hw\_0418  
1.  
mydata=read.csv("hw1\_0418.csv",header=T)  
  
ttest\_p=c()  
  
for (ii in 6:10){  
 ttest\_p[ii-5]=t.test(mydata[,ii]~mydata$Gender)$p.val  
}  
  
idx=which((ttest\_p<0.01)==TRUE)  
  
G0\_idx=1:500  
G1\_idx=501:1000  
  
permute\_p=c()  
  
for (ii in 1 : 100){  
 permute\_p[ii]=t.test(mydata[sample(G0\_idx,250),5+idx],mydata[sample(G1\_idx,250),5+idx])$p.val  
}  
  
sig\_num=table(permute\_p<0.05)  
  
jpeg("outpu1\_pie.JPG")  
pie(sig\_num,labels=c(paste("non-significant = ", (sig\_num[1]/100) ,sep=''),paste("significant = ", (sig\_num[2]/100),sep=''),main="HW0418\_1\_pie\_chart"))  
dev.off()  
  
  
png("outpu1\_barplot.PNG")  
barplot(sig\_num,names.arg=c("non-significant","significant"),main="HW0418\_1\_barplot")  
dev.off()  
  
2.  
  
mydata=read.csv("hw1\_0418.csv",header=T)  
  
anova\_p=c()  
  
for (ii in 6:10){  
 anova\_p[ii-5]=anova(lm(mydata[,ii]~factor(mydata$Hospital)))$"Pr(>F)"[1]  
}  
  
idx=which((anova\_p<0.01)==TRUE)  
  
pdf("output2.PDF")  
boxplot(G4~Hospital,xlab="Hospital",ylim=c(7,10),main="HW0418\_2\_boxplot",data=mydata)  
dev.off()  
  
3.  
  
mydata=read.csv("hw2\_0418.csv",header=T)  
  
ranksum\_p=c()  
  
for (ii in 6:10){  
 ranksum\_p[ii-5]=wilcox.test(mydata[,ii]~factor(mydata$Virus))$p.value  
}  
  
idx=which((ranksum\_p<0.01)==TRUE)  
  
xx=1:10  
  
bmp("output3.bmp")  
plot(xx,xx,type="n",xlim=c(0,11),ylim=c(0,15.1),xlab="X axis",ylab="Y axis")  
yy1=sort(mydata$G3[mydata$Virus==0])  
yy2=sort(mydata$G3[mydata$Virus==1])  
points(yy1,pch=1,col="Red")  
points(yy2,pch=2,col="Green")  
  
xx=1:10  
abline(lm(yy1~xx),lty=3)  
abline(lm(yy2~xx),lty=4)  
  
R1=lm(yy1~xx)  
text(6,15,paste("y=",round(R1$coefficients[2],4),"x+",round(R1$coefficients[1],4)))  
R2=lm(yy2~xx)  
text(8,2,paste("y=",round(R2$coefficients[2],4),"x+",round(R2$coefficients[1],4)))  
  
  
legend(1,15,legend=c("Virus=0","Virus=1"),pch=c(1,2),col=c("Red","Green"))  
dev.off()  
  
4.  
  
mydata=read.csv("hw3\_0418.csv",header=T)  
  
int\_p=c()  
  
for (ii in 6:10){  
 int\_p[ii-5]=summary(lm(mydata[,ii]~factor(mydata$Gender)+factor(mydata$Virus)+factor(mydata$Gender\*mydata$Virus)))$coefficients[4,4]  
}  
  
  
idx=which((int\_p<0.01)==TRUE)  
  
  
G0V0=mean(mydata$G1[(mydata$Gender==0) & (mydata$Virus==0)])  
G0V1=mean(mydata$G1[(mydata$Gender==0) & (mydata$Virus==1)])  
G1V0=mean(mydata$G1[(mydata$Gender==1) & (mydata$Virus==0)])  
G1V1=mean(mydata$G1[(mydata$Gender==1) & (mydata$Virus==1)])  
  
x\_value=c(1,2,1,2)  
y\_value=c(G1V0,G1V1,G0V0,G0V1)  
  
pdf("output4.pdf")  
plot(x\_value,y\_value,xaxt='n',xlim=c(0,3),ylim=c(5,6),xlab="Virus Infection",ylab="Gene Expression",pch=c(1,1,2,2),col=c("Blue","Blue","Brown","Brown"),main="Interaction Effect")  
  
axis(side=1, at=c(1,2), labels=c("0","1"))  
segments(x\_value[1],y\_value[1],x\_value[2],y\_value[2],col="Blue")  
segments(x\_value[3],y\_value[3],x\_value[4],y\_value[4],col="Brown")  
legend(0,5.8,legend=c("Gender 1","Gender 0"),pch=c(1,2),col=c("Blue","Brown"))  
  
dev.off()

大家好,

作業三已經改完

本次作業目的是讓大家練習一下簡單的抽樣和畫圖

沒有甚麼太大的問題

唯一提醒大家的事情是pie chart因為不會自動標比例上去

如果最後是各位的論文

要記得標數字上去

不然不是很容易看到比例

程式碼供各位參考

但有任何的寫法都是可以的

Cheers!