Savitribai Phule Pune University

Post Graduate Diploma in Data Analytics

LUNG CAPACITY ANALYSIS

1. ABSTRACT

Lung Capacity are also known as respiratory volumes. It refers to the volume of gas in the lungs at a given time during the respiratory cycle. Lung capacities are derived from summation of different lung volumes. The Average total lung capacity of an adult human male is about 6 liters of air. Lung Volumes measurement is an integral part of pulmonary function test. These volumes tend to vary, depending on the depth of respiration, ethnicity, gender age, body composition and in certain respiratory diseases. A number of the lung Volumes can be measured by Spirometry-Tidal volume, Inspiratory reserve volume, and expiratory reserve volume. However, measurement of Residual volume, Functional residual capacity, and Total Lung Capacity is through body plethysmography, nitrogen washout and helium dilution technique.

2. INTRODUCTION

Lung Capacity or total lung capacity (TLC) is the volume of air in the lungs upon the maximum effort of inspiration. Among healthy adults, the average lung capacity is about 6 liters. Lung Cap, Age, Gender, Height, Weight, Smoker or not, Caesarean or not are factors affecting the different ranges of lung capacity among individuals. TLCC rapid increases from birth to adolescence and plateaus at around 25 years old. Males tend to have a greater TLC than females, while individuals with tall stature tend to have greater TLC than those with short stature, and individuals with a high waist-to-hip ratio generally have a lower TLC. Individuals of African descent have a lower TLC compared to individuals of European descent. Additional factors that affect an individual’s Lung Capacity include the level of physical activity chest wall deformities, and respiratory diseases.

Clinicians can measure lung capacity by plethysmography, dilutional helium gas method, nitrogen gas washout method, or radiographically by a relatively new technique using by computed tomography (CT). Methodically, the TLC is calculated by measuring the lung capacities: inspiratory capacity (IC), functional residual capacity (FRC), and the vital capacity (VC). The lung capacities can be further divided into the following lung volumes: tidal volume (TV), inspiratory reserve volume (IRV), expiratory reserve volume (ERV), and the residual volume (RV). This analysis will not delve into definition of all the lung capacities and lung volumes but instead will outline the methods in which lung capacity is measured and discussed the clinical significance of TLC.

3. METHODOLOGY

3.1 DATASET

The Dataset is collected from Kaggle.com and it is showing Lung Capacity of smokers and non-smokers by their Age, Height, Weight, Gender and Caesarean. May be the Lung volume measured using above techniques but here we don't have clear information about how Lung capacity was measured in our dataset.

Why this particular Dataset has been selected?

This Particular dataset has been selected for Analysis as it includes maximum information which are useful of Statistical Analysis.

3.2 Data Analysis

For Lung Capacity Data Analysis I am using statistical technique including Exploratory Data Analysis, Visualization, Descriptive Statistics, Inferential Statistics, Probability Distribution, Simple Linear Regression, Multiple Linear Regression, and Logistic Regression. All the Data Analysis, computations and comparisons have been performed using R Language.

4. RESULT AND DISCUSSION

The present work encompasses Data analysis of Lung Capacity Dataset.

Set working Directory

```
setwd("C:\\Users\\VB\\Desktop\\PROJECTS")
```

Read Data

```
LungCapData <- read.csv("LungCapData.txt",header = T,sep = "\t")
```

```
attach(LungCapData)
```

Data Exploring

```
str(LungCapData)
```

```
## 'data.frame':    725 obs. of  6 variables:
##  $ LungCap  : num  6.47 10.12 9.55 11.12 4.8 ...
##  $ Age      : int  6 18 16 14 5 11 8 11 15 11 ...
##  $ Height   : num  62.1 74.7 69.7 71 56.9 58.7 63.3 70.4 70.5 59.2 ...
##  $ Smoke    : Factor w/ 2 levels "no","yes": 1 2 1 1 1 1 1 1 1 1 ...
##  $ Gender   : Factor w/ 2 levels "female","male": 2 1 1 2 2 1 2 2 2 2 ...
##  $ Caesarean: Factor w/ 2 levels "no","yes": 1 1 2 1 1 1 2 1 1 1 ...
```

```
dim(LungCapData)
```

```
## [1] 725   6
```

```
length(LungCapData)
```

```
## [1] 6
```

```
head(LungCapData)
```

```
##   LungCap Age Height Smoke Gender Caesarean
## 1   6.475   6   62.1    no   male        no
## 2  10.125  18   74.7   yes female        no
## 3   9.550  16   69.7    no female       yes
## 4  11.125  14   71.0    no   male        no
## 5   4.800   5   56.9    no   male        no
## 6   6.225  11   58.7    no female        no
```

```
tail(LungCapData)
```

```
##     LungCap Age Height Smoke Gender Caesarean
## 720   7.325   9   66.3    no   male        no
## 721   5.725   9   56.0    no female        no
## 722   9.050  18   72.0   yes   male       yes
## 723   3.850  11   60.5   yes female        no
## 724   9.825  15   64.9    no female        no
## 725   7.100  10   67.7    no   male        no
```

```
names(LungCapData)
```

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

```
levels(LungCapData$Smoke)
```

```
## [1] "no"  "yes"
```

```
class(LungCapData$LungCap)
```

```
## [1] "numeric"
```

Data Cleaning

TRAILING AND LEADING SPACES

```
LungCapData$Smoke <- trimws(LungCapData$Smoke,which = c("right"))
LungCapData$Smoke <- trimws(LungCapData$Smoke,which = c("left"))
```

HANDLING PUNCTUATION MARKS

```
LungCapData$smoke <- gsub("[[:punct:]]|[[:digit:]]|(http[[:alpha:]]*:\\/\\/)","",LungCapData$Smoke)
```

IDENTIFYING MISSING VALUES

```
library(mice)
```

```
##
## Attaching package: 'mice'
```

```
## The following objects are masked from 'package:base':
##
##     cbind, rbind
```

```
library(VIM)
```

```
## Loading required package: colorspace
```

```
## Loading required package: grid
```

```
## Loading required package: data.table
```

```
## VIM is ready to use.
##  Since version 4.0.0 the GUI is in its own package VIMGUI.
##
##           Please use the package to use the new (and old) GUI.
```

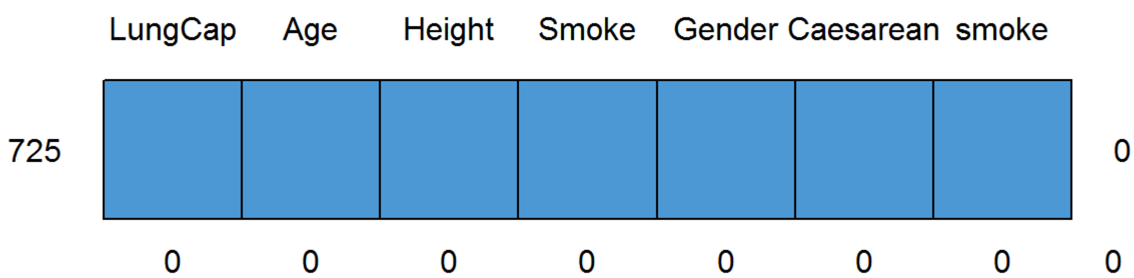
```
## Suggestions and bug-reports can be submitted at: https://github.com/alexkowa/VIM/issues
```

```
##
## Attaching package: 'VIM'
```

```
## The following object is masked from 'package:datasets':
##
##     sleep
```

```
md.pattern(LungCapData)
```

```
##  /\     /\
## {  `---'  }
## {  O   O  }
## ==>  V <==  No need for mice. This data set is completely observed.
##  \  \|/  /
##   `-----'
```




```
##     LungCap Age Height Smoke Gender Caesarean smoke
## 725       1   1      1     1      1         1     1 0
##           0   0      0     0      0         0     0 0
```

```
md.pairs(LungCapData)
```

```
## $rr
##           LungCap Age Height Smoke Gender Caesarean smoke
## LungCap       725 725    725   725    725       725   725
## Age           725 725    725   725    725       725   725
## Height        725 725    725   725    725       725   725
## Smoke         725 725    725   725    725       725   725
## Gender        725 725    725   725    725       725   725
## Caesarean     725 725    725   725    725       725   725
## smoke         725 725    725   725    725       725   725
##
## $rm
##           LungCap Age Height Smoke Gender Caesarean smoke
## LungCap         0   0      0     0      0         0     0
## Age             0   0      0     0      0         0     0
## Height          0   0      0     0      0         0     0
## Smoke           0   0      0     0      0         0     0
## Gender          0   0      0     0      0         0     0
## Caesarean       0   0      0     0      0         0     0
## smoke           0   0      0     0      0         0     0
##
## $mr
##           LungCap Age Height Smoke Gender Caesarean smoke
## LungCap         0   0      0     0      0         0     0
## Age             0   0      0     0      0         0     0
## Height          0   0      0     0      0         0     0
## Smoke           0   0      0     0      0         0     0
## Gender          0   0      0     0      0         0     0
## Caesarean       0   0      0     0      0         0     0
## smoke           0   0      0     0      0         0     0
##
## $mm
##           LungCap Age Height Smoke Gender Caesarean smoke
## LungCap         0   0      0     0      0         0     0
## Age             0   0      0     0      0         0     0
## Height          0   0      0     0      0         0     0
## Smoke           0   0      0     0      0         0     0
## Gender          0   0      0     0      0         0     0
## Caesarean       0   0      0     0      0         0     0
## smoke           0   0      0     0      0         0     0
```

```
p <- function(x){sum(is.na(x))/length(x)*100}
apply(LungCapData,2,p)
```

```
##   LungCap       Age    Height     Smoke    Gender Caesarean     smoke
##         0         0         0         0         0         0         0
```

```
apply(is.na(LungCapData),2,which)
```

```
## integer(0)
```

Exploratory Data Analysis

UNIVARITE ANALYSIS- *to check the summary of the data to get rough idea about Data.*

```
summary(LungCapData)
```

```
##     LungCap            Age            Height         Smoke          
##  Min.   : 0.507   Min.   : 3.00   Min.   :45.30   Length:725        
##  1st Qu.: 6.150   1st Qu.: 9.00   1st Qu.:59.90   Class :character  
##  Median : 8.000   Median :13.00   Median :65.40   Mode  :character  
##  Mean   : 7.863   Mean   :12.33   Mean   :64.84                     
##  3rd Qu.: 9.800   3rd Qu.:15.00   3rd Qu.:70.30                     
##  Max.   :14.675   Max.   :19.00   Max.   :81.80                     
##     Gender    Caesarean    smoke          
##  female:358   no :561   Length:725        
##  male  :367   yes:164   Class :character  
##                         Mode  :character  
##                                           
##                                           
## 
```

Frequency Distribution

to examine the outliers and significant trends are the relative abundance of each particular target data within dataset.

```
breaks <- seq(from=min(Age),to=max(Age),by=3)
pop <- cut(Age,breaks = breaks,right = TRUE,include.lowest = FALSE)
title <- (cbind(table(pop)))
colnames(title) <- c("frequency");title
```

```
##         frequency
## (3,6]          51
## (6,9]         118
## (9,12]        177
## (12,15]       189
## (15,18]       140
```

```
hist(title)
```

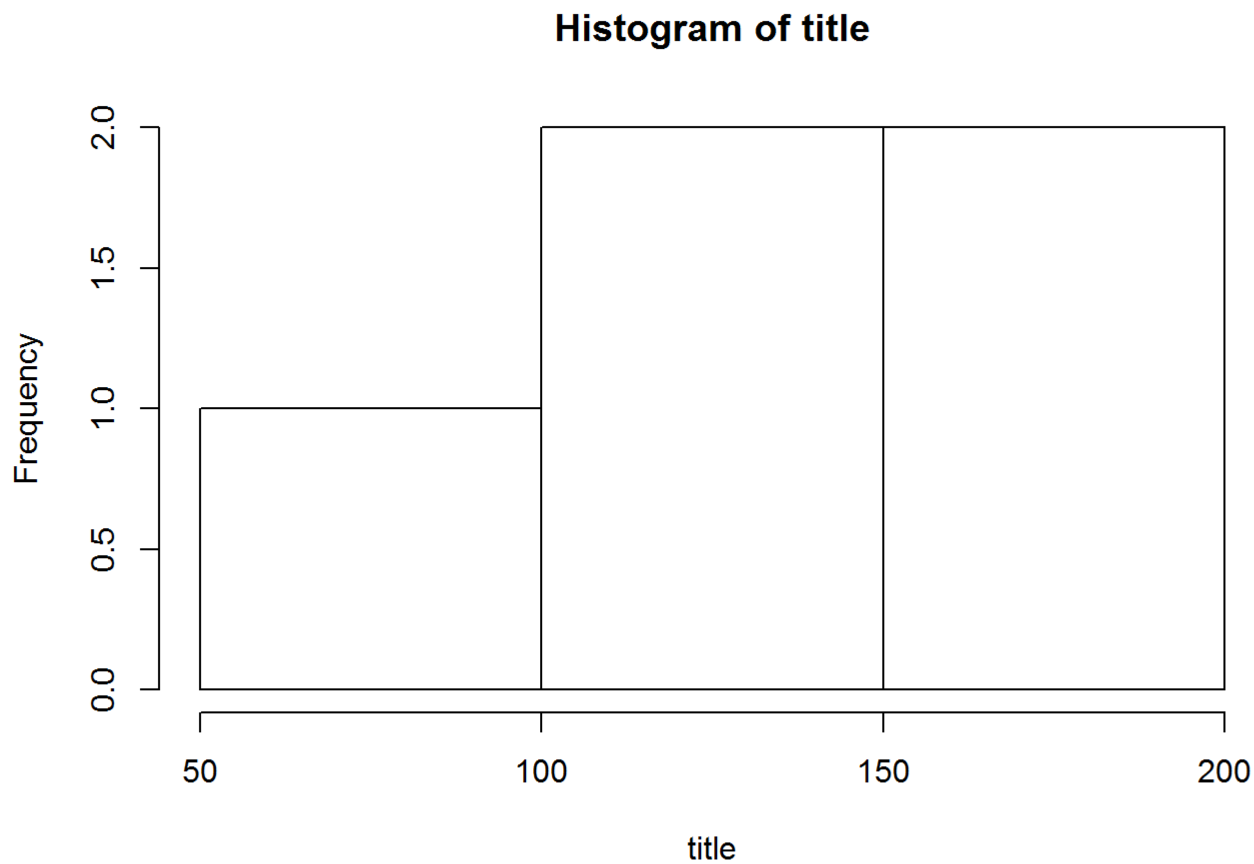


Table for proportion - *to examine the number of observations for a variables.*

```
table(Smoke)
```

```
## Smoke
##  no yes
## 648  77
```

```
table(Smoke)/length(Smoke)
```

```
## Smoke
##        no       yes
## 0.8937931 0.1062069
```

Create two way table or contigency table

```
table(Smoke,Gender)
```

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

Measures of Central Tendency

Calculate the count of variable which is going to analyze

```
length(LungCap)
```

```
## [1] 725
```

Calcualte the Sum of the LungCap

```
sum(LungCap)
```

```
## [1] 5700.782
```

Calculate the Mean of LungCap

```
mean(LungCap)
```

```
## [1] 7.863148
```

Calculate the Median of of Luncap

```
median(LungCap)
```

```
## [1] 8
```

Calculate the Mode of Luncap

```
mode <- function(x){
  ux <- unique(x)
  ux[which.max(tabulate(match(x,ux)))]
}
```

```
mode(LungCap)
```

```
## [1] 8.35
```

Measures of Dispersions

Calculate the Range of the LungCap

```
range(LungCap)
```

```
## [1]  0.507 14.675
```

Calculate quantile of the LungCap

```
quantile(LungCap)
```

```
##     0%    25%    50%    75%   100%
##  0.507  6.150  8.000  9.800 14.675
```

Calculate IQR of the LungCap

```
IQR(LungCap)
```

```
## [1] 3.65
```

Calculate min

```
min(LungCap)
```

```
## [1] 0.507
```

Calculate Max

```
max(LungCap)
```

```
## [1] 14.675
```

Calculate Variance

```
var(LungCap)
```

```
## [1] 7.086288
```

Calculate Standard Deviation

```
sd(LungCap)
```

```
## [1] 2.662008
```

Calculate Square root

```
sqrt(var(LungCap))
```

```
## [1] 2.662008
```

calculate probabilities

```
quantile(LungCap,probs = c(0.20,0.5,0.9,1))
```

```
##    20%    50%    90%   100%
##  5.645  8.000 11.205 14.675
```

