

# Machine Learning

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```
library(caret)
library(rpart.plot)
library(rattle)
library(calibrate)
library(randomForest)
```

## Decision Tree Example

### Problem Description

Given a data set that contains some observation and corresponding class label, can a machine learning algorithm be trained to determine the class label of any data set (not necessarily the data that was used for training) from its observation

### Solution using decision tree

```
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
```

Create data partition

```
inTrain <- createDataPartition(iris$Species, p = 0.6, list = FALSE)
trainData <- iris[inTrain,]
testData <- iris[-inTrain,]
```

Build a decision tree model and use it for prediction on test data set

```
treeModel <- train(Species ~ ., data = trainData, method = "rpart")
preClass <- predict(treeModel, newdata = testData)
cMatrix <- confusionMatrix(preClass, testData$Species)
cMatrix$table
```

```
##           Reference
## Prediction  setosa versicolor virginica
##   setosa      20         0         0
##   versicolor   0        19         3
##   virginica    0         1        17
```

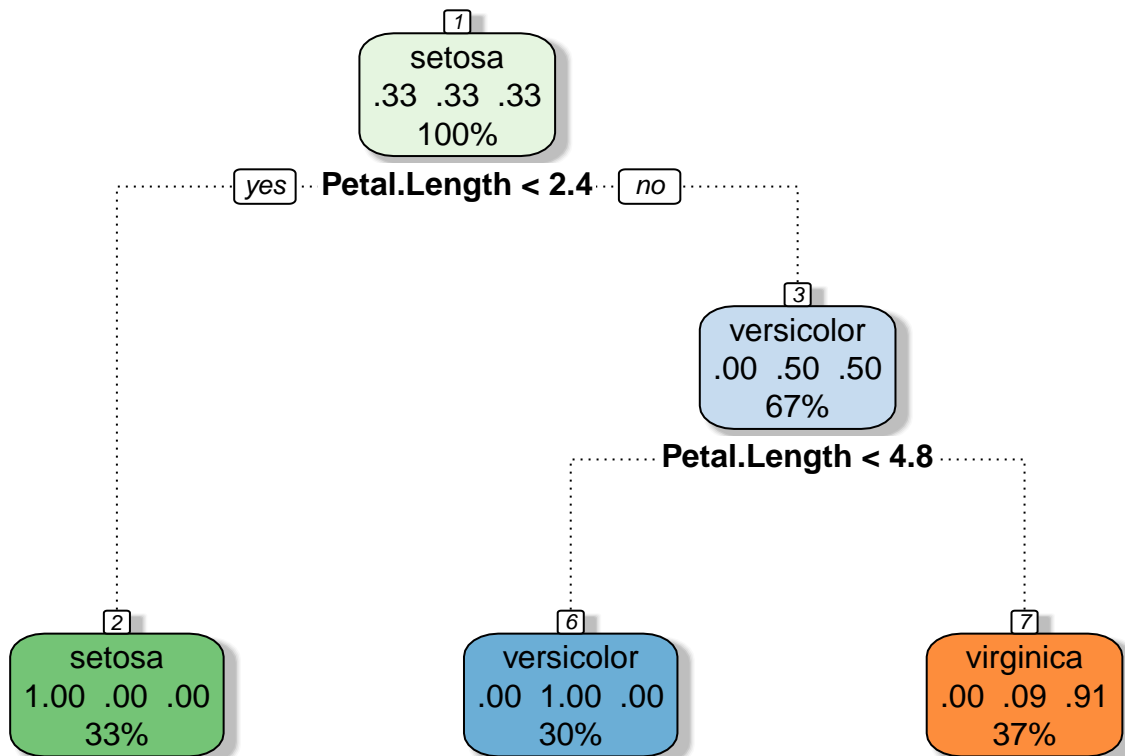
Look at what are the important variables

