**A hospital wants to determine whether there is any difference in the average Turn Around Time (TAT) of reports of the laboratories on their preferred list. They collected a random sample and recorded TAT for reports of 4 laboratories. TAT is defined as sample collected to report dispatch.**

**Analyze the data and determine whether there is any difference in average TAT among the different laboratories at 5% significance level.**

**Minitab File: LabTAT.mtw**

**#import the data set**

LabTAT<-read.csv(file.choose(),header = T)

View(LabTAT)

**#check weather the dat set contains null values**

sum(is.na(LabTAT)) #zero null values

# shows first six datas

head(LabTAT)

|  |
| --- |
| Laboratory.1 Laboratory.2 Laboratory.3 Laboratory.4  1 185.35 165.53 176.70 166.13  2 170.49 185.91 198.45 160.79  3 192.77 194.92 201.23 185.18  4 177.33 183.00 199.61 176.42  5 193.41 169.57 204.63 152.60  6 179.45 197.00 181.51 161.12 |
|  |
| |  | | --- | | > | |

**#in our data sets y is continous and x is discrete**

**#x= Laboratory.1 Laboratory.2 Laboratory.3 Laboratory.4**

**#Y= Values of X**

**# in our data set gives Four population**

**# compare four population with each other**

**#next step is to check weather data is normalized or not using shapiro test**

attach(LabTAT)

**# we have to set hypothesis**

**#H0: Data is normally distributed(p>0.05)**

**#H1: not normally distributed (p<0.05)**

shapiro.test(Laboratory.1)

Shapiro-Wilk normality test

data: Laboratory.1

W = 0.99018, p-value = 0.5508

shapiro.test(Laboratory.2)

Shapiro-Wilk normality test

data: Laboratory.2

W = 0.99363, p-value = 0.863

shapiro.test(Laboratory.3)

Shapiro-Wilk normality test

data: Laboratory.3

W = 0.98863, p-value = 0.4205

shapiro.test(Laboratory.4)

Shapiro-Wilk normality test

data: Laboratory.4

W = 0.99138, p-value = 0.6619

**# in all case p- values>0.05, so accept null hypothesis,**

**#that means all populations are normally distributed**

**# next step is to check the variance are equal**

**# here we have more than two population, so we have to perform Bartlet test**

**#for for finding equal variance**

**#for doing bartlet test we have to perform some data manipulations**

**# we have to convert four column data sets into two column set using stack operations**

**#convert data set into a stacked data**

stacked\_data<-stack(LabTAT)

View(stacked\_data)

head(stacked\_data,10)

|  |
| --- |
| values ind  1 185.35 Laboratory.1  2 170.49 Laboratory.1  3 192.77 Laboratory.1  4 177.33 Laboratory.1  5 193.41 Laboratory.1  6 179.45 Laboratory.1  7 191.37 Laboratory.1  8 166.81 Laboratory.1  9 158.81 Laboratory.1  10 165.88 Laboratory.1 |
|  |
| |  | | --- | | > | |

attach(stacked\_data)

**#check variance of all sample equal using bartlett.test**

**# we have to set hypothesis**

**#H0: Variance of sample are equal # p-value>0.05**

**#H1 : Variance of sample are not equal # p-value <0.05**

bartlett.test(values~ind, data=stacked\_data)

|  |
| --- |
| Bartlett test of homogeneity of variances  data: values by ind  Bartlett's K-squared = 6.0995, df = 3, p-value = 0.1069 |
|  |
| |  | | --- | | > | |

# p-value=0.1069 >0.05 **so p high null fly means reject alternatete hypothesis, accept**

**#null hypothesis, that means variance between populations are equal**

**#here we gets all samples variance are equal, so next step is to perform one way ANOVA test**

**# we have to set hypothesis**

**#H0:means sample are equal # p-value>0.05**

**#H1 :meanssample are not equal # p-value <0.05**

anova\_test<-aov(values~ind, data=stacked\_data)

summary(anova\_test)

|  |
| --- |
| Df Sum Sq Mean Sq F value Pr(>F)  ind 3 79979 26660 118.7 <2e-16 \*\*\*  Residuals 476 106905 225  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 |
|  |
| |  | | --- | | > | |

**# here we get very small p-value<0.05, so we can say that mean of all samples are different**

**# so we have to conclude that there is difference in average TAT among the different laboratories at 5% significance level.**