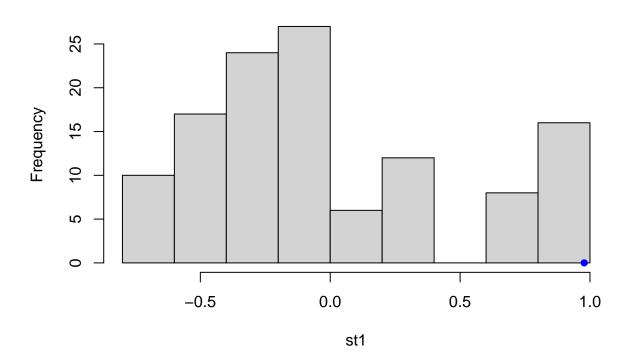
#### Problem-1

Samar Moussa/NIU:1661270 \_ Jamia Begum/NIU: 1676891

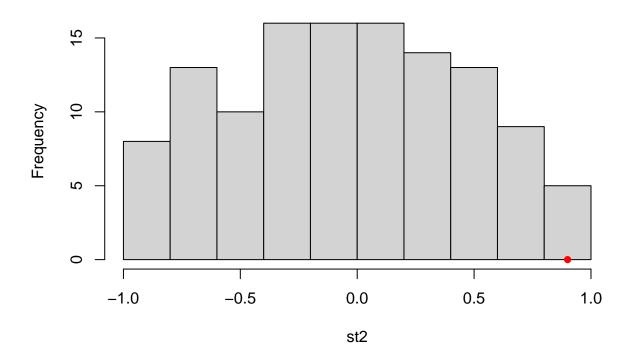
#### 2022-12-30

```
#exercise:1. Remember one of the examples presented in class:
#The first row is chest circumference (in inches) of five subjects.
#Let us call this X.
#The second row is the respective total volumes of air that can be breathed in
#and out in one minute (in liters) for the same five subjects. Let us call this Y.
#X: 39, 29, 60, 40, 32
#Y: 11, 5, 20, 8, 6
#Download the package combinat in order to use the function permn().
\#Perform\ an\ exact\ test\ for\ HO : = 0 against H1 : > 0.
#Use Pearson and Spearman correlation coefficient as well
\#Answer: suppose, \#\#The null hypothesis is, H0: rho = 0 (i.e X and Y are not correlated) \#\#The
Alternative hypothesis is,H1: rho>0 (i.e X and Y are positively correlated)
x = c(39, 29, 60, 40, 32)
y=c(11,5,20,8,6)
sttrue1= cor(x,y,method= "pearson") #taking statistic as the Pearson correlation coefficient
sttrue1
## [1] 0.9777792
sttrue2= cor(x,y,method= "spearman") #taking statistic as the spearman correlation coefficient
sttrue2
## [1] 0.9
n=length(y)
nr=fact(n) #number of rearrangements to be examined
st1=numeric(nr)
st2=numeric(nr)
cnt1=0 #for initiating counting
cnt2=0
d=permn(y) #Permuting randomly the Y column leaving the X fixed
for (i in 1:nr)
 { st1[i] <-cor(d[[i]],x,method= "pearson")
 if (st1[i] >=sttrue1)cnt1=cnt1+1 #comparing the true statistic and the evaluated statistic
  st2[i] <-cor(d[[i]],x,method= "spearman")
```

### Histogram of st1



# Histogram of st2



#in both cases, since the p-value is lower than 0.05, we have lower evidence to support the null hypothese #therefore, the null hypotheses is rejected, so we can conclude that #Chest circumference and volume of air are positively correlated

