

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 :

```

      Predicted \ Actual
      setosa versicolor virginica
setosa      14         0         0
versicolor   0        17         0
virginica    0         1        13
> 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 :

```
RStudio
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R 4.4.1 ~ /

Call:
rpart(formula = Species ~ ., data = train_data, method = "class")
n= 105

      CP nsplit  rel error    xerror    xstd
1 0.5294118      0 1.00000000 1.2058824 0.06232572
2 0.3970588      1 0.47058824 0.5441176 0.07198662
3 0.0300000      2 0.07352941 0.1176471 0.03997857

Variable importance
Petal.Width Petal.Length Sepal.Length Sepal.Width
          34           32            21            13

Node number 1: 105 observations,    complexity param=0.5294118
predicted class=virginica expected loss=0.647619 P(node) =1
class counts:    36    32    37
probabilities: 0.343 0.305 0.352
left son=2 (36 obs) right son=3 (69 obs)
Primary splits:
  Petal.Length < 2.45 to the left, improve=35.54783, (0 missing)
  Petal.Width < 0.8 to the left, improve=35.54783, (0 missing)
  Sepal.Length < 5.45 to the left, improve=24.79179, (0 missing)
  Sepal.Width < 3.25 to the right, improve=12.34670, (0 missing)
Surrogate splits:
  Petal.Width < 0.8 to the left, agree=1.000, adj=1.000, (0 split)
  Sepal.Length < 5.45 to the left, agree=0.924, adj=0.778, (0 split)
  Sepal.Width < 3.25 to the right, agree=0.819, adj=0.472, (0 split)

Node number 2: 36 observations
predicted class=setosa expected loss=0 P(node) =0.3428571
class counts:    36     0     0
probabilities: 1.000 0.000 0.000

Node number 3: 69 observations,    complexity param=0.3970588
predicted class=virginica expected loss=0.4637681 P(node) =0.6571429
class counts:     0    32    37
probabilities: 0.000 0.464 0.536
left son=6 (35 obs) right son=7 (34 obs)
Primary splits:
  Petal.Width < 1.75 to the left, improve=25.291950, (0 missing)
  Petal.Length < 4.75 to the left, improve=25.187810, (0 missing)
  Sepal.Length < 6.15 to the left, improve= 5.974246, (0 missing)
  Sepal.Width < 2.45 to the left, improve= 2.411006, (0 missing)
```

```

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Console Terminal Background Jobs
R 4.4.1: ~/...
predicted class=setosa expected loss=0 P(node) =0.542871
class counts: 36 0 0
probabilities: 1.000 0.000 0.000

Node number 3: 69 observations, complexity param=0.3970588
predicted class=virginica expected loss=0.4637681 P(node) =0.6571429
class counts: 0 32 37
probabilities: 0.000 0.464 0.536
left son=6 (35 obs) right son=7 (34 obs)
Primary splits:
Petal.Width < 1.75 to the left, improve=25.291950, (0 missing)
Petal.Length < 4.75 to the left, improve=25.187810, (0 missing)
Sepal.Length < 6.15 to the left, improve= 5.974246, (0 missing)
Sepal.Width < 2.45 to the left, improve= 2.411006, (0 missing)
Surrogate splits:
Petal.Length < 4.75 to the left, agree=0.913, adj=0.824, (0 split)
Sepal.Length < 6.15 to the left, agree=0.696, adj=0.382, (0 split)
Sepal.Width < 2.65 to the left, agree=0.638, adj=0.265, (0 split)

Node number 6: 35 observations
predicted class=versicolor expected loss=0.1142857 P(node) =0.3333333
class counts: 0 31 4
probabilities: 0.000 0.886 0.114

Node number 7: 34 observations
predicted class=virginica expected loss=0.02941176 P(node) =0.3238095
class counts: 0 1 33
probabilities: 0.000 0.029 0.971

> plot(tree_model)
> text(tree_model, pretty = 0)
> predictions <- predict(tree_model, newdata = test_data, type = "class")
> 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
> accuracy <- sum(diag(confusion_matrix)) / sum(confusion_matrix)
> cat("Accuracy:", accuracy * 100, "%\n")
Accuracy: 97.77778 %
>

```

Output

