

# Data Analysis on Iris Flowers

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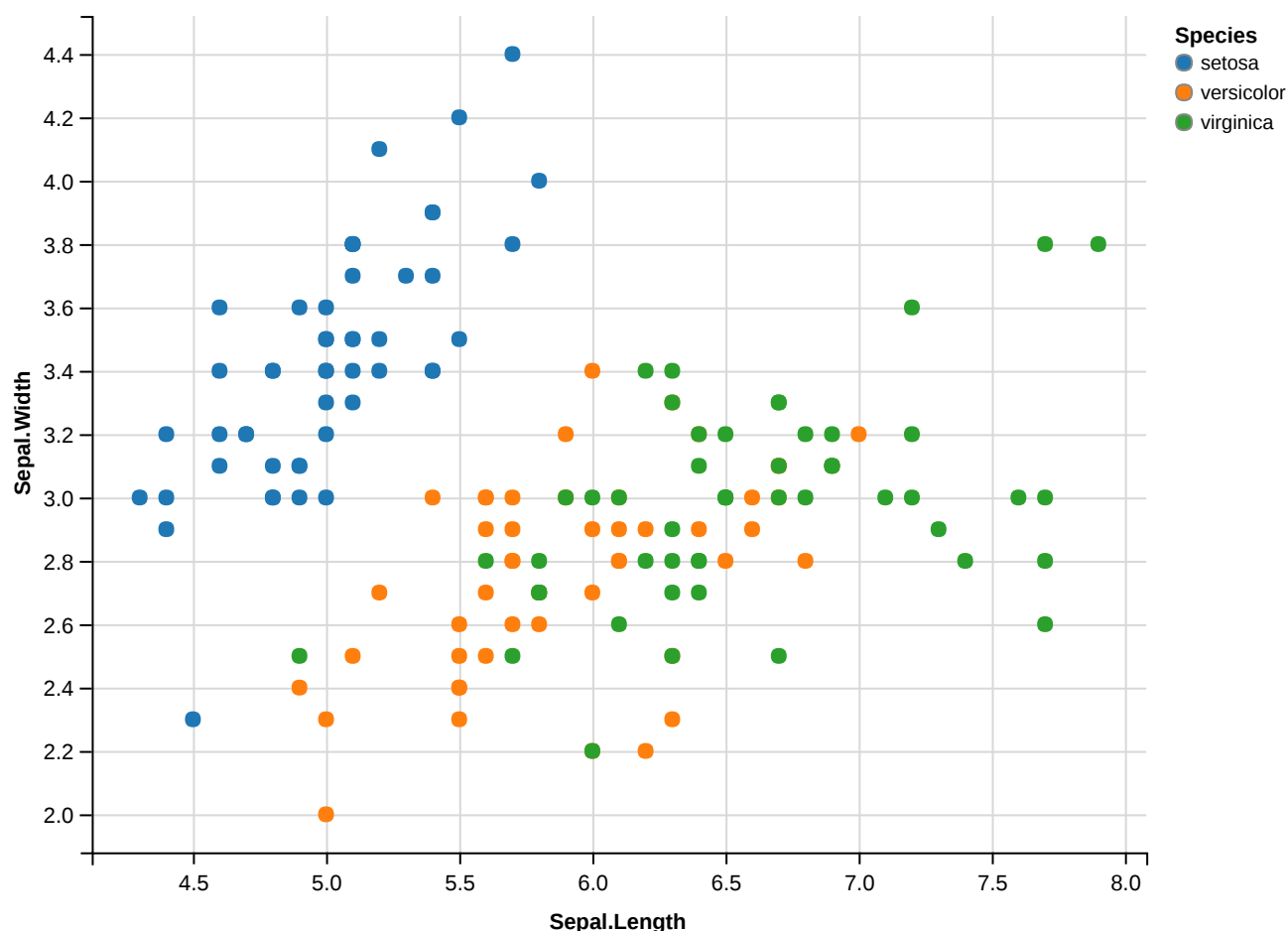
## Load the data

```
head(iris)
```

```
## 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
## 6          5.4          3.9          1.7          0.4  setosa
```