```
varImp(treeModel)
```

```
## rpart variable importance
##
##           Overall
## Petal.Length 100.00
## Petal.Width  95.87
## Sepal.Length  34.05
## Sepal.Width   0.00
```

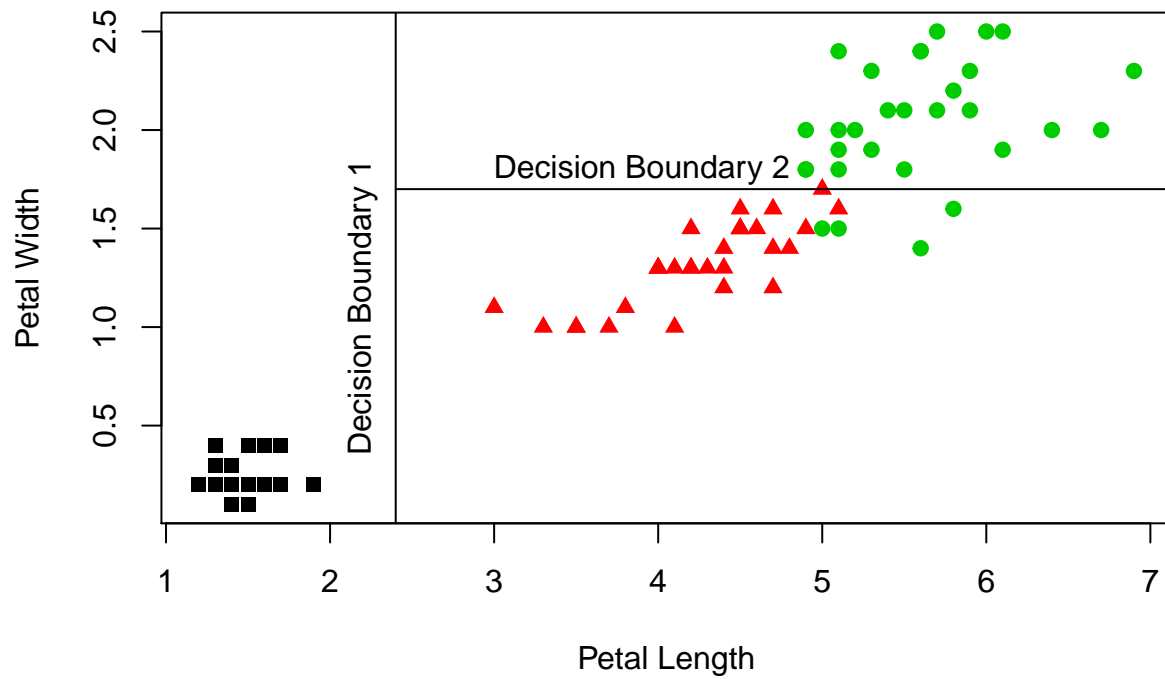
Visualization of the decision tree

