Statistical_testing_in_R.R

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```
###Independent T test

#The independent t test is used to test if there is any statistically
#significant difference between two means.
#Use of an independent t test requires several assumptions to be satisfied.
#The assumptions are listed below

#The variables are continuous and independent
#The variables are normally distributed
#The variances in each group are equal

#When these assumptions are satisfied the results of the t test are valid.
#Otherwise they are invalid and you need to use a non-parametric test.
#When data is not normally
#distributed you can apply transformations to make it normally distributed.


##the data to be used for these tests are goin to be mtcars

summary(mtcars)
```

```
##       mpg             cyl             disp             hp
##  Min.   :10.40   Min.   :4.000   Min.   : 71.1   Min.   : 52.0
##  1st Qu.:15.43   1st Qu.:4.000   1st Qu.:120.8   1st Qu.: 96.5
##  Median :19.20   Median :6.000   Median :196.3   Median :123.0
##  Mean   :20.09   Mean   :6.188   Mean   :230.7   Mean   :146.7
##  3rd Qu.:22.80   3rd Qu.:8.000   3rd Qu.:326.0   3rd Qu.:180.0
##  Max.   :33.90   Max.   :8.000   Max.   :472.0   Max.   :335.0
##       drat             wt             qsec             vs
##  Min.   :2.760   Min.   :1.513   Min.   :14.50   Min.   :0.0000
##  1st Qu.:3.080   1st Qu.:2.581   1st Qu.:16.89   1st Qu.:0.0000
##  Median :3.695   Median :3.325   Median :17.71   Median :0.0000
##  Mean   :3.597   Mean   :3.217   Mean   :17.85   Mean   :0.4375
##  3rd Qu.:3.920   3rd Qu.:3.610   3rd Qu.:18.90   3rd Qu.:1.0000
##  Max.   :4.930   Max.   :5.424   Max.   :22.90   Max.   :1.0000
##        am              gear            carb
##  Min.   :0.0000   Min.   :3.000   Min.   :1.000
##  1st Qu.:0.0000   1st Qu.:3.000   1st Qu.:2.000
##  Median :0.0000   Median :4.000   Median :2.000
##  Mean   :0.4062   Mean   :3.688   Mean   :2.812
##  3rd Qu.:1.0000   3rd Qu.:4.000   3rd Qu.:4.000
##  Max.   :1.0000   Max.   :5.000   Max.   :8.000
```

```
head(mtcars)
```

```
##                    mpg cyl disp  hp drat    wt  qsec vs am gear carb
## Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
## Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
## Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
## Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
## Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
## Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

```
colnames(mtcars)
```

```
##  [1] "mpg"  "cyl"  "disp" "hp"   "drat" "wt"   "qsec" "vs"   "am"   "gear"
## [11] "carb"
```

```
##creating labels for am variable

mtcars$am_label<-factor(mtcars$am,levels=c(0,1),labels=c("Automatic","Manual"))
mtcars[,c('am','am_label')]
```

```
##                     am  am_label
## Mazda RX4            1    Manual
## Mazda RX4 Wag        1    Manual
## Datsun 710           1    Manual
## Hornet 4 Drive       0 Automatic
## Hornet Sportabout    0 Automatic
## Valiant              0 Automatic
## Duster 360           0 Automatic
## Merc 240D            0 Automatic
## Merc 230             0 Automatic
## Merc 280             0 Automatic
## Merc 280C            0 Automatic
## Merc 450SE           0 Automatic
## Merc 450SL           0 Automatic
## Merc 450SLC          0 Automatic
## Cadillac Fleetwood   0 Automatic
## Lincoln Continental  0 Automatic
## Chrysler Imperial    0 Automatic
## Fiat 128             1    Manual
## Honda Civic          1    Manual
## Toyota Corolla       1    Manual
## Toyota Corona        0 Automatic
## Dodge Challenger     0 Automatic
## AMC Javelin          0 Automatic
## Camaro Z28           0 Automatic
## Pontiac Firebird     0 Automatic
## Fiat X1-9            1    Manual
## Porsche 914-2        1    Manual
## Lotus Europa         1    Manual
## Ford Pantera L       1    Manual
## Ferrari Dino         1    Manual
## Maserati Bora        1    Manual
## Volvo 142E           1    Manual
```

```
attach(mtcars)

##generating descriptive statistics for each group
#mean
aggregate(mtcars$mpg,by=list(mtcars$am_label),FUN=mean)
```

```
##     Group.1        x
## 1 Automatic 17.14737
## 2    Manual 24.39231
```

```
#range
aggregate(mtcars$mpg,by=list(mtcars$am_label),FUN=range)
```

```
##     Group.1  x.1  x.2
## 1 Automatic 10.4 24.4
## 2    Manual 15.0 33.9
```

```
##generating box plot for each group for each group to check the dist

boxplot(mpg~am_label,main="Distribution of two groups",xlab="am label",ylab="mpg range")

##to check the assumption that the two groups are normally dist

##perform shapiro wilk normality test

aggregate(mtcars$mpg,by=list(mtcars$am_label),FUN=function(x) shapiro.test(x))
```

