

COST PRACTICALS

1. Using R execute the basic commands ,array,lists and frames.

```

> msg="hello world"
> msg
[1] "hello world"
> i=10
> i
[1] 10
> f=22.5
> f
[1] 22.5
> |

```

```

msg="hello world"
> msg
[1] "hello world"
> i=10
> i
[1] 10
> f=22.5
> f
[1] 22.5

```

VECTORS→ARRAYS

```

> v=c(10,20,30)
> v
[1] 10 20 30>

```

Values with same list and different datatype:

```

l=list(10,10.5,'A')
> l
[[1]]
[1] 10

```

```

[[2]]
[1] 10.5

```

```

[[3]]
[1] "A"

```

Assigning vector earlier created

```

l2=list(10,10.5,'A',v)
> l2

```

```
[[1]]  
[1] 10
```

```
[[2]]  
[1] 10.5
```

```
[[3]]  
[1] "A"
```

```
[[4]]  
[1] 10 20 30
```

```
l2=list(10,10.5,'A',v,l)  
> l2  
[[1]]  
[1] 10
```

```
[[2]]  
[1] 10.5
```

```
[[3]]  
[1] "A"
```

```
[[4]]  
[1] 10 20 30
```

```
[[5]]  
[[5]][[1]]  
[1] 10
```

```
[[5]][[2]]  
[1] 10.5
```

```
[[5]][[3]]  
[1] "A"
```

MATRIX

```
> v=c(10,20,30,40)  
> v  
[1] 10 20 30 40  
> m=matrix(v,nrow=2)  
> m
```

```

      [,1] [,2]
[1,]  10  30
[2,]  20  40

```

For row wise representation

```

m=matrix(v,nrow=2,byrow="true")
> m
      [,1] [,2]
[1,]  10  20
[2,]  30  40
>

```

Changing elements in vectors

```

> v[2]=100
> v
[1] 10 100 30 40

```

```

> l[4]=20
> l
[[1]]
[1] 10

```

```

[[2]]
[1] 10.5

```

```

[[3]]
[1] "A"

```

```

[[4]]
[1] 20

```

```

> m=matrix(l,nrow=2,byrow="true")
> m
      [,1] [,2]
[1,] 10  10.5
[2,] "A"  20
>

```

vector	same	linear
list	different	linear
matrix	Different&same	2D

array	same	2D
-------	------	----

Arrays

```
a=array(1:12,dim=c(3,4,2))
```

```
> a
```

```
, , 1
```

```
  [,1] [,2] [,3] [,4]
[1,]  1  4  7 10
[2,]  2  5  8 11
[3,]  3  6  9 12
```

```
, , 2
```

```
  [,1] [,2] [,3] [,4]
[1,]  1  4  7 10
[2,]  2  5  8 11
[3,]  3  6  9 12
```

```
> a=array(c("red","blue"),dim=c(3,4,2))
```

```
> a
```

```
, , 1
```

```
  [,1] [,2] [,3] [,4]
[1,] "red" "blue" "red" "blue"
[2,] "blue" "red" "blue" "red"
[3,] "red" "blue" "red" "blue"
```

```
, , 2
```

```
  [,1] [,2] [,3] [,4]
[1,] "red" "blue" "red" "blue"
[2,] "blue" "red" "blue" "red"
[3,] "red" "blue" "red" "blue"
```

```
>
```

Merging 2 vectors and combining it into a table

```
Name=c("asmita","bharti","aditya")
```

```
> age=c(12,34,45)
```

```
> details=cbind(Name,age)
```

```
> details
```

```

      Name age
[1,] "asmita" "12"
[2,] "bharti" "34"
[3,] "aditya" "45"
>

```

DATA FRAMES

EXCEL FILE COMES TO R STUDIO IT SEES IT AS DATA FRAMES.

```

students<-data.frame(Name=c('a','b','c'),Age=c(23,45,45),Height=c(140,180,160))
> students
  Name Age Height
1  a  23   140
2  b  45   180
3  c  45   160
>

```

Create a data frame employee having vectors employee name ,emp;loyee id,emp_salary,emp_joining_date,emp_designation.

```

employee<-data.frame(emp_name=c('asmita','aditya','smita','anisha'),emp_id=c(1,4,5,6),emp
_salary=c(12000,40000,56000,89000),emp_joining_date=c('12/6/2022','23/8/2000','23/6/202
1','24/9/2023'),emp_designation=c('hacker','doctor','smoother','cobbler'))
employee

```

Output:

```

> employee
  emp_name emp_id emp_salary emp_joining_date emp_designation
1  asmita     1    12000     12/6/2022     hacker
2  aditya     4    40000     23/8/2000     doctor
3  smita      5    56000     23/6/2021    smoother
4  anisha      6    89000     24/9/2023     cobbler
>
>
>

```

Create vector of fruits and list of colors and merge them.

```

fruits=c('mango','banana','apple')
colors=list('yellow','yellow','red')
druy=cbind(fruits,colors)
druy

```

Output:

```

fruits colors

```

```
[1,] "mango" "yellow"  
[2,] "banana" "yellow"  
[3,] "apple" "red"  
>
```

Create a matrix of name, country and capital city of size 4*3

PRACTICAL 2

In the source window, select the code and run.

