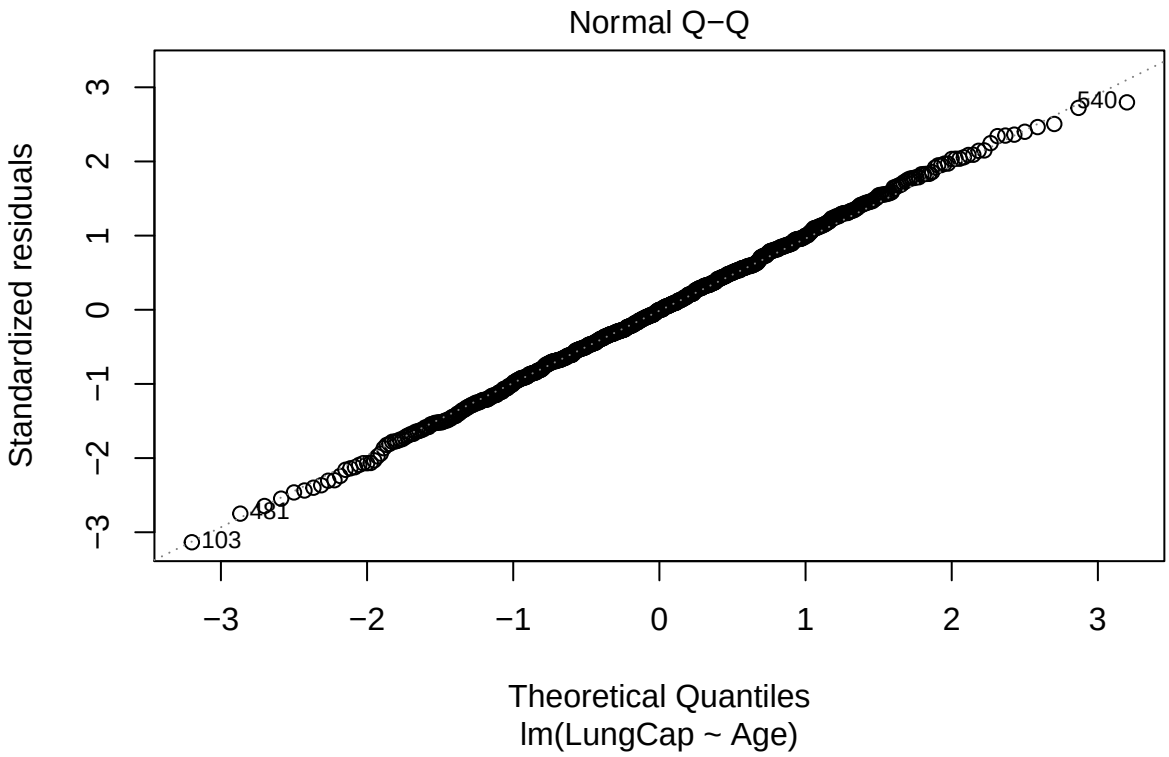
```
confint(model1)
```

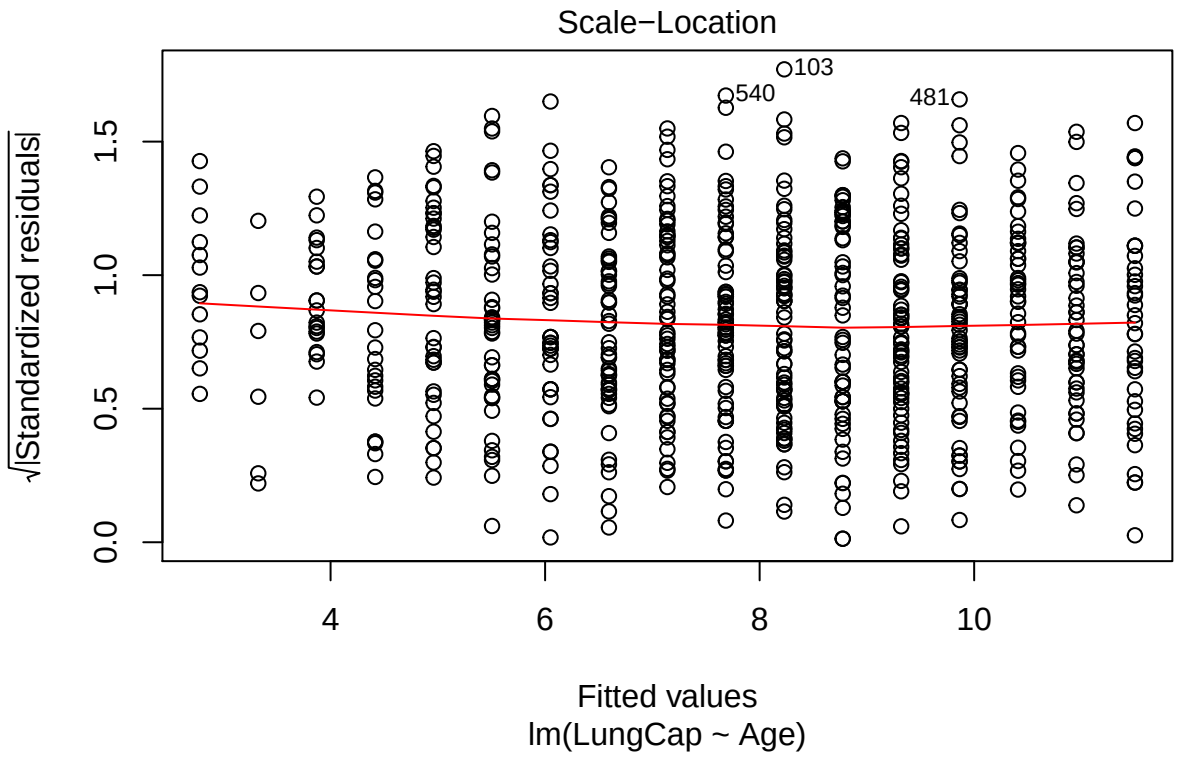
```
##                 2.5 %    97.5 %
## (Intercept) 0.7865454 1.5071702
## Age         0.5170471 0.5726497
```

