



Experiment 6

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Subject Name: Data Mining Lab

Subject Code: 20CSP-376

Aim: To perform classification using the Bayesian classification algorithm using R

Script and Output:

```
library(e1071)
```

```
library(gmodels)
```

```
library(dplyr) iris <-
```

```
read.csv('iris_1.csv')
```

```
str(iris)
```

```
summary(iris)
```



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```
index = sample(2,nrow(iris),prob=c(0.8,0.2),replace=TRUE)
```

```
set.seed(1234)
```

```
#training set train=
```

```
iris[index==1,]
```

```
#testing set test=
```

```
iris[index==2,]
```

```
#test_data will be given as an input to the model to predict species test_data
```

```
= test[1:4]
```

```
#test_labels are the actual values of species of the test data
```

```
test_label=test[,5]
```

```
print(test_label)
```



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```
model=naiveBayes(train$class~.,train)
```

```
model test_result=predict(model,test_data)
```

```
test_result
```

```
#compare the predicted and actual values
```

```
CrossTable(x=test_label, y=test_result)
```

OUTPUT:



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```
R 4.1.2 ~ / #
> library(e1071)
> library(gmodels)
> library(dplyr)
> iris <- read.csv('iris_1.csv')
> str(iris)
'data.frame': 150 obs. of 5 variables:
 $ sepal_length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ sepal_width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ petal_length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ petal_width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ class       : chr  "Iris-setosa" "Iris-setosa" "Iris-setosa" "Iris-setosa" ...
> summary(iris)
  sepal_length  sepal_width  petal_length  petal_width   class
Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100   Length:150
1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300   Class :character
Median :5.800   Median :3.000   Median :4.350   Median :1.300   Mode  :character
Mean   :5.843   Mean   :3.054   Mean   :3.759   Mean   :1.199
3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
>
> index = sample(2,nrow(iris),prob=c(0.8,0.2),replace=TRUE)
>
> set.seed(1234)
> #training set
> train= iris[index==1,]
> #testing set
> test= iris[index==2,]
> #test_data will be given as an input to the model to predict species
> test_data = test[1:4]
> #test_labels are the actual values of species of the test data
> test_label=test[,5]
> print(test_label)
 [1] "Iris-setosa"      "Iris-setosa"      "Iris-setosa"      "Iris-setosa"      "Iris-setosa"
 [6] "Iris-setosa"      "Iris-setosa"      "Iris-setosa"      "Iris-versicolor"  "Iris-versicolor"
[11] "Iris-versicolor"  "Iris-versicolor"  "Iris-versicolor"  "Iris-versicolor"  "Iris-versicolor"
[16] "Iris-virginica"   "Iris-virginica"   "Iris-virginica"   "Iris-virginica"   "Iris-virginica"
[21] "Iris-virginica"   "Iris-virginica"   "Iris-virginica"   "Iris-virginica"   "Iris-virginica"
[26] "Iris-virginica"   "Iris-virginica"
```



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```
> model=naiveBayes(train$class~.,train)
> model
```

Naive Bayes Classifier for Discrete Predictors

Call:
naiveBayes.default(x = X, y = Y, laplace = laplace)

A-priori probabilities:

```
Y
  Iris-setosa Iris-versicolor Iris-virginica
0.3414634    0.3495935    0.3089431
```

Conditional probabilities:

```
                sepal_length
Y                [,1]      [,2]
Iris-setosa     5.009524 0.3369950
Iris-versicolor 5.986047 0.5138934
Iris-virginica  6.586842 0.6597178
```

```
                sepal_width
Y                [,1]      [,2]
Iris-setosa     3.419048 0.3690714
Iris-versicolor 2.783721 0.2910819
Iris-virginica  2.968421 0.3425700
```

```
                petal_length
Y                [,1]      [,2]
Iris-setosa     1.473810 0.1767726
Iris-versicolor 4.295349 0.4765718
Iris-virginica  5.568421 0.5723849
```

```
                petal_width
Y                [,1]      [,2]
Iris-setosa     0.250000 0.1109823
Iris-versicolor 1.330233 0.1994455
Iris-virginica  2.023684 0.2755184
```

```
> test_result=predict(model,test_data)
> test_result
 [1] Iris-setosa    Iris-setosa    Iris-setosa    Iris-setosa    Iris-setosa
 [6] Iris-setosa    Iris-setosa    Iris-setosa    Iris-versicolor Iris-versicolor
[11] Iris-versicolor Iris-versicolor Iris-versicolor Iris-versicolor Iris-versicolor
[16] Iris-virginica Iris-virginica Iris-virginica Iris-virginica Iris-virginica
[21] Iris-virginica Iris-virginica Iris-versicolor Iris-virginica Iris-virginica
[26] Iris-virginica Iris-virginica
Levels: Iris-setosa Iris-versicolor Iris-virginica
> #compare the predicted and actual values
> CrossTable(x=test_label, y=test_result)
```

```
library(Iris)
setosa <- test_iris[1:8,]
versicolor <- test_iris[9:15,]
virginica <- test_iris[16:27,]
> #compare the predicted and actual values
> CrossTable(x=test_label, y=test_result)
```

Cell Contents

	N
Chi-square contribution	
N / Row Total	
N / Col Total	
N / Table Total	

Total Observations in Table: 27

test_label	test_result			Row Total
	Iris-setosa	Iris-versicolor	Iris-virginica	
Iris-setosa	8	0	0	8
	13.370	2.370	3.259	
	1.000	0.000	0.000	0.296
	1.000	0.000	0.000	
	0.296	0.000	0.000	
Iris-versicolor	0	7	0	7
	2.074	11.699	2.852	
	0.000	1.000	0.000	0.259
	0.000	0.875	0.000	
	0.000	0.259	0.000	
Iris-virginica	0	1	11	12
	3.556	1.837	7.639	
	0.000	0.083	0.917	0.444
	0.000	0.125	1.000	
	0.000	0.037	0.407	
Column Total	8	8	11	27
	0.296	0.296	0.407	

> |

4. Learning Outcome:

- Setting and getting directory path for R project.
- Creating and working with FP growth algorithm.
- Saving data frame in .csv file format in R.
- Loading .csv file in data frame and print it.
- Basic of the data frame and r studio uses in the data frame