NEW*

MATRIX

```
m1=matrix(1:9,nrow=3)  
> m2=matrix(10:18,nrow=3)  
> m1  
  [,1] [,2] [,3]  
[1,]  1  4  7  
[2,]  2  5  8  
[3,]  3  6  9  
> m2  
  [,1] [,2] [,3]  
[1,] 10 13 16  
[2,] 11 14 17  
[3,] 12 15 18
```

ADDITION OF A MATRIX

```
m=m1+m2  
> m  
  [,1] [,2] [,3]  
[1,] 11 17 23  
[2,] 13 19 25  
[3,] 15 21 27
```

```
>  
SUBTRACTION OF A MATRIX
```

```
m=m1-m2  
> m  
      [,1] [,2] [,3]  
[1,]  -9  -9  -9  
[2,]  -9  -9  -9  
[3,]  -9  -9  -9  
>
```

```
MULTIPLICATION OF A MATRIX.
```

```
m=m1*m2  
> m  
      [,1] [,2] [,3]  
[1,]   10   52  112  
[2,]   22   70  136  
[3,]   36   90  162
```

```
DIVISION OF A MATRIX
```

```
m=m1/m2  
> m  
      [,1] [,2] [,3]  
[1,] 0.1000000 0.3076923 0.4375000  
[2,] 0.1818182 0.3571429 0.4705882  
[3,] 0.2500000 0.4000000 0.5000000
```

```
TRANSPOSE OF A MATRIX -row to column and column to row.
```

```
tm=t(m1)  
> tm  
      [,1] [,2] [,3]  
[1,]    1    2    3  
[2,]    4    5    6  
[3,]    7    8    9  
>
```

```
INVERSE OF A MATRIX.
```

```
Determinant
```

```
det(m1)  
[1] 0  
> det(m2)  
[1] 5.329071e-15
```

NEW MATRIX.

```
m3=matrix(c(10,2,3,5),nrow=2)
```

```
> m3
```

```
      [,1] [,2]  
[1,]  10   3  
[2,]   2   5
```

```
> det(m3)
```

```
[1] 44
```

```
> solve(m3)
```

```
      [,1] [,2]  
[1,] 0.11363636 -0.06818182  
[2,] -0.04545455  0.22727273  
>
```

PRACTICAL 3 & PRACTICAL 4

Using R Execute the statistical functions: mean, median, mode, quartiles, range, inter quartile range histogram

1.CREATE EXCEL FILE.

2. ENTER THE DETAILS INTO THAT

3. SAVE THE FILE WITH .CSV(COMMA DELIMITED).

4. CLICK YES AND OK

5. AFTER THAT GO TO RSTUDIO

6. AND IN ENVIRONMENT SECTION GO TO IMPORT DATASET. AND FIND YOUR FILE AND IMPORT IT.

7. AFTER THAT IMPORT QUERIES

```
mean([filename]$(columnname))
```

```
ex)
```

MEAN:

NOTE: write code in source

```
mean(student$marks)
```

```
median(student$marks).
```

Code:

```
meanval=function(v)
```

```
+ {
```

```
+   l=length(v)
```

```
+   sum=0
```

```
+   for(i in v)
```

```
+   {
```

```
+     sum=sum+i
```



```
+ }
+ avg=sum/l
+ avg
+ }
> meanval(student$MARKS)
[1] 83.8
```

MEDIAN:

```
med=function(v)
+ {
+   l=length(v)
+   v=sort(v)
+   if(l%%2==0)
+   {
+     p=l/2
+     q=p+1
+     md=(v[p]+v[q])/2
+   }
+   else
+   {
+     p=(l+1)/2
+     md=v[p]
+   }
+   md
+ }
>
>
> med(student$MARKS)
[1] 93.5
> med(student$MARKS)
[1] 93.5
>
```

With vectors.

```
v=c(1,2,3,4,5)
med(v)
```

Output;

```
[1] 3
```

MODE:

UNIQUE- ONLY UNIQUE VALUES

MAX= MAXIMUM VALUE

TABLE= RETURN FREQUENCY

MATCH= CHECK X VALUES AND RETURN Y POSITION WITH RESPECT TO X

MATCH(X,Y)