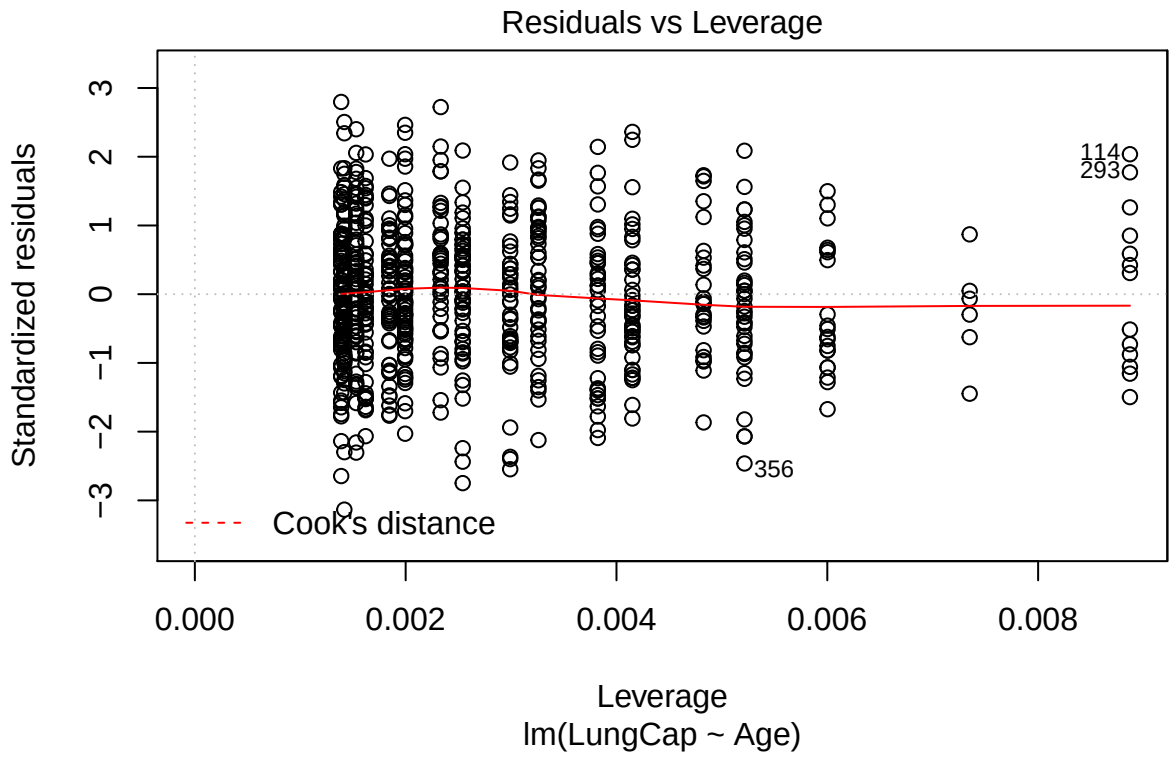
visualize the assumption

```
plot(model1)
```


Residuals vs Fitted
Residuals
Fitted values
lm(LungCap ~ Age)
540
103
481
4
6
8
10
−4
−2
0
2
4


Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(LungCap ~ Age)
103
481
540
−3
−2
−1
0
1
2
3


Scale−Location
103
540
481
√|Standardized residuals|
0.0
0.5
1.0
1.5
4
6
8
10
Fitted values
lm(LungCap ~ Age)



fit a model using Age Height as explanatory variables :

H0 B0=B1=B2= 0

```
mlr <- lm(LungCap~Age+Height , data = LungCapData)
summary(mlr)
```

```
##
## Call:
## lm(formula = LungCap ~ Age + Height, data = LungCapData)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.4080 -0.7097 -0.0078  0.7167  3.1679
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -11.747065   0.476899 -24.632  < 2e-16 ***
## Age           0.126368   0.017851   7.079 3.45e-12 ***
## Height        0.278432   0.009926  28.051  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.056 on 722 degrees of freedom
## Multiple R-squared:  0.843,  Adjusted R-squared:  0.8425
## F-statistic:  1938 on 2 and 722 DF,  p-value: < 2.2e-16
```

p-value < 0.05 , reject H0 84.25% of variation in lung capacity is explained by Age and Height increase in 1 year of Age with an increase in 0.126 of lung capacity adjusting for Height

pearson correlation between Age ,Height :

```
cor(Age , Height, method = "pearson")
```

```
## [1] 0.8357368
```

there is +ve strong correlation

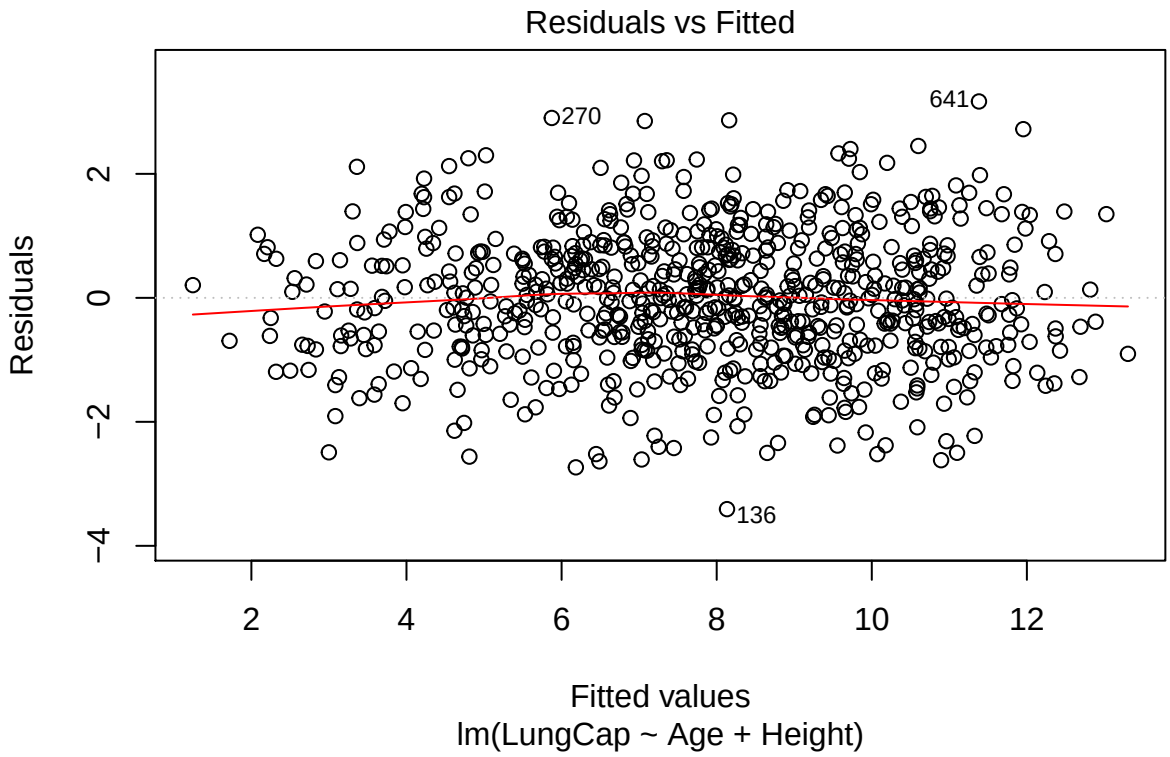
Getting the coeffecient confedience interval :