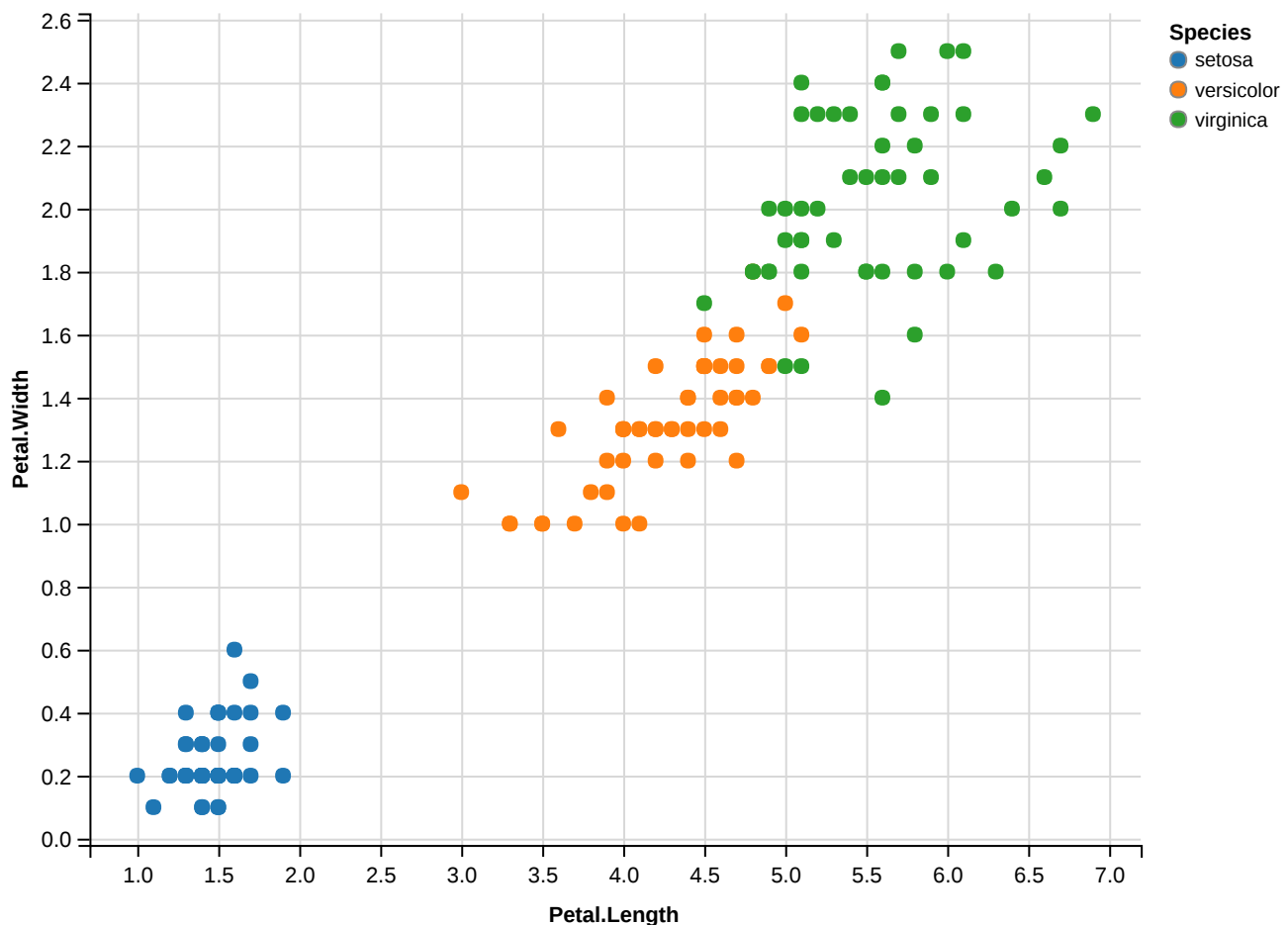
## Scatterplot

By using scatterplots, we can find how much the parameters are correlated



The Sepal Length and Sepal width are somewhat correlated but not that much, we can see that the setosa is completely separated since they have small sepal length and small sepal width than other species. But the real problem is that the virginica, versicolor species were mixed apart. Hence we move to the next parameters.

```
iris %>% ggvis(~Petal.Length,~Petal.Width,fill = ~Species) %>% layer_points()
```



Check this, this scatterplot is pretty good, which separates the species and forms a perfect correlation line.