2->1

WHICH PROPERTY- RETURN THE POSITION.

ex)

```
getmod=function(x)
{
  uniqx=unique(x)
  mod=uniqx[which.max(table(match(x,uniqx)))]
  mod
}
getmod(student$MARKS)
```

OUTPUT:

```
> getmod(student$MARKS)
[1] 99
>
```

EXPLANATION

x=(6,4,6,4,8,6)
uniqx=(6,4,8)

Match

6->1,4->2,6->1,4->2,8->3,6->1

Table

position-> occurrence

1->3

2->2

3->1

max=3 occurrence=1(position)

mod[1]

Therefore the mod is 6.

PRACTICAL 5

VARIANCE.- DIFFERENCE OF AVERAGE WITH RESPECT TO POSITION.

```
> var(student$MARKS)
[1] 573.2889
> var(student$MARKS)
[1] 573.2889
```

VARIANCE CODE:

```
varx=function(x)
{
  n=length(x)
  m=meanval(x)
  sum=0
  for(i in x)
  {
    sqdiff=(i-m)^2
    sum=sum+sqdiff
  }
  variance=sum/n
  variance
}
```

```
varx(student$MARKS)
```

OUTPUT:

```
> varx(student$MARKS)
[1] 515.96
> varx(student$MARKS)
[1] 515.96
>
```

PRACTICAL 5

COVARIANCE

```
covar=function(x,y)
{
  mk=meanval(x)
  at=meanval(y)
  n=length(x)
  sum=0
  for(i in seq_along(x))
  {
```

```

    cvmarks=x[i]-mk
    cvattd=y[i]-at
    mul=cvmarks*cvattd
    sum=sum+mul
  }
  cv=sum/(n-1)
  cv
}

```

OUTPUT:

```

> covar(stud45$MARKS,stud45$ATTENDANCE)
[1] 250.6889

> cov(stud45$MARKS,stud45$ATTENDANCE)
[1] 250.6889

```

STANDARD DEVIATION

```

std=function(x)
{
  v=var(x)
  s=sqrt(v)
  s
}

```

OUTPUT:

```

> std(stud45$MARKS)
[1] 28.22782

```

PRACTICAL 6

-0.5 to 0.5= fairly skewed
 -0.5 to -1=negatively moderately skewed
 -0.5 to 1=positively moderately skewed.

SKEWNESS

```

sk1=function(x)
{
  s=(3*meanval(x)-med(x))/std(x)
  s
}

```

OUTPUT:

```

> sk1(stud45$MARKS)

```

```
[1] 4.718576  
> sk(stud45$MARKS)
```

```
[1] 4.718576
```

PRACTICAL 7

HYPOTHESIS

QUESTION:

Mean weight=15.4kg
Sample Size=35
Sample mean=14.6kg
Sd=2.5

You can't say that your hypothesis is correct

PRACTICAL 3

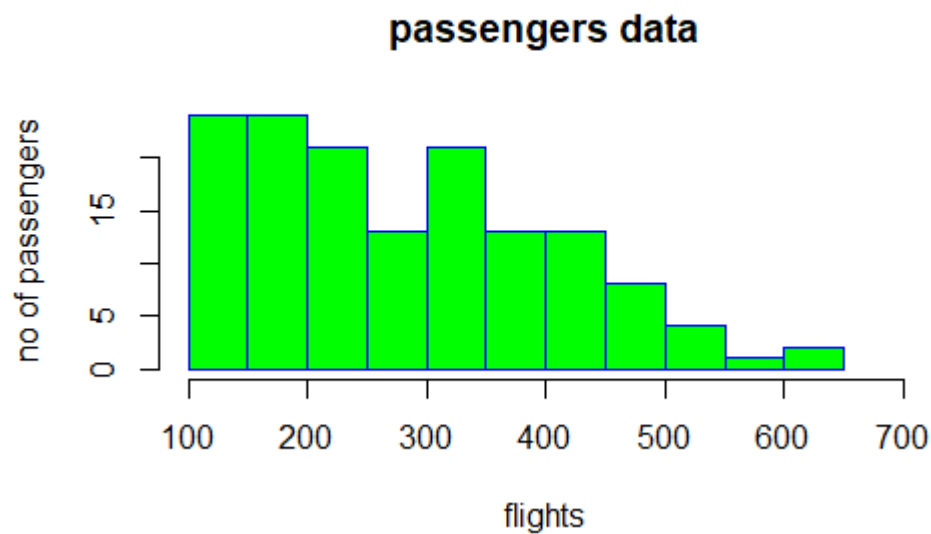
Using R Execute the statistical functions:mean, median, mode, quartiles, range, inter quartile range histogram