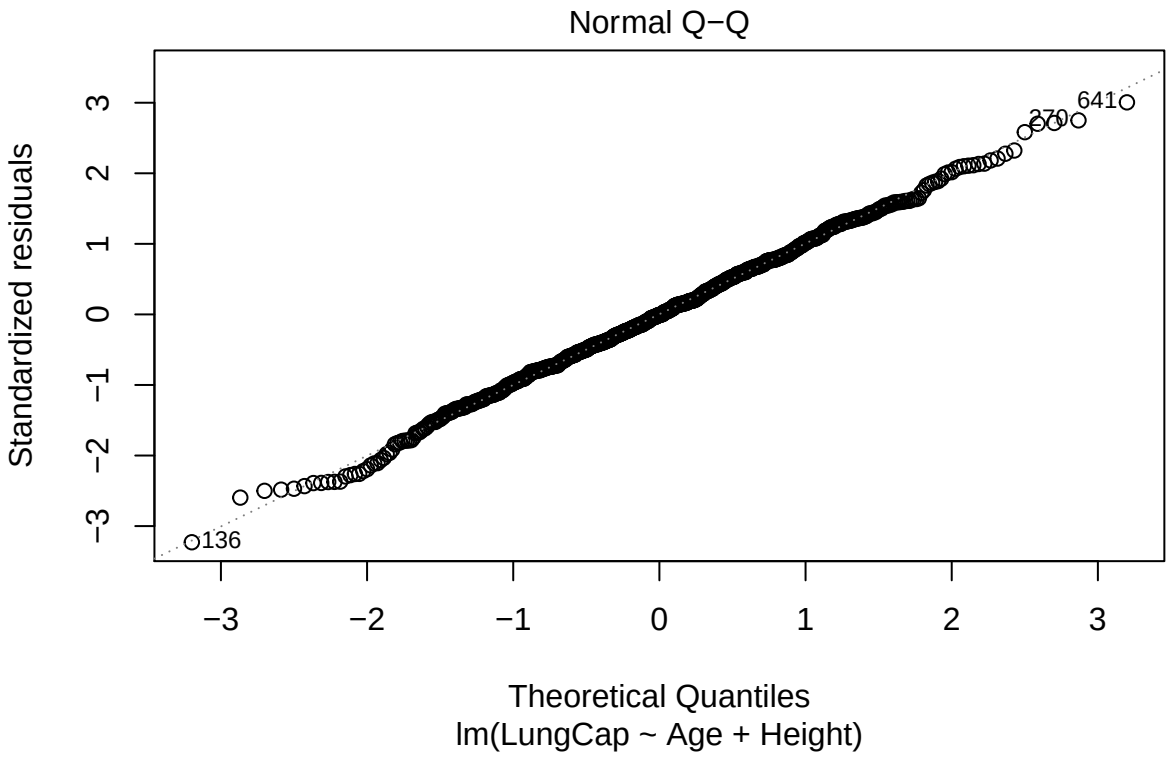
```
confint(mlr)
```

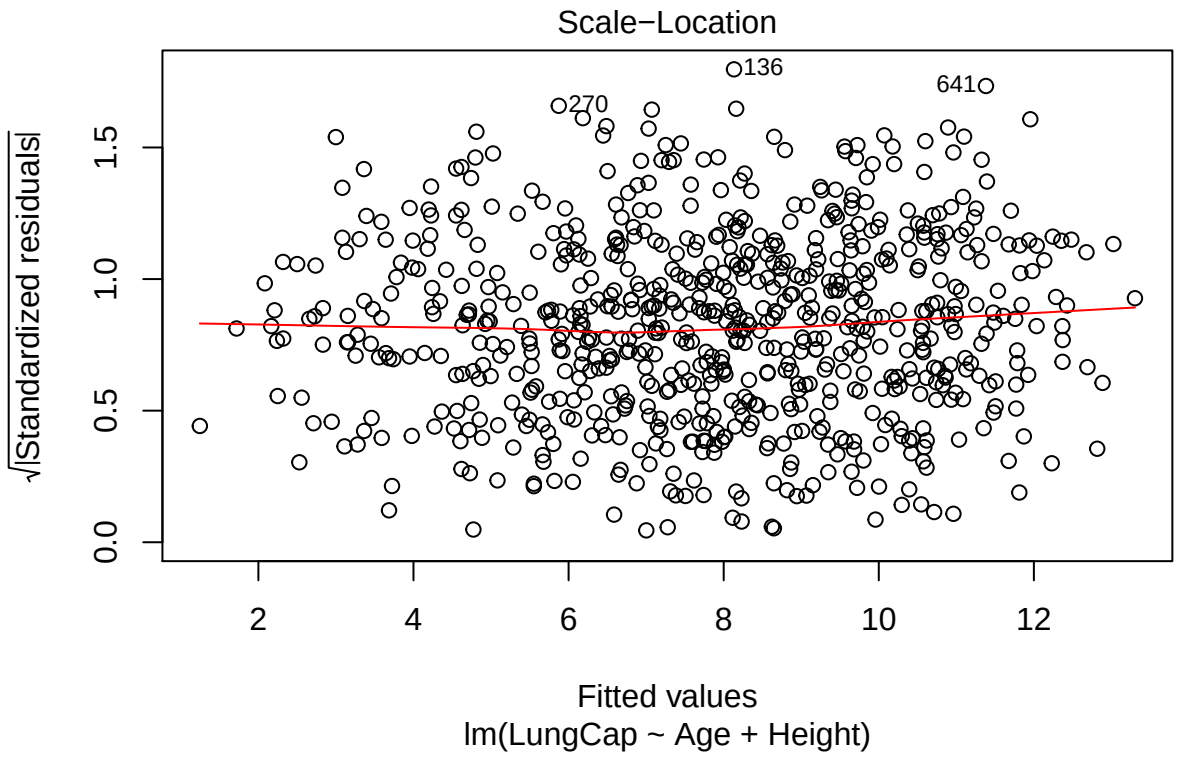
```
##                    2.5 %      97.5 %
## (Intercept) -12.68333877 -10.8107918
## Age           0.09132215   0.1614142
## Height        0.25894454   0.2979192
```

