NAME: G.NARAYANEE NIMESHIKA
REG NUM : 20BPS1111

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Activity Sheet - 9 - LARGE SAMPLE TEST

AIM: To find whether the hypothesis is accepted or rejected

1)

SYNTAX:

```
# Null hypothesis H0: mu =12.0
# Alternative Hypothesis: H1:mu ≠ 12.0
xbar=mean(x)
sd=sqrt(var(x))
n=length(x)
t=(xbar-mu)/(sd/sqrt(n))
t
tv=qt(1-a/2,df=n-1) #two tailed
tv
if (t<tv)
sprintf("We accept the null hypothesis H0")else
{
  sprintf("We reject the null hypothesis H0")
}
```

CODE:

```r
# Null hypothesis H0: mu =12.0
# Alternative Hypothesis: H1:mu ≠ 12.0
x=c(14.3,12.6,13.7,10.9,13.7,12.0,11.4,12.0,12.6,13.1)
mu=12
a =.05
xbar=mean(x)
sd=sqrt(var(x))
n=length(x)
t=(xbar-mu)/(sd/sqrt(n))
t
tv=qt(1-a/2,df=n-1) #two tailed
tv
if (t<tv)
sprintf("We accept the null hypothesis H0")else
{
  sprintf("We reject the null hypothesis H0")
}
```

OUTPUT:

```
> # Null hypothesis H0: mu =12.0
> # Alternative Hypothesis: H1:mu ≠ 12.0
> x=c(14.3,12.6,13.7,10.9,13.7,12.0,11.4,12.0,12.6,13.1)
> mu=12
> a =.05
> xbar=mean(x)
> sd=sqrt(var(x))
> n=length(x)
> t=(xbar-mu)/(sd/sqrt(n))
> t
[1] 1.835644
> tv=qt(1-a/2,df=n-1) #two tailed
> tv
[1] 2.262157
> if (t<tv)
+ sprintf("We accept the null hypothesis H0")else
+ {
+   sprintf("We reject the null hypothesis H0")
+ }
[1] "We accept the null hypothesis H0"
```

2)

H0: mu1 = mu2 there is no significant difference between the medicines A and B as regards on increase in weight.

H1: mu1 ≠ mu2 there is a significant difference between the medicines A and B

SYNTAX:

n1=length(a); n2=length(b)

al=0.01

tv=qf(1-al/2,n1-1,n2-1)

f=var(a)/var(b)

#alternative way

ft=var.test(a,b,alternative="two.sided")

CODE:

```r
a=c(42,39,38,60,41)
b=c(38, 42,56, 64, 68, 69, 62)
n1=length(a)
n2=length(b)
al=0.01
tv=qf(1-al/2,n1-1,n2-1)
f=var(a)/var(b)
f
#alternative way
ft=var.test(a,b,alternative="two.sided")
ft
```

OUTPUT:

```
> f
[1] 0.5345572
>
> #alternative way
> ft=var.test(a,b,alternative="two.sided")
> ft

        F test to compare two variances

data:  a and b
F = 0.53456, num df = 4, denom df = 6, p-value = 0.5668
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.08584285 4.91648918
sample estimates:
ratio of variances
         0.5345572
```

3) SYNTAX:

Null hypothesis H0:var1=var2

Alternative Hypothesis: H1:var1 ≠ var2

n1=length(a); n2=length(b)

al=0.05

tv=qf(1-al/2,n1-1,n2-1)

f=var(b)/var(a)

#alternative way

ft=var.test(a,b,alternative="two.sided")

CODE:

```r
# Null hypothesis H0:var1=var2
# Alternative Hypothesis: H1:var1 ≠ var2
a=c(6.21, 5.70, 6.04, 4.47, 5.22, 4.45, 4.84, 5.84, 5.88, 5.82, 6.09, 5.59,6.06, 5.59, 6.74, 5.55)
b=c(4.28 ,7.71 ,6.48 ,7.71, 7.37 ,7.20 ,7.06 ,6.40 ,8.93, 5.91, 5.51, 6.36)
n1=length(a)
n2=length(b)
al=0.05
tv=qf(1-al/2,n1-1,n2-1)
f=var(b)/var(a)
f
#alternative way
ft=var.test(a,b,alternative="two.sided")
ft
```