HISTOGRAM

CODE:

```
hist(AirPassengers,  
main="passengers data",  
xlab="flights",  
ylab="no of passengers",  
xlim=c(100,700),  
col="green",  
border="blue",  
breaks=10  
)
```

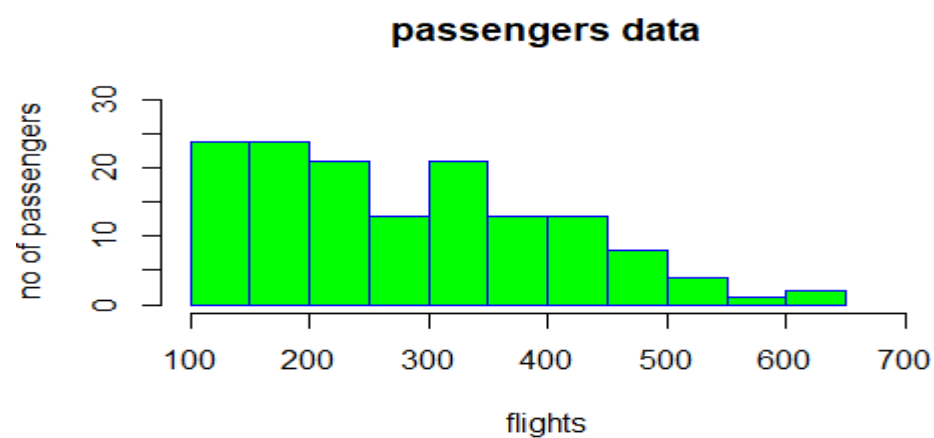
OUTPUT:



```

hist(AirPassengers,
main="passengers data",
xlab="flights",
ylab="no of passengers",
xlim=c(100,700),
ylim=c(0,30),
col="green",
border="blue",
breaks=10
)
    
```

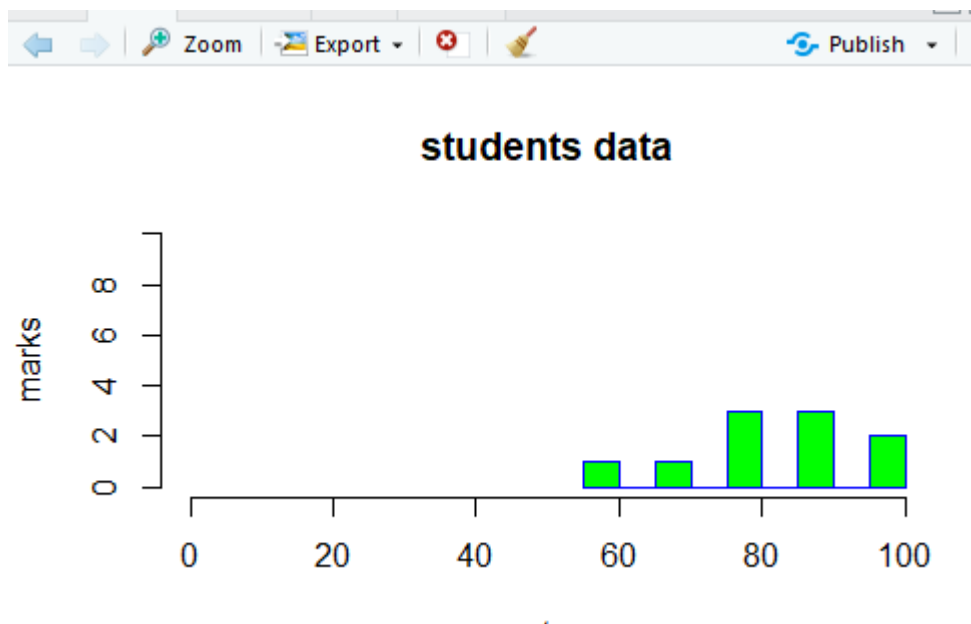
OUTPUT:



WITH STUDENTS DATA

```
hist(student$MARKS,  
main="students data",  
xlab="stu",  
ylab="marks",  
xlim=c(0,100),  
ylim=c(0,10),  
col="green",  
border="blue",  
breaks=10  
)
```

OUTPUT:



QUARTILES

```
quantile(student$MARKS)
```

OUTPUT

```
> quantile(student$MARKS)  
 0%   25%  50%  75% 100%  
56.00 77.25 83.50 90.00 100.00
```

InterQuartileRange:(Between 25% and 75%)(Subtraction)

```
IQR(student$MARKS)
```

OUTPUT:

```
> IQR(student$MARKS)
[1] 12.75
```

RANGE:

```
> range(student$MARKS)
[1] 56 100
```

PRACTICAL 7

Import the data from Excel / .CSV and perform the hypothetical testing.