```
fancyRpartPlot(treeModel$finalModel)
```

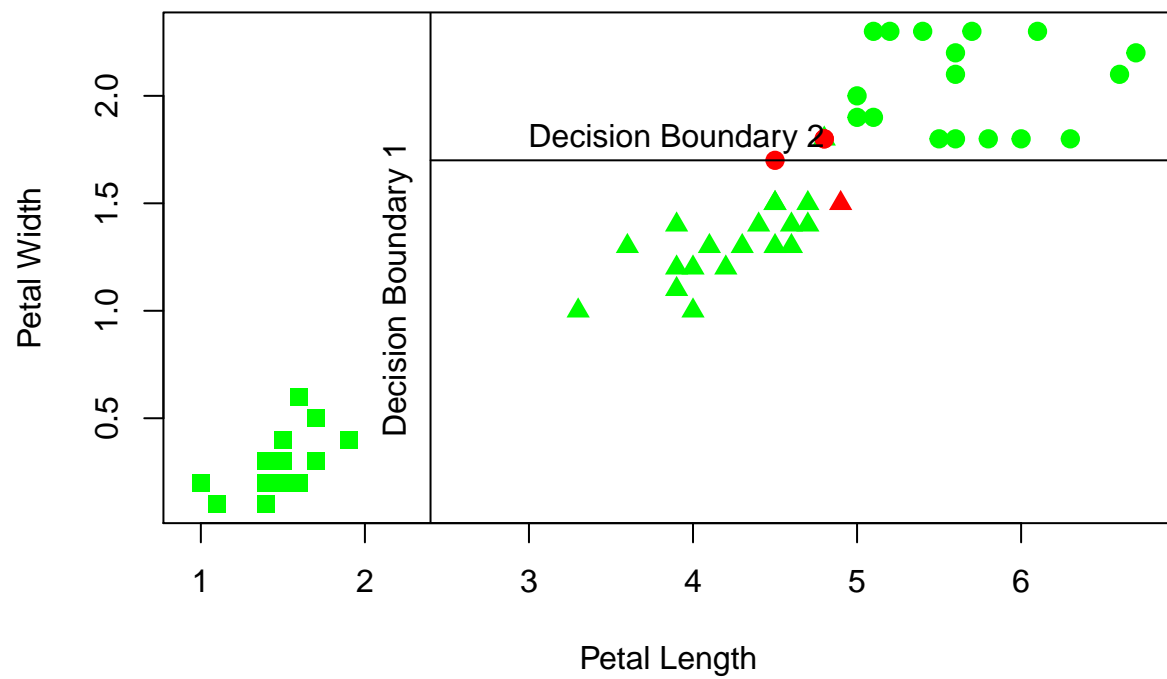


Rattle 2016-Jun-16 11:47:11 USER

Alternative visualization of the decision tree



Visualization of the prediction result

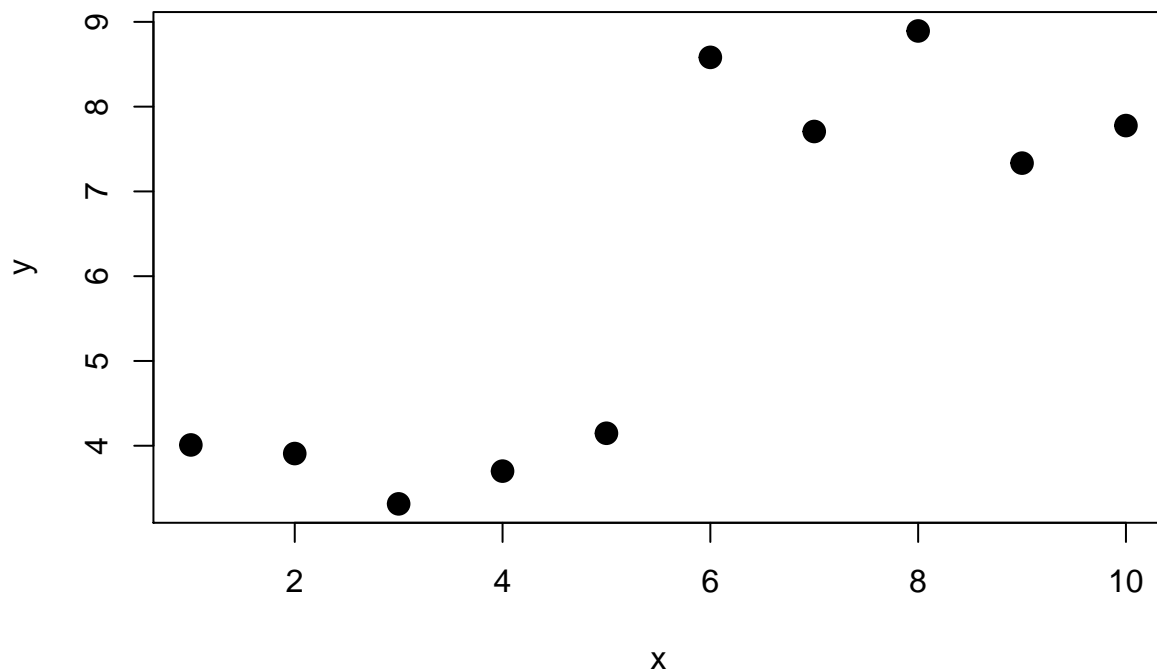


## Clustering Example

### K-means clustering

