**26th/July/2011**

**R Practical (RP1)**

**Q1.** The percentage potassium in blood serum was determined by three different analysts using the same method. The following results were obtained:

|  |
| --- |
| analyst A B C |
| 0.015 0.012 0.019  0.015 0.014 0.018  0.017 0.016 0.020  0.017 0.013 0.021  0.018 0.010 0.019  0.016 0.012 0.018 |

Draw box plots to represent the above data.

Use an analysis of variance technique to answer the following question:

Use Tukey’s method to test for a significant variance among the average results obtained by each of the three analysts. Use 1 % and 5% levels of significance

Setwd(C:\kilificourse")

getwd()

dir()

## Load some libraries

library(epicalc)

library(MASS)

# 1. Load the file into a data frame named df1 with the read.table function. As the first line in the file contains the column names, we set the header argument as TRUE.

df1 = read.table("oneway.txt", header=TRUE); df1

boxplot(df1, col=c(2:4), ylab="% potassium in blood serum", xlab="Analyst")

# 2. Concatenate the data rows of df1 into a single vector r .

r = c(t(as.matrix(df1))) ; r # response data

# 3. Assign new variables for the treatment levels and number of observations

f = c("A", "B", "C") # treatment levels

k = 3 # number of treatment levels

n = 6 # observations per treatment

# 4. Create a vector of treatment factors that corresponds to each element of r in step 3 with the gl function

tm = gl(k, 1, n\*k, factor(f)) ; tm # matching treatments

library(gplots)

plotmeans(r~tm, main="Mean plot with 95% CI")

# 5. Apply the function aov to a formula that describes the response r by the treatment factor tm.

av = aov(r ~ tm)

# 6. Print out the ANOVA table with the summary function.

summary(av)

## Use Tukey's method'

(m1<-TukeyHSD(av, conf.level=0.99))# at 1% significance level

(m2<-TukeyHSD(av)) # at 5% significance level

# X11(height=6, width=6)

op<-par(mfrow=c(2,2))

plot(av)

par(op)

graphics.off()

shapiro.qqnorm(r)

plot(m1)

plot(m2)

**Qn2.** Suppose that in a study to compare body sizes of three genotypes of fourth-instar silkworm, the mean length (in millimeters) for separately reared cocoons of heterozygous(HET), homozygous (HOM), and wild (WLD) silkworms was determined at five laboratory sites; the data are given in the table below.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  |  | sites |  |  |
| variable | 1 | 2 | 3 | 4 | 5 |
| HOM | 29.87 | 28.16 | 32.08 | 30.84 | 29.44 |
| HET | 32.51 | 30.82 | 34.17 | 33.46 | 32.99 |
| WLD | 35.76 | 33.14 | 36.29 | 34.95 | 35.89 |

Draw box plots to represent this data.

Carry out analysis of Variance. Use 1% and 5% Significance level to test the mean difference between the groups using the Tukey’s method.

rm(list=c()) # remove all existing objects

# 1. Load the file into a data frame named df2 with the read.table function.

df2 = read.table("block.txt", header=TRUE); df2

boxplot(df2, col=c(2:6), ylab="body sizes (mean length in mm)", xlab="Genotypes")

# 2. Concatenate the data rows in df2 into a single vector r .

r = c(t(as.matrix(df2))); r # response data

#3. Assign new variables for the treatment levels and number of control blocks

f = c("1", "2", "3","4","5")# treatment levels

k = 5 # number of treatment levels

n = 3# number of control blocks

# 4. Create a vector of treatment factors that corresponds to the each element in r of step 3 with the gl function. # number of control blocks

tm = gl(k, 1, n\*k, factor(f)) # matching treatment

library(gplots)

plotmeans(r~tm, main="Mean plot with 95% CI")

# 5. Similarly, create a vector of blocking factors for each element in the response data r.

blk = gl(n, k, k\*n) ;blk # blocking factor

# 6. Apply the function aov to a formula that describes the response r by both the treatment factor tm and the block control blk

av = aov(r ~ tm + blk)

# 7. Print out the ANOVA table with the summary function

summary(av)

#### Use Tukey's method to look at the differences between groups'

(m1<-TukeyHSD(av, conf.level=0.99))# at 1% significance level

(m2<-TukeyHSD(av)) # at 5% significance level

# X11(height=6, width=6)

op<-par(mfrow=c(2,2))

plot(av)

par(op)

graphics.off()

shapiro.qqnorm(r)

plot(m1)

plot(m2)