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 :

```
            Actual
Predicted    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**

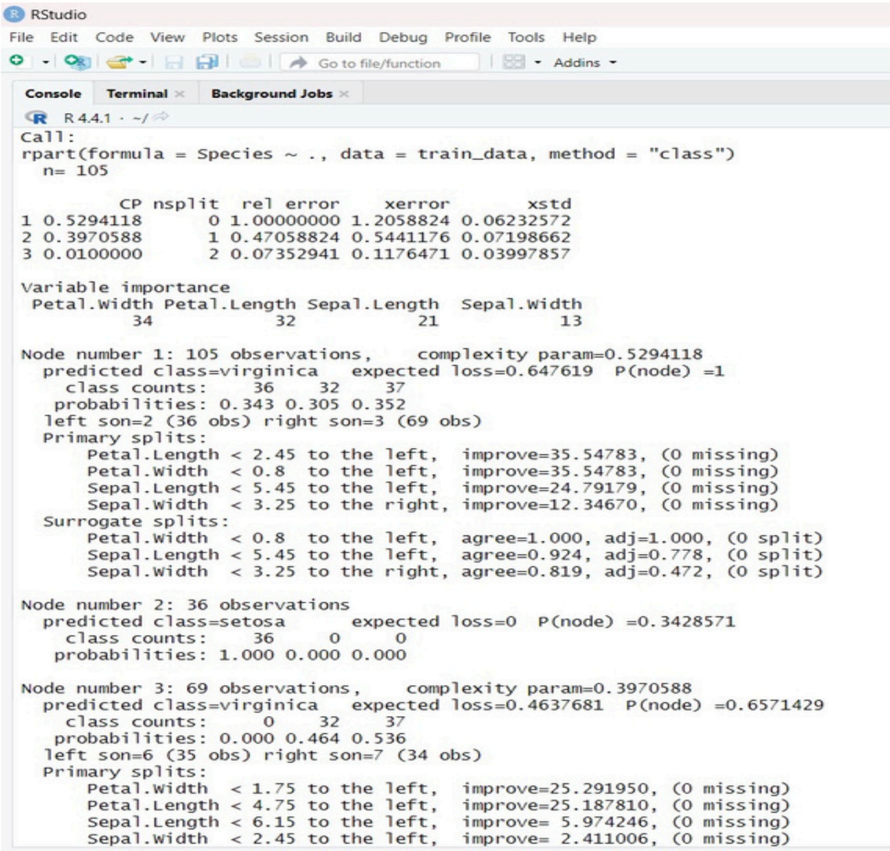
Install and load the rpart package (if not already installed) install.packages("rpart") library(rpart) # Load the iris dataset data(iris) # Split the data into training (70%) and testing (30%) sets set.seed(123) # For reproducibility sample_indices <- sample(1:nrow(iris), 0.7 * nrow(iris)) train_data <- 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 :



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```
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 0.0100000      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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```
  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)
  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