

Unsupervised Learning DBSCAN 1

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R Markdown

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
# Step 1: load fpc package
#install.packages("fpc")
library(fpc)
```

```
# Remove label from iris dataset
iris2 <- iris[-5] # remove class tags
```

```
# Step 2: Apply DbScan clustering
ds_model <- dbscan(iris2, eps=0.45, MinPts=5)
```

```
# Interpretation of Model
ds_model
```

```
## dbscan Pts=150 MinPts=5 eps=0.45
##      0  1  2
## border 24  4 13
## seed    0 44 65
## total   24 48 78
```

```
# 1 to 3 : identified clusters
# 0: noises or outliers, objects that are not assigned to any clusters
```

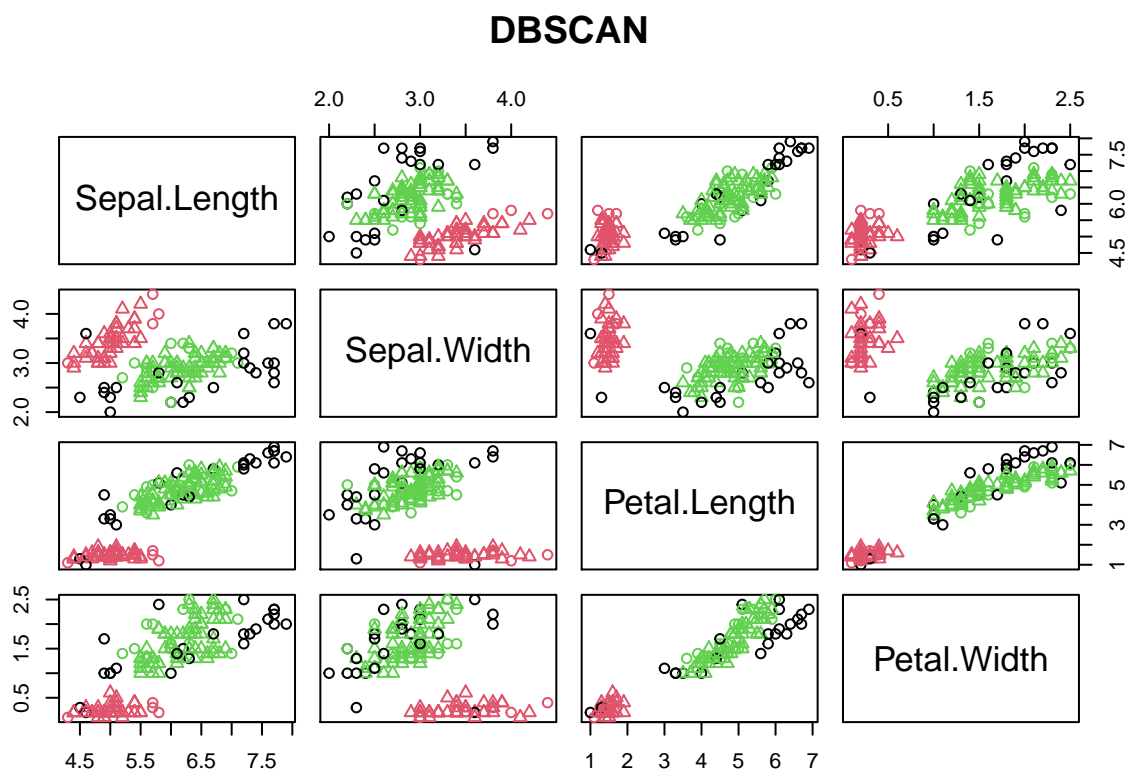
```
# Check the cluster
ds_model$cluster
```

```
##      [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1
##     [38] 1 1 1 1 0 1 1 1 1 1 1 1 1 2 2 2 2 2 2 0 2 2 0 2 0 2 2 2 2 2 0 2 2 2 2
##     [75] 2 2 2 2 2 2 2 2 2 2 2 2 2 0 2 2 2 2 2 0 2 2 2 2 2 2 2 2 0 0 0 0 2
##    [112] 2 2 2 0 2 2 0 0 2 2 2 0 2 2 0 2 2 2 0 0 2 2 0 0 2 2 2 2 2 2 2 2 2 2
##    [149] 2 2
```

```
# compare clusters with original class labels
table(ds_model$cluster, iris$Species)
```

```
##
##      setosa versicolor virginica
## 0         2          7         15
## 1        48          0          0
## 2         0         43         35
```

```
# Plot Cluster
plot(ds_model, iris2, main = "DBSCAN")
```



```
plot(ds_model, iris2[c(1,4)], main = "Petal Width vs Sepal Length")
```

