Exp. No : 8

# Implement SVM/Decision tree classification techniques

## 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 :**

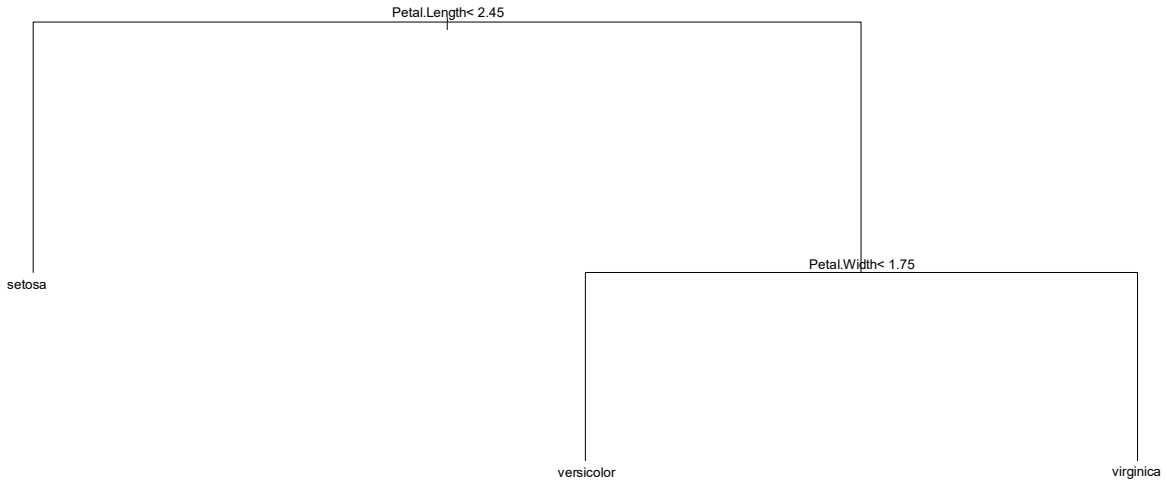
```
> print(confusion_matrix)
            Actual
Predicted    setosa versicolor virginica
  setosa         14          0         0
  versicolor      0         17         0
  virginica       0          1        13
> # Calculate accuracy
> accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix)
> cat("Accuracy:", accuracy * 100, "%\n")
Accuracy: 97.77778 %
>
```

### 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 :**

```
> 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)
           Actual
Predicted    setosa versicolor virginica
  setosa         14          0         0
  versicolor      0         18         1
  virginica       0          0        12
```


Petal.Length< 2.45
setosa
Petal.Width< 1.75
versicolor
virginica