Data Exploration in R

Rémi FERRARI

The following documents the data exploration of a clean flower dataset called Iris. The project also takes a dive into statistical modelling. The programming language used in this project was the R language. Writing and computation of the code was realized on “rstudio.cloud”.

Table of Contents

Importing Dataset

Importing Iris dataset

```
> library(datasets)
> data("iris")
>
```

Summary Statistics

Summary Statistics of Iris dataset

```
> head(iris, 5)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
> tail(iris, 5)
    Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
146          6.7         3.0          5.2         2.3 virginica
147          6.3         2.5          5.0         1.9 virginica
148          6.5         3.0          5.2         2.0 virginica
149          6.2         3.4          5.4         2.3 virginica
150          5.9         3.0          5.1         1.8 virginica
> summary(iris)
  Sepal.Length    Sepal.Width     Petal.Length    Petal.Width          Species
 Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100   setosa    :50
 1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300   versicolor:50
 Median :5.800   Median :3.000   Median :4.350   Median :1.300   virginica :50
 Mean   :5.843   Mean   :3.057   Mean   :3.758   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

> library(skimr)
> skim(iris)
── Data Summary ────────────────────────
                           Values
Name                       iris
Number of rows             150
Number of columns          5

_________________________
Column type frequency:
  factor                   1
  numeric                  4

_________________________
Group variables            None

── Variable type: factor ──────────────────◆◆◆──────────────────────────────────────────────
  skim_variable n_missing complete_rate ordered n_unique top_counts
1 Species               0             1 FALSE          3 set: 50, ver: 50, vir: 50

── Variable type: numeric ──────────────────────────────────────────────────────◆◆──────────
  skim_variable n_missing complete_rate mean    sd  p0 p25  p50 p75 p100 hist
1 Sepal.Length          0             1 5.84 0.828 4.3 5.1 5.8  6.4  7.9 ▆▇▇▅▂
2 Sepal.Width           0             1 3.06 0.436 2   2.8 3    3.3  4.4 ▁▆▇▂▁
3 Petal.Length          0             1 3.76 1.77  1   1.6 4.35 5.1  6.9 ▇▁▂▅▅
4 Petal.Width           0             1 1.20 0.762 0.1 0.3 1.3  1.8  2.5 ▇▁▂▅▃
```

Grouping by species

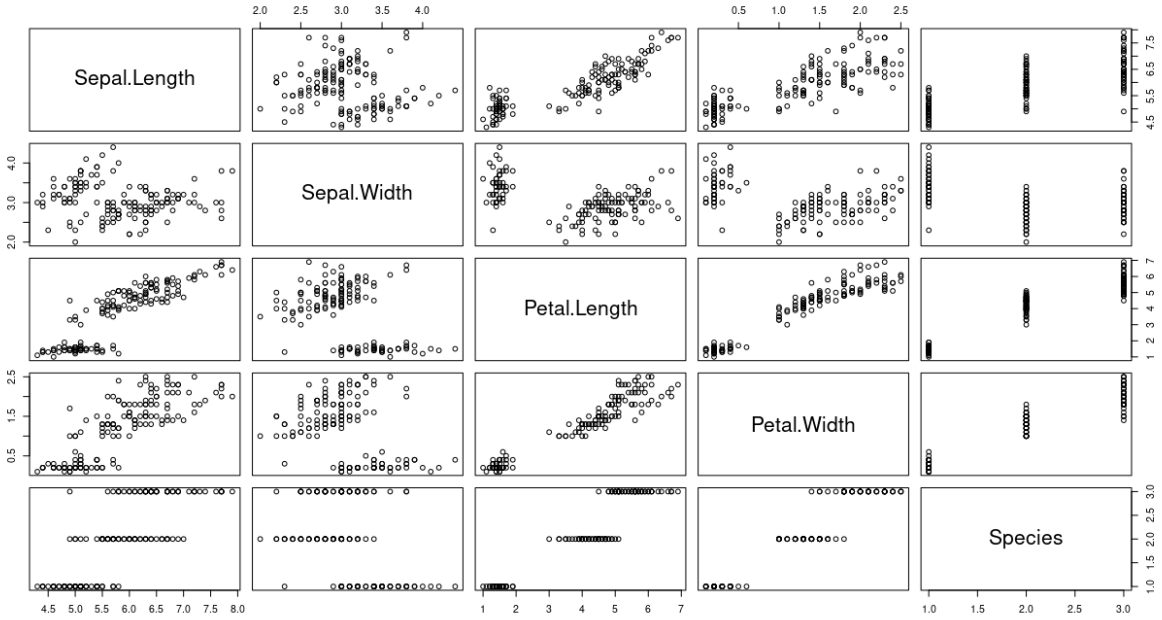
```
> iris %>%
+   dplyr::group_by(Species) %>%
+   skim()
── Data Summary ────────────────────────
                           Values
Name                       Piped data
Number of rows             150
Number of columns          5
_____________________
Column type frequency:
  numeric                  4
_____________________
Group variables            Species

── Variable type: numeric ──────────────────────────────────────────────────────
   skim_variable Species    n_missing complete_rate  mean    sd  p0  p25  p50  p75 p100
 1 Sepal.Length  setosa             0             1 5.01  0.352 4.3 4.8  5    5.2   5.8
 2 Sepal.Length  versicolor         0             1 5.94  0.516 4.9 5.6  5.9  6.3   7
 3 Sepal.Length  virginica          0             1 6.59  0.636 4.9 6.22 6.5  6.9   7.9
 4 Sepal.Width   setosa             0             1 3.43  0.379 2.3 3.2  3.4  3.68  4.4
 5 Sepal.Width   versicolor         0             1 2.77  0.314 2   2.52 2.8  3     3.4
 6 Sepal.Width   virginica          0             1 2.97  0.322 2.2 2.8  3    3.18  3.8
 7 Petal.Length  setosa             0             1 1.46  0.174 1   1.4  1.5  1.58  1.9
 8 Petal.Length  versicolor         0             1 4.26  0.470 3   4    4.35 4.6   5.1
 9 Petal.Length  virginica          0             1 5.55  0.552 4.5 5.1  5.55 5.88  6.9
10 Petal.Width   setosa             0             1 0.246 0.105 0.1 0.2  0.2  0.3   0.6
11 Petal.Width   versicolor         0             1 1.33  0.198 1   1.2  1.3  1.5   1.8
12 Petal.Width   virginica          0             1 2.03  0.275 1.4 1.8  2    2.3   2.5
   hist
 1 ▁▃▇▃▁
 2 ▁▃▇▇▂
 3 ▁▂▇▅▁
 4 ▁▃▇▃▁
 5 ▁▂▇▅▂
 6 ▁▃▇▃▁
 7 ▁▂▇▃▁
 8 ▁▃▇▇▂
 9 ▁▃▇▃▁
10 ▇▂▁▁▁
11 ▁▃▇▂▁
12 ▁▂▇▇▂
```

