```
#extracting samples having class setosa
setos<-iris[iris[,5]=="setosa",]
mean_setosa<-as.matrix(colMeans(setos[,1:4]))
cov_setosa<-as.matrix(cov(setos[,1:4]))

#extracting samples having class versicolor
versicol<- iris[iris[,5]=="versicolor",]
mean_versicol<-as.matrix(colMeans(versicol[,1:4]))
cov_versicol=as.matrix(cov(versicol[,1:4]))

#extracting samples having class verginica
vergin=iris[iris[,5]=="virginica",]
mean_vergin=as.matrix(colMeans(vergin[,1:4]))
cov_vergin=as.matrix(cov(vergin[,1:4]))


#converting mean to a vector
mean_setosa<-as.vector(mean_setosa)
mean_vergin<-as.vector(mean_vergin)
mean_versicol<-as.vector(mean_versicol)
vec<-NULL
v1<-NULL
k=1

for(i in 1:length(rownames(iris)))
{

  d<-iris[i,1:4]
  d<-as.vector(unlist(d))

  #calculating multivariate density for class setosa
  a=dmvnorm(d,mu=mean_setosa,Sigma = cov_setosa)

  #calculating multivariate density for class versicolor
  b=dmvnorm(d,mu=mean_versicol,Sigma = cov_versicol)

  #calculating multivariate density for class virginica
  c=dmvnorm(d,mu=mean_vergin,Sigma = cov_vergin)
  vec<-c(a,b,c)

  #finding the highest density value among the three.
  v1[k]<-which.max(vec)


  k=k+1
}
h=1
ii1<-NULL
for(i in 1:length(rownames(iris)))
{
  if(iris[i,5]=="setosa")
  {
    ii1[h]<-1
    h=h+1
  }
  else if(iris[i,5]=="versicolor")
  {
    ii1[h]<-2
    h=h+1
  }
  else
  {
    ii1[h]<-3
    h=h+1
  }
}
count=0



for(i in 1:length(ii1))
{
  #doing this to plot the values in green and red color and calculating the accuracy using count.
  if(v1[i]==ii1[i])
  {
    v1[i]="green"
    count=count+1
  }
  else
    v1[i]="red"
}

#printing the accuracy
print(count)
print(count/150)
```