```
head(obs)
```

```
##    x      y
## 1 1 4.009373
## 2 2 3.907874
## 3 3 3.314335
## 4 4 3.700416
## 5 5 4.147273
## 6 6 8.581343
```



Create 2 clusters

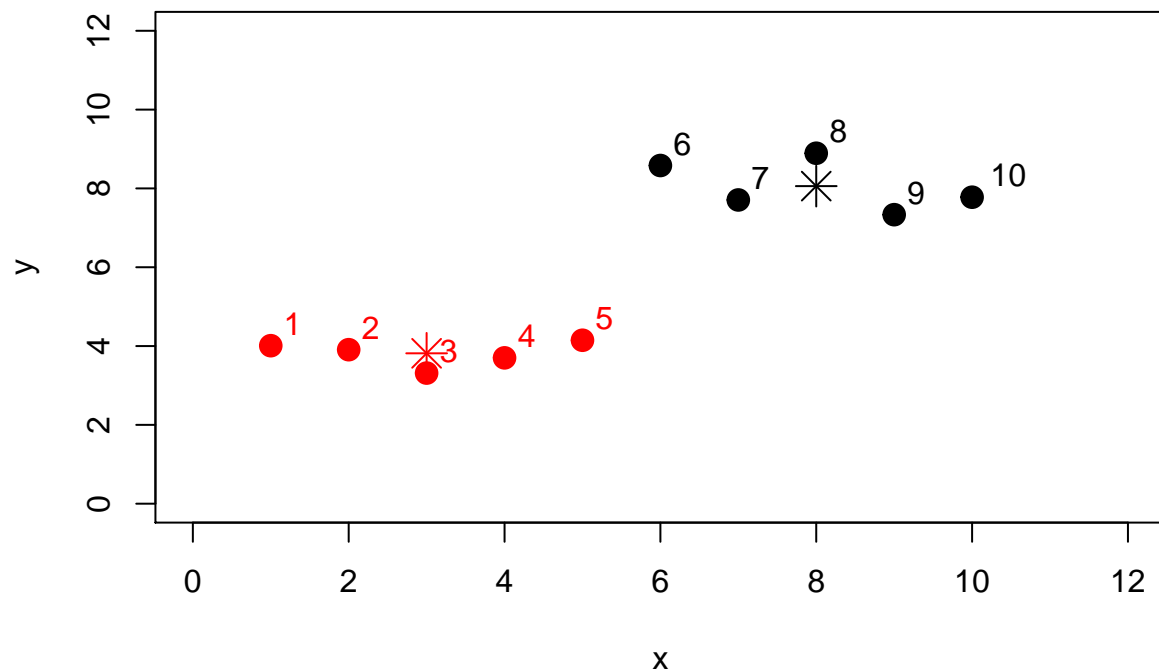
```
kmeansObj <- kmeans(obs, centers = 2)
data.frame(obs, cluster = kmeansObj$cluster)
```

```
##    x      y cluster
## 1 1 4.009373      2
## 2 2 3.907874      2
## 3 3 3.314335      2
## 4 4 3.700416      2
```

```
## 5 5 4.147273 2
## 6 6 8.581343 1
## 7 7 7.707038 1
## 8 8 8.892733 1
## 9 9 7.333703 1
## 10 10 7.776717 1
```

```
kmeansObj$centers
```

```
## x y
## 1 8 8.058307
## 2 3 3.815854
```



Create 4 clusters

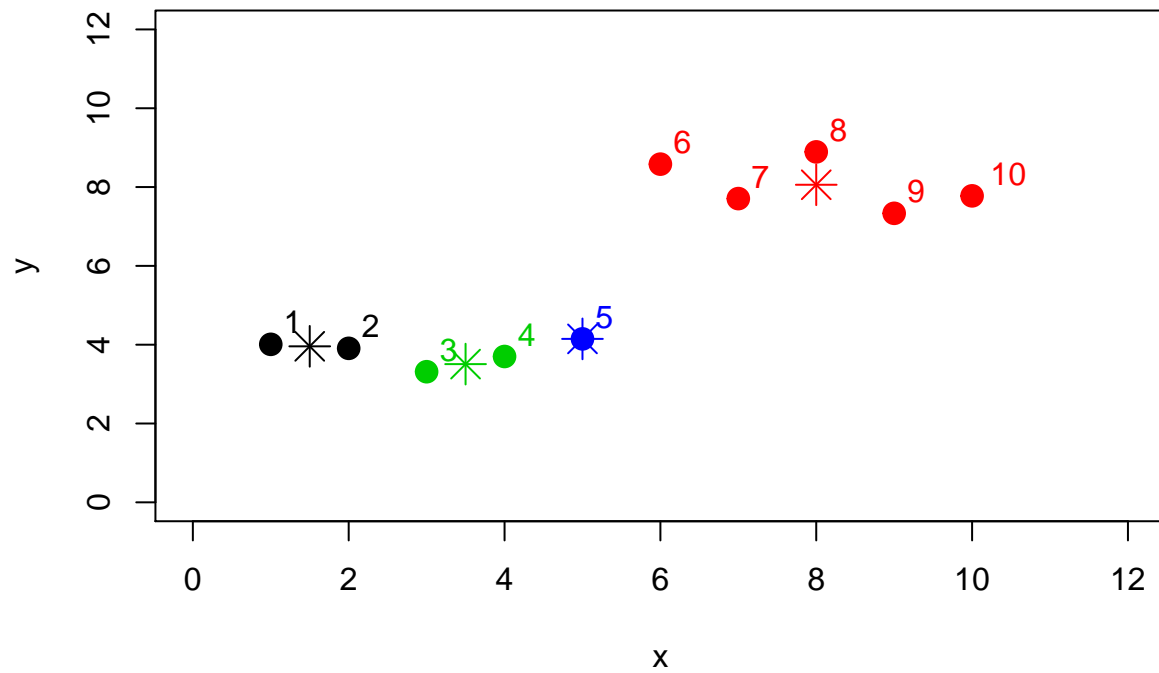
```
kmeansObj <- kmeans(obs, centers = 4)
data.frame(obs, cluster = kmeansObj$cluster)
```