Measures of Shapes

Measures of Shapes - *Describe the distribution of the data within dataset.*

Calculate the Skewness

```
library(e1071)
skewness(LungCap)
```

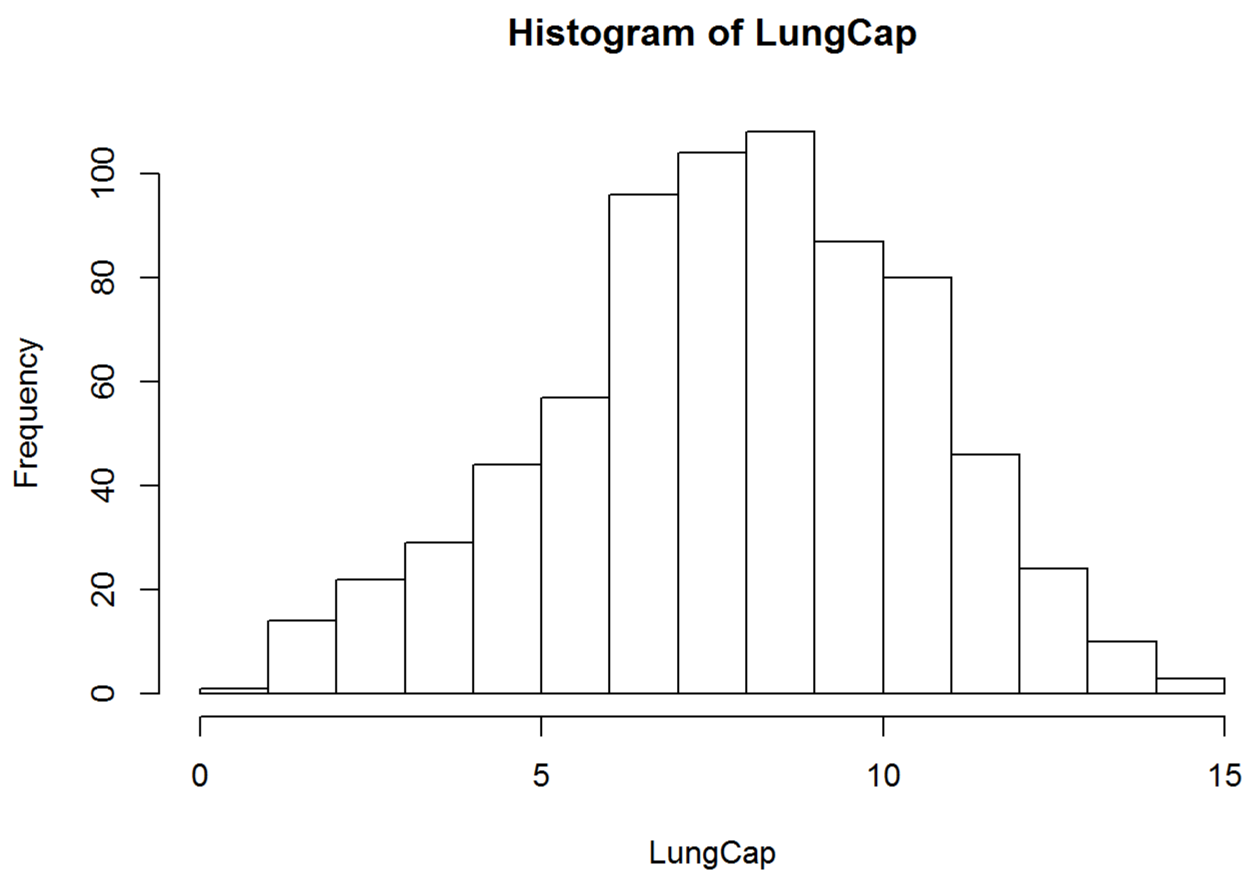
```
## [1] -0.2269314
```

Shapiro test is used to check normality.

```
shapiro.test(LungCap)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  LungCap
## W = 0.99305, p-value = 0.001886
```

```
hist(LungCap)
```

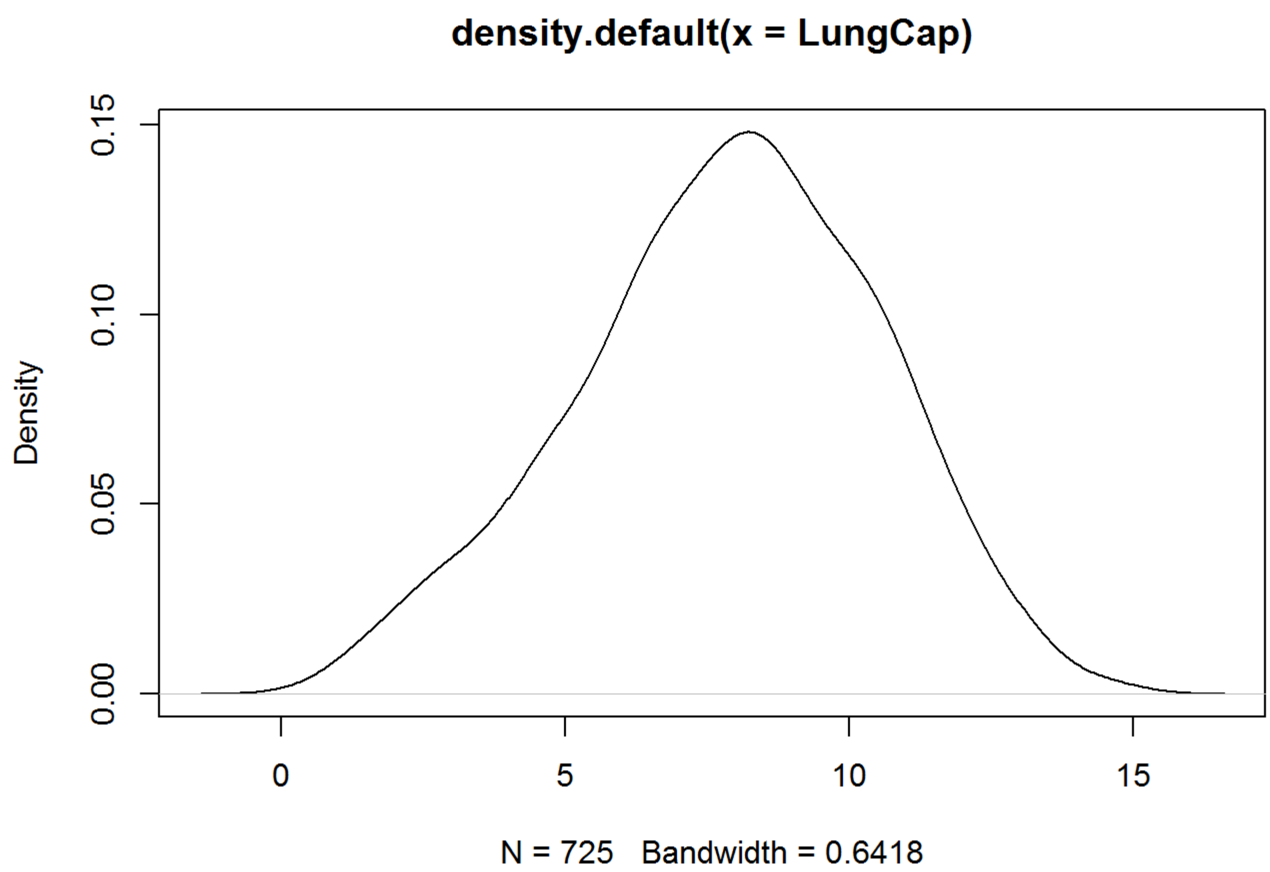


Calculate the Kurtosis

```
kurtosis(LungCap)
```

```
## [1] -0.3259122
```

```
plot(density(LungCap))
```



BIVARIATE ANALYSIS

Bivariate Analysis Deals with two sets of data. this paired data come from related sources or samples.

Correlation - *is a parametric measure of the linear association between 2 numeric variables.*

```
cor(LungCap,Height)
```

```
## [1] 0.9121873
```

```
cor(LungCap,Age)
```

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

Covariance - *measure of how much two random variables vary together.*

```
cov(LungCap,Age)
```

```
## [1] 8.738289
```

Calculating Corrlation matrix

```r
cor(LungCapData[,1:3])
```

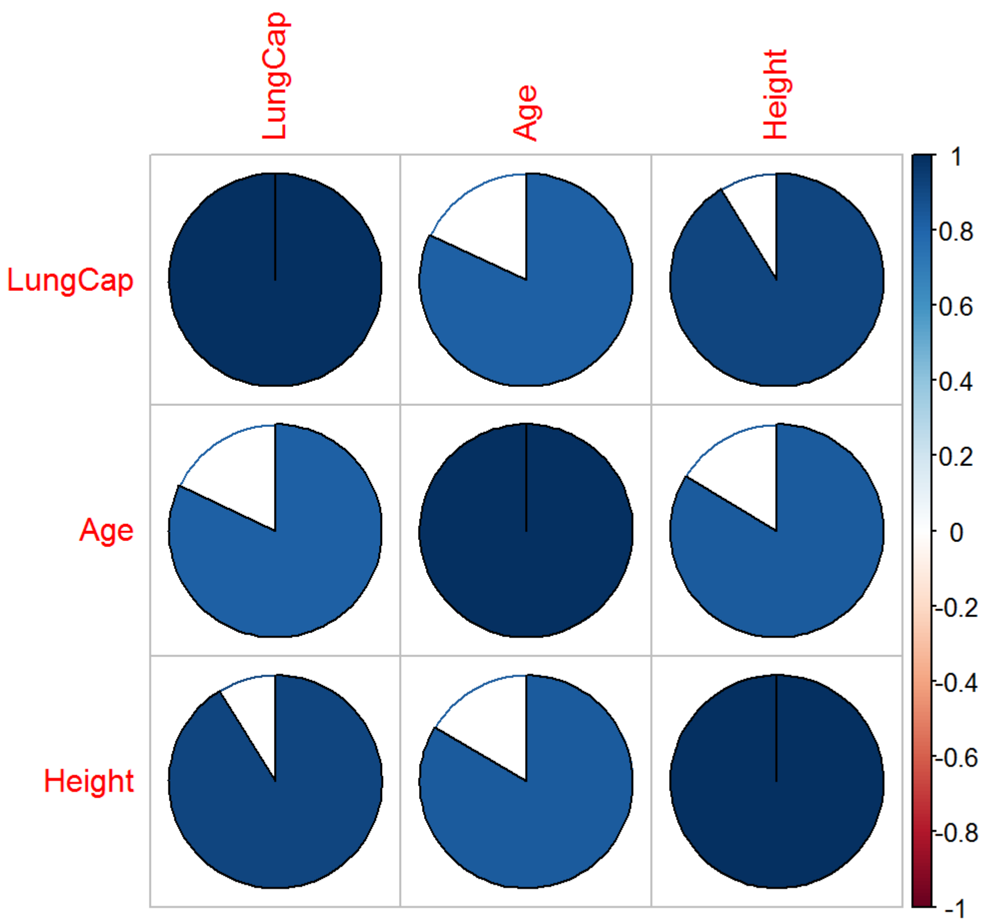
```
##           LungCap       Age    Height
## LungCap 1.0000000 0.8196749 0.9121873
## Age     0.8196749 1.0000000 0.8357368
## Height  0.9121873 0.8357368 1.0000000
```

corrlation matrix plot

```r
library(corrplot)
```

```
## corrplot 0.84 loaded
```

```r
corrplot(cor(LungCapData[,1:3]),method = 'pie')
```



pair plot

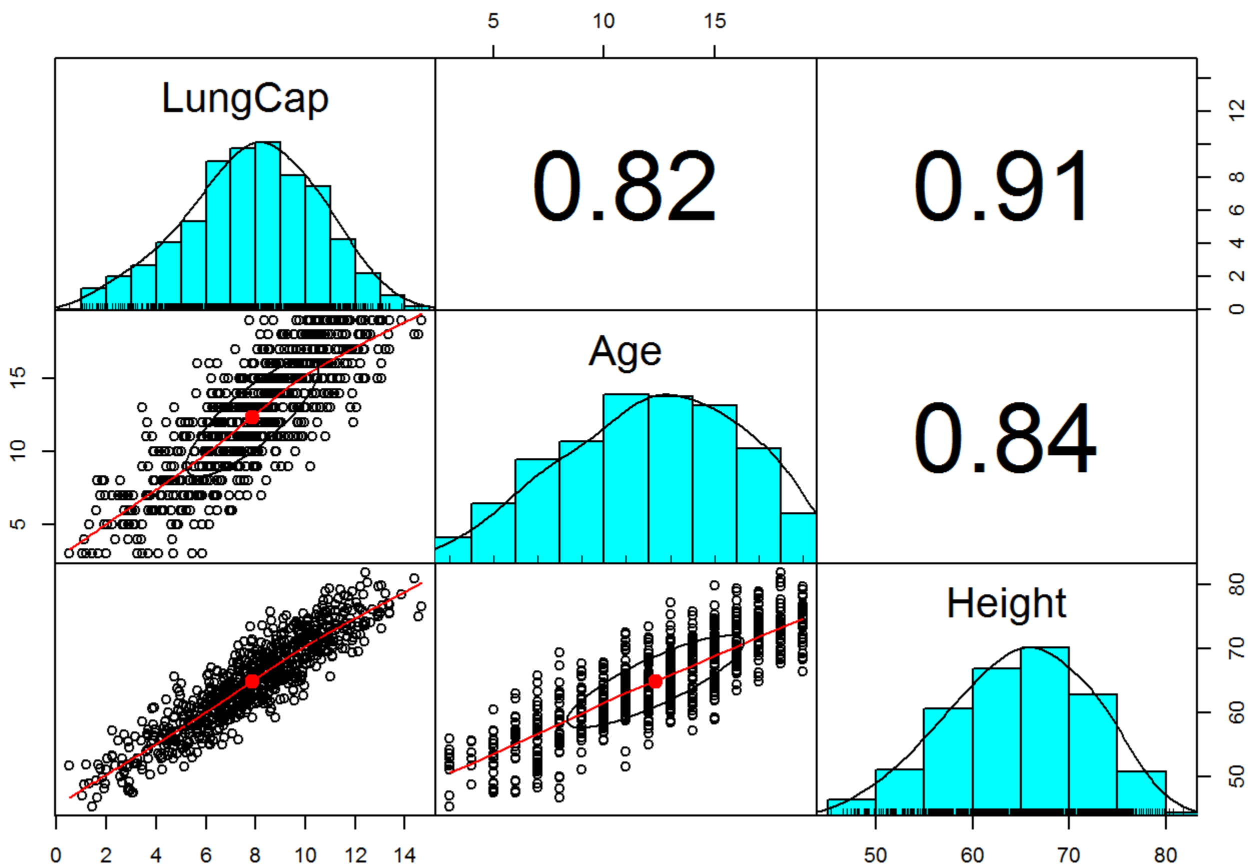
Pair plots are way to visualize relationship between each variables. It produces a matrix of relationship between each variable for an instant examination of our data.

```r
library(psych)
library(ggplot2)
```

```
##
## Attaching package: 'ggplot2'
```

```
## The following objects are masked from 'package:psych':
##
##     %+%, alpha
```

```
pairs.panels(LungCapData[c(1:3)],gap=0,bg=c("red","yellow","blue")[LungCapData$Smoke],pch=21)
```



Multivariate Analysis

You try to understand a sense of relationship of all variables with one another.

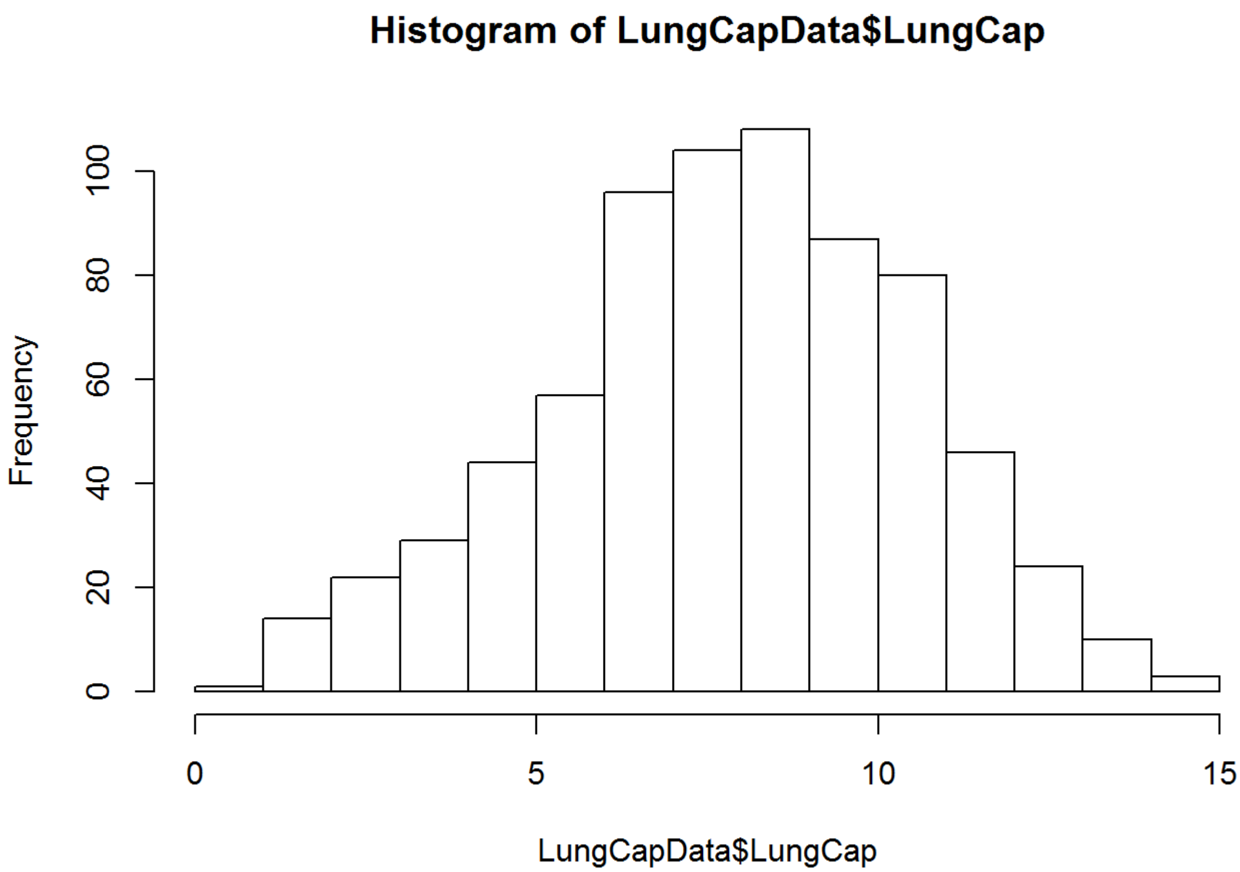
```
aggregate(data.frame("LungCap"=LungCapData$LungCap,"Age"=LungCapData$Age,"Height(cm)"=LungCapDat
a$Height), by=list(Smoke=LungCapData$Smoke), FUN=mean)
```

```
##   Smoke  LungCap      Age Height.cm.
## 1    no 7.770188 12.03549   64.39830
## 2   yes 8.645455 14.77922   68.52208
```