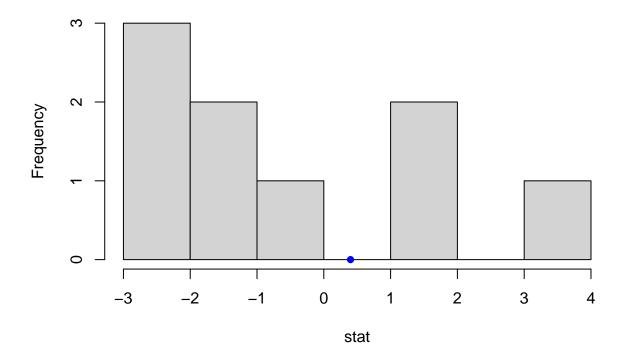
#### Problem-2

```
#install.packages("R.utils")
library(R.utils)
## Warning: package 'R.utils' was built under R version 4.2.2
## Loading required package: R.oo
## Loading required package: R.methodsS3
## R.methodsS3 v1.8.2 (2022-06-13 22:00:14 UTC) successfully loaded. See ?R.methodsS3 for help.
## R.oo v1.25.0 (2022-06-12 02:20:02 UTC) successfully loaded. See ?R.oo for help.
## Attaching package: 'R.oo'
## The following object is masked from 'package:R.methodsS3':
##
##
       throw
  The following objects are masked from 'package:methods':
##
##
       getClasses, getMethods
## The following objects are masked from 'package:base':
##
##
       attach, detach, load, save
## R.utils v2.12.2 (2022-11-11 22:00:03 UTC) successfully loaded. See ?R.utils for help.
##
## Attaching package: 'R.utils'
## The following object is masked from 'package:utils':
##
##
       timestamp
## The following objects are masked from 'package:base':
##
##
       cat, commandArgs, getOption, isOpen, nullfile, parse, warnings
```

```
Standard= c(2.5, 3.4, 2.9, 4.1, 5.3, 3.4, 1.9, 3.3, 1.8)
Additive=c(3.5, 6.3, 4.2, 4.3, 3.8, 5.7, 4.4, 0, 0)
diff=Additive - Standard
sttrue= mean(diff)
n=length(diff)
nf=2^n-1
st=numeric(nf)
stat = numeric(n)
for (i in 0:nf)
  { rearr=intToBin(i)
nn=nchar(rearr)
u=strrep("0", n-nn)
rearr=paste(u,rearr,sep="")
for (j in 1:n){stat[j]=ifelse(substr(rearr,j,j)==0, diff[j], -diff[j])}
st[i]=mean(stat)
pvalue <-length(st[st<=sttrue])/(2^n) # p-value</pre>
pvalue
```

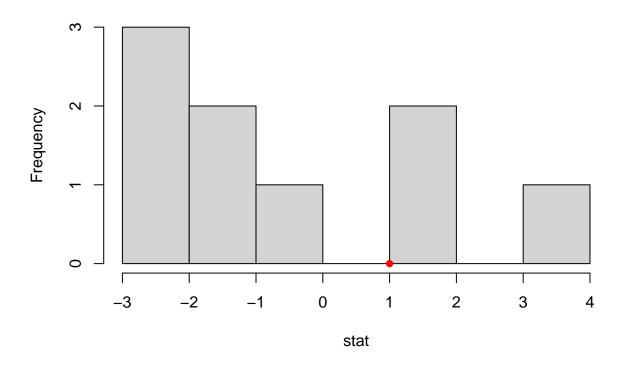
#### ## [1] 0.7167969

### Histogram of stat



```
#since the p-value is larger, we have enough evidence to support the
#null hypothesis therefore, the null hypothesis is not rejected, so we can conclude
# that the additive is not effective.
#(b) Explore several statistics in order to perform the permutation test.
#What is the final conclusion?
#we are going to use several statistic like pearson correlation coefficient and
#spearman correlation coefficient
Standard= c(2.5, 3.4, 2.9, 4.1, 5.3, 3.4, 1.9, 3.3, 1.8)
Additive=c(3.5, 6.3, 4.2, 4.3, 3.8, 5.7, 4.4, 0, 0)
diff=Additive - Standard
n=length(diff)
sttrue1= median(diff)
n=length(diff)
nf=2^n-1
st1=numeric(nf)
stat = numeric(n)
for (i in 0:nf)
{ rearr=intToBin(i)
nn=nchar(rearr)
u=strrep("0", n-nn)
rearr=paste(u,rearr,sep="")
for (j in 1:n){stat[j]=ifelse(substr(rearr,j,j)==0, diff[j], -diff[j])}
st1[i]=median(stat)
}
pvalue1 <-length(st1[st1<=sttrue1])/(2^n) # p-value</pre>
pvalue1
## [1] 0.7714844
```

# Histogram of stat



#in this case, using different statistic the p-value is also larger, we
#have enough evidence to support the null hypothesis
#therefore, the null hypothesis is not rejected, so we can conclude that
#there does not exist a significant difference before and after the additive
#that is the additive is not effective

