library("e1071")

library("caret")

install.packages("readr")

library(readr)

v=read\_csv("Bcancer.csv")

m=v

m=data.frame(m[,2:32])

class  = rep(0,nrow(m))

class = ifelse(m$diagnosis =="M",1,0)

index=sample(1:nrow(m),size = 0.7\*nrow(m))

train  = m[index,2:31]

test = m[-index,2:31]

classtrain = class[index]

classtest = class[-index]

model = svm(train,classtrain,type = "C-classification")

predi  = predict(model , test)

t1 = table(pred = predi ,true = classtest )

1 - sum(diag(t1))/sum(t1)

pcm =v

pcm =data.frame(pcm[3:31])

m=prcomp(t(pcm),scale=true,center=true)

ind=sample(which(m$sdev > 1))

sort(ind)

m = m$rotation[,1:length(ind)]

index=sample(1:nrow(m),size = 0.7\*nrow(m))

train  = m[index,]

nrow(train)

test = m[-index,]

nrow(test)

classtrain = class[index]

classtest = class[-index]

model = svm(train,classtrain,type = "C-classification")

predi  = predict(model , test)

t3 =table(pred = predi ,true = classtest )

t3

1 - sum(diag(t1))/sum(t1)

install.packages("GGally")

library(GGally)

require(GGally)

data(v, package="reshape")

#plot fot selected variables

ggpairs(data=v, # data.frame with variables

        columns=3:13, # columns to plot, default to all.

        title="Cancer data", # title of the plot

        mapping=ggplot2::aes(colour = diagnosis)) # aesthetics, ggplot2 style

summary(v)

corrplot(v)

install.packages("corrplot")

library(corrplot)

vw=v[,3:32]

M=cor(vw)

#plot for correlation of all variables

corrplot(cor(vw), order="hclust", addrect=2,t1.col="black",tl.srt=45)

install.packages("pROC")

library('pROC')

#plot for class

plot(class,col=class+10,pch=class+10)