Visual insight

Panel Plot

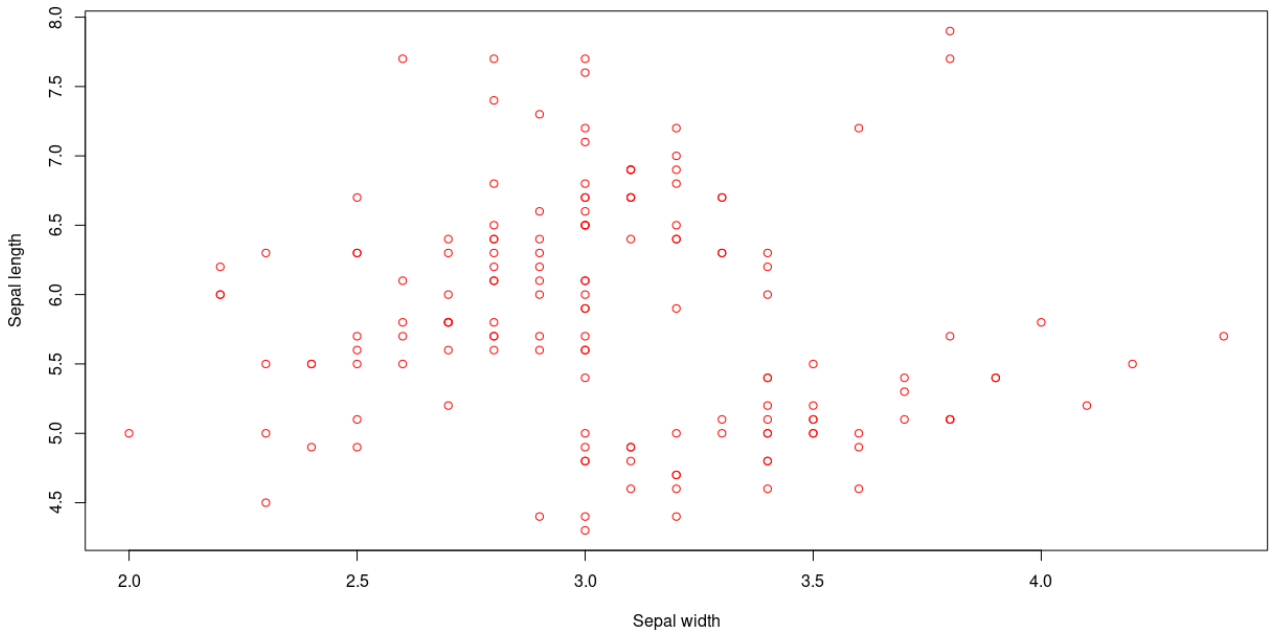
```
> plot(iris)
```



Scatter Plot

```
> plot(iris$Sepal.Width, iris$Sepal.Length)
>
> plot(iris$Sepal.Width, iris$Sepal.Length, col = "red")
>
> plot(iris$Sepal.Width, iris$Sepal.Length, col = "red",
ls
+      xlab = "Sepal width", ylab = "Sepal length")
```