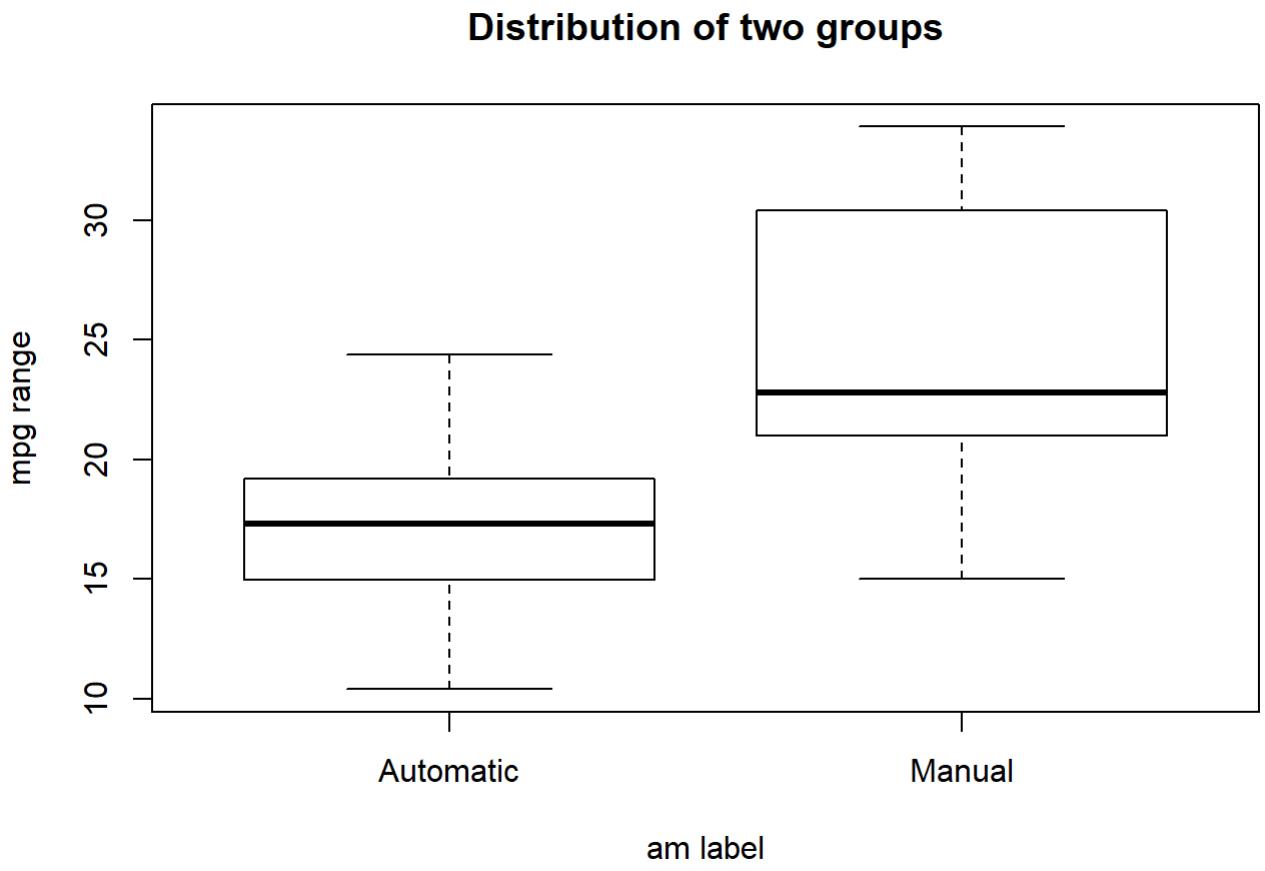
```
## Warning in format.data.frame(x, digits = digits, na.encode = FALSE):
## corrupt data frame: columns will be truncated or padded with NAs
```

```
##     Group.1         x
## 1 Automatic 0.9767743
## 2    Manual 0.9458037
```

```
##computing the p value for this test

aggregate(mtcars$mpg,by=list(mtcars$am_label),FUN=function(x) shapiro.test(x)$p.value)
```

```
##     Group.1         x
## 1 Automatic 0.8987358
## 2    Manual 0.5362729
```

```
##in this test the null hypothesis is the dist is normal..since we see that
##at 0.05 significance level the value is greater than 0.05 we accept the null
##hypothesis and hence the two samples are normally dist


##now we check the assumption of variance

##performing levene test

library(car)
```




```
leveneTest(mtcars$mpg~mtcars$am_label)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value  Pr(>F)
## group  1  4.1876 0.04957 *
##       30
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##the null hypothesis is the variance is equal
##since p value is less than 0.05 we accept the alternate hypothesis and hence
##the variance is not equal

##alternately we also perform var.test that computes f test

##inorder to stabilize the data variance we should take the log transformation

mtcars$log_mpg<-log(mpg)
leveneTest(mtcars$log_mpg~mtcars$am_label)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.3902 0.5369
##       30
```

```
##now the variance is equal

##since all the assumptions are satisfied we can perform the t test

t.test(mtcars$log_mpg~mtcars$am_label, var.equal=TRUE)
```

```
##
##  Two Sample t-test
##
## data:  mtcars$log_mpg by mtcars$am_label
## t = -3.9087, df = 30, p-value = 0.0004905
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.5277597 -0.1655209
## sample estimates:
## mean in group Automatic    mean in group Manual
##                2.816692                3.163332
```

```
###We see that p-value is less than 0.05 so we reject the null hypothesis
##thus the means of the two samples are statistically different



################################################################################




#Paired sample T testing

#The paired samples t test is used to check if there are any differences in
#the mean of the same sample at two different time points.
#For example a medical researcher collects data on the same patients
#before and after a therapy. A paired t test will show if the therapy
#improves patient outcomes.

#There are several assumptions that need to be satisfied so that
#results of a paired t test are valid. They are listed below

#The measured variable is continuous
#The differences between the two groups are approximately normally distributed
#We should not have any outliers in our data
#An adequate sample size is required


library(MASS)

head(anorexia)
```

```
##   Treat Prewt Postwt
## 1  Cont  80.7   80.2
## 2  Cont  89.4   80.1
## 3  Cont  91.8   86.4
## 4  Cont  74.0   86.3
## 5  Cont  78.1   76.1
## 6  Cont  88.3   78.1
```

```
library(psych)
```

```
##
## Attaching package: 'psych'
```