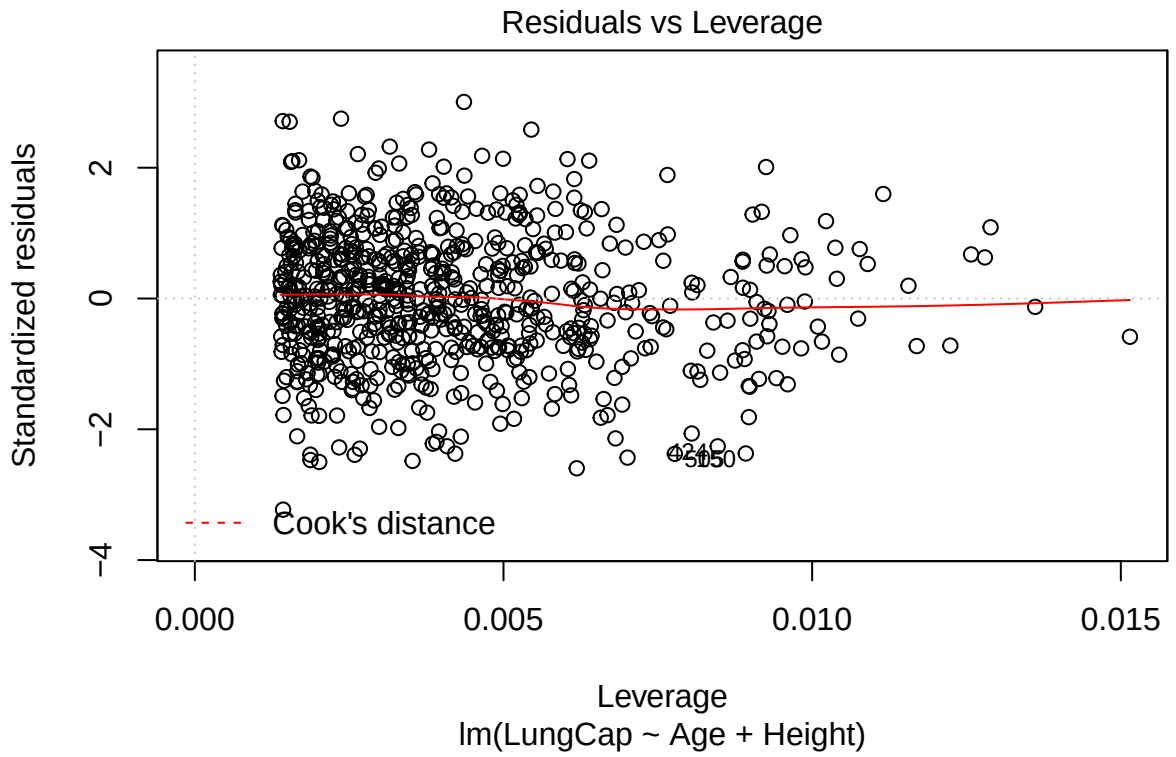
visualize the assumption

```
plot(mlr)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(LungCap ~ Age + Height)
136
641
−3
−2
−1
0
1
2
3


Scale−Location
136
641
270
√|Standardized residuals|
0.0
0.5
1.0
1.5
2
4
6
8
10
12
Fitted values
lm(LungCap ~ Age + Height)



fit model for all variables

