

Exp.No: 8**IMPLEMENT SVM/DECISION TREE CLASSIFICATION TECHNIQUES****AIM:**

To write an R code to implement SVM/decision tree classification techniques.

PROCEDURE:

1. Install and load the required packages (e1071 for SVM and rpart for Decision Tree) and load the iris dataset.
2. Split the dataset into training (70%) and testing (30%) sets using a reproducible random sampling method.
3. Fit the SVM model with a radial kernel using the training data, print the model summary, and evaluate its performance using a confusion matrix and accuracy calculation.
4. Fit the Decision Tree model using the rpart function with the training data, print the model summary, visualize the tree, and evaluate its performance using a confusion matrix and accuracy calculation.
5. Predict the test set results for both SVM and Decision Tree models and assess their accuracy.

PROGRAM CODE:**a) SVM IN R**

```
# Install and load the e1071 package (if not already installed)
install.packages("e1071") library(e1071)

# Load the iris dataset data(iris)

# Inspect the first few rows of the dataset head(iris)

# Split the data into training (70%) and testing (30%) sets set.seed(123)
# For reproducibility
sample_indices <- sample(1:nrow(iris), 0.7 * nrow(iris)) train_data
<- iris[sample_indices, ]
test_data <- iris[-sample_indices, ]

# Fit the SVM model svm_model <- svm(Species ~ ., data =
train_data, kernel = "radial")
```

```
# Print the summary of the model summary(svm_model)

# Predict the test set predictions <- predict(svm_model,
newdata = test_data)

# Evaluate the model's performance
confusion_matrix <- table(Predicted = predictions, Actual = test_data$Species)
print(confusion_matrix)

# Calculate accuracy
accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix) cat("Accuracy:",
accuracy * 100, "%\n")
```

OUTPUT:

The screenshot shows the RStudio interface with the following components:

- Script Editor:** Contains the R code for training and evaluating an SVM model.
- Console:** Displays the output of the code, including the SVM formula, parameters, support vectors, and a confusion matrix.
- Environment:** Lists the objects in the global environment, including data, iris, linear_model, logistic_model, mtcars, svm_model, test_data, and train_data.
- Packages:** Shows the installed system libraries, including base, BH, BioManager, BioParallel, BioVersion, boot, class, cdi, and cluster.

Console Output:

```
svm(formula = Species ~ ., data = train_data, kernel = "radial")

Parameters:
SVM-Type: C-classification
SVM-Kernel: radial
cost: 1

Number of Support Vectors: 45
( 7 18 20 )

Number of Classes: 3

Levels:
setosa versicolor virginica

> # Predict the test set
> predictions <- predict(svm_model, newdata = test_data)
> # Evaluate the model's performance
> confusion_matrix <- table(Predicted = predictions, Actual = test_data$Species)
> print(confusion_matrix)
      Actual
Predicted setosa versicolor virginica
setosa      14         0         0
versicolor  0         17         0
virginica   0          1        13

> # Calculate accuracy
> accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix)
> cat("Accuracy:", accuracy * 100, "%\n")
Accuracy: 97.77778 %
>
```

Environment:

Object	Details
data	7 obs. of 2 variables
iris	150 obs. of 5 variables
linear_model	List of 12
logistic_model	List of 30
mtcars	32 obs. of 11 variables
svm_model	List of 31
test_data	45 obs. of 5 variables
train_data	105 obs. of 5 variables

Values:

Variable	Value
accuracy	0.977777777777778
confusion_matrix	'table' int [1:3, 1:3] 14 0 0 0 17 1 0 0 13
heights	num [1:7] 150 160 165 170 175 180 185
predicted_probs	Named num [1:32] 0.461 0.461 0.598 0.492 0.297 ...
predictions	Factor w/ 3 levels "setosa","versicolor",...: 1 1 1 1 1 ...
sample_indices	int [1:105] 14 50 118 43 150 148 90 91 143 92 ...
weights	num [1:7] 55 60 62 68 70 75 80

System Library:

Name	Description	Version
base	The R Base Package	4.4.1
BH	Boost C++ Header Files	1.84.0-0
BioManager	Access the Bioconductor Project Package Repository	1.30.25
BioParallel	Bioconductor facilities for parallel evaluation	1.38.0
BioVersion	Set the appropriate version of Bioconductor packages	3.19.1
boot	Bootstrap Functions (Originally by Angelo Canty for S)	1.3-31
class	Functions for Classification	7.3-22
cdi	Helpers for Developing Command Line Interfaces	3.6.3
cluster	"Finding Groups in Data": Cluster Analysis Extended	2.1.6

b) Decision tree in R

```
# Install and load the rpart package (if not already installed)
install.packages("rpart") library(rpart)

# Load the iris dataset data(iris)

# Split the data into training (70%) and testing (30%) sets set.seed(123)
# For reproducibility
sample_indices <- sample(1:nrow(iris), 0.7 * nrow(iris)) train_data
<- iris[sample_indices, ]
```

```

test_data <- iris[-sample_indices, ]

# Fit the Decision Tree model
tree_model <- rpart(Species ~ ., data = train_data, method = "class")

# Print the summary of the model summary(tree_model)

# Plot the Decision Tree plot(tree_model)
text(tree_model, pretty = 0)

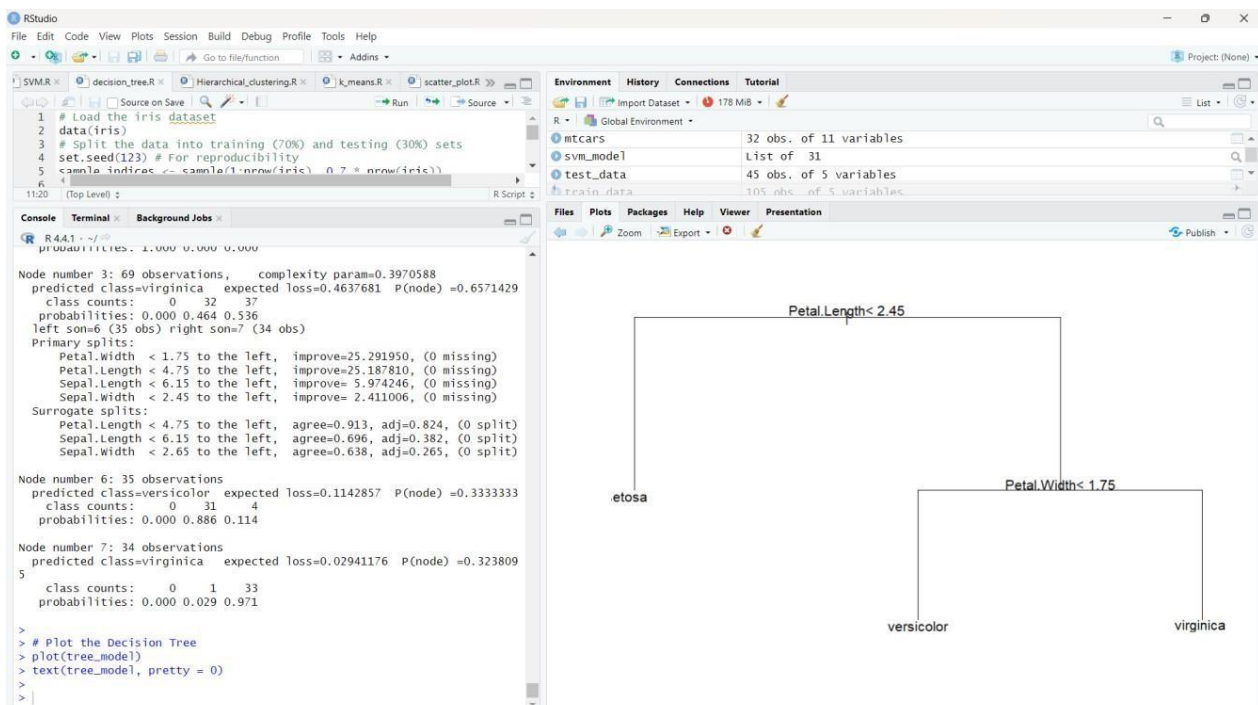
# Predict the test set predictions <- predict(tree_model, newdata =
test_data, type = "class")

# Evaluate the model's performance
confusion_matrix <- table(Predicted = predictions, Actual = test_data$Species)
print(confusion_matrix)

# Calculate accuracy
accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix) cat("Accuracy:",
accuracy * 100, "%\n")

```

OUTPUT:



RESULT:

Thus the R program to implement SVM/decision tree classification techniques has been executed and verified successfully.