### prpblem-3

#### 2023-01-15

```
#Problem-3:Assume that during a three-hour period spent outside, a person
#recorded the temperature, the amount of time they mowed the
#grass, and their water consumption. The experiment was conducted
#on 7 randomly selected days during the summer.
#(a) Fit the Water Consumption as a linear function of the Temperature
#(T) and the Time mowing the grass (TMG) by
#means of a multiple regression model. Hint: Use function
#lm in R.
library(combinat)
## Attaching package: 'combinat'
## The following object is masked from 'package:utils':
##
##
       combn
df=data.frame(T=c(75,83,85,85,92,97,99), W=c(16,20,25,27,32,48,48),
              TMG=c(1.85,1.25,1.5,1.75,1.15,1.75,1.6))
df
##
     T W TMG
## 1 75 16 1.85
## 2 83 20 1.25
## 3 85 25 1.50
## 4 85 27 1.75
## 5 92 32 1.15
## 6 97 48 1.75
## 7 99 48 1.60
model<-lm(W~ T+TMG,data=df)</pre>
an<-anova(model)</pre>
an
## Analysis of Variance Table
## Response: W
            Df Sum Sq Mean Sq F value
              1 905.53 905.53 584.316 1.737e-05 ***
## T
## TMG
             1 65.13
                        65.13 42.029 0.002918 **
## Residuals 4 6.20
                        1.55
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
```

```
FTtrue<-an$"F value"[1] #True F value of T before permutation test
FTMGtrue<-an$"F value"[2] #gives the significance between TMG and W
FTtrue
```

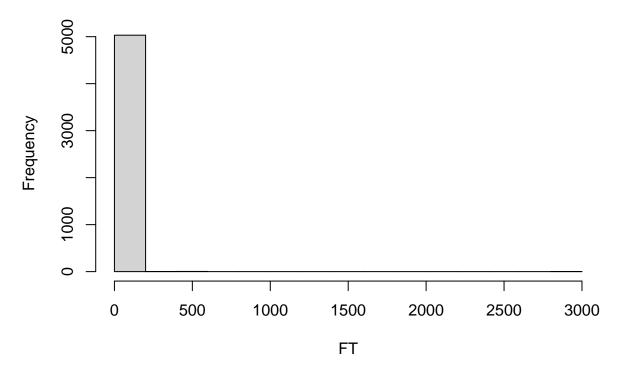
## [1] 584.3158

FTMGtrue

## [1] 42.02869

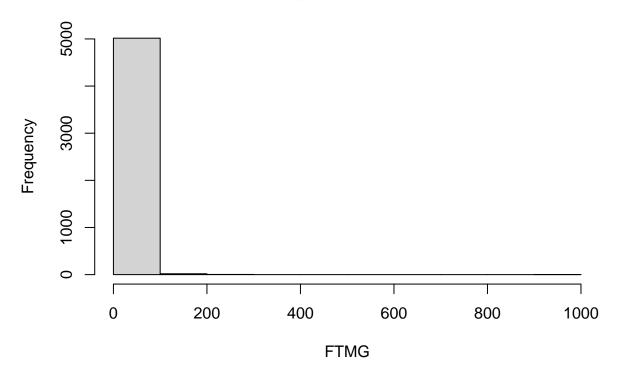
```
#F-value of the variable TR without permutation testis 584.3158
#F-value for the variable TMG without permutation test is 42.02869
#(b) Test the significance of the variables T and TMG using an
#exact permutation test. Compare the results with those obtained
#with the multiple regression model.
#exact test
T=c(75,83,85,85,92,97,99)
W=c(16,20,25,27,32,48,48)
TMG=c(1.85,1.25,1.5,1.75,1.15,1.75,1.6)
df=data.frame(T=c(75,83,85,85,92,97,99),W=c(16,20,25,27,32,48,48),
              TMG=c(1.85,1.25,1.5,1.75,1.15,1.75,1.6))
n = length(T)
nr=fact(n) #number of rearrangements to be examined
FT=numeric(nr)
FTMG=numeric(nr)
for (i in 1:nr){
 newW<- permn(W)</pre>
 newW
 model1<- lm(newW[[i]]~ T+TMG, data=df)</pre>
  an1<-anova(model1)
  FT[i]<-an1$"F value"[1]</pre>
  FTMG[i] <- an1$"F value"[2]</pre>
}
hist(FT, main = " Histogram of the FT")
```

# Histogram of the FT



hist(FTMG, main = " Histogram of the FTMG")

### **Histogram of the FTMG**



```
an1
## Analysis of Variance Table
## Response: newW[[i]]
            Df Sum Sq Mean Sq F value
##
              1 815.03 815.03 115.124 0.0004276 ***
## TMG
              1 133.51
                       133.51 18.858 0.0122283 *
## Residuals 4 28.32
                          7.08
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
# F value of T after permutation test
FT1<-an1$"F value"[1]
                        #gives the significance between T and W
\#\ F\ value\ of\ TMG\ after\ permutation\ test
FTMG1<-an$"F value"[2] #gives the significance between TMG and W
## [1] 115.124
```

FTMG1

## [1] 42.02869

 $\hbox{\it \#the $f$-values are different after doing exact test than the obtained values from $$\#$the multiple linear regression model}$