```
mlr1 <- lm(LungCap~ Age+Height+Smoke+Gender+Caesarean,data = LungCapData)
summary(mlr1)
```

```
##
## Call:
## lm(formula = LungCap ~ Age + Height + Smoke + Gender + Caesarean,
##     data = LungCapData)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3388 -0.7200  0.0444  0.7093  3.0172
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -11.32249    0.47097 -24.041  < 2e-16 ***
## Age            0.16053    0.01801   8.915  < 2e-16 ***
## Height         0.26411    0.01006  26.248  < 2e-16 ***
## Smokeyes      -0.60956    0.12598  -4.839 1.60e-06 ***
## Gendermale     0.38701    0.07966   4.858 1.45e-06 ***
## Caesareanyes  -0.21422    0.09074  -2.361   0.0185 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 1.02 on 719 degrees of freedom
## Multiple R-squared:  0.8542, Adjusted R-squared:  0.8532
## F-statistic: 842.8 on 5 and 719 DF,  p-value: < 2.2e-16
```

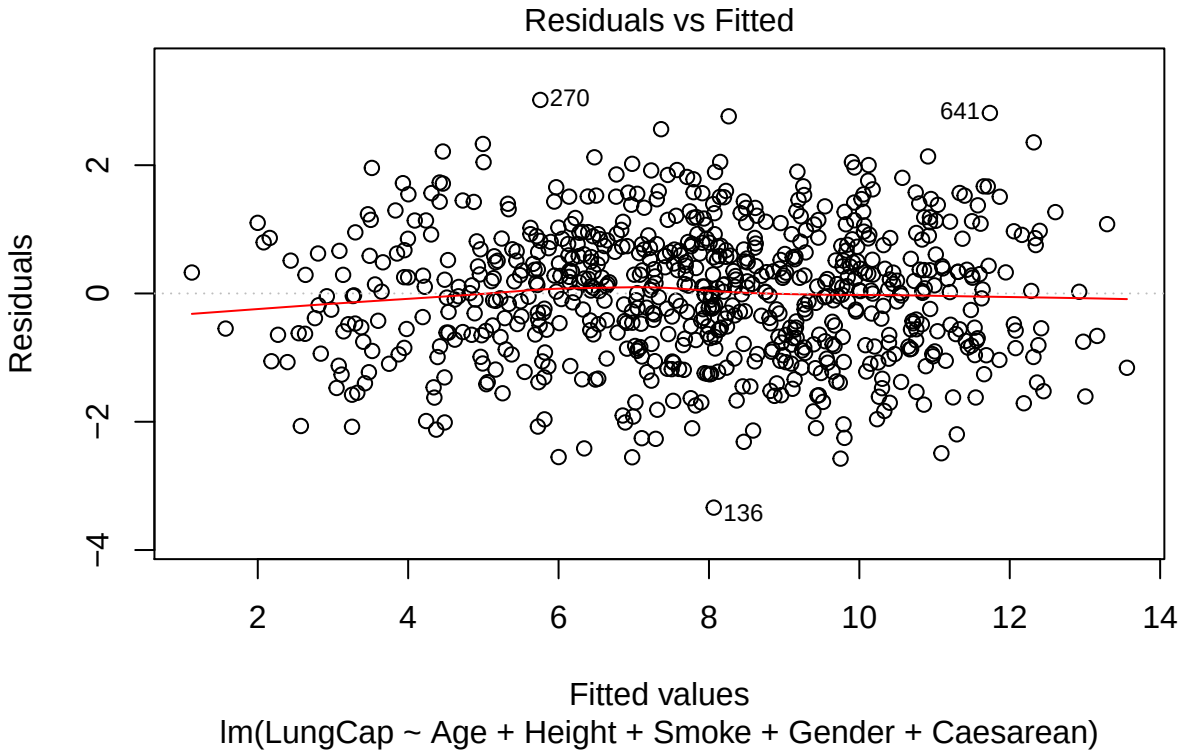
Getting the coeffecient confedience interval :

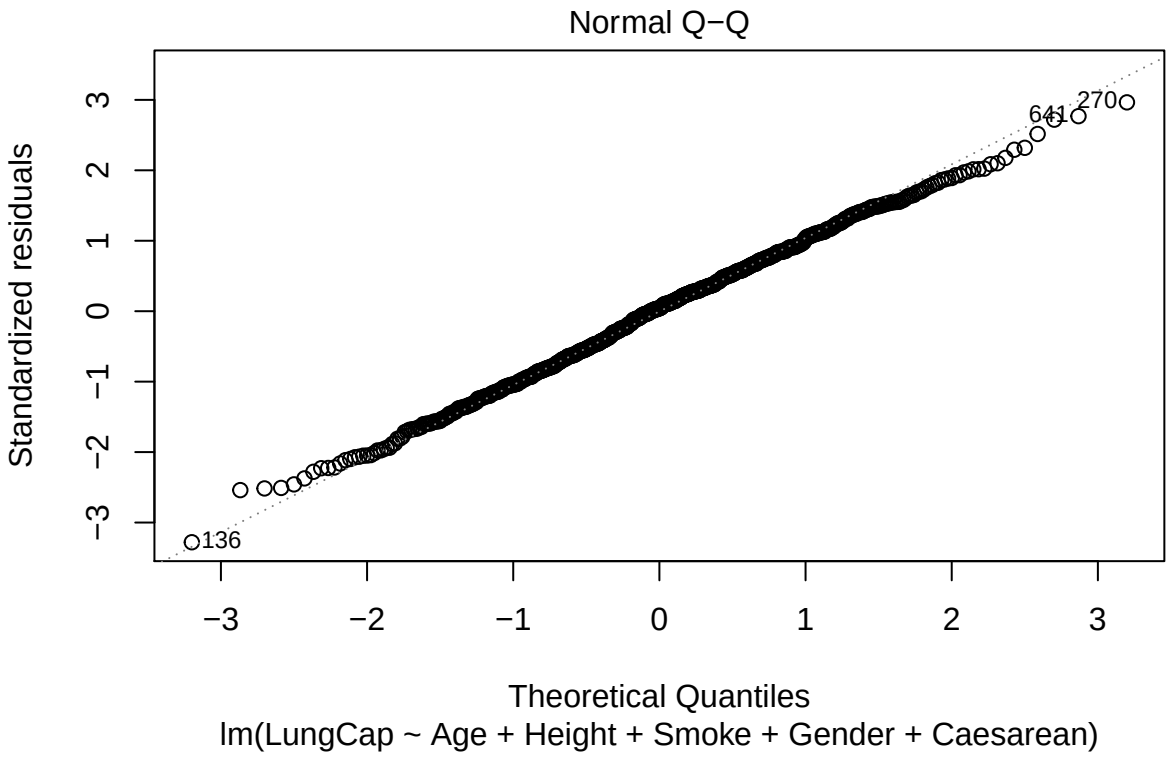
```
confint(mlr1)
```

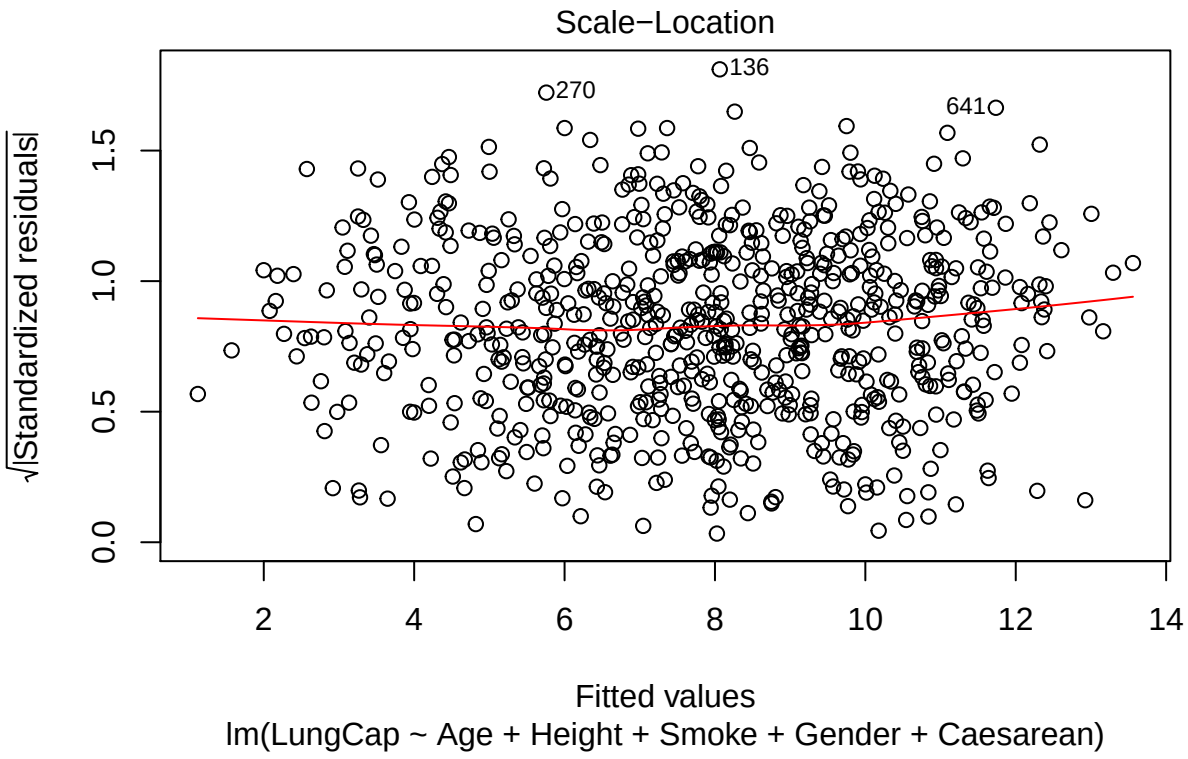
```
##                    2.5 %       97.5 %
## (Intercept)  -12.2471338 -10.39783728
## Age            0.1251765   0.19588271
## Height         0.2443581   0.28386751
## Smokeyes      -0.8568861  -0.36223237
## Gendermale     0.2306230   0.54340035
## Caesareanyes  -0.3923590  -0.03607738
```

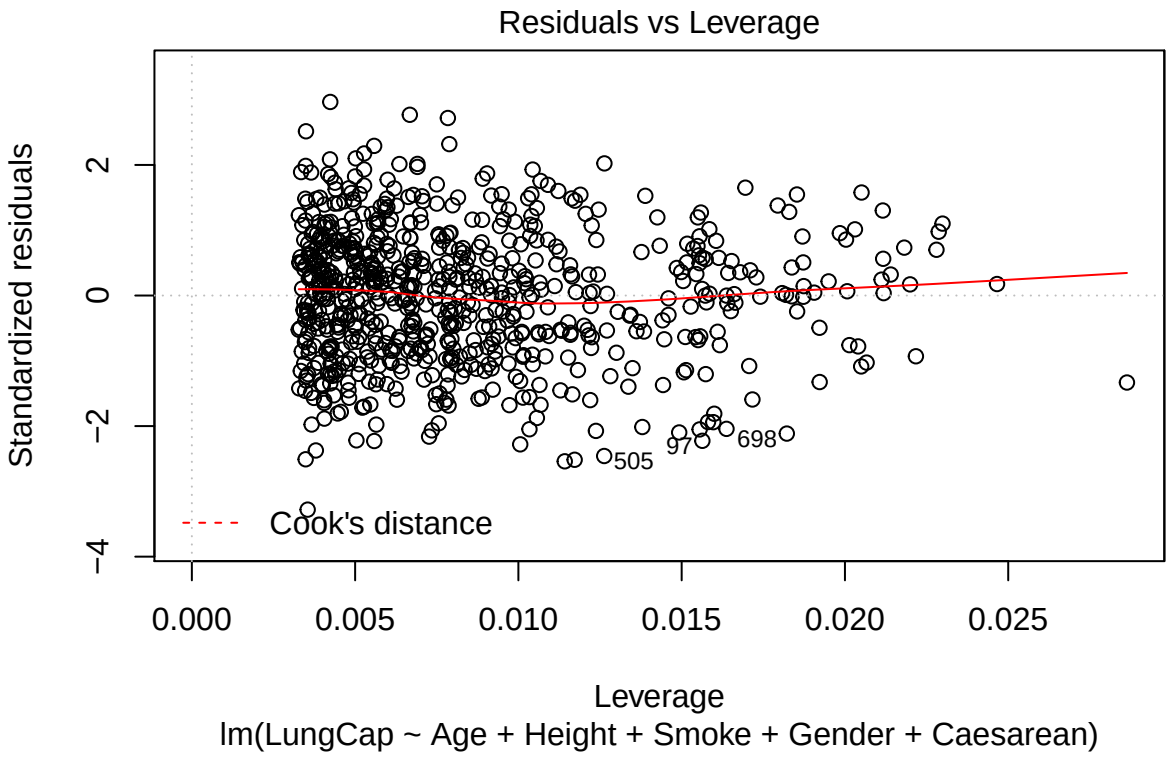
visualize the assumption

```
plot(mlr1)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(LungCap ~ Age + Height + Smoke + Gender + Caesarean)
136
641
270


Scale−Location
136
270
641
√|Standardized residuals|
0.0
0.5
1.0
1.5
2
4
6
8
10
12
14
Fitted values
lm(LungCap ~ Age + Height + Smoke + Gender + Caesarean)


Residuals vs Leverage
Standardized residuals
2
0
−2
−4
0.000
0.005
0.010
0.015
0.020
0.025
505
97
698
Cook's distance
Leverage
lm(LungCap ~ Age + Height + Smoke + Gender + Caesarean)