OUTPUT:

```
> f
[1] 3.741404
> #alternative way
> ft=var.test(a,b,alternative="two.sided")
> ft

        F test to compare two variances

data:  a and b
F = 0.26728, num df = 15, denom df = 11, p-value = 0.01972
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.08026564 0.80393023
sample estimates:
ratio of variances
         0.2672793
```

INFERENCE : Hypothesis H0 is rejected

4)

SYNTAX:

```
x=c(49, 53 ,51, 52, 47, 50 ,52 ,53)
y=c(52, 55 ,52, 53, 50 ,54 ,54, 53)
t.test(x, y, paired = TRUE, alternative = "two.sided")
#alternate
n=length(x)
d=(x-y)
a=0.05
mean=mean(d)
sd=sd(d)
tc=abs(mean/(sd/sqrt(n)))
tv=qt(1-a/2,df=n-1) #two tailed
if (tc<tv)
  sprintf("We accept the null hypothesis H0")else
  {
    sprintf("We reject the null hypothesis H0")
  }
```

CODE:

```r
x=c(49, 53 ,51, 52, 47, 50 ,52 ,53)
y=c(52, 55 ,52, 53, 50 ,54 ,54, 53)
t.test(x, y, paired = TRUE, alternative = "two.sided")
#alternate
n=length(x)
d=(x-y)
a=0.05
mean=mean(d)
sd=sd(d)
tc=abs(mean/(sd/sqrt(n)))
n
mean
sd
tc
tv=qt(1-a/2,df=n-1) #two tailed
tv
if (tc<tv)
  sprintf("We accept the null hypothesis H0")else
  {
    sprintf("We reject the null hypothesis H0")
  }
```

OUTPUT:

```
> x=c(49, 53 ,51, 52, 47, 50 ,52 ,53)
> y=c(52, 55 ,52, 53, 50 ,54 ,54, 53)
> t.test(x, y, paired = TRUE, alternative = "two.sided")

        Paired t-test

data:  x and y
t = -4.3205, df = 7, p-value = 0.003478
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -3.0946083 -0.9053917
sample estimates:
mean of the differences
                     -2
```

```
> #alternate
> n=length(x)
> d=(x-y)
> a=0.05
> mean=mean(d)
> sd=sd(d)
> tc=abs(mean/(sd/sqrt(n)))
> n
[1] 8
> mean
[1] -2
> sd
[1] 1.309307
```

```
> tc
[1] 4.320494
> tv=qt(1-a/2,df=n-1) #two tailed
> tv
[1] 2.364624
> if (tc<tv)
+   sprintf("We accept the null hypothesis H0")else
+   {
+     sprintf("We reject the null hypothesis H0")
+   }
[1] "We reject the null hypothesis H0"
```

5)

AIM: To test if there is any association between the attribute independence of attribute and goodness of fit using chi Square distribution

SYNTAX:

```
o=c(404,420,400,376)

e=c(400,400,400,400)

xsq=sum((o-e)^2/e)

xsq

cv=qchisq(p=0.05,df=3,lower.tail=FALSE)

cv

if(cv>xsq){

  print("H0 IS ACCEPTED")

}else{

  print(" H1 IS ACCEPTED")

}

data=matrix(c(404,420,400,376),ncol=4,byrow=T)

data

chisq.test(data)
```

CODE:

```
o=c(404,420,400,376)
e=c(400,400,400,400)
xsq=sum((o-e)^2/e)
xsq
cv=qchisq(p=0.05,df=3,lower.tail=FALSE)
cv
if(cv>xsq){
  print("H0 IS ACCEPTED")
}else{
  print(" H1 IS ACCEPTED")
}
data=matrix(c(404,420,400,376),ncol=4,byrow=T)
data
chisq.test(data)
```

OUTPUT:

```
> o=c(404,420,400,376)
> e=c(400,400,400,400)
> xsq=sum((o-e)^2/e)
> xsq
[1] 2.48
> cv=qchisq(p=0.05,df=3,lower.tail=FALSE)
> cv
[1] 7.814728
> if(cv>xsq){
+   print("H0 IS ACCEPTED")
+ }else{
+   print(" H1 IS ACCEPTED")
+ }
[1] "H0 IS ACCEPTED"
> data=matrix(c(404,420,400,376),ncol=4,byrow=T)
> data
     [,1] [,2] [,3] [,4]
[1,]  404  420  400  376
> chisq.test(data)

        Chi-squared test for given probabilities

data:  data
X-squared = 2.48, df = 3, p-value = 0.4789
```