VISUALIZATION

Histogram -*is a quick way to get information about a sample distribution without detaild statistical Analysis.*

```
hist(LungCapData$LungCap)
```



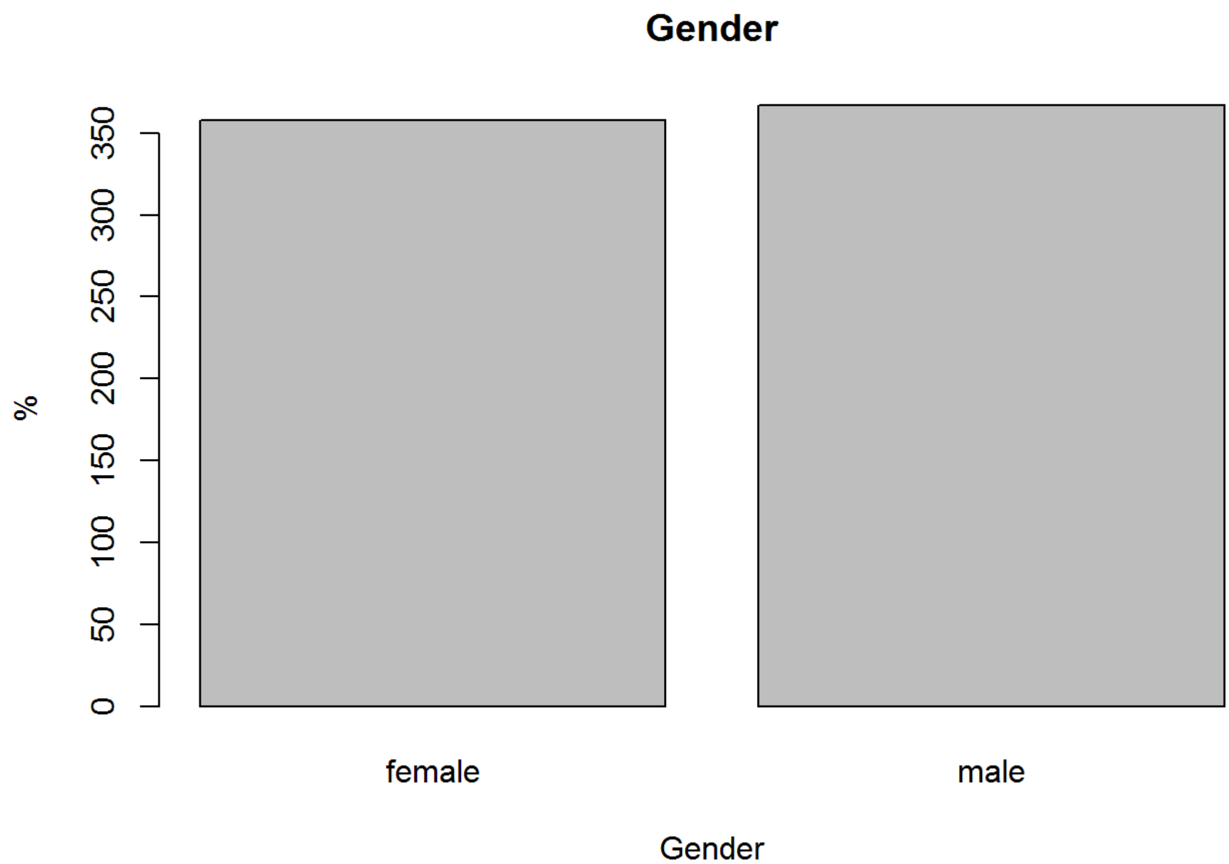
Barplot

Barplot is appropriate for summarizing the distribution of a categorical variables.

```
count <- table(Gender); count
```

```
## Gender
## female   male
##    358    367
```

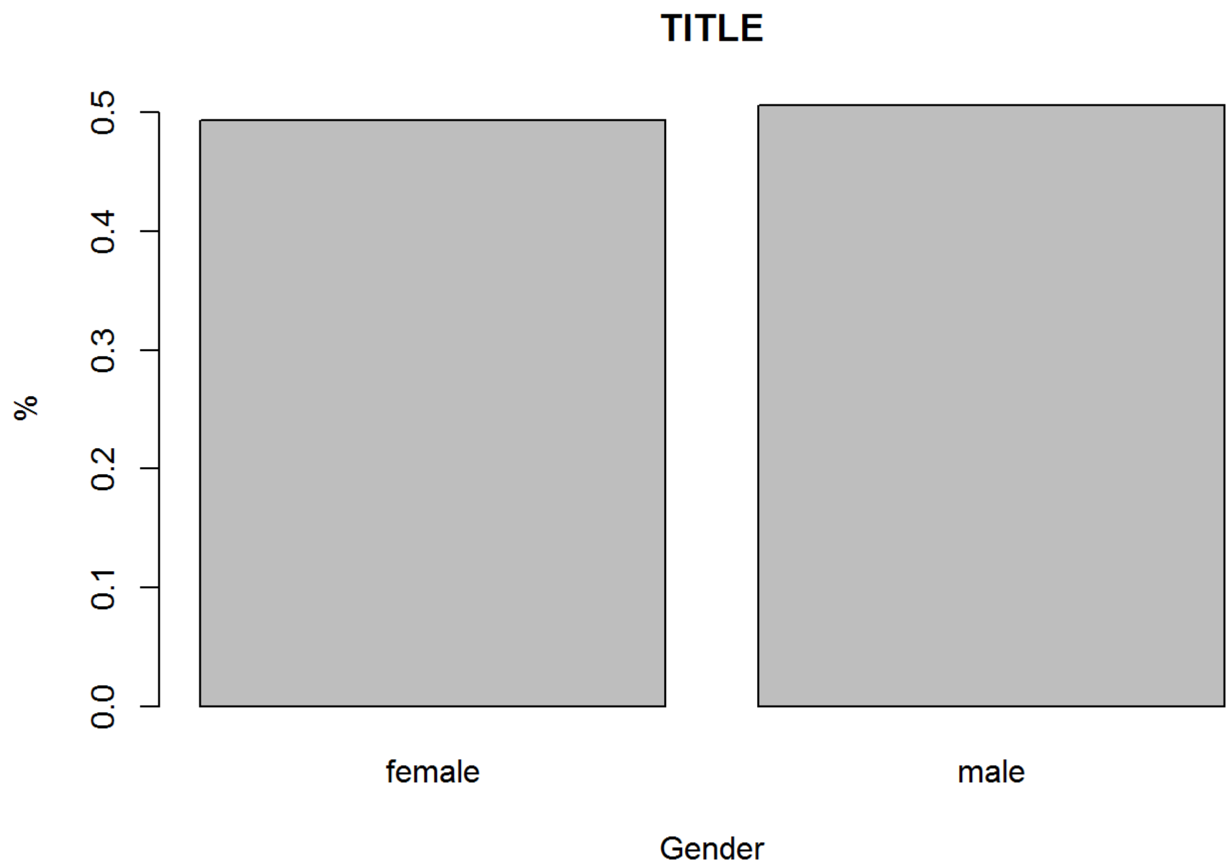
```
barplot(count,main = "Gender",xlab = "Gender",ylab = "%")
```




```
percentage <- table(Gender)/length(Gender)
```

Adding Titles to the plot

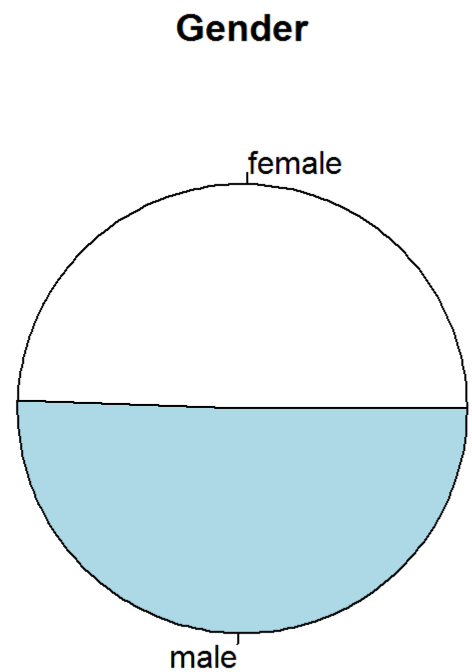
```
barplot(percentage,main = "TITLE",xlab = "Gender",ylab = "%")
```



Pie Charts

Pie chart is appropriate for summarizing the distribution of a categorical variables.

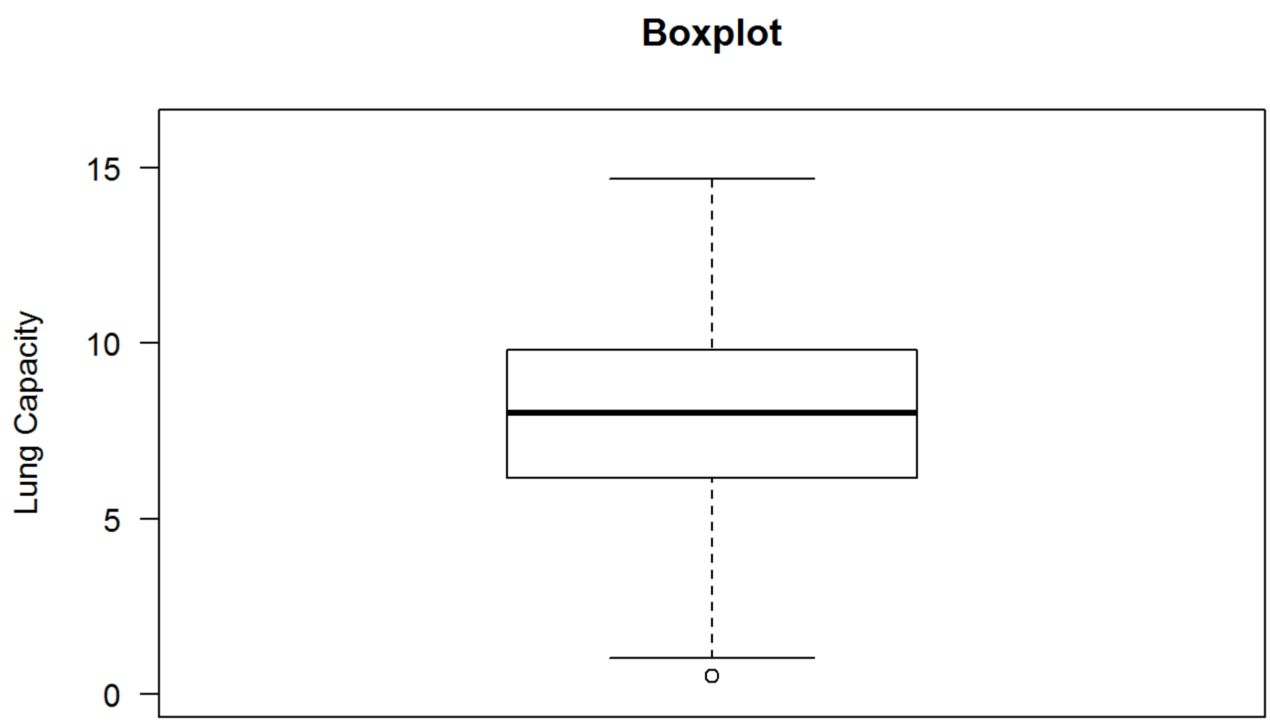
```
pie(count, main = "Gender")
```



Boxplot

Boxplot is appropriate for summarizing the distribution of a numerical variables.

```
boxplot(LungCap,main='Boxplot',ylab='Lung Capacity',ylim=c(0,16),las=1)
```

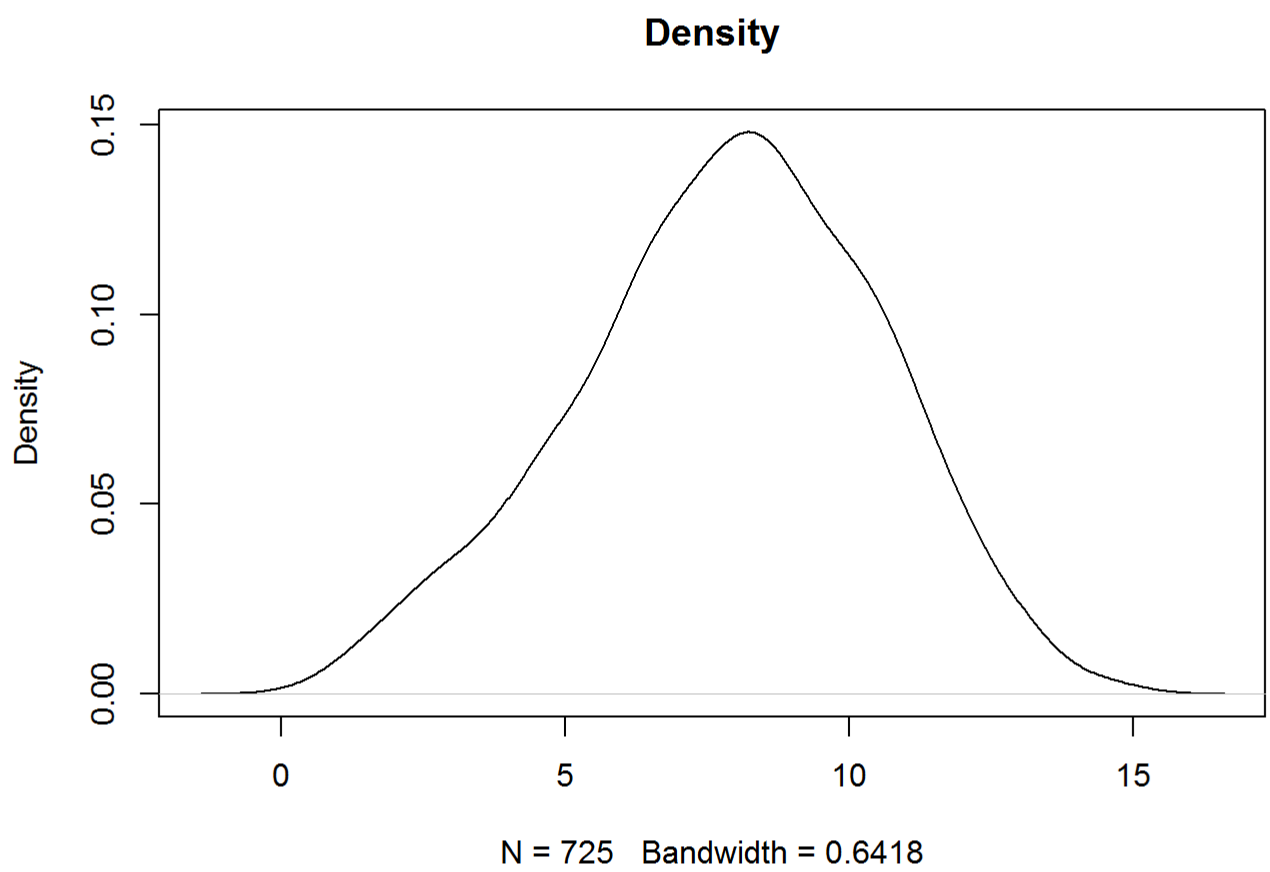


Density plot

Density plot is appropriate for summarizing the distribution of a numerical variables.

```
d <- density(LungCap)
```

```
plot(d, main = 'Density')
```



Stratified Boxplot

is useful for examining the relationship between a categorical variable and numerica variable with strata or groupe.

```
AgeGroups <- cut(Age,breaks = c(0,13,15,17,25),labels = c("<13","14/15","15/17","18"))
```

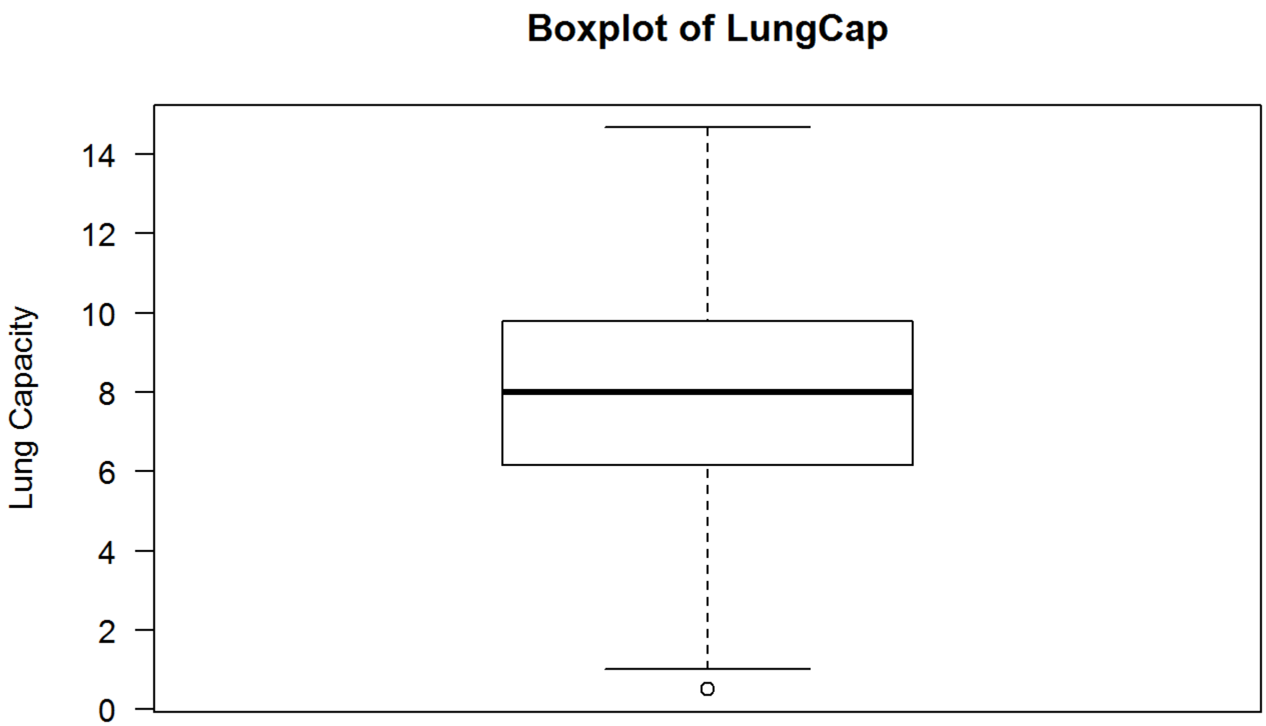
```
Age[1:5]
```

```
## [1]  6 18 16 14  5
```

