Experiment No: 03

Experiment Name: A herd of 1500 steer was fed to special high protein gain for a month. A random sample of 29 was weighted and had gained an average of 6.7 pounds. If the sd of weight gain for the entire herd is 7.1. Test the hypothesis at 5% level of significance that the average weight gain per steer for the month was more than 5 pounds. Also comments on the test using the p-value. Create the confidence interval

Objectives:

1. To construct the average weight gain per steer for the month. ~~was~~
2. To create the confidence interval
3. To construct p-value.
4. To comment on the data.

Procedure :

Step-1: state the null hypothesis and alternative hypothesis.
The alternate hypothesis was more than 5 pounds.
So, H1 : mu >5
H0 : mu <=5

Step-2: Select the level of significance.
The significance level is ~~are~~ selected 0.05.

Step-3: select the test statistic.
Hence, the standard deviation are known, so we use z-test.

$$Z = \frac{\bar{x} - \mu}{\sigma/\sqrt{n}}$$

$$\bar{x} = \frac{1}{n} \Sigma x_i$$

Step-4: Formulate the decision rule.
If the tabulated value of z is greater than calculated value of z then null

hypothesis is accepted, otherwise null hypothesis is rejected.

R Source code :

```
H0: mu<=5
H1: mu>5
x.bar <-6.7
mu <-5
sd <- 7.1
n <-29
z<-(x.bar - mu) / (sd / sqrt(n))
alpha = 0.05
ztab<-qnorm(0.05, lower.tail = FALSE)
# p-value
pvalue <-pnorm(z, lower.tail = FALSE)
H0: mu is not equal 5
ztab1 <-qnorm (0.025 )
ztab2 <-qnorm (0.975)
p.value<-2 * pnorm (z, lower.tail = FALSE)
CI<-c (x.bar+ztab1*sd/sqrt(n),
      x.bar+ ztab2*sd/sqrt(n) )
```

Input and output:

x.bar

6.7

mu

5

sd

7.1

n

29

z

1.28

alpha

0.05

ztab = 1.64

pvalue = 0.098

ztab1 = -1.96

ztab2 = 1.96

p.value = 0.19

CI = 4.1159 , 9.2840

Comment: From the R code we can see that, ztab > zcal and also see that pvalue > alpha. So H0 is accepted. The average weight gain per steer for the month was less than 5 pounds.

Experiment No : 04

Experiment Name: In order to find out whether children with chronic diarrhea have the same average hemoglobin level (Hb) that is normally seen in healthy children in the same area, a random sample of 10 children with chronic diarrhea are selected and their Hb levels<g/dl are obtained as follows : 12.3, 11.4, 14.2, 15.3, 14.8, 13.8, 11.1, 15.1, 15.8, 13.2. Do the data provide sufficient evidence to indicate that the mean Hb level for children with chronic diarrhea is less than the normal value of 14.6 (g/dl)? Test at 0.01 level of significance. Draw a boxplot and normal plot for this data and comments.

Objectives:

1. To Calculate the mean Hb level for Children with chronic diarrhea is less than the normal value of 14.6 (g/dl).

2. To draw a boxplot and normal plot for this data.

3. To comments for this data.

Procedure:

Step-1: State the null hypothesis and alternate hypothesis. The alternate hypothesis is less than the normal value of 14.6. So the null hypothesis is greater than or equal 14.6.

H0: $\mu >= 14.6$

H1: $\mu < 14.6$

Step-2: Select the level of significance. The significance level is selected 0.01.

Step-3: Select the test statistic.
The sample size is less 30 and population standard deviation are unknown. so we use t-test.

$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}}$$

$$s^2 = \frac{1}{n-1}\left[\Sigma x_i^2 - \frac{(\Sigma x_i)^2}{n}\right]$$

Step-4: Formulate the decision rule.
If the tabulated value of t is greater than calculated value of t then H0 is accepted, otherwise rejected.