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

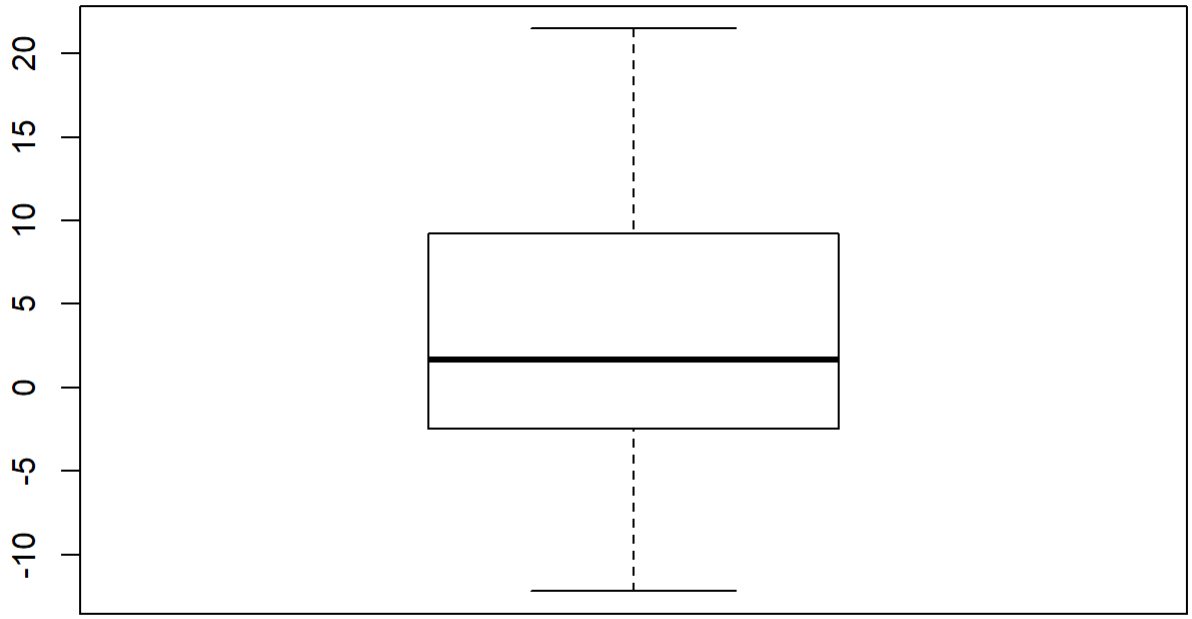
```
describe(anorexia)
```

```
##        vars  n  mean   sd median trimmed  mad  min   max range  skew
## Treat*    1 72  1.83 0.79   2.00    1.79 1.48  1.0   3.0   2.0  0.29
## Prewt     2 72 82.41 5.18  82.30   82.47 5.49 70.0  94.9  24.9 -0.05
## Postwt    3 72 85.17 8.04  84.05   84.82 9.56 71.3 103.6  32.3  0.36
##        kurtosis   se
## Treat*    -1.35 0.09
## Prewt     -0.16 0.61
## Postwt    -0.81 0.95
```

```
##computing mean using apply function

apply(anorexia[,c(2,3)],2,mean)
```

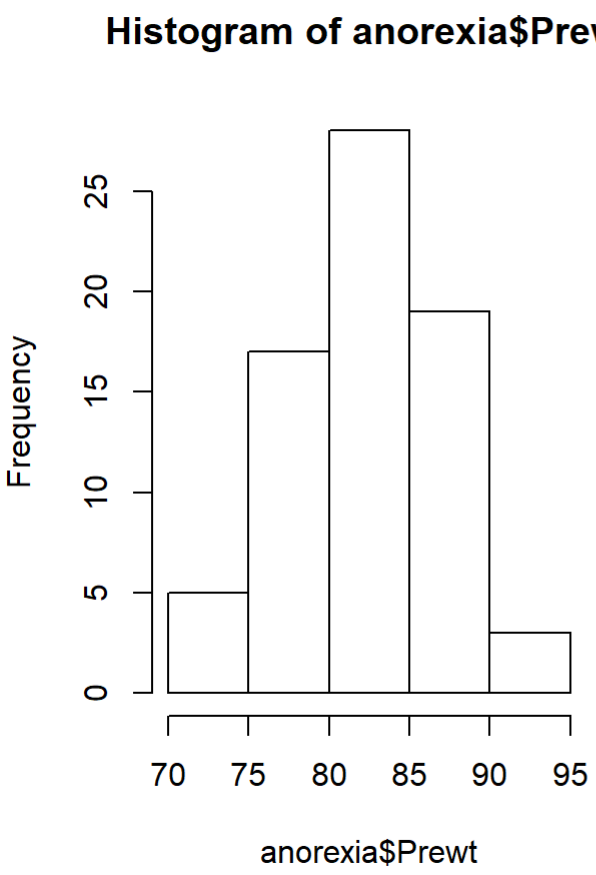
```
##    Prewt   Postwt
## 82.40833 85.17222
```