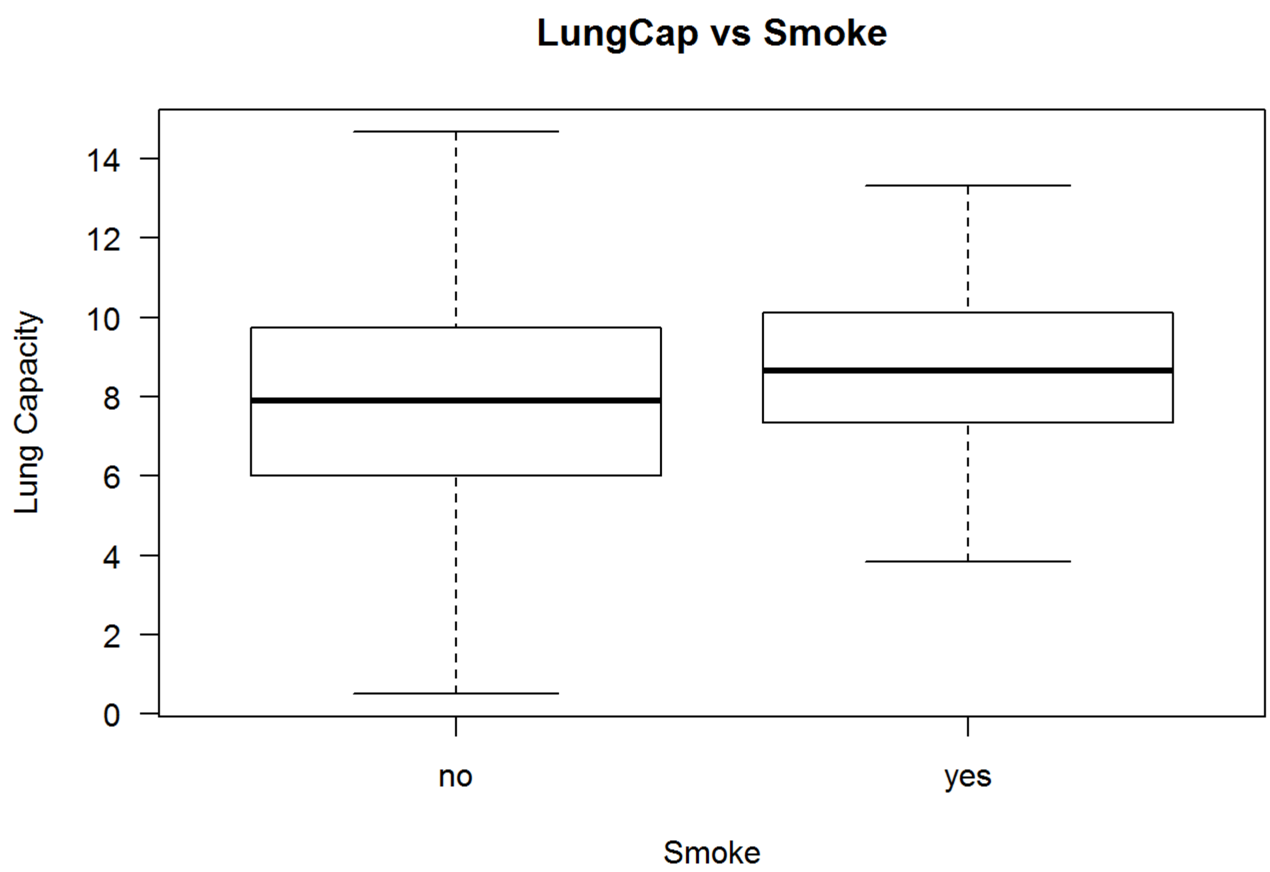
```
AgeGroups[1:5]
```

```
## [1] <13   18    15/17 14/15 <13
## Levels: <13 14/15 15/17 18
```

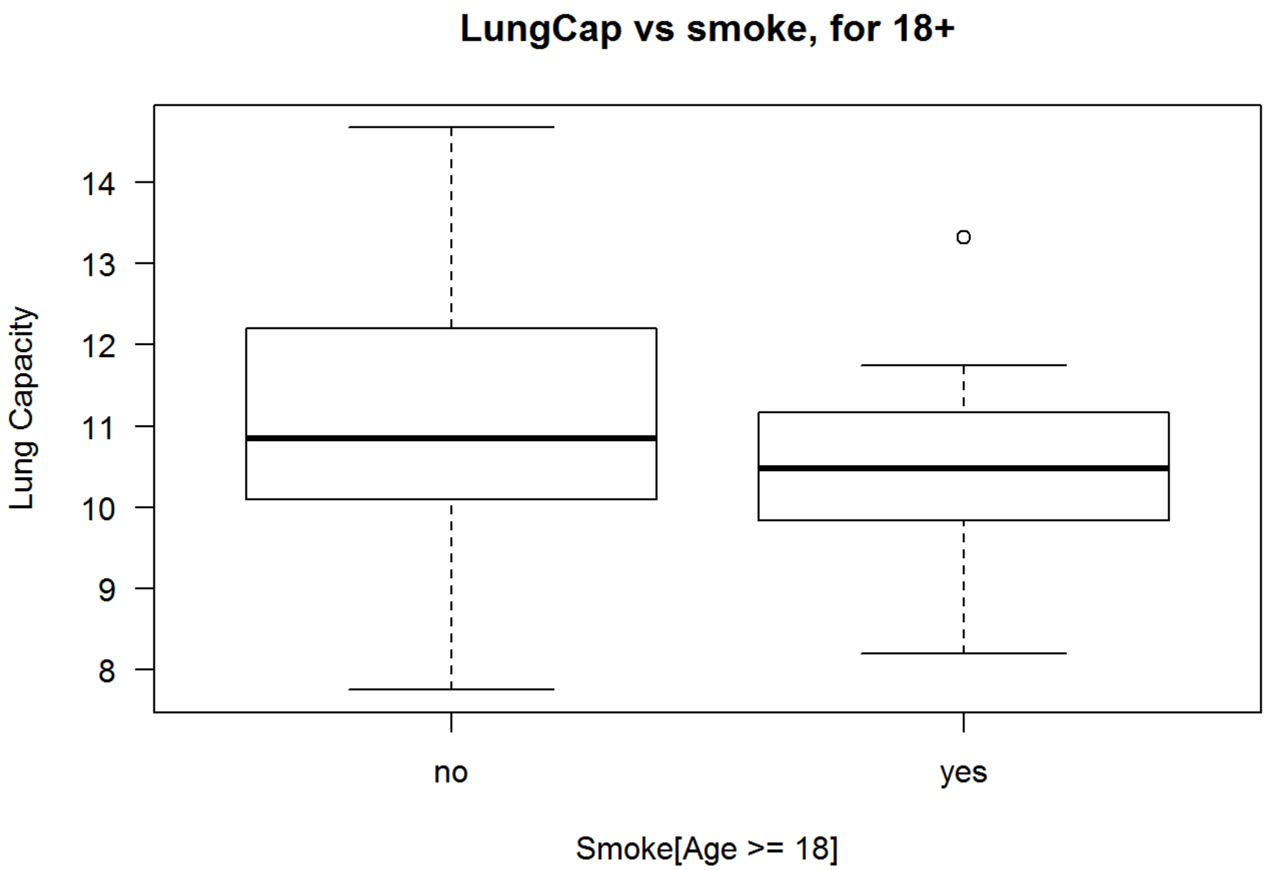
```
boxplot(LungCap,ylab='Lung Capacity',main="Boxplot of LungCap",las = 1)
```



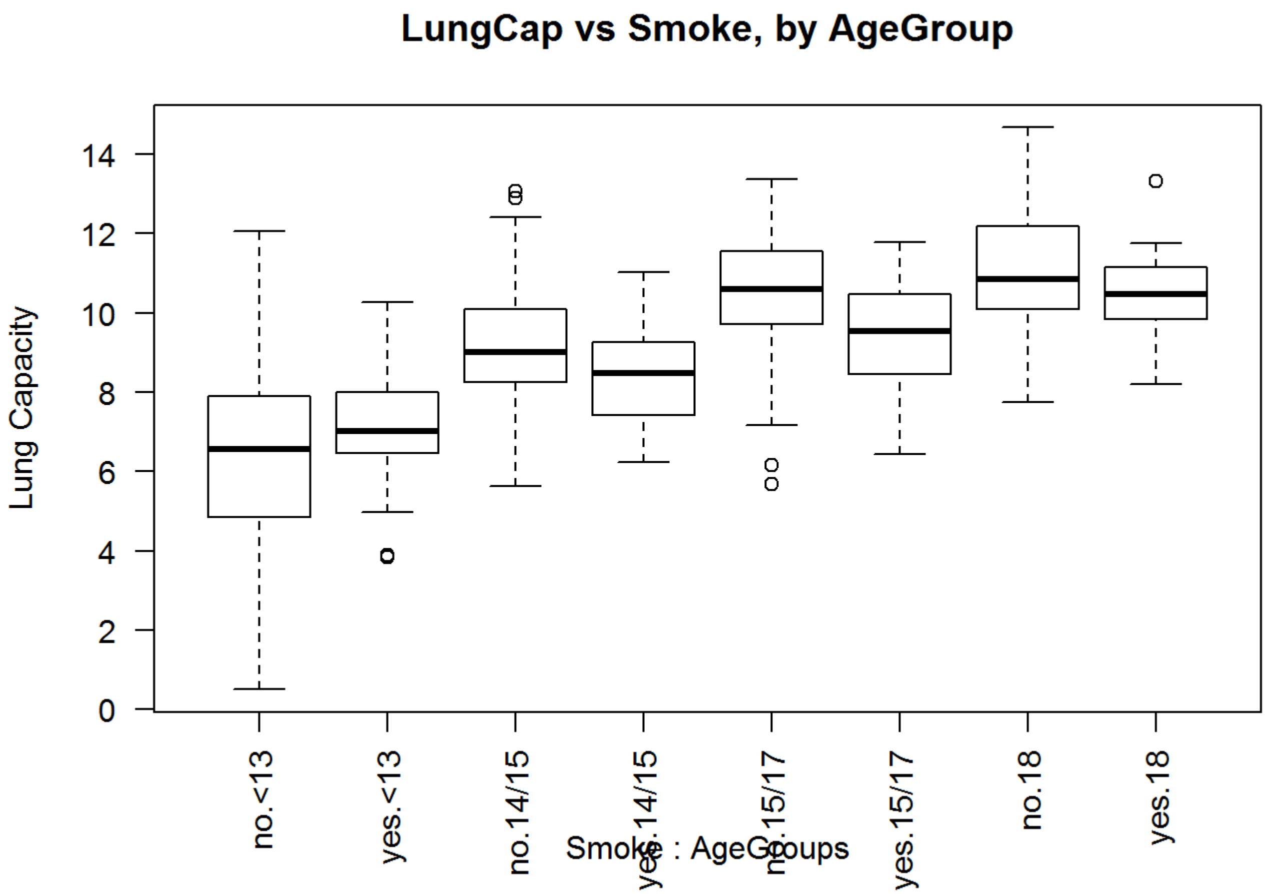

```
boxplot(LungCap ~ Smoke,ylab = "Lung Capacity",main="LungCap vs Smoke",las = 1)
```




```
boxplot(LungCap[Age >= 18] ~ Smoke[Age >= 18],ylab = "Lung Capacity",main = "LungCap vs smoke, f
or 18+",las=1)
```




```
boxplot(LungCap ~ Smoke * AgeGroups,ylab = "Lung Capacity", main = "LungCap vs Smoke, by AgeGrou
p",las = 2)
```



Steam and Leaf Plot

is appropriate for summarizing the distribution of a numberic variables and are most appropriate for smaller datasets.

```
femaleLungCap <- LungCap[Gender == "female"]
```

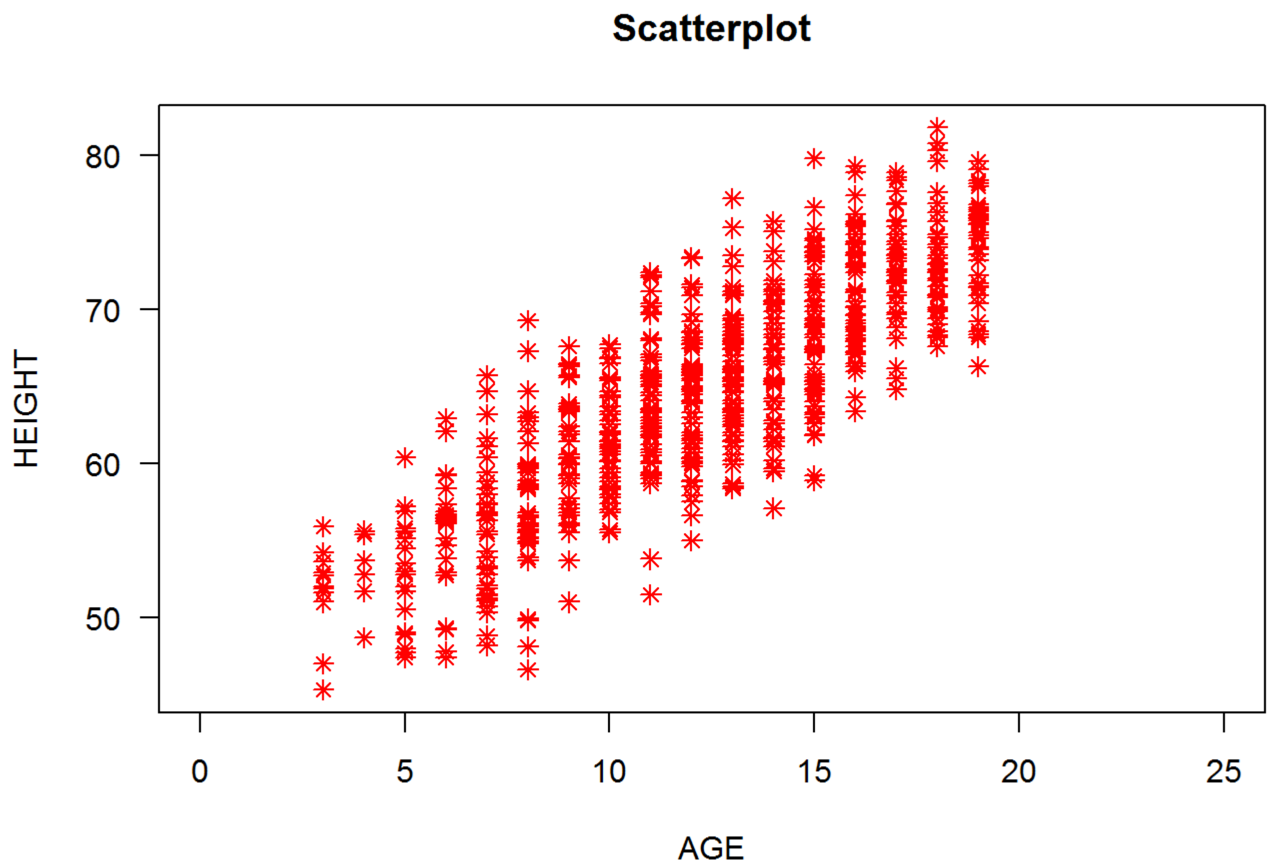
```
stem(femaleLungCap,scale = 2)
```

```
##
##   The decimal point is at the |
##
##    0 | 5
##    1 | 013
##    1 | 5689
##    2 | 00334
##    2 | 56777789999
##    3 | 01224
##    3 | 57788999999
##    4 | 012333344
##    4 | 555556666677777899
##    5 | 00001222223344
##    5 | 66666777778999
##    6 | 0001111112222222223334
##    6 | 5555556666667777777788888999999
##    7 | 00012333444444444
##    7 | 5555666667778888888999999
##    8 | 000000001111122222333333444444
##    8 | 55555666666666677777788888888899
##    9 | 0000000011122223333344
##    9 | 555566667777888889999999
##   10 | 00001111122233444
##   10 | 5555666777778899
##   11 | 00111223
##   11 | 556678888
##   12 | 12224
##   12 | 79
##   13 | 1
```

Scatterplot

is appropriate for examining the relationship between 2 numerica variable

```
plot(Age,Height,main = 'Scatterplot',xlab='AGE',ylab = 'HEIGHT',las=1,xlim = c(0,25),pch=8,col=2
)
```