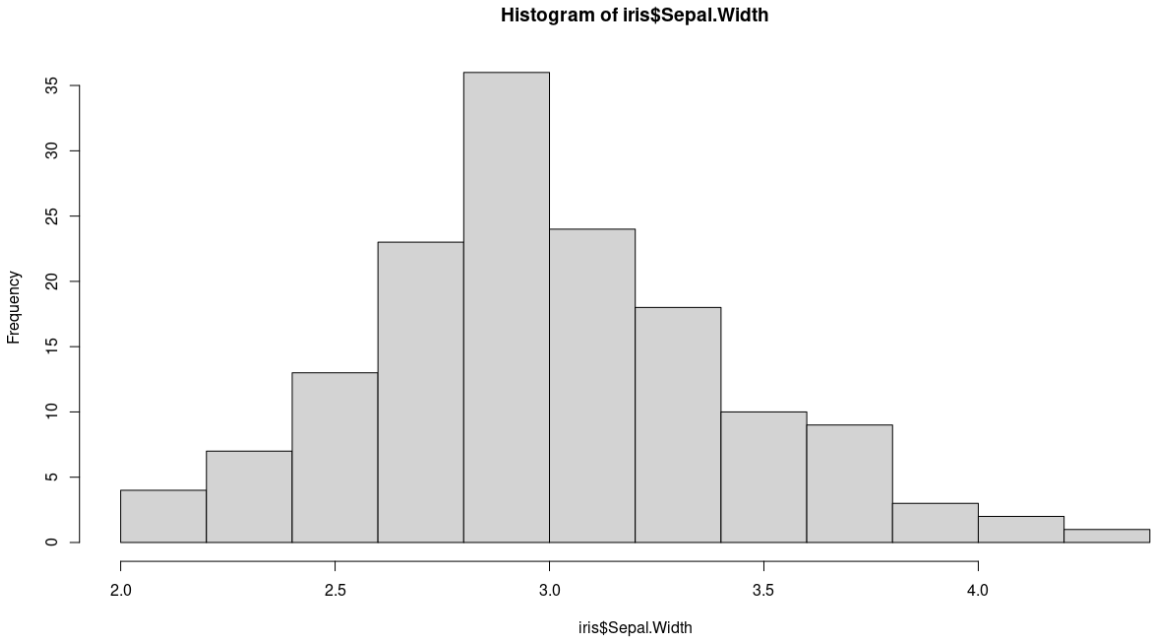
(For output, see below)



Histogram

Sepal Width

```
> hist(iris$Sepal.Width)
>
```

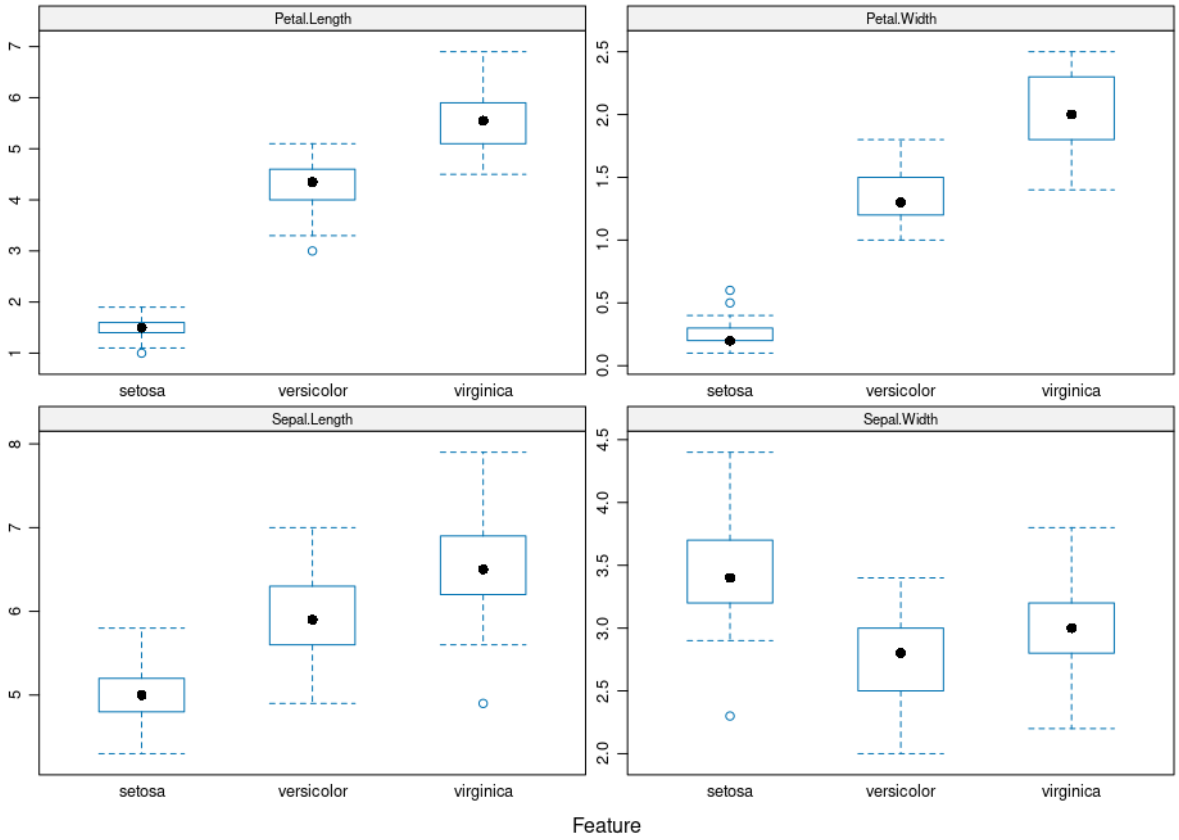


Observations:

Distribution seems normal. Most frequent Sepal Width sits around 3cm with a frequency of 35. Width range spans from 2 to 4.5cm.

Feature Plot

```
> library(caret)
Loading required package: ggplot2
Loading required package: lattice
>
> featurePlot(x = iris[,1:4],
+             y = iris$Species,
+             plot = "box",
+             strip=strip.custom(par.strip.text=list(cex=.7)),
+             scales = list(x = list(relation="free"),
+                           y = list(relation="free")))
>
```



Observations:

We can observe that Virginica species is generally lengthier in sepal and petal length. It is generally wider in petal width. Throughout petal length, petal width, and sepal length we can observe several common characteristics: Virginica species is, in general, the larger species followed up by the versicolor species. Same can be said when observing the range of the species throughout the different metrics. These characteristics are not shown in sepal width with the setosa species showcasing similar range to the other species and a generally greater value.

Classification Model Construction & Observation

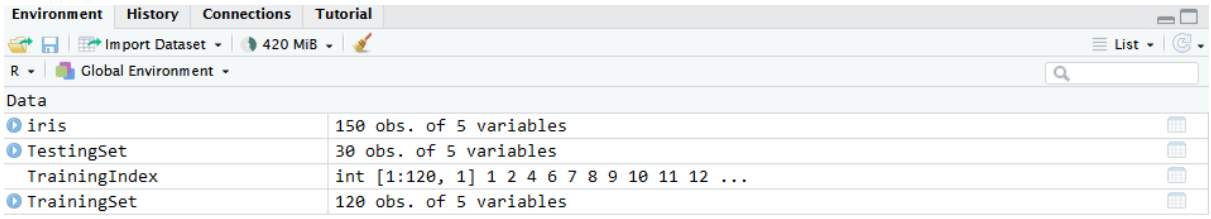
Setting random seed number, separating and observing training and testing data

```
set.seed(100)

TrainingIndex <- createDataPartition(iris$Species, p=0.8, list = FALSE)
TrainingSet <- iris[TrainingIndex,]
TestingSet <- iris[-TrainingIndex,]
```

```
> View(TrainingSet)
> View(TestingSet)
```

Testing and training set can be observed below with a 4:1 training set to testing set ratio. Two bottom figures showcase training (left) and testing data (right)



	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
7	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa
9	4.4	2.9	1.4	0.2	setosa
10	4.9	3.1	1.5	0.1	setosa
11	5.4	3.7	1.5	0.2	setosa
12	4.8	3.4	1.6	0.2	setosa
13	4.8	3.0	1.4	0.1	setosa
14	4.3	3.0	1.1	0.1	setosa
15	5.8	4.0	1.2	0.2	setosa
16	5.7	4.4	1.5	0.4	setosa
18	5.1	3.5	1.4	0.3	setosa
19	5.7	3.8	1.7	0.3	setosa
20	5.1	3.8	1.5	0.3	setosa
21	5.4	3.4	1.7	0.2	setosa
22	5.1	3.7	1.5	0.4	setosa
23	4.6	3.6	1.0	0.2	setosa
25	4.8	3.4	1.9	0.2	setosa
26	5.0	3.0	1.6	0.2	setosa
27	5.0	3.4	1.6	0.4	setosa
29	5.2	3.4	1.4	0.2	setosa
30	4.7	3.2	1.6	0.2	setosa
31	4.8	3.1	1.6	0.2	setosa
33	5.2	4.1	1.5	0.1	setosa
34	5.5	4.2	1.4	0.2	setosa

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
3	4.7	3.2	1.3	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
17	5.4	3.9	1.3	0.4	setosa
24	5.1	3.3	1.7	0.5	setosa
28	5.2	3.5	1.5	0.2	setosa
32	5.4	3.4	1.5	0.4	setosa
39	4.4	3.0	1.3	0.2	setosa
45	5.1	3.8	1.9	0.4	setosa
46	4.8	3.0	1.4	0.3	setosa
50	5.0	3.3	1.4	0.2	setosa
52	6.4	3.2	4.5	1.5	versicolor
56	5.7	2.8	4.5	1.3	versicolor
61	5.0	2.0	3.5	1.0	versicolor
63	6.0	2.2	4.0	1.0	versicolor
67	5.6	3.0	4.5	1.5	versicolor
80	5.7	2.6	3.5	1.0	versicolor
81	5.5	2.4	3.8	1.1	versicolor
84	6.0	2.7	5.1	1.6	versicolor
90	5.5	2.5	4.0	1.3	versicolor
95	5.6	2.7	4.2	1.3	versicolor
107	4.9	2.5	4.5	1.7	virginica
109	6.7	2.5	5.8	1.8	virginica
113	6.8	3.0	5.5	2.1	virginica
124	6.3	2.7	4.9	1.8	virginica
125	6.7	3.3	5.7	2.1	virginica
129	6.4	2.8	5.6	2.1	virginica
132	7.9	3.8	6.4	2.0	virginica
136	7.7	3.0	6.1	2.3	virginica

