NAÏVE BAYES CLASSIFIER

```
library("e1071")
ir=iris
train=ir[1:100,]
test=ir[101:50,]
model=naiveBayes(Species~.,data=train)
pred=predict(model,test)
pred
table(pred)
table(test$Species)
table(pred,test$Species)
```

LINEAR REGRESSION

```
bankloan=read.csv("E:\\Dataset\\R\\bank_loan.csv",header=T)
str(bankloan)
bk=bankloan[1:700,]


riskmodel<-glm(default~age+employ+address+debtinc+othdebt,
        family=binomial,data=bk)
summary(riskmodel)


library(ROCR)


bk$predprob<-fitted(riskmodel)


 pred<-prediction(bk$predprob,bk$default)


 perf<-performance(pred,"tpr","fpr")


 plot(perf)
```

```
 abline(0,1)
```

KNN

```r
data<-iris
row_labels=data[,5]
data$Species=as.numeric(data$Species)
data[,1:4]=scale(data[,1:4])
set.seed(123)
size=floor(0.8*nrow(data))
train_ind=sample(seq_len(nrow(data)),size=size)
train_label=data[train_ind,5]
test_label<-row_labels[-train_ind]
data_train=data[train_ind,1:4]
data_test=data[-train_ind,1:4]

library(class)
pred_model=knn(train=data_train,test=data_test,cl=train_label,k=round(sqrt(nrow(data_train))))

plot_predictions<-data.frame(data_test$Sepal.Length,data_test$Sepal.Width,
          data_test$Petal.Length,data_test$Petal.Width,predicted=pred_model)

colnames(plot_predictions)<-c("Sepal.Length","Sepal.Width","Petal.Length","Petal.Width","Class")

library(ggplot2)
library(gridExtra)
pl<-ggplot(plot_predictions,aes(Sepal.Length,Sepal.Width,color=predicted,fill=predicted))+

geom_point(size=5)+geom_text(aes(label=test_label),hjust=1,vjust=2)+ggtitle("Predicted
relationship between Sepal Length and Sepal Width")+

          theme(plot.title=element_text(hjust=0.5))+theme(legend.position="none")
```

KMEANS CLUSTERING

```r
library("e1071")
Iris.Features=iris
Iris.Features$Species<-NULL
View(Iris.Features)
results=kmeans(Iris.Features,3)
results
results$size
results$cluster
table(iris$Species,results$cluster)
plot(iris[c("Petal.Length","Petal.Width")],col=results$cluster)
plot(iris[c("Petal.Length","Petal.Width")],col=iris$Species)
plot(iris[c("Sepal.Length","Sepal.Width")],col=results$cluster)
```

HAC CLUSTER

```r
library(factoextra)
iris_data=iris[1:4]
iris_data_std=scale(iris_data)
iris_dist=dist(iris_data_std)
iris_dist
myclust=hclust(iris_dist,method="complete")


plot(myclust)


rect.hclust(myclust,k=5,border=2.5)
iris.cluster=cutree(myclust,k=3)
rownames(iris_data_std)<-paste(iris$Species,1:dim(iris)[1],sep="-")
fviz_cluster(list(data=iris_data_std,cluster=iris.cluster))
```

APRIORI

```r
mydata=read.csv("E:\\Dataset\\R\\Cosmetics.csv",header="T",colClasses="factor")
View(mydata)
```

```
library("arules")

rules=apriori(mydata)

summary(rules)

rules=apriori(mydata,parameter=list(minlen=2,maxlen=3,supp=0.7))

inspect(rules)

library("arulesViz")

plot(rules)
```

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