INFERENTIAL STATISTICS

Hypothesis Testing *Parametric Test*

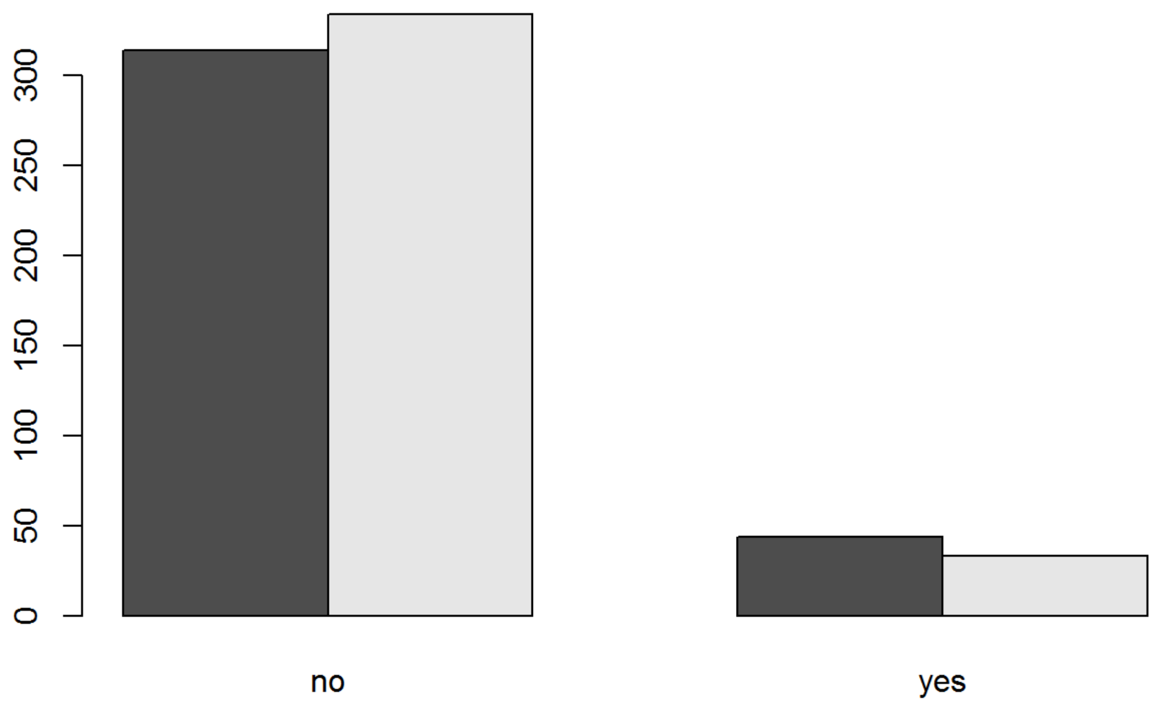
Z-test one-sided

```
# H0 : Male smoker is greater than female smoker.
# CI : 95 %

t <- table(Gender,Smoke);t
```

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

Make a Barplot to examine the distribution of data

```
barplot(t,beside = TRUE)
```




```
prop.test(t,correct = FALSE,alternative = 'greater')
```

```
##
##  2-sample test for equality of proportions without continuity
##  correction
##
## data:  t
## X-squared = 2.0773, df = 1, p-value = 0.9252
## alternative hypothesis: greater
## 95 percent confidence interval:
##  -0.07064256  1.00000000
## sample estimates:
##    prop 1    prop 2
## 0.8770950 0.9100817
```

Z-test two-sided

```
# H0 : female smoker is equal to male smoker
# CI : 95%

prop.test(t,correct = FALSE)
```

```
##
##  2-sample test for equality of proportions without continuity
##  correction
##
## data:  t
## X-squared = 2.0773, df = 1, p-value = 0.1495
## alternative hypothesis: two.sided
## 95 percent confidence interval:
##  -0.07785641  0.01188287
## sample estimates:
##    prop 1    prop 2
## 0.8770950 0.9100817
```

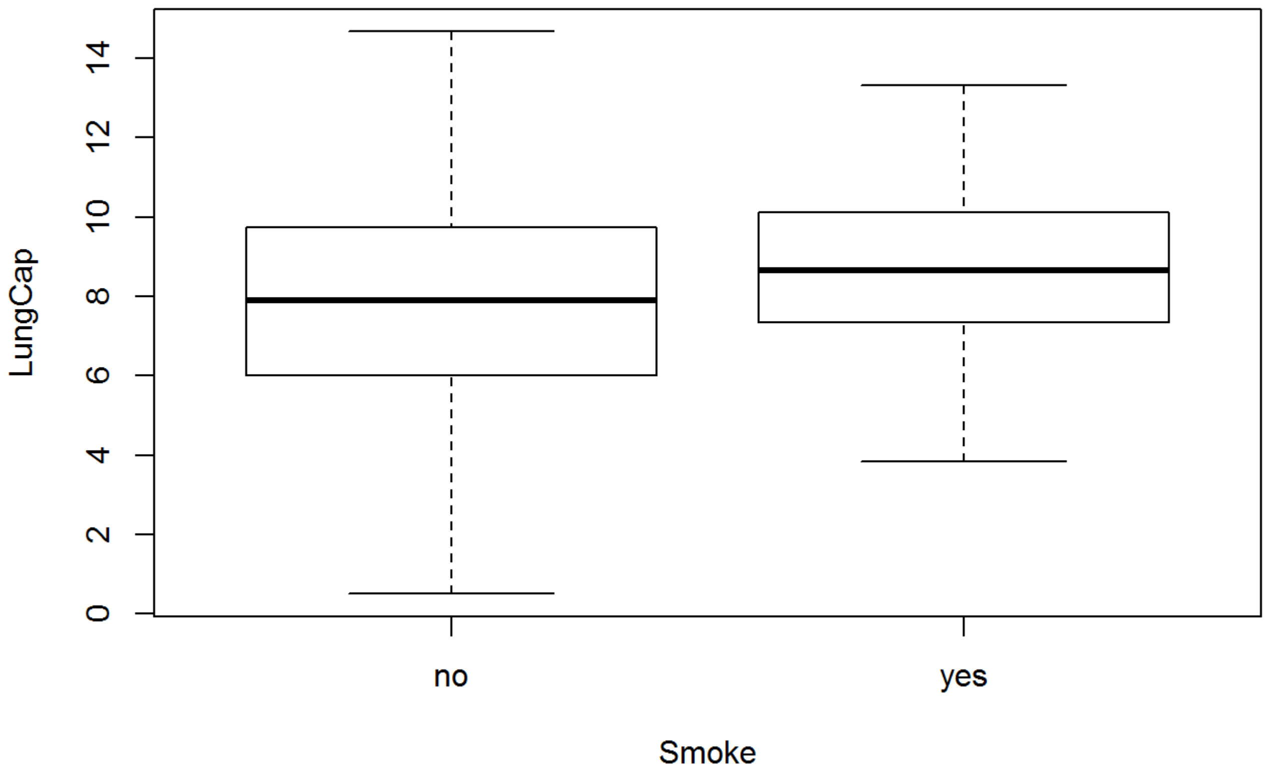
T-test one-side

```
# H0 : mu < 8
# one sided 95% cI for mu

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

```
##
##  One Sample t-test
##
## data:  LungCap
## t = -1.3842, df = 724, p-value = 0.08336
## alternative hypothesis: true mean is less than 8
## 95 percent confidence interval:
##      -Inf 8.025974
## sample estimates:
## mean of x
##  7.863148
```

t-test two-side - is parametric methods appropriate for examining the difference in means for 2 population.

```
boxplot(LungCap ~ Smoke)
```

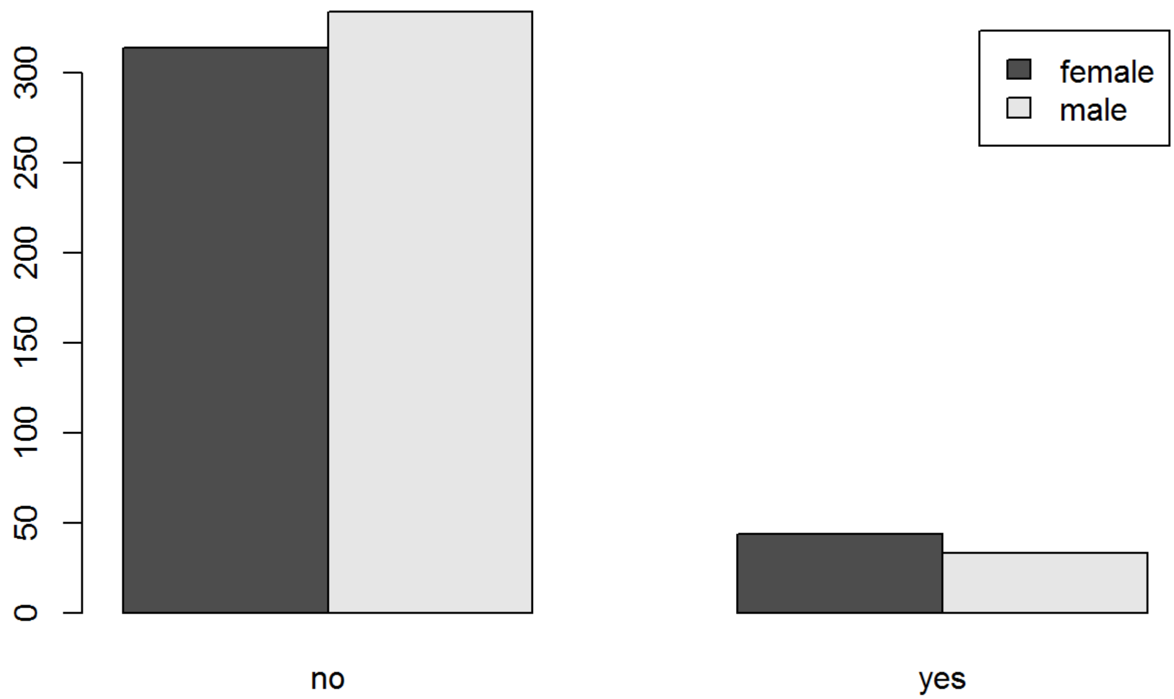



```
# Ho : mean lung cap of smokers = of non-smokers
# assume non-equal variances

t.test(LungCap ~ Smoke,mu=0,alt='two.side',conf=0.95,var.eq=F,paired =F)
```

```
##
##  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
```

Chi-square - Appropriate for testing independence between two categorical variables.

```
# For chi-square test produce a contigency table

TAB <- table(Gender,Smoke)

# produce a barplot to check the distribution.

barplot(TAB,beside = T,legend=T)
```



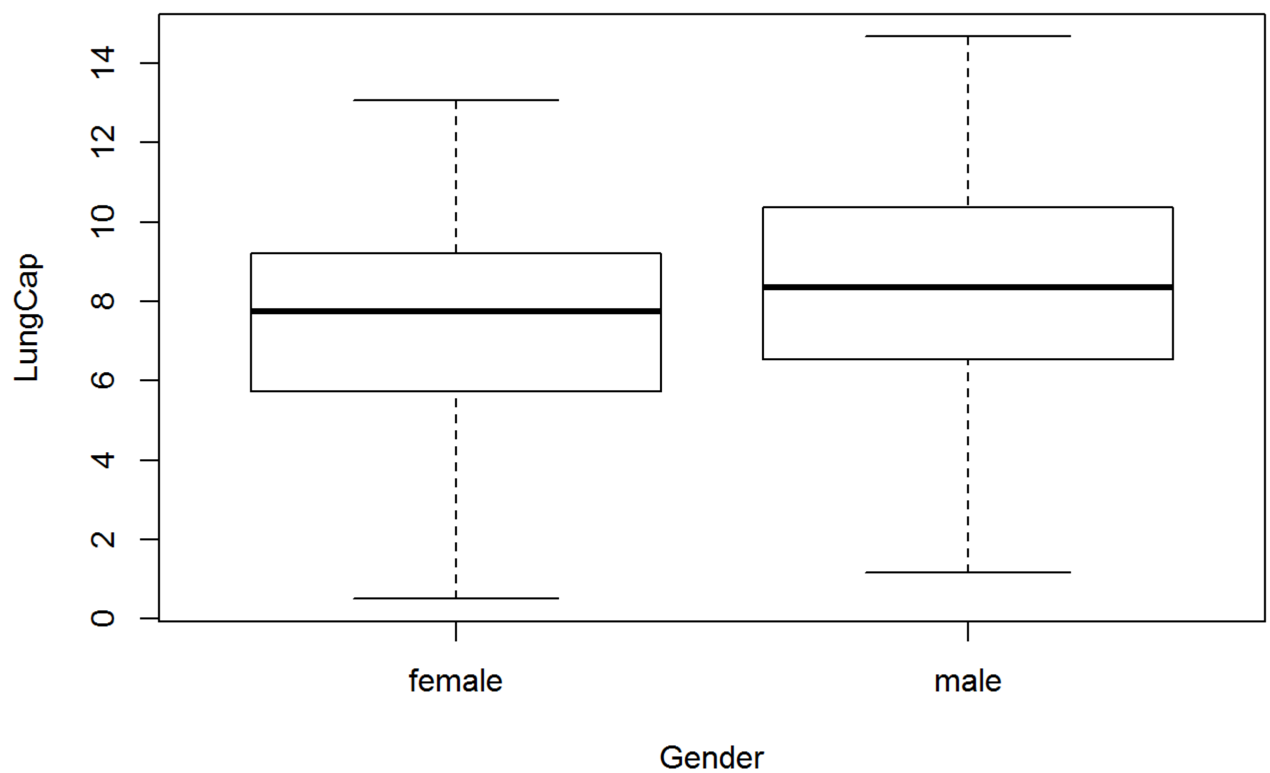

```
CHI <- chisq.test(TAB,correct = T)
CHI
```

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

F-Test

ANOVA - appropriate for comparing the means for 2 or more independent populations.

```
# produce a box plot to check the distribution of Lung cap variable and gender variable.

boxplot(LungCap ~ Gender)
```



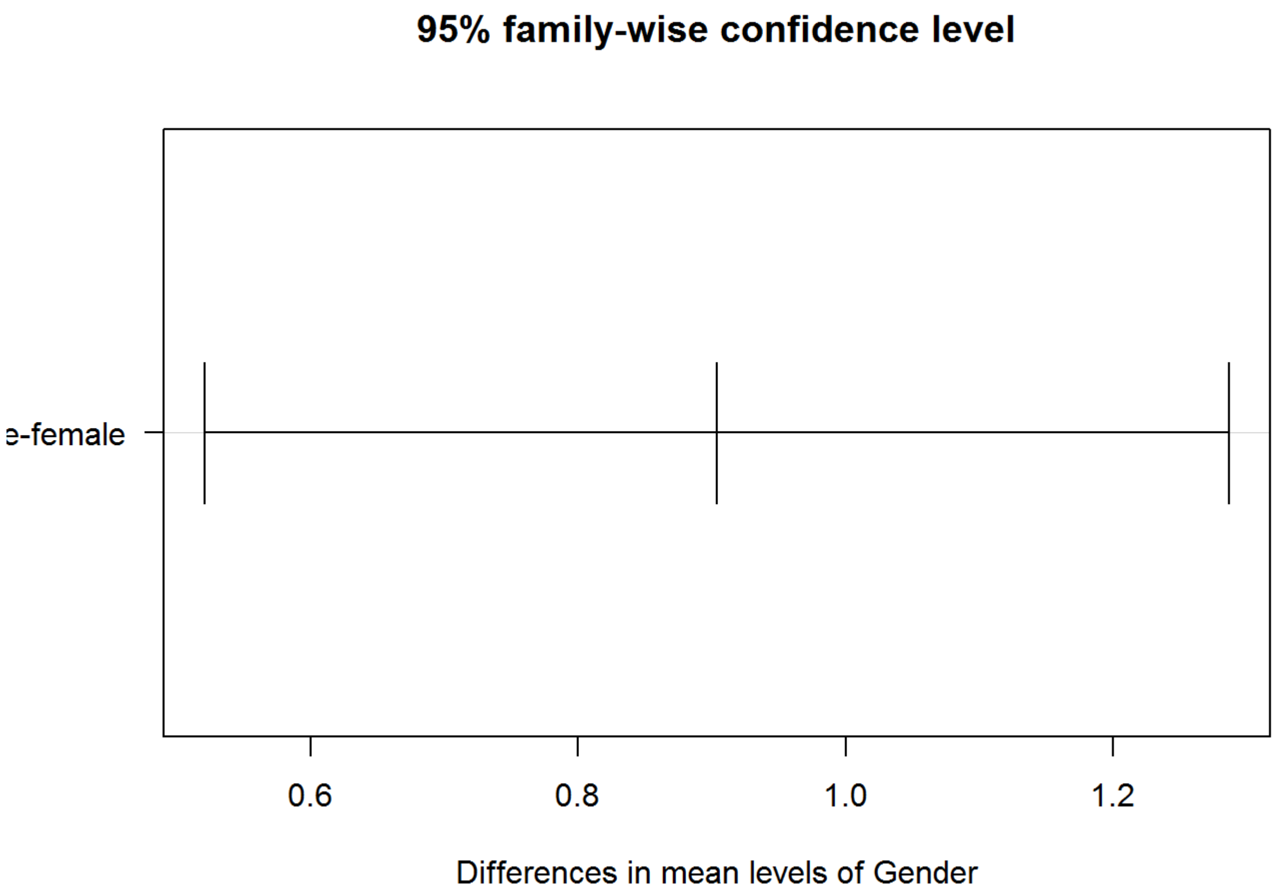

```r
# H0 : Mean Lungcap  is the same for all Genders

ANOVA1 <-  aov(LungCap ~ Gender)
summary(ANOVA1)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)    
## Gender        1    148  147.96   21.47 4.26e-06 ***
## Residuals   723   4983    6.89                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
TukeyHSD(ANOVA1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
## 
## Fit: aov(formula = LungCap ~ Gender)
## 
## $Gender
##                  diff       lwr      upr   p adj
## male-female 0.9035866 0.5207397 1.286434 4.3e-06
```

```r
plot(TukeyHSD(ANOVA1),las=1)
```



Non-Parametric Test

Wilcoxon Signed Rank Test - *Appropriate for examining the median Difference in observations for 2 populations.*

Mann-Whitney U Test A.K.A Wilcoxon Rank sum test - *appropriate for examining the difference in Medians for 2 independent populations*