## Correlations

Let's check the numerical correlations of the parameters

```
print(cor(iris$Sepal.Length,iris$Sepal.Width))
```

```
## [1] -0.1175698
```

```
print(cor(iris$Petal.Length,iris$Petal.Width))
```

```
## [1] 0.9628654
```

## Correlation matrix

For each property the correlations are identified for different species i.e, setosa, versicolor, virginica

```
type <- levels(iris$Species)
print(type[1])
```

```
## [1] "setosa"
```

```
cor(iris[iris$Species==type[1],1:4])
```

```
##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## Sepal.Length      1.0000000    0.7425467    0.2671758    0.2780984
## Sepal.Width       0.7425467    1.0000000    0.1777000    0.2327520
## Petal.Length      0.2671758    0.1777000    1.0000000    0.3316300
## Petal.Width       0.2780984    0.2327520    0.3316300    1.0000000
```

```
print(type[2])
```

```
## [1] "versicolor"
```

```
cor(iris[iris$Species==type[3],1:4])
```

```
##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## Sepal.Length      1.0000000    0.4572278    0.8642247    0.2811077
## Sepal.Width       0.4572278    1.0000000    0.4010446    0.5377280
## Petal.Length      0.8642247    0.4010446    1.0000000    0.3221082
## Petal.Width       0.2811077    0.5377280    0.3221082    1.0000000
```

```
print(type[3])
```

```
## [1] "virginica"
```

```
cor(iris[iris$Species==type[3],1:4])
```

```
##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## Sepal.Length      1.0000000    0.4572278    0.8642247    0.2811077
## Sepal.Width       0.4572278    1.0000000    0.4010446    0.5377280
## Petal.Length      0.8642247    0.4010446    1.0000000    0.3221082
## Petal.Width       0.2811077    0.5377280    0.3221082    1.0000000
```

## Knowing the data

```
head(iris)
```

```
##   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
## 6           5.4           3.9           1.7           0.4   setosa
```

## Structure of the data

```
str(iris)
```

```
## 'data.frame': 150 obs. of 5 variables:
## $ Sepal.Length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ Petal.Length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ Petal.Width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
## $ Species : Factor w/ 3 levels "setosa","versicolor",...: 1 1 1 1 1 1 1 1 1 1
## ...
```

## Tabulations

```
table(iris$Species)
```

```
##
##      setosa versicolor virginica
##         50         50         50
```

```
round(prop.table(table(iris$Species)) * 100, digits = 1)
```

```
##
##      setosa versicolor virginica
##      33.3      33.3      33.3
```

```
summary(iris)
```

```
##      Sepal.Length      Sepal.Width      Petal.Length      Petal.Width
## Min.      :4.300    Min.      :2.000    Min.      :1.000    Min.      :0.100
## 1st Qu.:5.100    1st Qu.:2.800    1st Qu.:1.600    1st Qu.:0.300
## Median :5.800    Median :3.000    Median :4.350    Median :1.300
## 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
##      Species
## setosa      :50
## versicolor:50
## virginica   :50
##
##
##
```

```
summary(iris[c("Petal.Width", "Sepal.Width")])
```

```
##      Petal.Width      Sepal.Width
## Min.      :0.100    Min.      :2.000
## 1st Qu.:0.300    1st Qu.:2.800
## Median :1.300    Median :3.000
## Mean      :1.199    Mean      :3.057
## 3rd Qu.:1.800    3rd Qu.:3.300
## Max.      :2.500    Max.      :4.400
```

## Normalization

The normalization/feature scaling is not necessary but still, it improves the accuracy of this classification system. Here normalization process makes all the columns to be in the range of 0 to 1.

```
library(class)
normalize <- function(x) {
  num <- x - min(x)
  denom <- max(x) - min(x)
  return (num/denom)
}

iris_norm <- as.data.frame(lapply(iris[1:4], normalize))

summary(iris_norm)
```

```
##      Sepal.Length      Sepal.Width      Petal.Length      Petal.Width
## Min.      :0.0000    Min.      :0.0000    Min.      :0.0000    Min.      :0.00000
## 1st Qu.:0.2222    1st Qu.:0.3333    1st Qu.:0.1017    1st Qu.:0.08333
## Median :0.4167    Median :0.4167    Median :0.5678    Median :0.50000
## Mean      :0.4287    Mean      :0.4406    Mean      :0.4675    Mean      :0.45806
## 3rd Qu.:0.5833    3rd Qu.:0.5417    3rd Qu.:0.6949    3rd Qu.:0.70833
## Max.      :1.0000    Max.      :1.0000    Max.      :1.0000    Max.      :1.00000
```

## Training and Testing sets

The dataset is divided into two parts 1) Training set : To train the classifier, it contains 2/3 of the dataset. 2) Testing set : To test the classifier, it contains 1/3 of the dataset.