```
## x y cluster
## 1 1 4.009373 1
## 2 2 3.907874 1
## 3 3 3.314335 3
## 4 4 3.700416 3
## 5 5 4.147273 4
## 6 6 8.581343 2
```

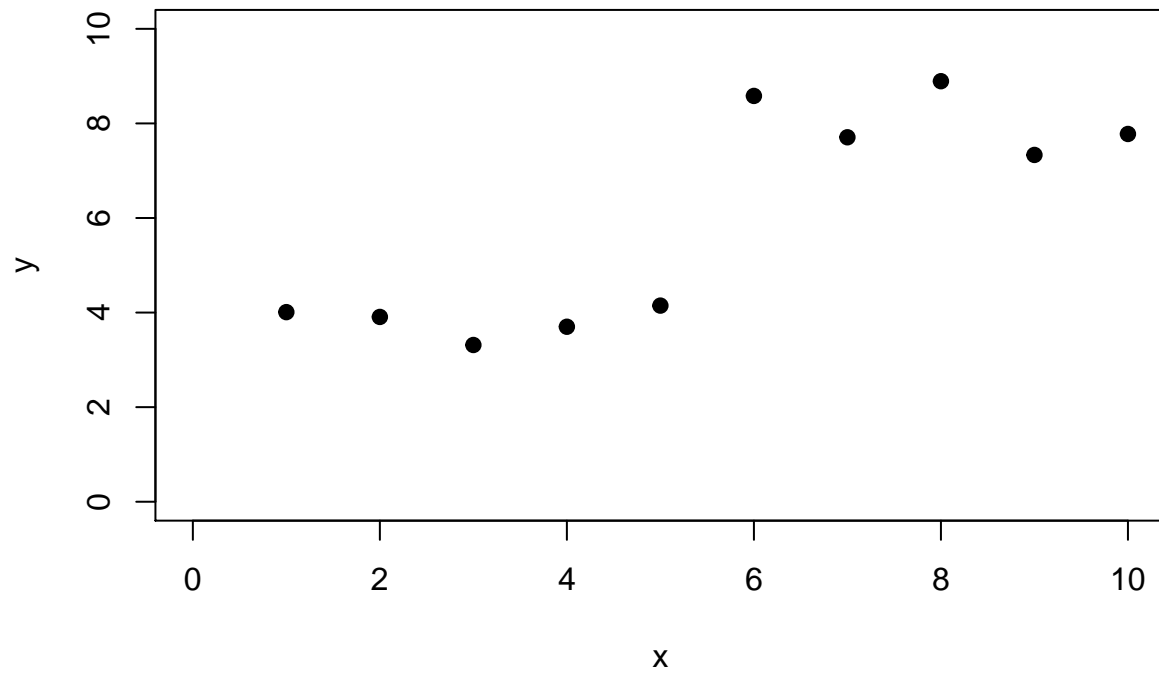
```
## 7  7 7.707038      2
## 8  8 8.892733      2
## 9  9 7.333703      2
## 10 10 7.776717     2
```

```
kmeansObj$centers
```

```
##      x      y
## 1 1.5 3.958623
## 2 8.0 8.058307
## 3 3.5 3.507375
## 4 5.0 4.147273
```



## Hierarchical Clustering