```
# Ho : Median Lung Capacity of Smokers  = that of non smokers
# two sided test

wilcox.test(LungCap ~ Smoke,mu=0,alt='two.sided',conf.int=T,conf.level = 0.95,paired=F,exact=F,c
orrect =T)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  LungCap by Smoke
## W = 20128, p-value = 0.005538
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -1.3999731 -0.2499419
## sample estimates:
## difference in location
##             -0.8000564
```

Kruskal Wallis Test - *equivalent to one-way Analysis of Variance*

```
kruskal.test(LungCap ~ Gender)
```

```
## 
##  Kruskal-Wallis rank sum test
## 
## data:  LungCap by Gender
## Kruskal-Wallis chi-squared = 18.325, df = 1, p-value = 1.862e-05
```

Fisher's Exact test* - *alternative to the chi-square test, it is used when the assumptions of chi-square test not met.we may consider using Fisher's Exact Test*

```
fisher.test(TAB,conf.int = T,conf.level = 0.99)
```

```
## 
##  Fisher's Exact Test for Count Data
## 
## data:  TAB
## p-value = 0.1845
## alternative hypothesis: true odds ratio is not equal to 1
## 99 percent confidence interval:
##  0.3625381 1.3521266
## sample estimates:
## odds ratio 
##  0.7054345
```

PROBABILITY DISTRIBUTION

Binomial Distribution - *X is Binomially Distributed with n = 20 trials and p = 1/6 prob of success.*

```
# In R dbinom command is used to find values for the probability density function of x, f(x)
# suppose 80%  adults are smoker and out of 10 are caesarean what
# is the probability that they are male exactly seven
# observations is n = 10
# success or events of male is x = 7
# p=0.8

dbinom(x=7,size = 10,prob = 0.8)
```

```
## [1] 0.2013266
```

```
# Probability of having exactly 7 males is 20.13%
```

Possion Distribution - *is the probability distribution of independent occurances in an interval.*

```
# support there are 12 adults smoking per minute on an average,
# find the probability of having seventeen or more adults smoking in a
# particular minutes

# probability of haveing sixteen or less adults smoking in a particular
# minute is given by the fuction ppois.

ppois(16,lambda = 12) # lower tail
```

```
## [1] 0.898709
```

```
# Here, the probability of having seventeen or more adults smoking in a # minute is in the upper tail of the probability density function

ppois(16,lambda = 12,lower = FALSE) # UPPER TAIL
```

```
## [1] 0.101291
```

```
# if there are twelve adults smoking per minute on an average, the probability of having seventeen ore more adults smoking in a particuler minute is 10.1%
```

Normal Distribution

```
# the mean of Lung capacity is 7, and standard deviation is 2.66.
# What is the percentage of Lung capacity of female which has 9 or more lung cap.

pnorm(9,mean = 7,sd=2.66, lower.tail = FALSE)
```

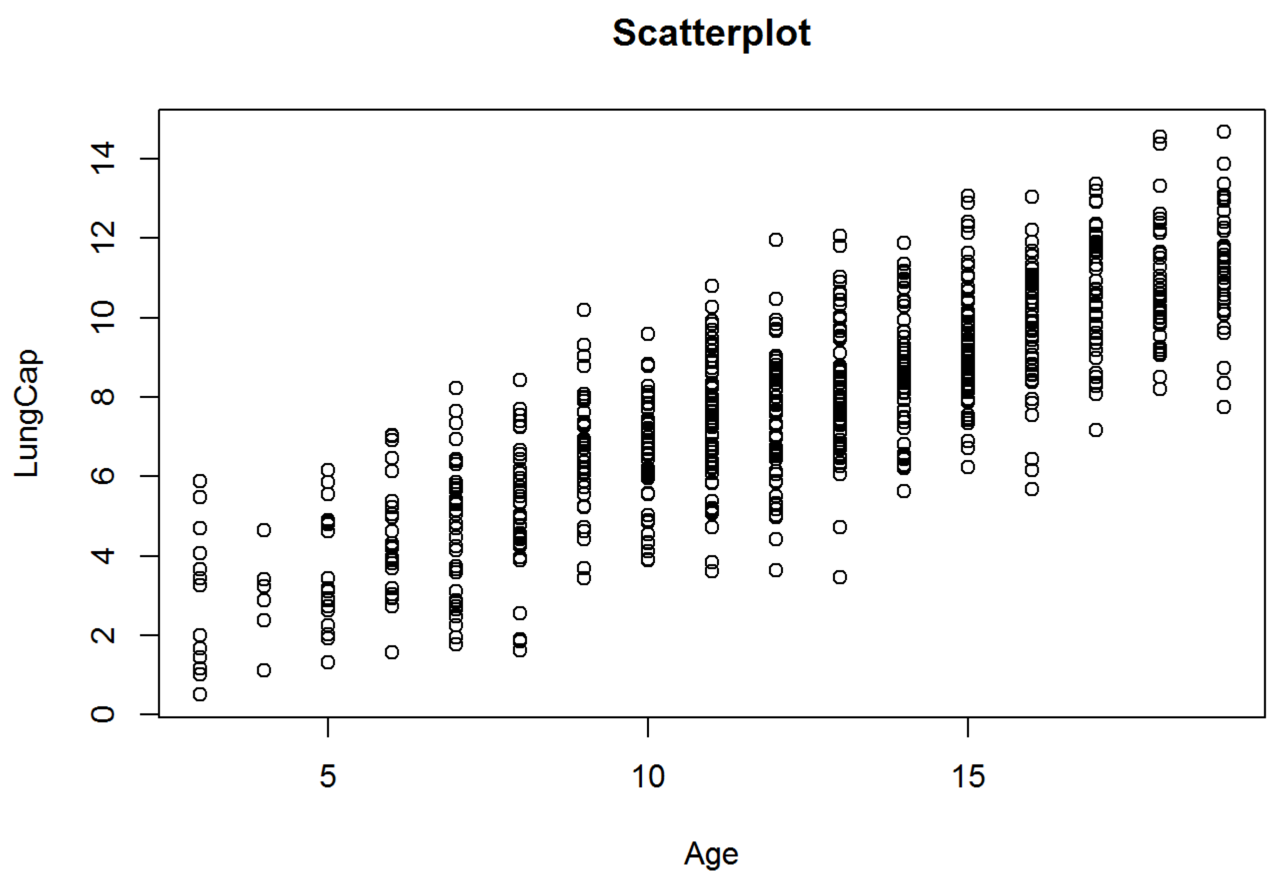
```
## [1] 0.2260617
```

```
# The percentage of female having Lung cap 9 or more is 22.6%
```

MODELLING

Simple Linear Regression - *useful for examining or modelling the relationship between 2 numeric variables.*

```
# Model the relationship between Age and Lung Capacity

plot(Age,LungCap,main = "Scatterplot")
```




```
# Calculate the correlation

cor(Age,LungCap)
```

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

```
# Fit a Linear Model

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

```r
# Model Evaluation
# Function that returns Root Mean Squared Error

rmse <- function(error)
{
    sqrt(mean(error^2))
}

# Function that returns Mean Absolute Error

mae <- function(error)
{
    mean(abs(error))
}
```

```r
rmse(mod$residuals)/100
```

```
## [1] 0.01523824
```

```r
mae(mod$residuals)/100
```

```
## [1] 0.01218942
```

```r
summary(mod)
```

```
##
## 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
```

```r
# Predict the Model

predict(mod, data.frame(Age = 16))
```

```
##        1
## 9.864432
```

Multiple Linear Regression -

useful for modelling the relationship between more than 2 numeric variables.

```
# Fit model

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

```
# Summary

summary(model1)
```

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

```
# Calculate Pearson's correlation between Age and Height

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

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

```
# ask for confidence intervals for the model coefficients

confint(model1,conf.level=0.95)
```

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

MODEL DIAGNOSTIC

Check Outliers

```
library(car)
```

```
## Loading required package: carData
```

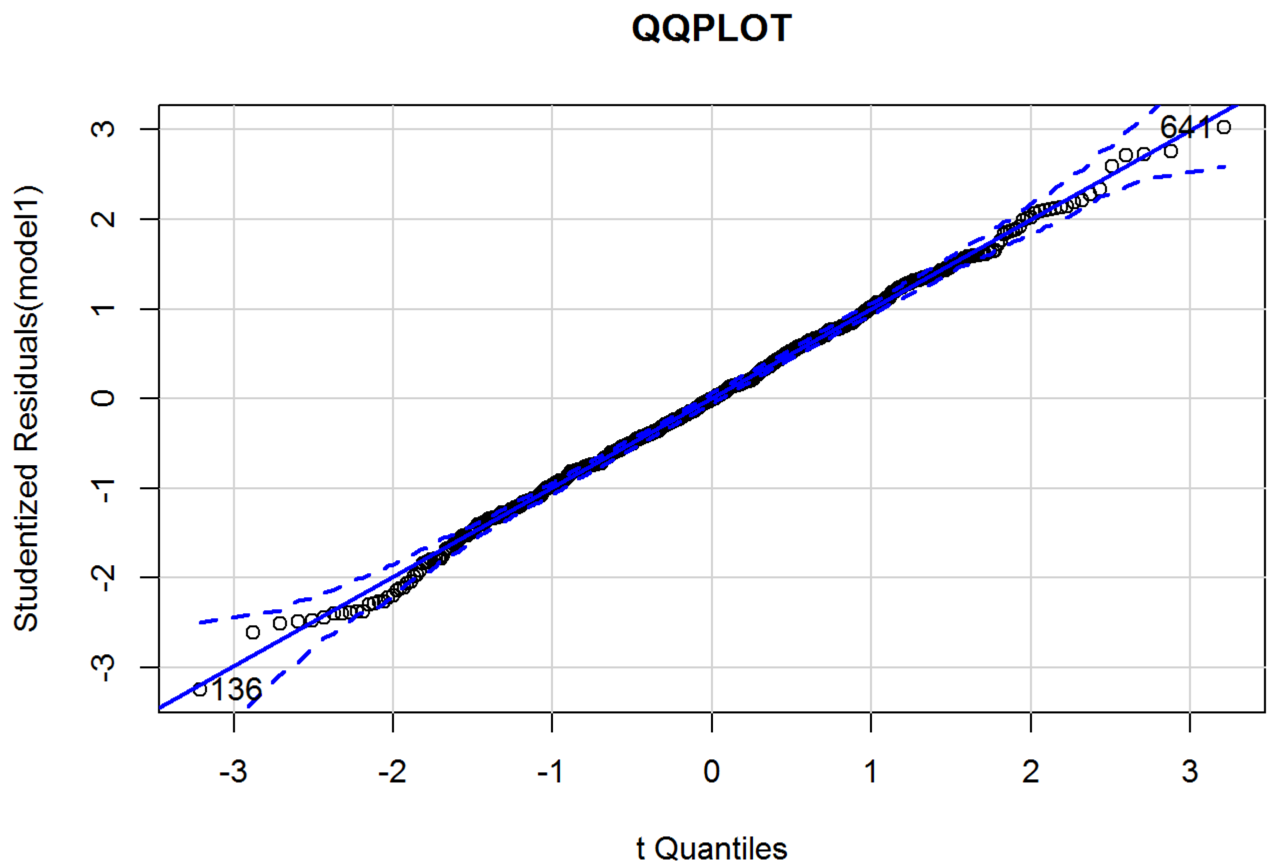
```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:psych':
##
##     logit
```

```
outlierTest(model1)
```

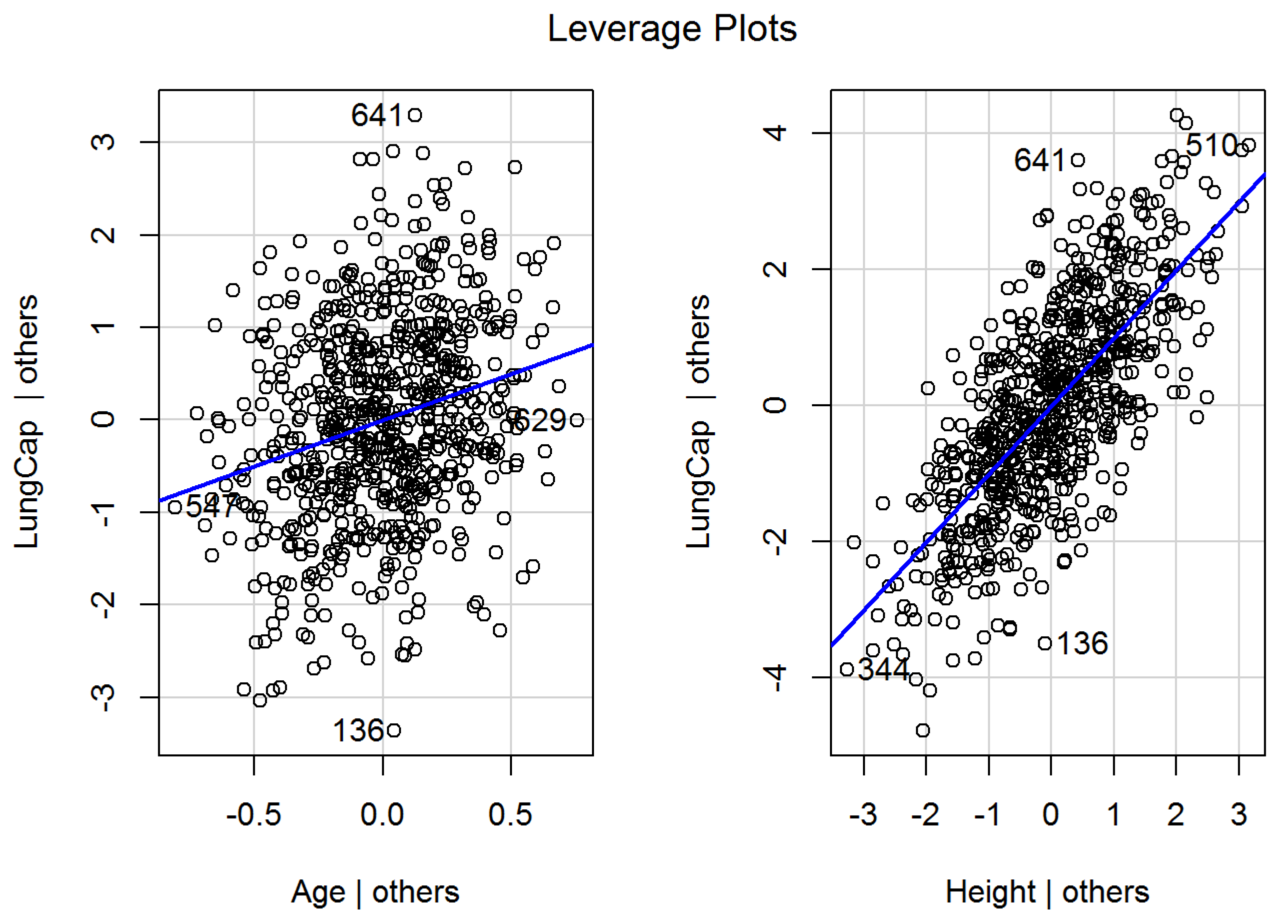
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 136 -3.250022          0.0012075      0.87547
```

```
qqPlot(model1,main="QQPLOT")
```




```
## [1] 136 641
```

```
leveragePlots(model1)
```



Examine the multicollinarity problem in the model

```
vif(model1)  # Variable value should be less than 10 then we can conclude there is no Multicolli
narity issue.
```

```
##      Age   Height
## 3.316266 3.316266
```

Checking the Heteroscadasticity problem in the model

```
ncvTest(model1)  # P-value should be less than 0.05 then we can conclude there is no heteroscada
sticity
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 1.347551, Df = 1, p = 0.24571
```

