**6304 Module 9**

**R Script File**

**rm(list=ls())**

**library(rio)**

**library(car)**

**cats1=import("6304 Module 9 Data Set.xlsx",**

**sheet="One Way Cats")**

**cats1$Flavor=as.factor(cats1$Flavor)**

**# Equality of variances test.**

**leveneTest(Eaten~Flavor,data=cats1)**

**boxplot(Eaten~Flavor,**

**main="Cats1, Five Food Flavors",**

**col="red",**

**data=cats1)**

**aggregate(Eaten~Flavor,cats1,var)**

**gilligan=aggregate(Eaten~Flavor,cats1,var)**

**gilligan**

**max(gilligan$Eaten)**

**min(gilligan$Eaten)**

**max(gilligan$Eaten)/min(gilligan$Eaten)**

**rm(gilligan)**

**# One Way ANOVA Cats.**

**cats1.out=aov(Eaten~Flavor,data=cats1)**

**summary(cats1.out)**

**names(cats1.out)**

**cats1.out$coefficients**

**gilligan=aggregate(Eaten~Flavor,cats1,mean)**

**gilligan**

**gilligan$Eaten[2]**

**gilligan$Eaten[1]**

**gilligan$Eaten[2]-gilligan$Eaten[1]**

**cats1.out$coefficients**

**rm(gilligan)**

**gilligan=TukeyHSD(cats1.out)**

**gilligan**

**plot(gilligan)**

**# par(mar sets the margins on the upcoming plot.**

**# Order of values is: bottom, left, top, right.**

**# Default values are 5.1,4.1,4.1,2.1**

**# Set, plot, reset.**

**par(mar=c(5.1,8,4.1,2.1))**

**plot(gilligan,las=2)**

**par(mar=c(5.1,4.1,4.1,2.1))**

**# Releveling Command**

**cats1a=cats1**

**cats1a$Flavor=relevel(cats1a$Flavor,"Kidney")**

**cats1a.out=aov(Eaten~Flavor,data=cats1a)**

**summary(cats1a.out)**

**cats1.out$coefficients**

**cats1a.out$coefficients**

**skipper=TukeyHSD(cats1a.out)**

**par(mar=c(5.1,8,4.1,2.1))**

**plot(skipper,las=2)**

**par(mar=c(5.1,4.1,4.1,2.1))**

**par(mfrow=c(2,1))**

**par(mar=c(5.1,8,4.1,2.1))**

**plot(gilligan,las=2,cex.axis=.6)**

**plot(skipper,las=2,cex.axis=.6)**

**par(mar=c(5.1,4.1,4.1,2.1))**

**par(mfrow=c(1,1))**

**# Two Way Anova Cats**

**cats2=import("6304 Module 9 Data Set.xlsx",**

**sheet="Two Way Cats")**

**cats2$Flavor=as.factor(cats2$Flavor)**

**cats2$Cat=as.factor(cats2$Cat)**

**levels(cats2$Flavor)**

**levels(cats2$Cat)**

**leveneTest(Eaten~Flavor,data=cats2)**

**leveneTest(Eaten~Cat,data=cats2)**

**aggregate(Eaten~Flavor,cats2,var)**

**aggregate(Eaten~Cat,cats2,var)**

**boxplot(Eaten~Flavor,**

**main="Cats2, Five Food Flavors",**

**col="red",**

**data=cats2)**

**boxplot(Eaten~Cat,**

**main="Cats2, Five Food Flavors",**

**col="red",pch=19,cex.axis=.8,**

**data=cats2)**

**cats2.out=aov(Eaten~Flavor+Cat,data=cats2)**

**summary(cats2.out)**

**cats2.out$coefficients**

**ginger=TukeyHSD(cats2.out)**

**ginger**

**par(mfrow=c(1,2))**

**par(mar=c(5.1,6,4.1,2.1))**

**plot(ginger,las=2,cex.axis=.6)**

**par(mfrow=c(1,1))**

**par(mar=c(5.1,4.1,4.1,2.1))**

**# Reading in cats3 data.**

**cats3=import("6304 Module 9 Data Set.xlsx",**

**sheet="Two Way Extra Cats")**

**cats3$Flavor=as.factor(cats3$Flavor)**

**cats3$Cat=as.factor(cats3$Cat)**

**levels(cats3$Cat)**

**aggregate(Eaten~Cat,cats3,var)**

**mr.smooches=subset(cats3,Cat=="Mr. Smooches")**

**itty.bitty=subset(cats3,Cat=="Itty-Bitty")**

**pork.chop=subset(cats3,Cat=="Pork Chop")**

**hist(pork.chop$Eaten,col="green",**

**xlim=c(0,3),**

**main="Comparing Cats")**

**hist(mr.smooches$Eaten,xlim=c(0,3),col="red",**

**add=TRUE)**

**hist(itty.bitty$Eaten,col="blue",add=TRUE)**

**# Equality of Variances**

**boxplot(Eaten~Cat,**

**main="Cats3, Five Food Flavors",**

**col="red",pch=19,cex.axis=.55,**

**data=cats3)**

**aggregate(Eaten~Cat,cats3,var)**

**leveneTest(Eaten~Flavor,data=cats3)**

**leveneTest(Eaten~Cat,data=cats3)**

**# Conducting the ANOVA on cats3.