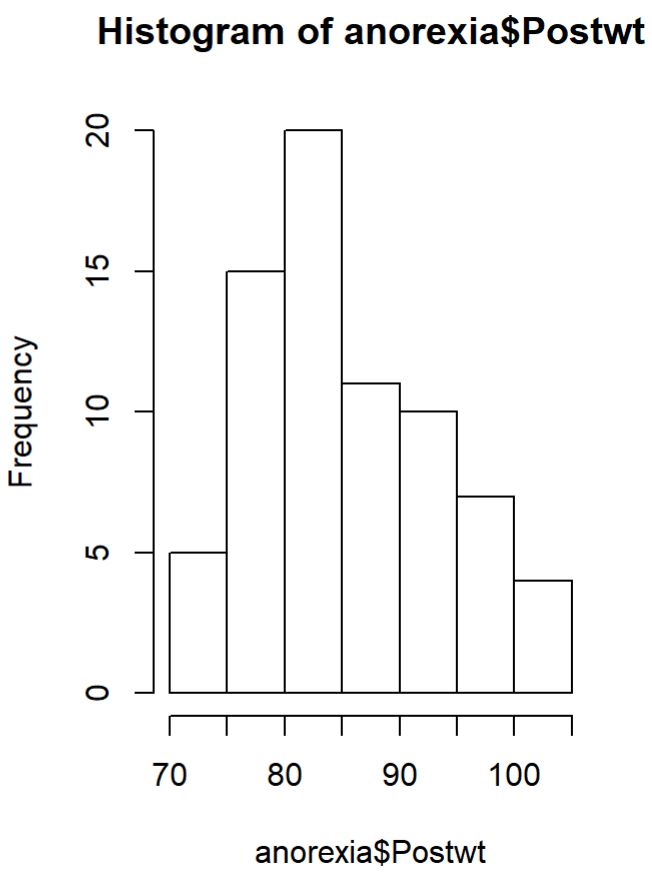
```
##creating a variable to check the diff

anorexia$diff=anorexia$Postwt-anorexia$Prewt

##creating a box plot
boxplot(anorexia$diff,xlab="The diff")
```