```
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

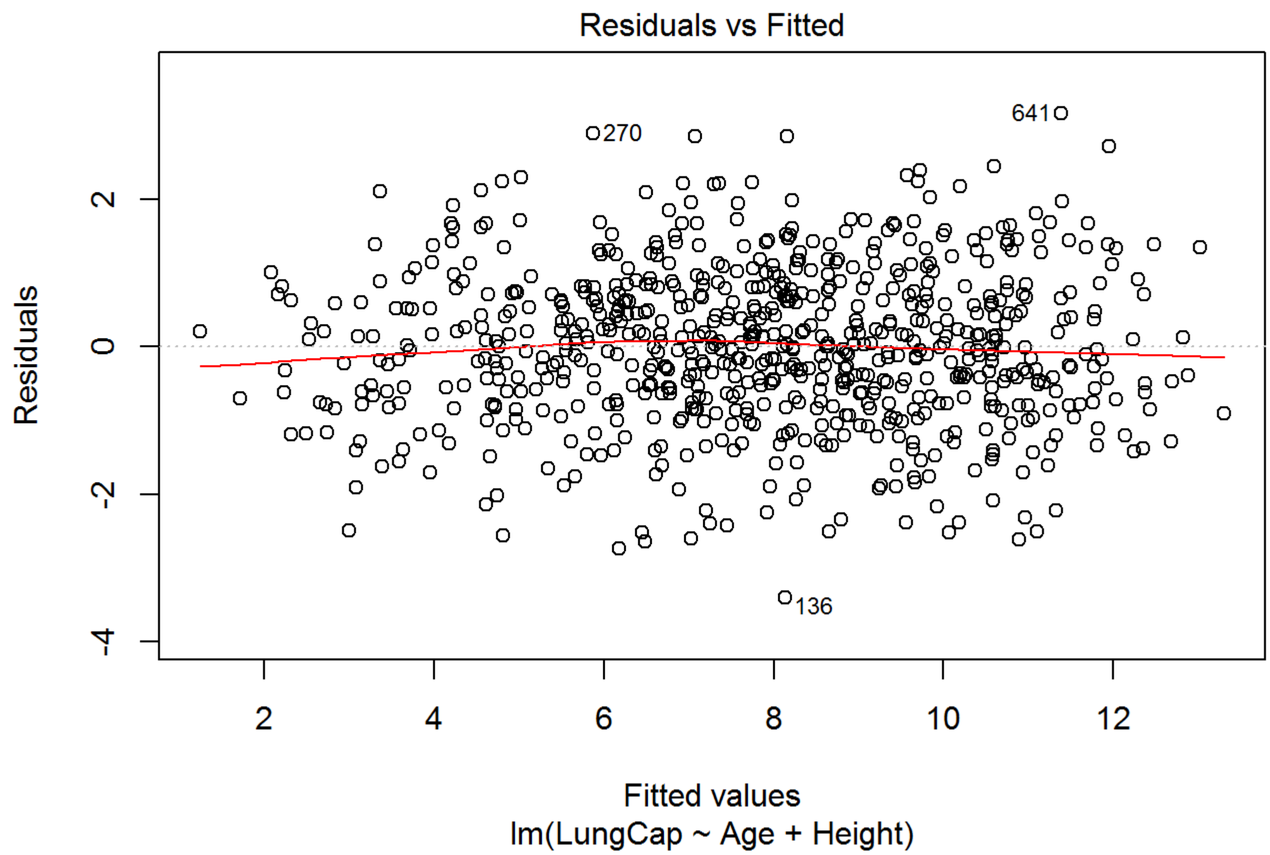
```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

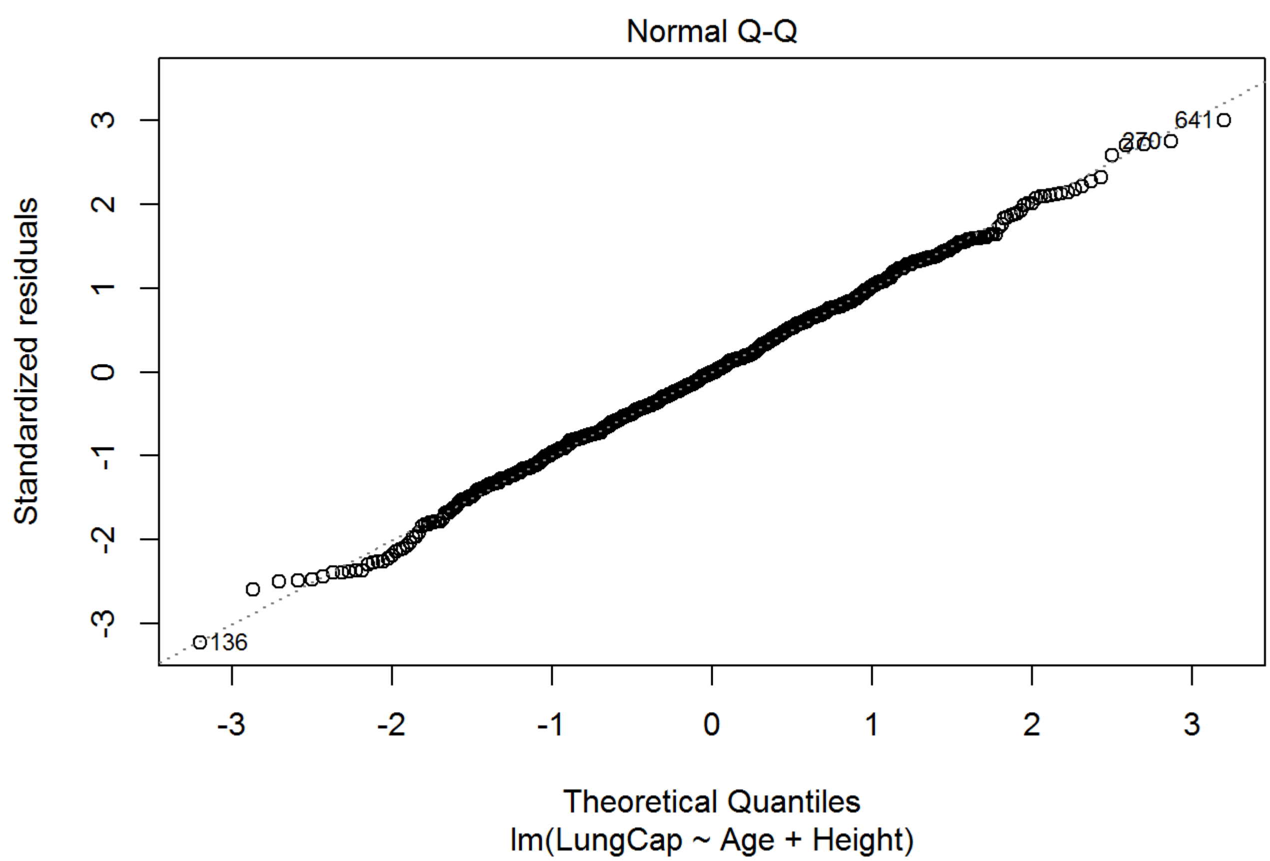
```
bptest(model1)
```

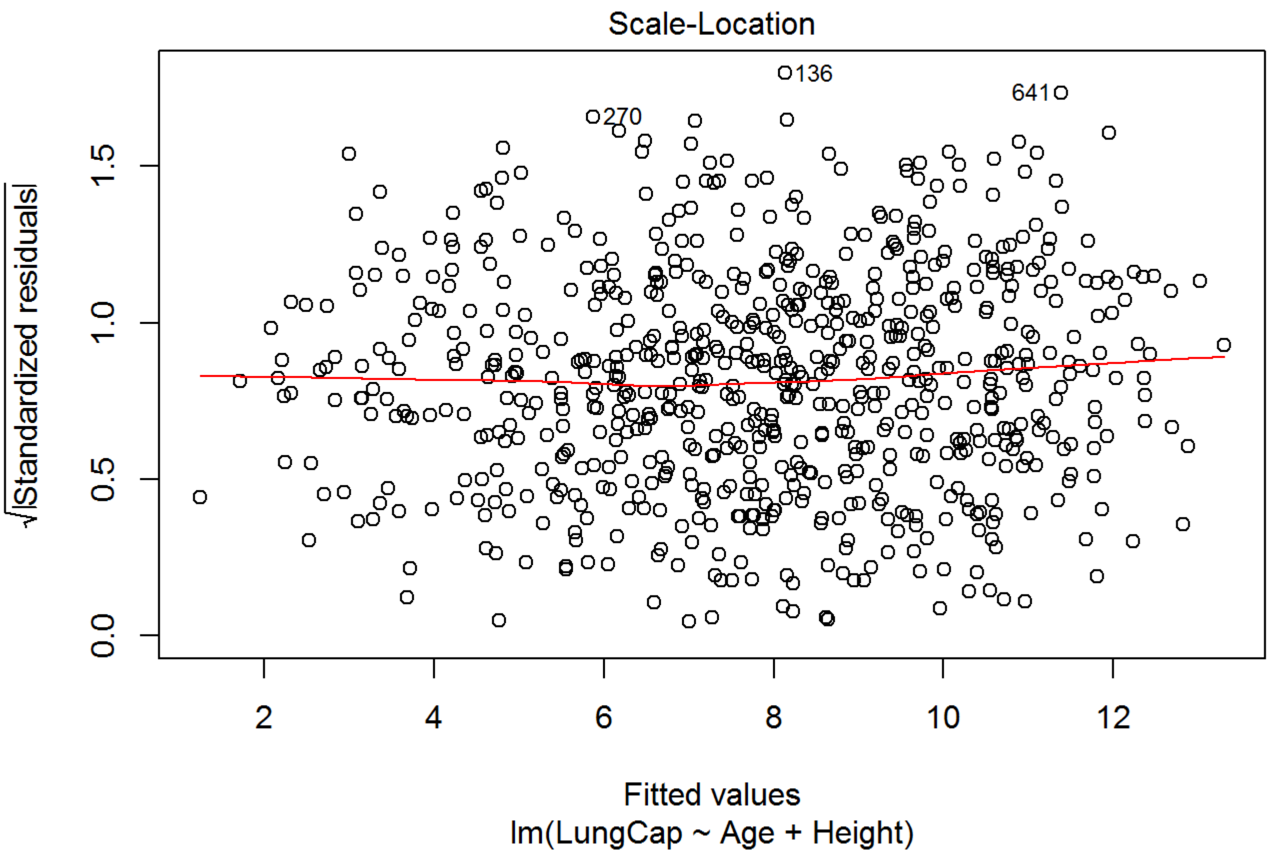
```
##
##  studentized Breusch-Pagan test
##
## data:  model1
## BP = 1.7152, df = 2, p-value = 0.4242
```

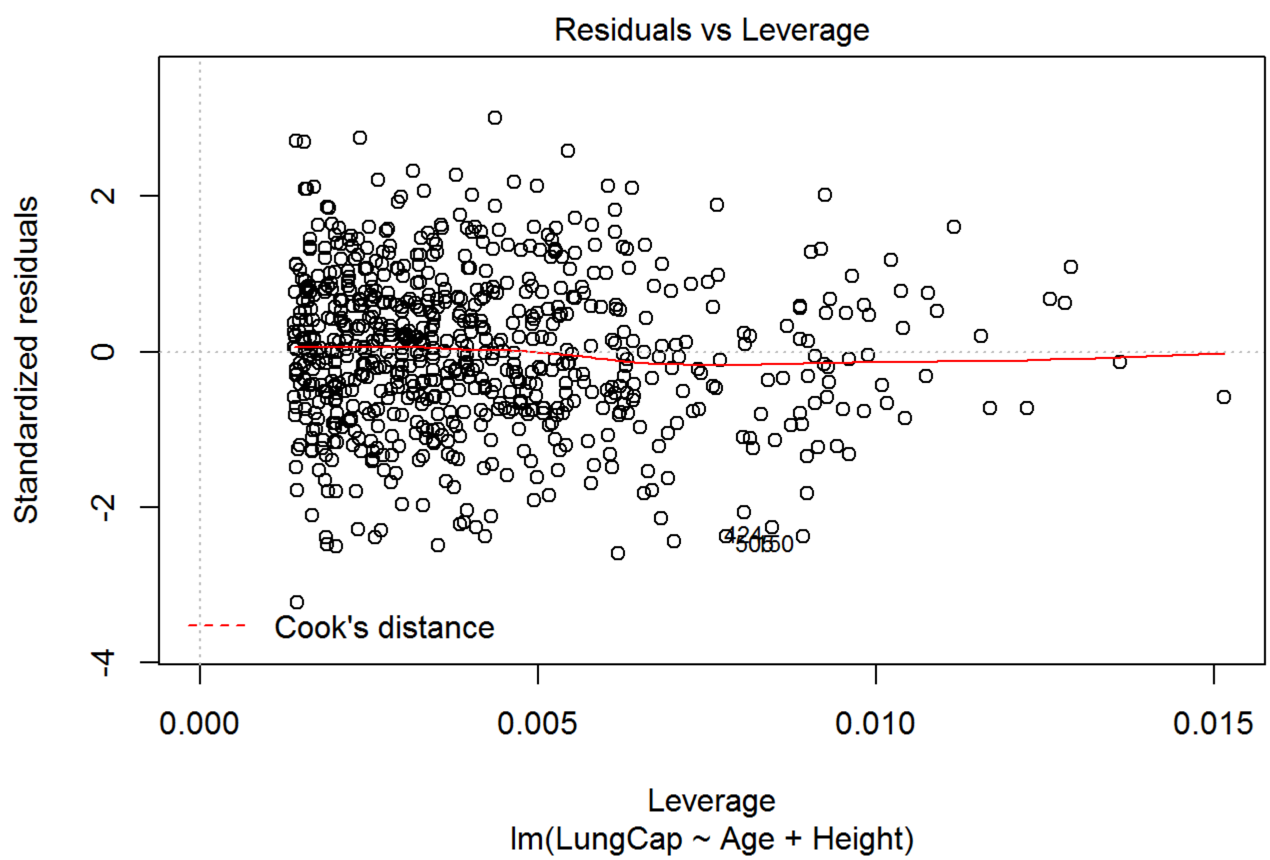
Checking Non-Linearity problem in the model

```
library(corrplot)
plot(model1)
```


Residuals vs Fitted
Residuals
Fitted values
lm(LungCap ~ Age + Height)
270
641
136
-4
-2
0
2
2
4
6
8
10
12


Normal Q-Q
Standardized residuals
Theoretical Quantiles
lm(LungCap ~ Age + Height)
641
270
136
-3
-2
-1
0
1
2
3





Checking AUtocorrelation problem in the model

```
dwtest(model1)
```

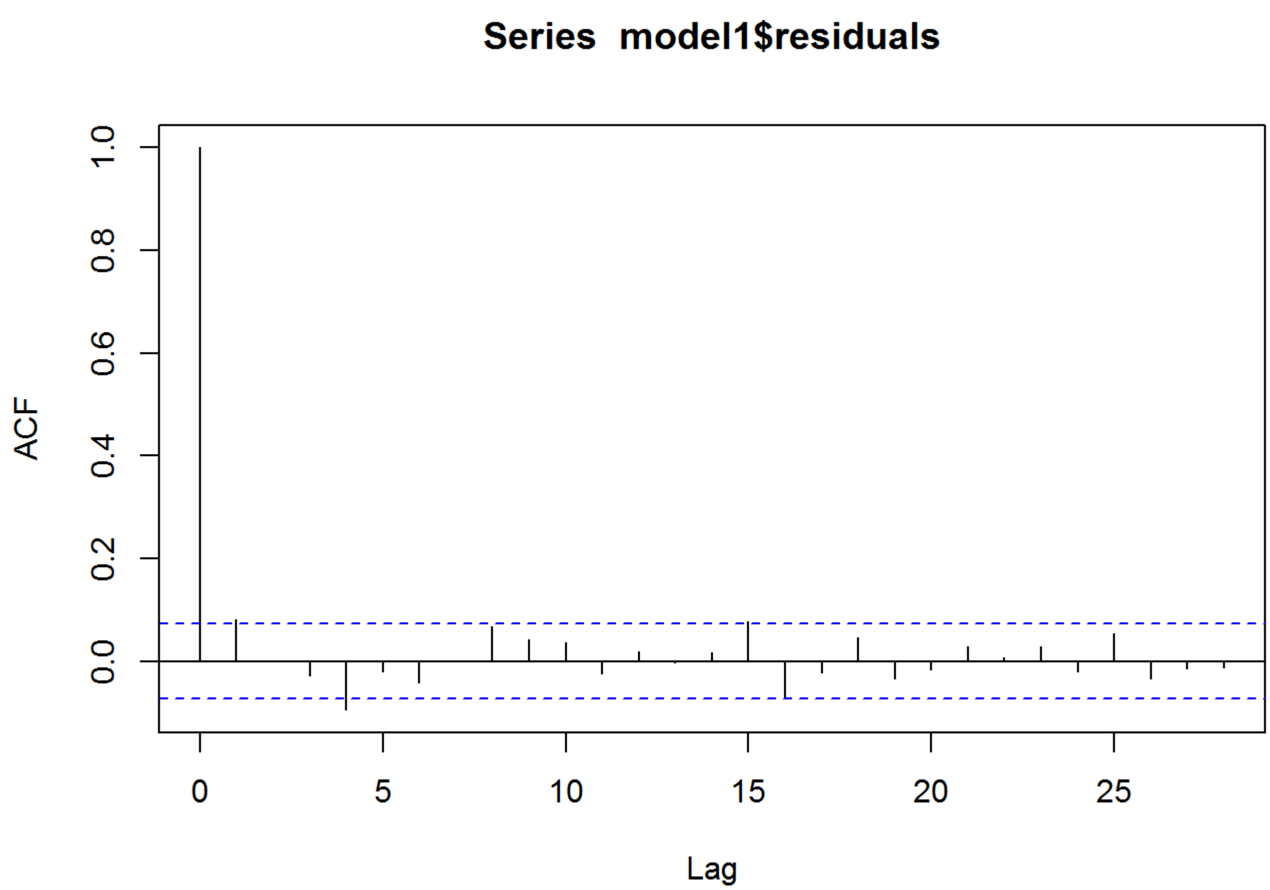
```
##
##  Durbin-Watson test
##
## data:  model1
## DW = 1.8348, p-value = 0.01296
## alternative hypothesis: true autocorrelation is greater than 0
```

```
# p-value is < 2.0 hence we accept Ha, can conclude there is no autocorrelation in this model
```

```
durbinWatsonTest(model1)
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1       0.0815809       1.83481   0.018
##  Alternative hypothesis: rho != 0
```

```
acf(model1$residuals)
```



```
# we see all the vertical lines are within significance bounce except 0 and more or less line 4
 is crossing the significance bounce but not so high. wc can conclude there is no autocorrelatio
n in the model.
```

```
bgtest(model1)
```

```
##
##  Breusch-Godfrey test for serial correlation of order up to 1
##
## data:  model1
## LM test = 4.8678, df = 1, p-value = 0.02736
```

```
# p value is < 2.0 hence we accept Ha, can conclude there is no autocorrelation in this model
```

```
bgtest(model1,order = 2)
```

```
##
##  Breusch-Godfrey test for serial correlation of order up to 2
##
## data:  model1
## LM test = 4.8876, df = 2, p-value = 0.08683
```