**

**cats3.out=aov(Eaten~Flavor+Cat,data=cats3)**

**summary(cats3.out)**

**cats3.out$coefficients**

**maryann=TukeyHSD((cats3.out))**

**maryann**

**par(mfrow=c(1,2))**

**par(mar=c(5.1,6,4.1,2.1))**

**plot(maryann,las=2,cex.axis=.5)**

**par(mar=c(5.1,4.1,4.1,2.1))**

**# Cats3 releveled for Mr. Smooches**

**cats3a=cats3**

**cats3a$Cat=relevel(cats3a$Cat,"Mr. Smooches")**

**cats3a.out=aov(Eaten~Flavor+Cat,data=cats3a)**

**summary(cats3a.out)**

**cats3a.out$coefficients**

**lovey=TukeyHSD((cats3a.out))**

**par(mfrow=c(1,2))**

**par(mar=c(5.1,6,4.1,2.1))**

**plot(lovey,las=2,cex.axis=.6)**

**par(mar=c(5.1,4.1,4.1,2.1))**

**par(mfrow=c(1,1))**

**# Cats3 releveled for Itty-Bitty**

**cats3b=cats3**

**cats3b$Cat=relevel(cats3b$Cat,"Itty-Bitty")**

**cats3b.out=aov(Eaten~Flavor+Cat,data=cats3b)**

**summary(cats3b.out)**

**cats3b.out$coefficients**

**thurston=TukeyHSD((cats3b.out))**

**par(mfrow=c(1,2))**

**par(mar=c(5.1,6,4.1,2.1))**

**plot(thurston,las=2,cex.axis=.6)**

**par(mar=c(5.1,4.1,4.1,2.1))**

**par(mfrow=c(1,1))**

**# Now Notice What Happens in the Plot**

**cats3c=cats3**

**cats3c$Cat=relevel(cats3c$Cat,"Mr. Smooches")**

**cats3c$Cat=relevel(cats3c$Cat,"Itty-Bitty")**

**cats3c.out=aov(Eaten~Flavor+Cat,data=cats3c)**

**summary(cats3c.out)**

**cats3c.out$coefficients**

**professor=TukeyHSD((cats3c.out))**

**par(mfrow=c(1,2))**

**par(mar=c(5.1,6,4.1,2.1))**

**plot(professor,las=2,cex.axis=.6)**

**par(mar=c(5.1,4.1,4.1,2.1))**

**par(mfrow=c(1,1))**

**# Changing Data Sets**

**# Heart Disease**

**rm(list=ls())**

**disease=import("6304 Module 9 Data Set.xlsx",**

**sheet="Heart Disease")**

**colnames(disease)=tolower(make.names(colnames(disease)))**

**names()**

**# Make Some Variables Factors**

**str(disease)**

**#disease$agecat=as.factor(disease$agecat)**

**#disease$gender=as.factor(disease$gender)**

**#disease$chest.pain=as.factor(disease$chest.pain)**

**#disease$exercise=as.factor(disease$exercise)**

**#disease$heart=as.factor(disease$heart)**

**Factors=c("agecat","gender","chest.pain",**

**"exercise","heart")**

**disease[Factors]=lapply(disease[Factors],factor)**

**str(disease)**

**attach(disease)**

**names(disease)**

**# Explore the Data a Bit**

**summary(hdl)**

**table(agecat)**

**table(agecat,heart)**

**table(heart,agecat)**

**# Focus on HDL (High Density Lipoprotein**

**# "Good" Cholesterol)**

**aggregate(hdl~heart,disease,mean)**

**aggregate(hdl~heart,disease,var)**

**leveneTest(hdl,heart)**

**gilligan=aov(hdl~heart,data=disease)**

**summary(gilligan)**

**skipper=TukeyHSD(gilligan)**

**plot(skipper)**

**# What About Blood Pressure and Age?**

**aggregate(bp~agecat,disease,mean)**

**aggregate(bp~agecat,disease,var)**

**leveneTest(bp~agecat)**

**gilligan=aov(bp~agecat,data=disease)**

**summary(gilligan)**

**skipper=TukeyHSD(gilligan)**

**plot(skipper)**

**par(mar=c(5.1,10,4.1,2.1))**

**plot(skipper,las=2)**

**par(mar=c(5.1,4.1,4.1,2.1))**