Question1: (WEIGHTS OF PENGUINS)

$\mu = 15.4\text{kg}$

$n = 35$

$\bar{x} = 14.6\text{kg}$

$sd = 2.5$

Level of significance = 0.05

a) $H_0: \mu \geq 15.4$ (lower tail test)

b) $H_0: \mu \leq 15.4$ (Upper tail test)

c) $H_0: \mu = 15.4$ (Equality test)-it doesn't matter whether it is greater or lesser but is there is a change or not.

SOLUTION:

a) $H_0: \mu \geq 15.4$

$H_1: \mu < 15.4$

$\mu = 15.4$

$n = 35$

$\bar{x} = 14.6$

$sd = 2.5$

$t = (\bar{x} - \mu) / (sd / \sqrt{n})$

t

$p = pt(t, df = n - 1)$

p

OUTPUT:


```
> t
[1] -1.893146
> p=pt(t,df=n-1)
> p
[1] 0.03343776 // 3%
>
```

THIS NULL HYPOTHESIS IS REJECTED

b)(STUDENTS SLEEP HOURS)

$H_0 = w \leq 15.4$

$H_1 = w > 15.4$

```
p=pt(t,df=n-1,lower.tail=FALSE)
P
```

OUTPUT:

```
> p=pt(t,df=n-1,lower.tail=FALSE)
> p
[1] 0.9665622 // 96%
```

THIS NULL HYPOTHESIS IS ACCEPTED

c)

$H_0 = w = 15.4$

$H_1 = w \neq 15.4$

```
p=2*pt(t,df=n-1)
p
```

OUTPUT:

```
> p=2*pt(t,df=n-1)
> p
[1] 0.06687552
```

Question 2:

$x = 7.24$

$u = 7$

$n = 22$

$sd = 1.93$

Significance level = 5%

Solution:

H0:hrs<=7

H1:hrs>7

CODE:

u=7

n=22

x=7.24

sd=1.93

t=(x-u)/(sd/sqrt(n))

t

p=pt(t,df=n-1,lower.tail=FALSE)

p

OUTPUT:

> u=7

> n=22

> x=7.24

> sd=1.93

> t=(x-u)/(sd/sqrt(n))

> t

[1] 0.5832641

> p=pt(t,df=n-1,lower.tail=FALSE)

> p

[1] 0.2829637 // 28%

THIS NULL HYPOTHESIS IS ACCEPTED.

Question 3:go for sample sd not for population

x=46500

u=50000

n=28

sd=9800

Significance level =5%

Solution:

HO=L>=50000

H1=L<50000

CODE:

```
u=50000
n=28
x=46500
sd=9800
t=(x-u)/(sd/sqrt(n))
t
p=pt(t,df=n-1)
p
```

OUTPUT:

```
> u=50000
> n=28
> x=46500
> sd=9800
> t=(x-u)/(sd/sqrt(n))
> t
[1] -1.889822
> p=pt(t,df=n-1)
> p
[1] 0.03478162 //3%
>
```

THIS NULL HYPOTHESIS IS REJECTED.

Question 4

```
x=18.1
u=19
n=40
sd=1.3
Significance level=5%
```

Solution:

H0: age \geq 19

H1: age $<$ 19

CODE:

```
u=18.1
n=19
x=40
sd=1.3
t=(x-u)/(sd/sqrt(n))
t
p=pt(t,df=n-1)
p
```

OUTPUT:

```

> u=18.1
> n=19
> x=40
> sd=1.3
> t=(x-u)/(sd/sqrt(n))
> t
[1] 73.43068
> p=pt(t,df=n-1)
> p
[1] 1

```

THIS HYPOTHESIS WILL BE REJECTED.

PRACTICAL 8

CHI SQUARED TEST- It is done when columns contain limited data
 Test for 2 categorical variables to check whether they are related or not
 Ex male and female(2 categories)

CODE:

```

library(MASS)
print(str(survey))