Realizing and observing scatterplots for training and testing sets in the purpose of gaining insight on training vs testing sets distribution differences. (Not all scatterplots are shown)

```
> plot(TrainingSet$Sepal.Width, TrainingSet$Sepal.Length, xlab = "Sepal Width", ylab = "Sepal Length")
> plot(TestingSet$Sepal.Width, TestingSet$Sepal.Length, xlab = "Sepal Width", ylab = "Sepal Length")
```

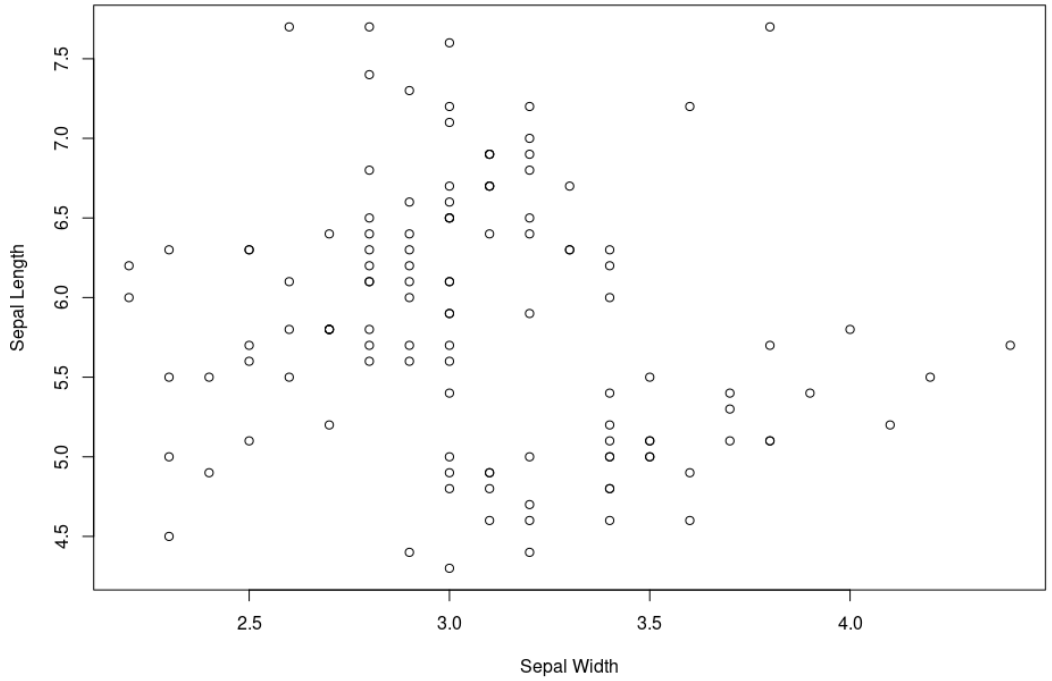


Figure 1: Training Set: Sepal Width vs Sepal Length

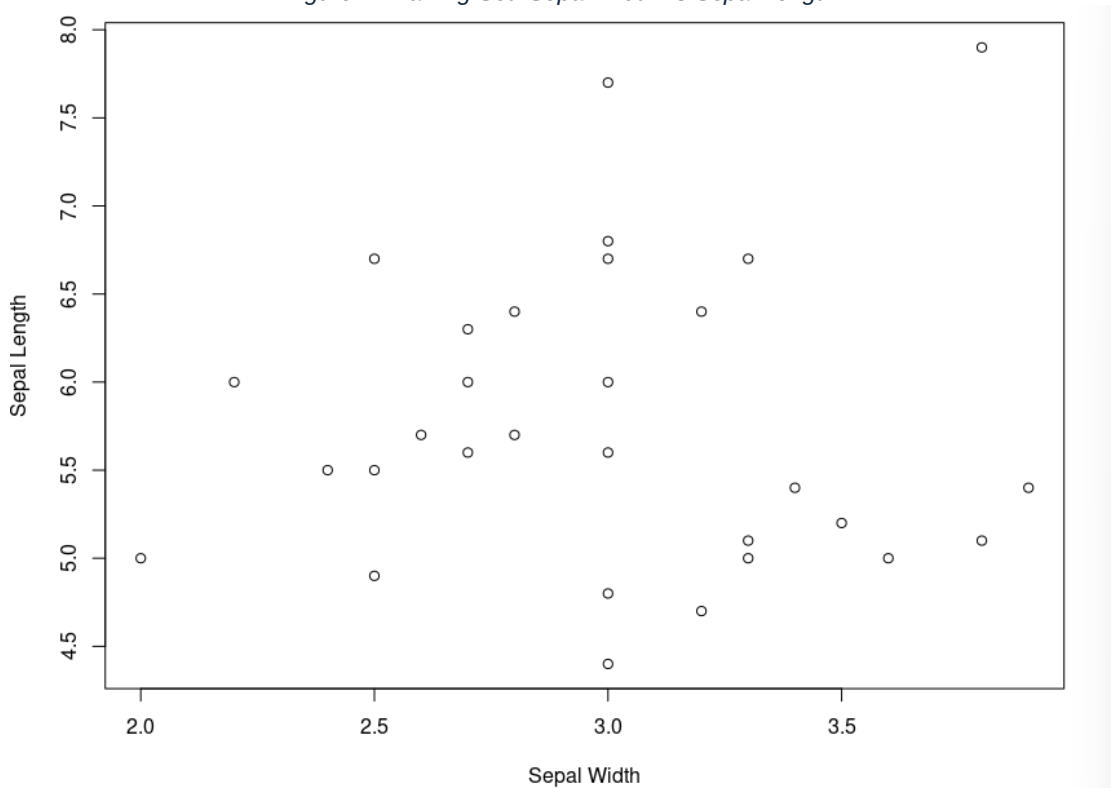


Figure 2: Testing Set: Sepal Width vs Sepal Length

Training Model

A training model is a machine learning model that is created by learning patterns from a labeled dataset (training data). The purpose of a training model is to adjust its parameters to minimize errors and improve performance, enabling it to make accurate predictions on new, unseen data.

```
> Model <- train(Species ~ ., data = TrainingSet,
+                method = "svmPoly",
+                na.action = na.omit,
+                preProcess=c("scale","center"),
+                trControl= trainControl(method="none"),
+                tuneGrid = data.frame(degree=1,scale=1,C=1)
+ )
```

Cross-Valdiation Model

A cross-validation model is a technique used to evaluate the generalizability of a machine learning model by splitting the data into multiple subsets (folds). The purpose of cross-validation is to assess how well the model will perform on independent datasets, helping to avoid overfitting and ensure robust performance across different data samples.

```
> Model.cv <- train(Species ~ ., data = TrainingSet,
+                   method = "svmPoly",
+                   na.action = na.omit,
+                   preProcess=c("scale","center"),
+                   trControl= trainControl(method="cv", number=10),
+                   tuneGrid = data.frame(degree=1,scale=1,C=1)
+ )
```

Applying Model for Prediction and Observation of Results

```
> Model.training <-predict(Model, TrainingSet)
> Model.testing <-predict(Model, TestingSet)
> Model.cv <-predict(Model.cv, TrainingSet)
```

Values	
Model.cv	Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
Model.testing	Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
Model.training	Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...

(See output below)

```
> print(Model.training.confusion)
Confusion Matrix and Statistics

            Reference