The diff

```
##checking the assumption to see if both the samples are normally dist
##visually

par(mfrow=c(1,2))


hist(anorexia$Prewt)
hist(anorexia$Postwt)
```






```
#pre treatment is normally dist but post treatment is not normally dist

##checking through normality test

shapiro.test(anorexia$Prewt)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  anorexia$Prewt
## W = 0.99248, p-value = 0.9484
```

```
shapiro.test(anorexia$Postwt)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  anorexia$Postwt
## W = 0.9673, p-value = 0.05781
```

```
shapiro.test(anorexia$diff)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  anorexia$diff
## W = 0.97466, p-value = 0.1544
```

```
#the diff is normally distributed




#Perform a power analysis to check the sample size has adequate power to detect a difference if
 it exists
#install package pwr and load it
library(pwr)
```

```
## Warning: package 'pwr' was built under R version 3.4.4
```

```
pwr.t.test(n=72,d=0.5,sig.level = 0.05,type = c("paired"))
```

```
##
##      Paired t test power calculation
##
##               n = 72
##               d = 0.5
##       sig.level = 0.05
##           power = 0.9869471
##     alternative = two.sided
##
## NOTE: n is number of *pairs*
```

```
#we see the power of the test is 98% hence the sample size is appropriate

var.test(anorexia$Prewt,anorexia$Postwt)
```

```
##
##  F test to compare two variances
##
## data:  anorexia$Prewt and anorexia$Postwt
## F = 0.41599, num df = 71, denom df = 71, p-value = 0.000288
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.2602635 0.6648930
## sample estimates:
## ratio of variances
##          0.4159896
```

```
#performing paired t test

t.test(anorexia$Prewt,anorexia$Postwt,paired = TRUE)
```

```
##
##  Paired t-test
##
## data:  anorexia$Prewt and anorexia$Postwt
## t = -2.9376, df = 71, p-value = 0.004458
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -4.6399424 -0.8878354
## sample estimates:
## mean of the differences
##               -2.763889
```

```
##the two sample means are statistically different


#All assumptions required were satisfied
#There were no outliers, data was normally distributed and the t test had adequate power
#The difference in weight before and after treatment was statistically significant at 5% LOs.









###chisqaure test of independence


data("trees")
head(trees)
```

```
##   Girth Height Volume
## 1   8.3     70   10.3
## 2   8.6     65   10.3
## 3   8.8     63   10.2
## 4  10.5     72   16.4
## 5  10.7     81   18.8
## 6  10.8     83   19.7
```

```
##creating a two way frequency table

mytable<-table(trees$Height,trees$Volume)
mytable
```

```
##
##      10.2 10.3 15.6 16.4 18.2 18.8 19.1 19.7 19.9 21 21.3 21.4 22.2 22.6
##   63    1    0    0    0    0    0    0    0    0  0    0    0    0    0
##   64    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##   65    0    1    0    0    0    0    0    0    0  0    0    0    0    0
##   66    0    0    1    0    0    0    0    0    0  0    0    0    0    0
##   69    0    0    0    0    0    0    0    0    0  0    1    0    0    0
##   70    0    1    0    0    0    0    0    0    0  0    0    0    0    0
##   71    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##   72    0    0    0    1    0    0    0    0    0  0    0    0    0    0
##   74    0    0    0    0    0    0    0    0    0  0    0    0    1    0
##   75    0    0    0    0    1    0    1    0    1  0    0    0    0    0
##   76    0    0    0    0    0    0    0    0    0  1    0    1    0    0
##   77    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##   78    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##   79    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##   80    0    0    0    0    0    0    0    0    0  0    0    0    