```

```

> print(str(survey))
'data.frame': 237 obs. of 12 variables:
 $ Sex : Factor w/ 2 levels "Female","Male": 1 2 2 2 2 1 2 1 2 2 ...
 $ Wr.Hnd: num 18.5 19.5 18 18.8 20 18 17.7 17 20 18.5 ...
 $ NW.Hnd: num 18 20.5 13.3 18.9 20 17.7 17.7 17.3 19.5 18.5 ...
 $ W.Hnd : Factor w/ 2 levels "Left","Right": 2 1 2 2 2 2 2 2 2 2 ...
 $ Fold : Factor w/ 3 levels "L on R","Neither",...: 3 3 1 3 2 1 1 3 3 3 ...
 $ Pulse : int 92 104 87 NA 35 64 83 74 72 90 ...
 $ Clap : Factor w/ 3 levels "Left","Neither",...: 1 1 2 2 3 3 3 3 3 3 ...
 $ Exer : Factor w/ 3 levels "Freq","None",...: 3 2 2 2 3 3 1 1 3 3 ...
 $ Smoke : Factor w/ 4 levels "Heavy","Never",...: 2 4 3 2 2 2 2 2 2 2 ...
 $ Height: num 173 178 NA 160 165 ...
 $ M.I : Factor w/ 2 levels "Imperial","Metric": 2 1 NA 2 2 1 1 2 2 2 ...
 $ Age : num 18.2 17.6 16.9 20.3 23.7 ...
NULL
> stu_data=data.frame(survey$Smoke,survey$Smoke)

```

```

stu_data=data.frame(survey$Smoke,survey$Exer)
stu_data=table(survey$Smoke,survey$Exer)
print(stu_data)

```

OUTPUT:

```
> print(stu_data)
```

	Freq	None	Some
Heavy	7	1	3
Never	87	18	84
Occas	12	3	4
Regul	9	1	7

```
> |
```

```
print (chisq.test(stu_data,correct = FALSE))
```

```
Pearson's Chi-squared test
```

```
data: stu_data
X-squared = 5.4885, df = 6, p-value = 0.4828
```

```
.. .
```

Q.RELATION BETWEEN THE SURVEY FOLD AND EXERCISES

```
ho=smoking<>Exercise accept
```

```
h1=Smoking~=Exercise
```

```
stu_data=data.frame(survey$Fold,survey$Exer)
```

```
stu_data=table(survey$Fold,survey$Exer)
```

```
print(stu_data)
```

```
print (chisq.test(stu_data,correct = FALSE))
```

```
> print (chisq.test(stu_data,correct = FALSE))
```

```
Pearson's Chi-squared test
```

```
data: stu_data
X-squared = 1.2213, df = 4, p-value = 0.8746
```

```
.. .
```

```
print(str(oats))
```

```
print(str(Melanoma))
```

```

Chi-squared approximation may be incorrect
> print(str(oats))
'data.frame': 72 obs. of 4 variables:
 $ B: Factor w/ 6 levels "I","II","III",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ V: Factor w/ 3 levels "Golden.rain",...: 3 3 3 3 1 1 1 1 2 2 ...
 $ N: Factor w/ 4 levels "0.0cwt","0.2cwt",...: 1 2 3 4 1 2 3 4 1 2 ...
 $ Y: int 111 130 157 174 117 114 161 141 105 140 ...
NULL
> print(str(Melanoma))
'data.frame': 205 obs. of 7 variables:
 $ time : int 10 30 35 99 185 204 210 232 232 279 ...
 $ status : int 3 3 2 3 1 1 1 3 1 1 ...
 $ sex : int 1 1 1 0 1 1 1 0 1 0 ...
 $ age : int 76 56 41 71 52 28 77 60 49 68 ...
 $ year : int 1972 1968 1977 1968 1965 1971 1972 1974 1968 1971 ...

```

```

Mel_data=data.frame(Melanoma$status,Melanoma$sex)
Mel_data=table(Melanoma$status,Melanoma$sex)
print(Mel_data)
print(chisq.test(Mel_data))

```

```

> Mel_data=table(Melanoma$status,Melanoma$sex)
> print(Mel_data)

```

```

  0  1
1 28 29
2 91 43
3  7  7

```

```

> print(chisq.test(Mel_data))

```

Pearson's Chi-squared test

```

data: Mel_data
X-squared = 6.793, df = 2, p-value = 0.03349

```

```

> |

```

REJECT THE NULL HYPOTHESIS

Q.RELATION BETWEEN CARS TYPE AND ENGINESIZE

```

print(str(Cars93))
car_data=data.frame(Cars93$Type,Cars93$EngineSize)
car_data=table(Cars93$Type,Cars93$EngineSize)
print(car_data)
print(chisq.test(car_data))