Prediction   setosa versicolor virginica
  setosa         40          0         0
  versicolor      0         40         1
  virginica       0          0        39

Overall Statistics

               Accuracy : 0.9917
                 95% CI : (0.9544, 0.9998)
    No Information Rate : 0.3333
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.9875

 Mcnemar's Test P-Value : NA

Statistics by Class:

                     Class: setosa Class: versicolor Class: virginica
Sensitivity                 1.0000            1.0000           0.9750
Specificity                 1.0000            0.9875           1.0000
Pos Pred Value              1.0000            0.9756           1.0000
Neg Pred Value              1.0000            1.0000           0.9877
Prevalence                  0.3333            0.3333           0.3333
Detection Rate              0.3333            0.3333           0.3250
Detection Prevalence        0.3333            0.3417           0.3250
Balanced Accuracy           1.0000            0.9938           0.9875
```

Overall, the model performs exceptionally well on the training set, with high accuracy, sensitivity, specificity, and balanced accuracy for all classes. The results indicate that the model has learned to classify the iris species very effectively, with minimal errors.

```
> print(Model.testing.confusion)
Confusion Matrix and Statistics

            Reference
Prediction   setosa versicolor virginica
  setosa         10          0         0
  versicolor      0          9         0
  virginica       0          1        10

Overall Statistics

               Accuracy : 0.9667
                 95% CI : (0.8278, 0.9992)
    No Information Rate : 0.3333
    P-Value [Acc > NIR] : 2.963e-13

                  Kappa : 0.95

 Mcnemar's Test P-Value : NA

Statistics by Class:

                     Class: setosa Class: versicolor Class: virginica
Sensitivity                 1.0000            0.9000           1.0000
Specificity                 1.0000            1.0000           0.9500
Pos Pred Value              1.0000            1.0000           0.9091
Neg Pred Value              1.0000            0.9524           1.0000
Prevalence                  0.3333            0.3333           0.3333
Detection Rate              0.3333            0.3000           0.3333
Detection Prevalence        0.3333            0.3000           0.3667
Balanced Accuracy           1.0000            0.9500           0.9750
```