R Source code:

```
H0: mu>=14.6
H1: mu<14.6
mu<-14.6
data<-c(12.3, 11.4, 14.2, 15.3, 14.8, 13.8, 11.1,
15.1, 15.8, 13.2)
n<-length(data)
```

```
x.bar <- mean(data)
Sd.est <- sd(data)
t <- (x.bar - mu)/(sd.est/sqrt(n))
tab <- qt(0.01, n-1)
Pvalue.t <- pt(t, df=n-1)
boxplot(data, ylab="Hb lebel", col="gray")
qqnorm(data, main="Normal Q-Q plot
of Hb level")
qqline(data)
```

Input and output:

mu = 14.6

n = 10

x.bar = 13.7

Sd.est = 1.655

t = -1.71

tab = -2.82

Pvalue.t = 0.059

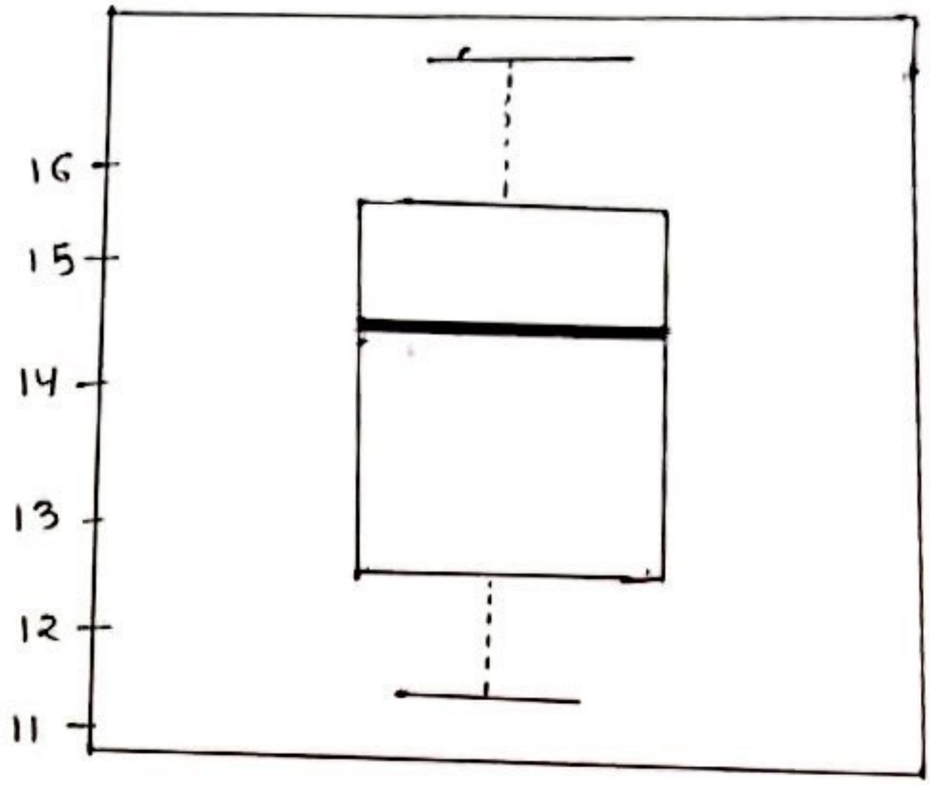

Fig: Boxplot

Normal Q-Q plot of Hb level

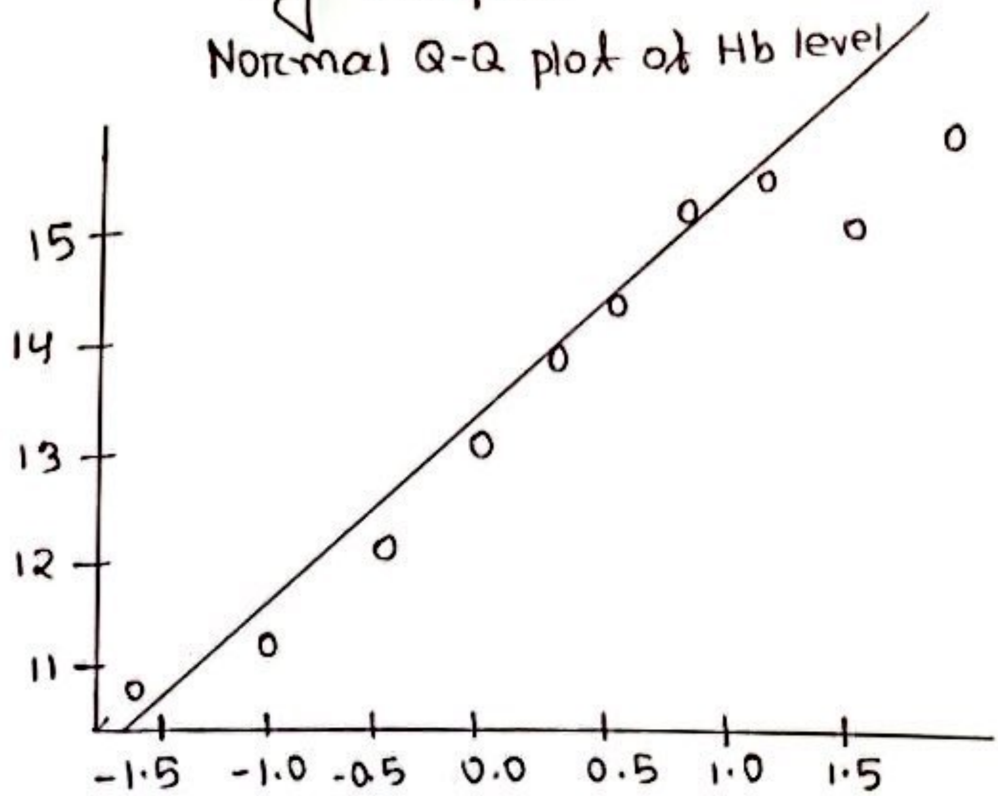

Fig: Normal plot

Comment: From the R code we can see that tab > tcal and also pvalue > alpha so H0 is accepted. Then the mean Hb level for children with chronic diarrhea is more than the normal value of 14.6.

Experiment No: 05

Experiment Name: In order to find out wheather children with chronic diarrhea have the same average hemoglobin level (Hb) that is normally seen in healthy children in the same area a random sample of 10 children with chronic diarrhea are selected and their Hb level (g/dl) are obtained as follows: 12.3, 11.4, 14.2, 15.3, 14.8, 13.8, 11.1, 15.1, 15.8, 13.2 another random sample of 12 children with chronic diarrhea are 11.1, 17.2, 13.4, 15.2, 14.1, 13.0, 12.5, 11.5, 12.7, 14.5, 15.3, 14.0. Is there any difference in the mean Hb label between the two groups of children

Objectives:

1. To calculate any difference in the mean Hb label between the two groups of children.

2. To comment on the data.

Procedure:

Step-1: state that the null hypothesis the mean Hb lebel between the two group of children is equal and the alternate hypothesis state that the mean Hb lebel between two group of children is not equal.