```

```

> car_data=data.frame(Cars93$Type,Cars93$EngineSize)
> car_data=table(Cars93$Type,Cars93$EngineSize)
> print(car_data)

      1 1.2 1.3 1.5 1.6 1.8 1.9 2 2.1 2.2 2.3 2.4 2.5 2.8 3 3.2 3.3 3.4 3.5 3.8 4.3 4.5 4.6
Compact 0  0  0  0  0  0  0  0  2  1  4  4  1  2  1  1  0  0  0  0  0  0  0
Large   0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  2  0  1  3  0  0  2
Midsize 0  0  0  0  0  0  0  0  1  0  4  0  1  1  5  2  0  1  1  3  0  1  1
Small   1  1  2  6  3  6  1  0  0  1  0  0  0  0  0  0  0  0  0  0  0  0  0
Sporty  0  0  1  1  2  1  0  1  0  1  2  0  0  1  1  0  0  2  0  0  0  0  0
Van     0  0  0  0  0  0  0  0  0  0  0  1  1  0  4  0  0  0  0  2  1  0  0

      4.9 5 5.7
Compact  0 0  0
Large    1 1  1
Midsize  0 0  0
Small     0 0  0
Sporty   0 0  1
Van      0 0  0
> print(chisq.test(car_data))

Pearson's Chi-squared test

data:  car_data
X-squared = 201.26, df = 125, p-value = 1.814e-05

Warning message:
In chisq.test(car_data) : Chi-squared approximation may be incorrect

```

REJECT THE NULL HYPOTHESIS

PRACTICAL 9

BINOMIAL DISTRIBUTION

Pdimom -cumulative

dbinom=specific

```

dbinom(4,size=12,prob=0.2)
[1] 0.1328756
> pbinom(4,size=12,prob=0.2)
[1] 0.9274445
> dbinom(4,size=12,prob=0.8)
[1] 0.0005190451
> pbinom(4,size=12,prob=0.8)
[1] 0.0005812429
> dbinom(4,size=12,prob=0.8)+
+ pbinom(3,size=12,prob=0.8)+
+ pbinom(2,size=12,prob=0.2)+
+ pbinom(1,size=12,prob=0.2)+
+ pbinom(0,size=12,prob=0.2)
[1] 0.9025244
> dbinom(4,size=12,prob=0.8)+
+ pbinom(3,size=12,prob=0.8)+
+ pbinom(2,size=12,prob=0.8)+
+ pbinom(1,size=12,prob=0.8)+
+ pbinom(0,size=12,prob=0.8)

```

```
[1] 0.0005859738
> dbinom(4,size=12,prob=0.8)+
+ dbinom(3,size=12,prob=0.8)+
+ dbinom(2,size=12,prob=0.8)+
+ dbinom(1,size=12,prob=0.8)+
+ dbinom(0,size=12,prob=0.8)
[1] 0.0005812429
>
```

Question 1

```
dbinom(6,size=10,prob=0.5)
pbinom(6,size=10,prob=0.5)
```

```
[1] 0.0005812429
> dbinom(6,size=10,prob=0.5)
[1] 0.2050781
> pbinom(6,size=10,prob=0.5)
[1] 0.828125
>
```

Microsoft Store

```
dbinom(0,size=9,prob=0.8)
dbinom(9,size=9,prob=0.2)
```

Mens question

NORMAL DISTRIBUTION

```
pno,m
pnorm(20.08,mean=20.05,sd=0.02)-
pnorm(20.03,mean=20.05,sd=0.02)
```

```
> pnorm(20.08,mean=20.05,sd=0.02)-
[1] 0.4331928
> pnorm(20.08,mean=20.05,sd=0.02)-
+ pnorm(20.03,mean=20.05,sd=0.02)
[1] 0.7745375
> |
```

File Explorer

```
pnorm(20.00,20.05,0.02)
1-pnorm(20.09,20.05,0.02)
1-pnorm(84,72,15.2)
```



```

> pnorm(20.00,20.05,0.02)
[1] 0.006209665
> 1-pnorm(20.09,20.05,0.02)
[1] 0.02275013
> 1-pnorm(84,72,15.2)
[1] 0.2149176
>

```

PRACTICAL 10

LINEAR REGRESSION - PREDICTION

```

sumxy=function(x,y)
{
  n=length(x)
  sum=0
  for(i in seq_along(x))
  {
    sum=sum + x[i]*y[i]
  }
  sum
}

```

```

v=c(1,2,3,4,5)
v
x=c(2,4,6,8,10)
x
sumxy(v,x)