So for the division purpose we need random rows, that's why we are using seed() method.

```
set.seed(1234)
ind <- sample(2, nrow(iris), replace=TRUE, prob=c(0.67, 0.33))
ind
```

```
##      [1] 1 1 1 1 2 1 1 1 1 1 2 1 1 2 1 2 1 1 1 1 1 1 1 2 1 2 2 1 1 1 1 1
##      [36] 2 1 1 2 2 1 1 1 1 1 2 1 1 2 1 1 2 1 1 1 1 2 1 2 2 1 1 1 1 2 1 1 1
##      [71] 1 2 1 2 1 1 1 1 1 1 2 1 1 1 1 2 1 1 1 2 1 1 1 1 1 1 1 2 1 1 1 1
##     [106] 1 1 1 1 1 2 1 2 1 1 2 2 1 1 2 2 2 2 2 1 1 1 1 1 1 2 1 1 1 2 1 2 1 1 2
##     [141] 1 2 1 1 1 1 2 1 2 1
```

```
iris.training <- iris[ind==1, 1:4]
```

```
head(iris.training)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1          5.1          3.5          1.4          0.2
## 2          4.9          3.0          1.4          0.2
## 3          4.7          3.2          1.3          0.2
## 4          4.6          3.1          1.5          0.2
## 6          5.4          3.9          1.7          0.4
## 7          4.6          3.4          1.4          0.3
```

```
iris.test <- iris[ind==2, 1:4]
```

```
head(iris.test)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 5          5.0          3.6          1.4          0.2
## 11         5.4          3.7          1.5          0.2
## 14         4.3          3.0          1.1          0.1
## 16         5.7          4.4          1.5          0.4
## 26         5.0          3.0          1.6          0.2
## 28         5.2          3.5          1.5          0.2
```

Here the data is being separated!with the above found random possibilities.

```
iris.trainLabels <- iris[ind==1,5]
```

```
print(iris.trainLabels)
```

```
## [1] setosa setosa setosa setosa setosa setosa
## [7] setosa setosa setosa setosa setosa setosa
## [13] setosa setosa setosa setosa setosa setosa
## [19] setosa setosa setosa setosa setosa setosa
## [25] setosa setosa setosa setosa setosa setosa
## [31] setosa setosa setosa setosa setosa setosa
## [37] setosa setosa versicolor versicolor versicolor versicolor
## [43] versicolor versicolor versicolor versicolor versicolor versicolor
## [49] versicolor versicolor versicolor versicolor versicolor versicolor
## [55] versicolor versicolor versicolor versicolor versicolor versicolor
## [61] versicolor versicolor versicolor versicolor versicolor versicolor
## [67] versicolor versicolor versicolor versicolor versicolor versicolor
## [73] versicolor versicolor versicolor versicolor virginica virginica
## [79] virginica virginica virginica virginica virginica virginica
## [85] virginica virginica virginica virginica virginica virginica
## [91] virginica virginica virginica virginica virginica virginica
## [97] virginica virginica virginica virginica virginica virginica
## [103] virginica virginica virginica virginica virginica virginica
## [109] virginica virginica
## Levels: setosa versicolor virginica
```

```
iris.testLabels <- iris[ind==2, 5]

print(iris.testLabels)
```

```
## [1] setosa      setosa      setosa      setosa      setosa      setosa
## [7] setosa      setosa      setosa      setosa      setosa      setosa
## [13] versicolor versicolor versicolor versicolor versicolor versicolor
## [19] versicolor versicolor versicolor versicolor versicolor versicolor
## [25] virginica   virginica   virginica   virginica   virginica   virginica
## [31] virginica   virginica   virginica   virginica   virginica   virginica
## [37] virginica   virginica   virginica   virginica
## Levels: setosa versicolor virginica
```