The model performs excellently on the testing set, with high accuracy and robust classification performance across all classes.

```
> print(Model.cv.confusion)
Confusion Matrix and Statistics

            Reference
Prediction   setosa versicolor virginica
  setosa         40          0         0
  versicolor      0         40         1
  virginica       0          0        39

Overall Statistics

               Accuracy : 0.9917
                 95% CI : (0.9544, 0.9998)
    No Information Rate : 0.3333
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.9875

 Mcnemar's Test P-Value : NA

Statistics by Class:

                     Class: setosa Class: versicolor Class: virginica
Sensitivity                 1.0000            1.0000           0.9750
Specificity                 1.0000            0.9875           1.0000
Pos Pred Value              1.0000            0.9756           1.0000
Neg Pred Value              1.0000            1.0000           0.9877
Prevalence                  0.3333            0.3333           0.3333
Detection Rate              0.3333            0.3333           0.3250
Detection Prevalence        0.3333            0.3417           0.3250
Balanced Accuracy           1.0000            0.9938           0.9875
```

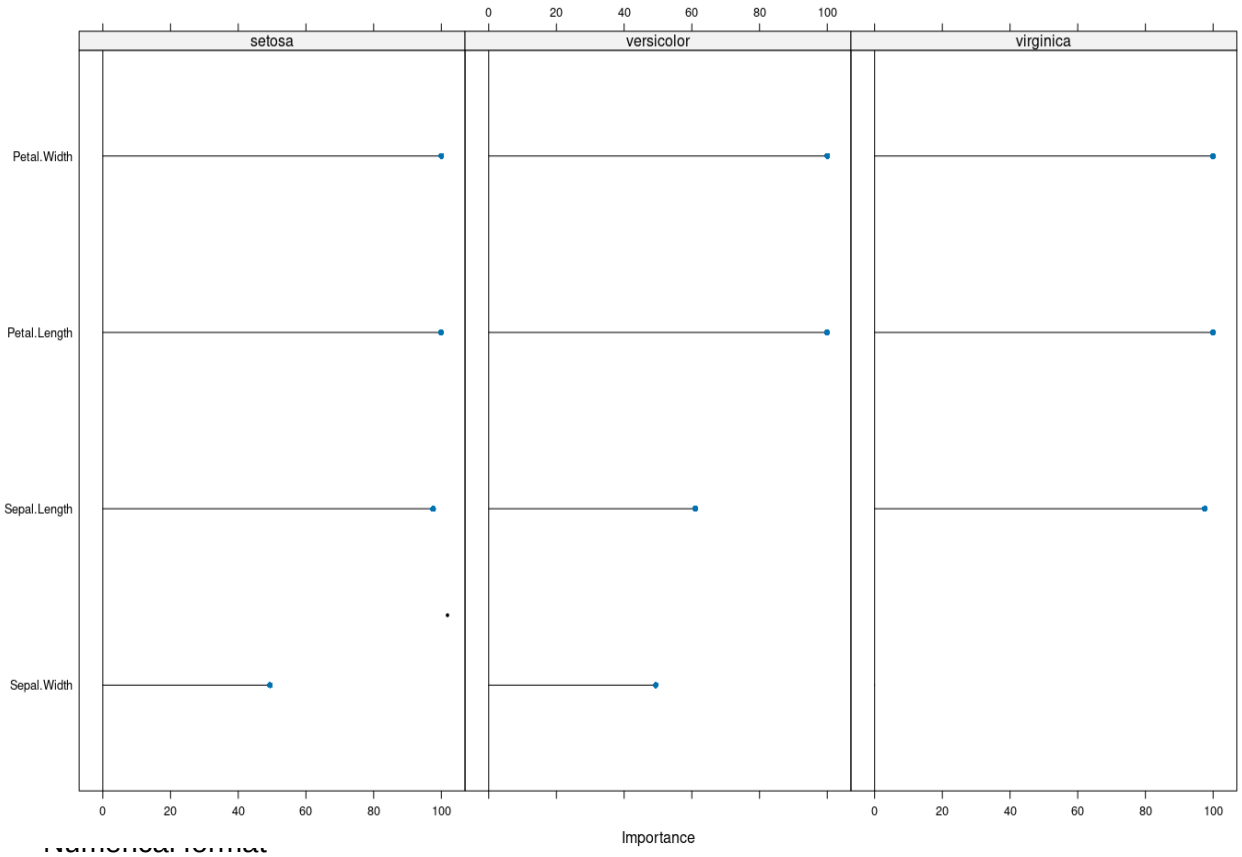
The cross-validation results show that the model has high accuracy and performs excellently across all classes, demonstrating robust and reliable classification performance.

Feature Importance

```
> Importance <- varImp(Model)
> plot(Importance)
> plot(Importance)
```

(see below for output)

Graph




```
> importance <- varImp(Model, scale = FALSE)
> print(importance)
ROC curve variable importance

  variables are sorted by maximum importance across the clas
             setosa versicolor virginica
Petal.Length 1.0000     1.0000    1.0000
Petal.Width  1.0000     1.0000    1.0000
Sepal.Length 0.9959     0.9350    0.9959
Sepal.Width  0.9156     0.9156    0.8334
```

Observation:

Petal Length and Petal Width are the most important features for predicting the species in the Iris dataset, based on the ROC curve analysis.