```

```

sum=function(v)
{
  s=0
  for (i in v)
  {
    s=s + i
  }
  s
}

```

```
sum(v)
```

```

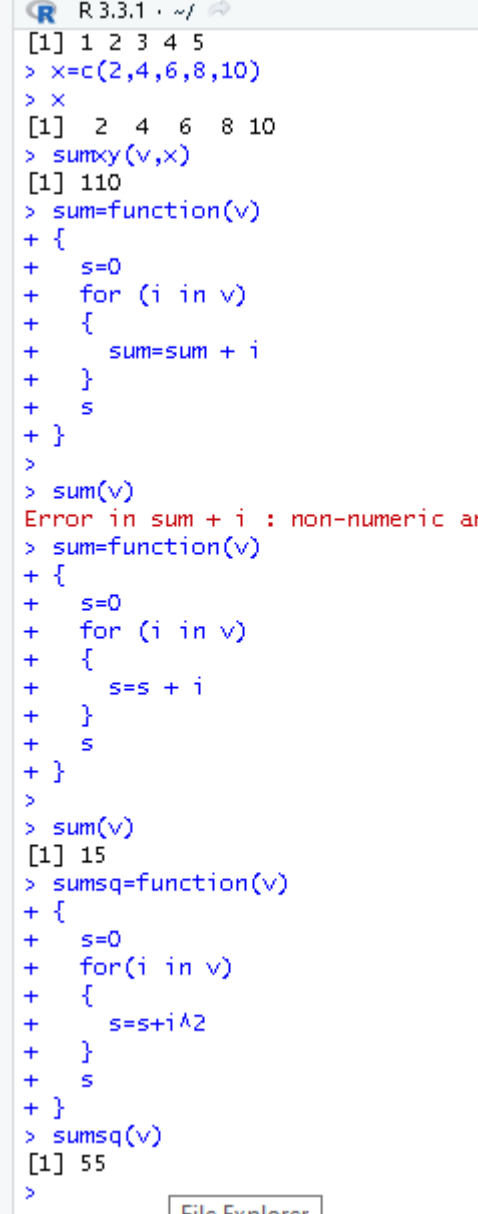
sumsq=function(v)
{
  s=0
  for(i in v)

```

```

{
  s=s+i^2
}
s
}
sumsq(v)
}
}

```



```

R 3.3.1 ~f
[1] 1 2 3 4 5
> x=c(2,4,6,8,10)
> x
[1] 2 4 6 8 10
> sumxy(v,x)
[1] 110
> sum=function(v)
+ {
+   s=0
+   for (i in v)
+   {
+     sum=sum + i
+   }
+   s
+ }
>
> sum(v)
Error in sum + i : non-numeric ar
> sum=function(v)
+ {
+   s=0
+   for (i in v)
+   {
+     s=s + i
+   }
+   s
+ }
>
> sum(v)
[1] 15
> sumsq=function(v)
+ {
+   s=0
+   for(i in v)
+   {
+     s=s+i^2
+   }
+   s
+ }
> sumsq(v)
[1] 55
>

```

File Explorer

```

n=length(v)
n
txy=sumxy(v,x)
txy
psxy=sum(v)*sum(x)
psxy

```

```
tsqx=sumsq(v)
tsqx
sqsx=sum(v)*sum(v)
sqsx
```

```
> n
[1] 5
> txy=sumxy(v,x)
> txy
[1] 110
> psxy=sum(v)*sum(x)
> psxy
[1] 450
> tsqx=sumsq(v)
> tsqx
[1] 55
> sqsx=sum(v)*sum(v)
> sqsx
[1] 225
> |
```

Microsof

```
tx=sum(v)
tx
ty=sum(x)
ty
```

```
b=((n*txy)-psxy)/((n*tsqx)-sqsx)
b
```

```
a=((ty*tsqx)-tx*txy)/((n*tsqx)-sqsx)
a
```

```
> tx=sum(v)
> tx
[1] 15
> ty=sum(x)
> ty
[1] 30
> b=((n*txy)-psxy)/((n*tsqx)-sqsx)
> b
[1] 2
> a=((ty*tsqx)-tx*txy)/((n*tsqx)-sqsx)
> a
[1] 0
> |
```

Type here to search

```
y=a+b*6
```

y

```
[1] 12 12 12
> y=a+b*6
> y
[1] 12
> |
```

PRACTICAL 11 & 12

Least square means-bls

Less error nice prediction

```
bls=(ty-(b*tx))/n
bls
```

```
x=50
y=b*50+0
y
```

```
[1] 12
> bls=(ty-(b*tx))/n
> bls
[1] 0
> y=b*50+0
> y
[1] 100
> |
```

```
error=function(x,y)
{
  yn=0
  for(i in seq_along(x))
  {
    yn=b*i+bls
    cat(sprintf("error for %d is %f:\n",i,yn-y[i]))
  }
}
error(v,x)
```

```
T      cat(sprintf('error for %d is\n', i))
+      }
+ }
> error(v,x)
error for 1 is -5.800000:
error for 2 is 2.300000:
error for 3 is 6.400000:
error for 4 is 3.500000:
error for 5 is -6.400000:
> |
```

Google Chrc