## Classification

Here the k-Nearest Neighbour Classification is applied, with the training set and the testing set and the species were predicted. The `knn()` method does a good job by predicting the species based on the training set and they were tested by the testing set.

```
iris_pred <- knn(train = iris.training, test = iris.test, cl = iris.trainLabels, k=3)
iris_pred
```

```
## [1] setosa      setosa      setosa      setosa      setosa      setosa
## [7] setosa      setosa      setosa      setosa      setosa      setosa
## [13] versicolor versicolor versicolor versicolor versicolor versicolor
## [19] versicolor versicolor versicolor versicolor versicolor versicolor
## [25] virginica   virginica   virginica   virginica   versicolor virginica
## [31] virginica   virginica   virginica   virginica   virginica   virginica
## [37] virginica   virginica   virginica   virginica
## Levels: setosa versicolor virginica
```

## Comparison

We need to make sure that our classifier has classified the species correctly, in order to do that we merge the real species name and the predicted name. As a result we find something unusual.

```
irisTestLabels <- data.frame(iris.testLabels)

merge <- data.frame(iris_pred, iris.testLabels)

names(merge) <- c("Predicted Species", "Observed Species")

merge
```

##	Predicted Species	Observed Species
## 1	setosa	setosa
## 2	setosa	setosa
## 3	setosa	setosa
## 4	setosa	setosa
## 5	setosa	setosa
## 6	setosa	setosa
## 7	setosa	setosa
## 8	setosa	setosa
## 9	setosa	setosa
## 10	setosa	setosa
## 11	setosa	setosa
## 12	setosa	setosa
## 13	versicolor	versicolor
## 14	versicolor	versicolor
## 15	versicolor	versicolor
## 16	versicolor	versicolor
## 17	versicolor	versicolor
## 18	versicolor	versicolor
## 19	versicolor	versicolor
## 20	versicolor	versicolor
## 21	versicolor	versicolor
## 22	versicolor	versicolor
## 23	versicolor	versicolor
## 24	versicolor	versicolor
## 25	virginica	virginica
## 26	virginica	virginica
## 27	virginica	virginica
## 28	virginica	virginica
## 29	versicolor	virginica
## 30	virginica	virginica
## 31	virginica	virginica
## 32	virginica	virginica
## 33	virginica	virginica
## 34	virginica	virginica
## 35	virginica	virginica
## 36	virginica	virginica
## 37	virginica	virginica
## 38	virginica	virginica
## 39	virginica	virginica
## 40	virginica	virginica

The classifier did a small mistake i.e, instead of versicolor,it predicted as virginica. This k-NN classification is not 100 % percent accurate.

## Proper summary

```
library(gmodels)
CrossTable(x = iris.testLabels, y = iris_pred, prop.chisq=FALSE)
```



```
##
##
##      Cell Contents
## |-----|
## |                N |
## |      N / Row Total |
## |      N / Col Total |
## |      N / Table Total |
## |-----|
##
##
## Total Observations in Table:  40
##
##
##      iris.testLabels | iris_pred
##      iris.testLabels |      setosa | versicolor | virginica | Row Total |
## -----|-----|-----|-----|-----|
##      setosa |      12 |      0 |      0 |      12 |
##      |      1.000 |      0.000 |      0.000 |      0.300 |
##      |      1.000 |      0.000 |      0.000 |      |
##      |      0.300 |      0.000 |      0.000 |      |
## -----|-----|-----|-----|
##      versicolor |      0 |      12 |      0 |      12 |
##      |      0.000 |      1.000 |      0.000 |      0.300 |
##      |      0.000 |      0.923 |      0.000 |      |
##      |      0.000 |      0.300 |      0.000 |      |
## -----|-----|-----|-----|
##      virginica |      0 |      1 |      15 |      16 |
##      |      0.000 |      0.062 |      0.938 |      0.400 |
##      |      0.000 |      0.077 |      1.000 |      |
##      |      0.000 |      0.025 |      0.375 |      |
## -----|-----|-----|-----|
##      Column Total |      12 |      13 |      15 |      40 |
##      |      0.300 |      0.325 |      0.375 |      |
## -----|-----|-----|-----|
##
##
```