Sepal Length is also important but slightly less influential.

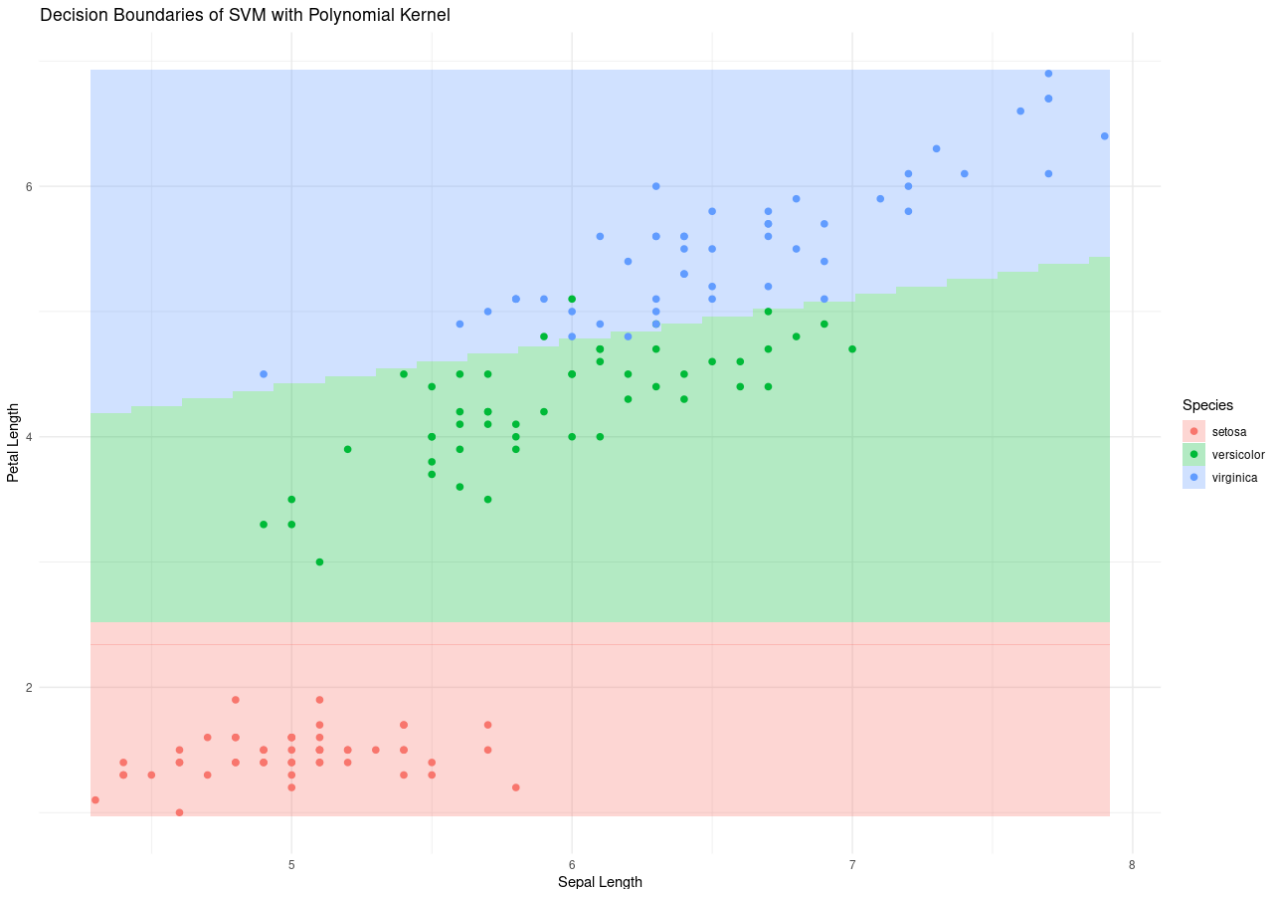
Sepal Width is the least important feature, although it still plays a role in the model's predictions.

These results suggest that the petal measurements (length and width) are much more crucial for distinguishing between the species compared to the sepal measurements.

Observing Model Decision Boundaries

Model Decision Boundaries

Please note that the decision boundaries graphics below are based upon a model utilizing the same method but restricted to two features.



Observations:

Model predicts that the Setosa species area remains between a petal length of 4cm and a sepal length of 8cm (this last number is most probably way off and showcases limits of the model and data). Versicor species ranges in petal length from 4 to 5.5cm as a linear function to Sepa length which ranges from 4 to 8cm. Setosa species ranges in sepal length from 4 to 8cm and petal length from 4 and above. All flowers of the virginica family where correctly identified. Several flowers from the Versicolor and Virginica where incorrectly identified. Overall, the majority of flowers where correctly identified. Please note that further information must be observed in order to correctly assess the model’s predictive capacity.