```
# p value is < 2.0 hence we accept Ha, can conclude there is no autocorrelation in this model
```

REGRESSION ASSUMPTIONS

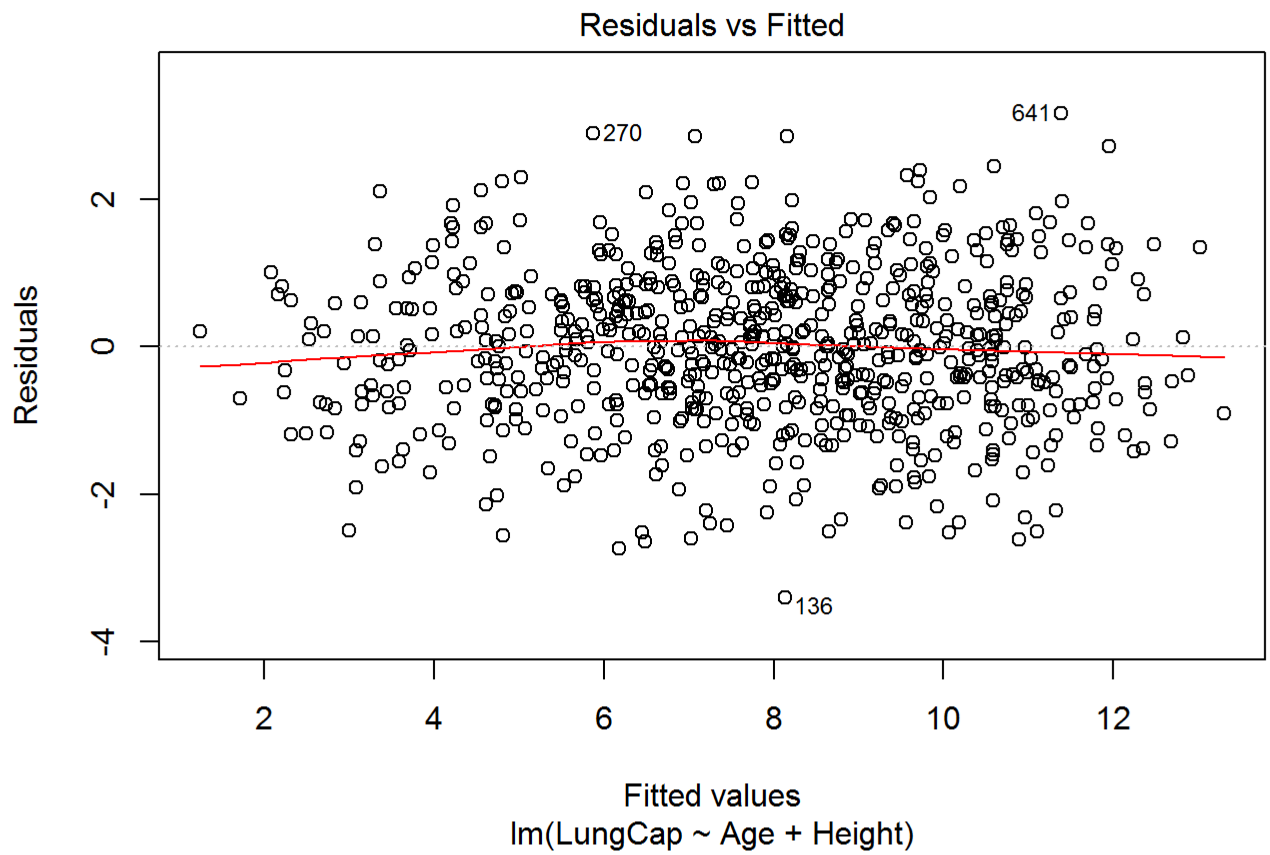
1 Assumption : The Y-values (or the errors, “e”) are independent!

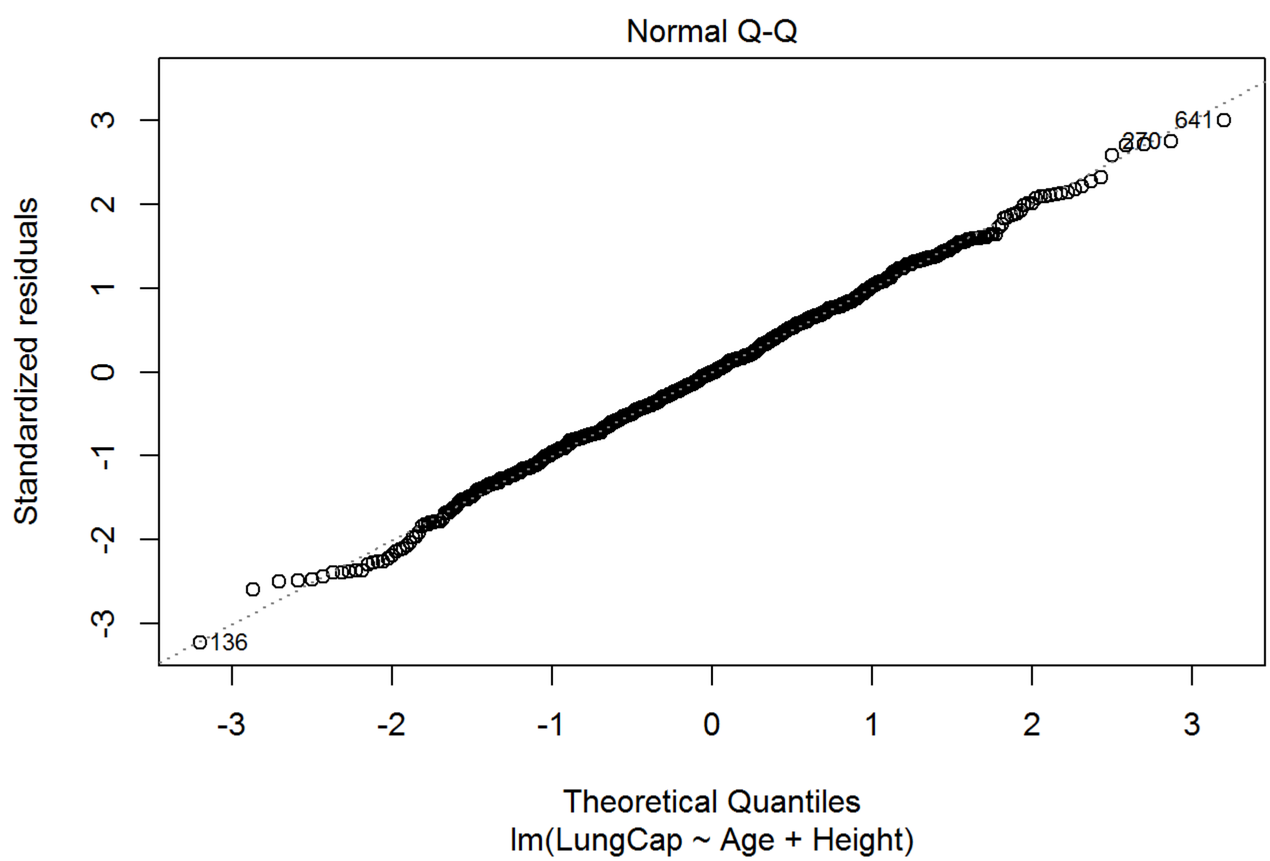
2 Assumption : The Y-values can be expressed as a linear function of the X variables

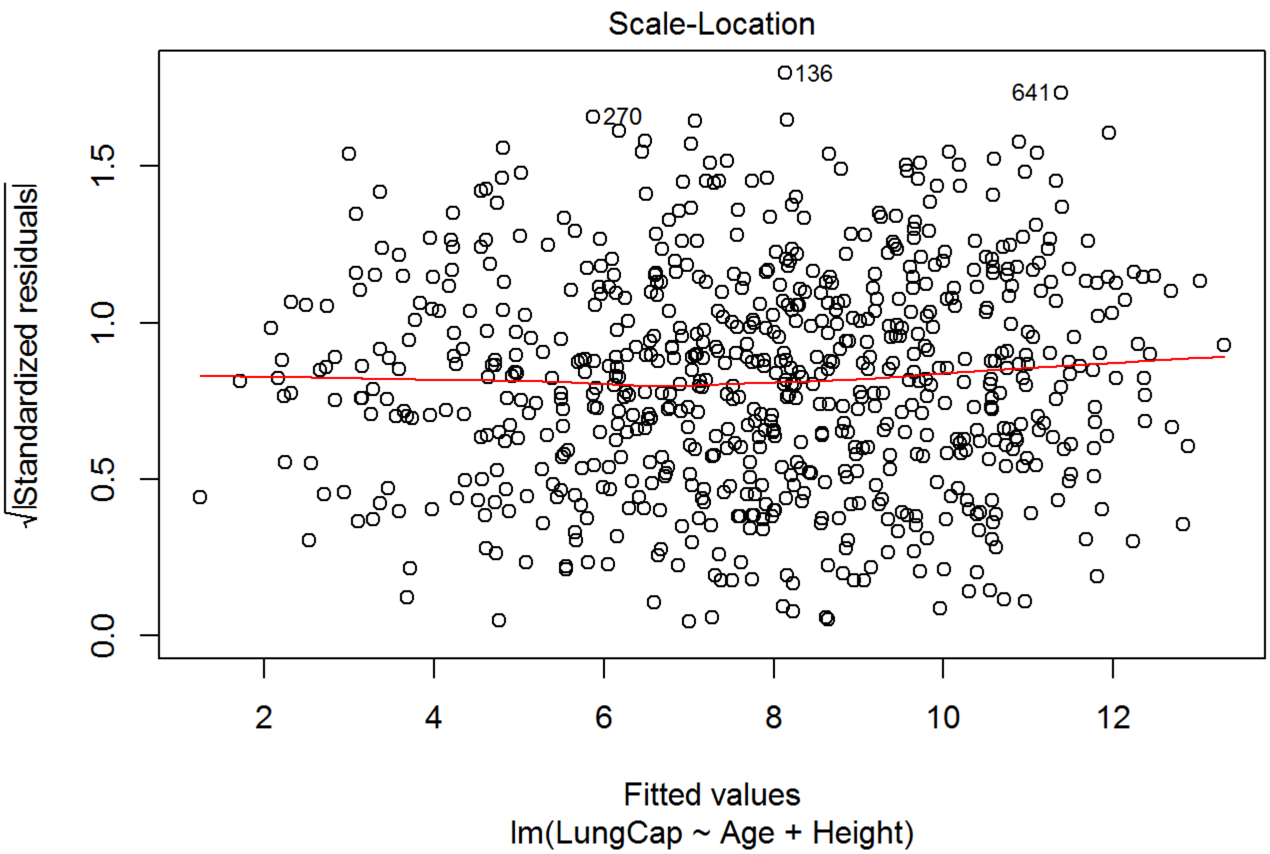
3 Assumption : Variation of observations around the regression line (the residual SE is constant (homoscedasticity)

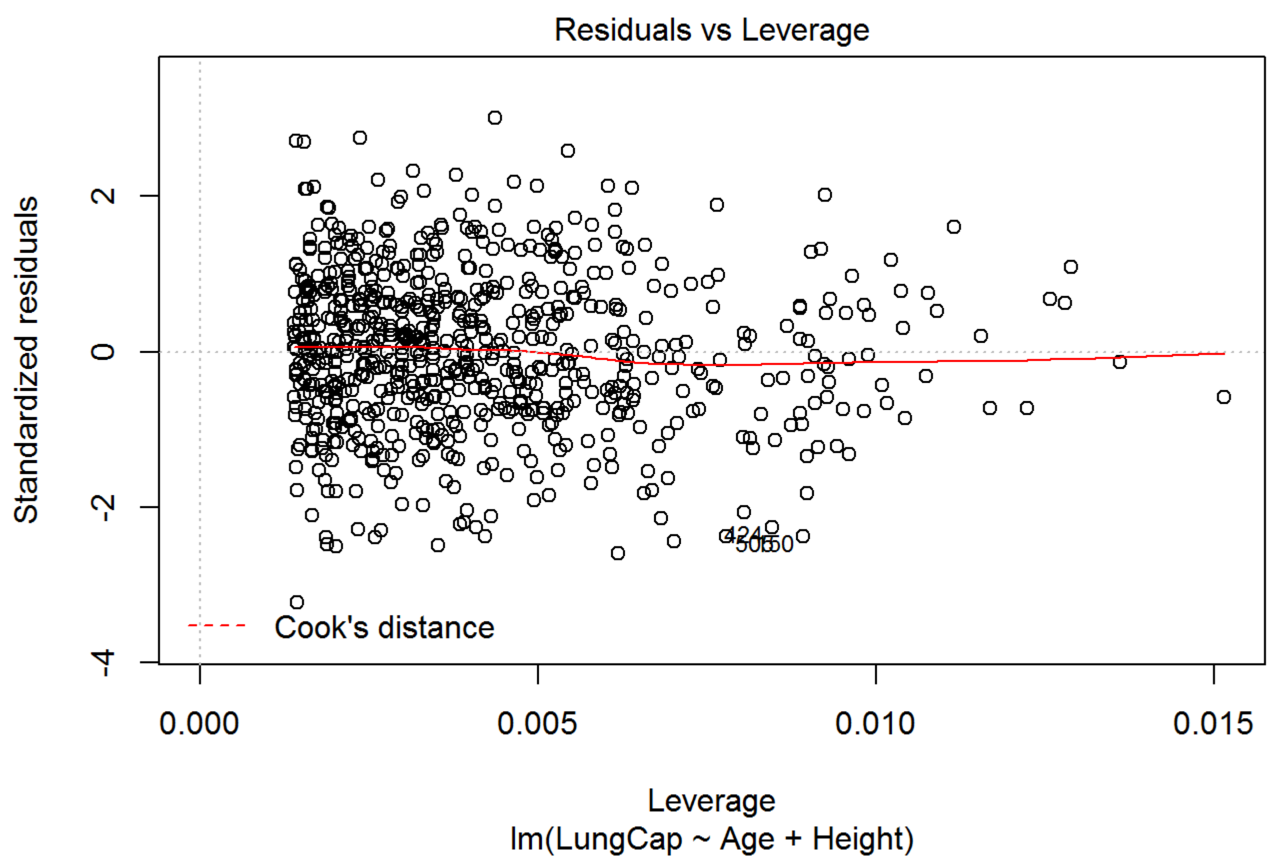
4 Assumption : for given values of X,Y values (or the error) are Normally distributed

```
plot(model1)
```


Residuals vs Fitted
Residuals
Fitted values
lm(LungCap ~ Age + Height)
270
641
136


Normal Q-Q
Standardized residuals
Theoretical Quantiles
lm(LungCap ~ Age + Height)
641
270
136


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


Residuals vs Leverage
Standardized residuals
Leverage
lm(LungCap ~ Age + Height)
Cook's distance
424
506
550
-4
-2
0
2
0.000
0.005
0.010
0.015

LOGISTIC REGRESSION - *is used to describe data and to explain the relationship between one dependent binary variable and one or more nominal, ordinal, interval or ratio-level independent variables.*

```
# Read Data

data <- read.csv("LungCapData.txt",header = T,sep = "\t")
str(data)
```

```
## 'data.frame':    725 obs. of  6 variables:
##  $ LungCap  : num  6.47 10.12 9.55 11.12 4.8 ...
##  $ Age      : int  6 18 16 14 5 11 8 11 15 11 ...
##  $ Height   : num  62.1 74.7 69.7 71 56.9 58.7 63.3 70.4 70.5 59.2 ...
##  $ Smoke    : Factor w/ 2 levels "no","yes": 1 2 1 1 1 1 1 1 1 1 ...
##  $ Gender   : Factor w/ 2 levels "female","male": 2 1 1 2 2 1 2 2 2 2 ...
##  $ Caesarean: Factor w/ 2 levels "no","yes": 1 1 2 1 1 1 2 1 1 1 ...
```

```
data <- data[c(1:4)]
```

```
# Normalize Data

data$LungCap <- scale(data$LungCap)
data$Age <- scale(data$Age)
data$Height <- scale(data$Height)
```

```
# Convert data to binary

levels(data$Smoke)=0:1
head(data)
```

```
##      LungCap        Age     Height Smoke
## 1 -0.5214663 -1.5798483 -0.3799252     0
## 2  0.8496790  1.4165938  1.3695539     1
## 3  0.6336766  0.9171868  0.6753161     0
## 4  1.2253352  0.4177798  0.8558180     0
## 5 -1.1506905 -1.8295518 -1.1019324     0
## 6 -0.6153804 -0.3313307 -0.8520068     0
```

```
# Check the class imbalance

table(data$Smoke)
```

```
##
##   0   1
## 648  77
```

```
# Data Partition

set.seed(1234)
ind <- sample(2,nrow(data),replace = T,prob = c(0.8,0.2))
train <- data[ind == 1,]
test <- data[ind == 2,]
```

```
# Handling Class Imbalance

library(ROSE)
```

```
## Loaded ROSE 0.0-3
```

```
both <- ovun.sample(Smoke ~., data = train,method = 'both',p=0.5,seed=222,N=573)$data
table(both$Smoke)
```

```
##
##   0   1
## 287 286
```

```
over <- ovun.sample(Smoke ~.,data = train,method = 'over',N=1296)$data
table(over$Smoke)
```

```
##
##   0   1
## 511 785
```

```
under <- ovun.sample(Smoke ~., data = train,method = 'under',N=154)$data
table(under$Smoke)
```

```
##
##  0  1
## 92 62
```

```
# Build a Model

mymodel <- glm(Smoke ~ LungCap + Age + Height,data = both, family = 'binomial')
```

```
# Predict Model on Training Dataset

p <- predict(mymodel,both,type = 'response')
pred <- ifelse(p>0.5,1,0)
tab <- table(Predicted=pred,Actual=both$Smoke)
1-sum(diag(tab))/sum(tab)
```

```
## [1] 0.2879581
```

```
# Predict model on test data

p1 <- predict(mymodel,test,type = 'response')
pred1 <- ifelse(p1 >0.5,1,0)
tab1 <- table(Predicted= pred1, Actual=test$Smoke)
1-sum(diag(tab1))/sum(tab1)
```

```
## [1] 0.2960526
```

5. CONCLUSION

With the help of R Statistical analysis and graphical representations, I can easily analysis the Lung Capacity data in the Smokers and non-smokers by their age, gender and Height.

6.REFERENCES

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