$H0: \mu_1 = \mu_2$

$H_A: \mu_1 \neq \mu_2$

Step-2: Select the level of significance. The selected level of significance is 0.05.

step-3: Select the test statistics.
The sample size is less than 30 and population standard deviation is unknown also the variance is ~~not~~ equal of the two groups of data. so we use t-test.

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{s^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}}$$

$$\bar{x}_1 = \frac{1}{n_1} \Sigma x_{i1}$$

$$\bar{x}_2 = \frac{1}{n_2} \Sigma x_{i2}$$

$$s_1^2 = \frac{1}{n_1-1}\left[\Sigma x_{i1}^2 - \frac{(\Sigma x_{i1})^2}{n_1}\right]$$

$$s_2^2 = \frac{1}{n_2-1}\left[\Sigma x_{i2}^2 - \frac{(\Sigma x_{i2})^2}{n_2}\right]$$

$$s^2 = \frac{(n_1-1)s_1^2 + (n_2-1)s_2^2}{n_1+n_2-2}$$

step-4: Formulate the decision rule.
The tabulated value of t is greater than the calculated value than the null hypothesis is accepted, otherwise rejected.

R-source code:

```
X1<-C(12.3, 11.4, 14.2, 15.3, 14.8, 13.8, 11.1, 15.1,
15.8, 13.2)
x2<-c(11.1, 17.2, 13.4, 15.2, 14.1, 13.0, 12.5, 11.5,
12.7, 14.5, 15.3, 14.0)

s1<-sd(x1)
s2<-sd(X2)
s1/s2

n1<-length(x1)
n2<-length(x2)
x1.bar<-mean(X1)
x2.bar<-mean(x2)
x1.var<-var(X1)
x1.var<-var(x2)
sp<-(((n1-1)*x1.var+(n2-1)*x2.var)/
                              (n1+n2-2))
t<-(X1.bar-x2.bar)/sqrt(sp*(1/n1+1/n2))
```

```
alpha = 0.05
t.tab<- qt( alpha/2, n1+n2-2 )
```

Input and output:

S1 = 1.65

S2 = 1.72

S1/S2 = 0.96

n1 = 10

n2 = 12

x1.bar = ~~2.74~~ 13.7

x2.bar = ~~2.96~~ 13.708

x1.var = 2.74

x2.var = 2.96

Sp = 2.86

t = -0.011

alpha = 0.05

t.tab = - 2.085

Comment: From the R code we can see that t.tab > t cal . so H0 is accepted. So we can say There is no difference in the mean Hb label between the two groups of children.