0    1
##   81    0    0    0    0    0    1    0    0    0  0    0    0    0    0
##   82    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##   83    0    0    0    0    0    0    0    1    0  0    0    0    0    0
##   85    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##   86    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##   87    0    0    0    0    0    0    0    0    0  0    0    0    0    0
##
##      24.2 24.9 25.7 27.4 31.7 33.8 34.5 36.3 38.3 42.6 51 51.5 55.4 55.7
##   63    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##   64    0    1    0    0    0    0    0    0    0    0  0    0    0    0
##   65    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##   66    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##   69    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##   70    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##   71    0    0    1    0    0    0    0    0    0    0  0    0    0    0
##   72    0    0    0    0    0    0    0    0    1    0  0    0    0    0
##   74    0    0    0    0    0    0    0    1    0    0  0    0    0    0
##   75    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##   76    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##   77    0    0    0    0    0    0    0    0    0    1  0    0    0    0
##   78    0    0    0    0    0    0    1    0    0    0  0    0    0    0
##   79    1    0    0    0    0    0    0    0    0    0  0    0    0    0
##   80    0    0    0    0    1    0    0    0    0    0  1    1    0    0
##   81    0    0    0    0    0    0    0    0    0    0  0    0    1    0
##   82    0    0    0    0    0    0    0    0    0    0  0    0    0    1
##   83    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##   85    0    0    0    0    0    1    0    0    0    0  0    0    0    0
##   86    0    0    0    1    0    0    0    0    0    0  0    0    0    0
##   87    0    0    0    0    0    0    0    0    0    0  0    0    0    0
##
##      58.3 77
##   63    0  0
##   64    0  0
##   65    0  0
##   66    0  0
##   69    0  0
```

```
##   70    0  0
##   71    0  0
##   72    0  0
##   74    0  0
##   75    0  0
##   76    0  0
##   77    0  0
##   78    0  0
##   79    0  0
##   80    1  0
##   81    0  0
##   82    0  0
##   83    0  0
##   85    0  0
##   86    0  0
##   87    0  1
```

```
##generating individual freq using margin table

margin.table(mytable,1)
```

```
##
## 63 64 65 66 69 70 71 72 74 75 76 77 78 79 80 81 82 83 85 86 87
##  1  1  1  1  1  1  1  2  2  3  2  1  1  1  5  2  1  1  1  1  1
```

```
margin.table(mytable,2)
```

```
##
## 10.2 10.3 15.6 16.4 18.2 18.8 19.1 19.7 19.9   21 21.3 21.4 22.2 22.6 24.2
##    1    2    1    1    1    1    1    1    1    1    1    1    1    1    1
## 24.9 25.7 27.4 31.7 33.8 34.5 36.3 38.3 42.6   51 51.5 55.4 55.7 58.3   77
##    1    1    1    1    1    1    1    1    1    1    1    1    1    1    1
```

```
#creating a new col called a

a=c(70, 65, 63, 72, 80, 83, 66, 75, 80, 75, 79, 76, 76, 69, 75, 74, 85, 8, 71,
      63, 78, 80, 74, 72, 77, 81, 82, 80, 86, 80, 87)

trees=cbind(trees,a)
length(trees$a)
```

```
## [1] 31
```

```
mytable2<-table(trees$Height,trees$a)

chisq.test(mytable)
```

```
## Warning in chisq.test(mytable): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  mytable
## X-squared = 589, df = 580, p-value = 0.3888
```

```
##we observe that the p value is greater than 0.05 and hence we accept the null
#hypothesis that the columns are independent of each other

chisq.test(mytable2)
```

```
## Warning in chisq.test(mytable2): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  mytable2
## X-squared = 571.64, df = 400, p-value = 3.495e-08
```

```
#we observe that the p value is much lesser than 0.05 and hence we
#reject the null hypothesis
```