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> library(rJava,xlsxjars,xlsx)

> irisData<-read.xlsx("E:\\BIG DATA\\AMA-II SEM\\Data Set\\irisd.xlsx", sheetName = "Sheet1", header
= TRUE)

> library(car); library(ggplot2); library(MASS); library(mvoutlier); library(mvnormtest); library(pastecs);
library(reshape)

> irisData$Groups<-
factor(irisData$Groups,levels=c("1","2","3"),labels=c("setosa","versicolor","virginica"))

> by(irisData$Sepal.Length, irisData$Groups, stat.desc, basic = FALSE)

> by(irisData$Sepal.Width, irisData$Groups, stat.desc, basic = FALSE)

> by(irisData$Petal.Width, irisData$Groups, stat.desc, basic = FALSE)

> by(irisData$Petal.Length, irisData$Groups, stat.desc, basic = FALSE)

> library(biotools)

> HV<-boxM(irisData[, 1:4], irisData[, "Groups"])

> HV

> set<-irisData[which(irisData$Groups=='setosa'),]

> set1<-set[1:4]

> setr<-t(set1)

> ver<-irisData[which(irisData$Groups=='versicolor'),]

> ver1<-ver[1:4]

> vert<-t(ver1)

> vir<-irisData[which(irisData$Groups=='virginica'),]

> vir1<-vir[1:4]

> virt<-t(vir1)

> mshapiro.test(setr)

> mshapiro.test(vert)

> mshapiro.test(virt)

> aq.plot(irisData[1:4])
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> outcome<-  
cbind(irisData$Sepal.Length,irisData$Sepal.Width,irisData$Petal.Length,irisData$Petal.Width)  
  
> irisModel<-manova(outcome~Groups, data=irisData)  
  
> summary(irisModel, intercept = TRUE, test = "Wilks")  
  
> summary(irisModel, intercept = TRUE, test = "Pillai")  
  
> summary(irisModel, intercept = TRUE, test = "Hotelling")  
  
> summary(irisModel, intercept = TRUE, test = "Hotelling")  
  
> summary(irisModel, intercept = TRUE, test = "Roy")  
  
> irisDFA<-lda(Groups~Sepal.Length+Sepal.Width+Petal.Length+Petal.Width,data=irisData)  
  
> irisDFA
```