```
distM <- dist(obs)
clusters <- hclust(distM, method = "ward.D")
```

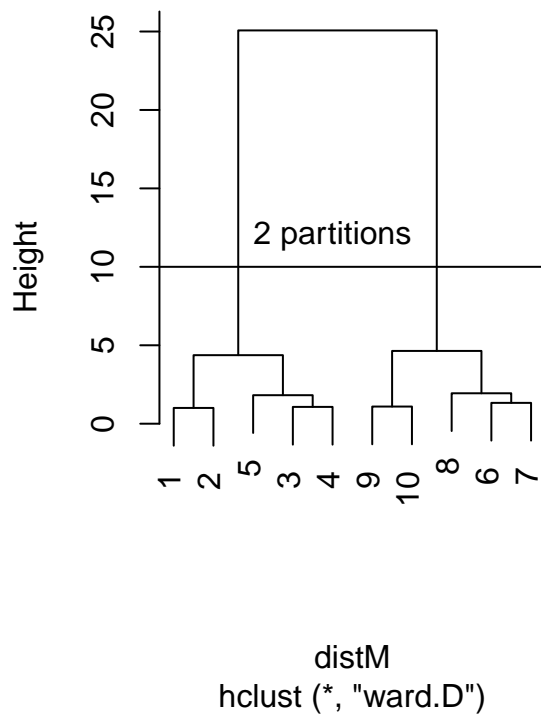


Create 2 partitions

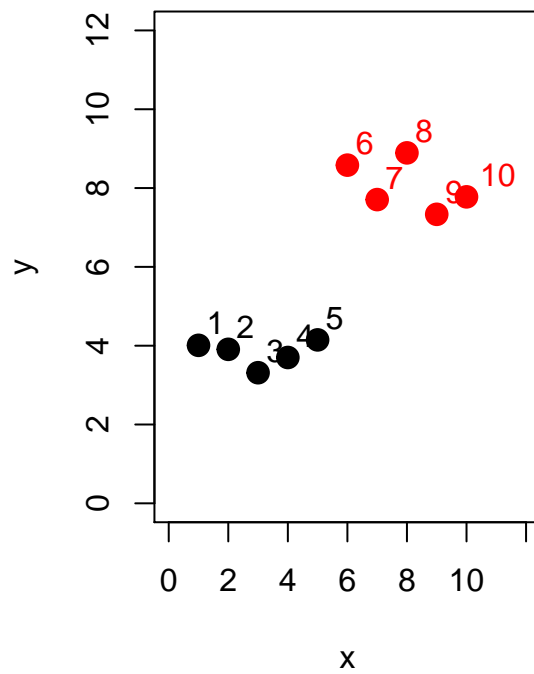
```
mem <- cutree(clusters, k = 2)
data.frame(obs, cluster = mem)
```

##	x	y	cluster
## 1	1	4.009373	1
## 2	2	3.907874	1
## 3	3	3.314335	1
## 4	4	3.700416	1
## 5	5	4.147273	1
## 6	6	8.581343	2
## 7	7	7.707038	2
## 8	8	8.892733	2
## 9	9	7.333703	2
## 10	10	7.776717	2

**Cluster Dendrogram**



**Same color points form a group**

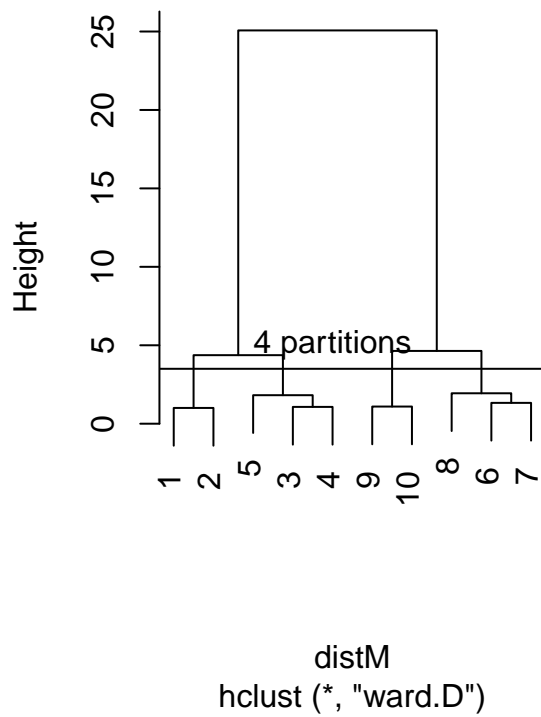


Create 4 partitions

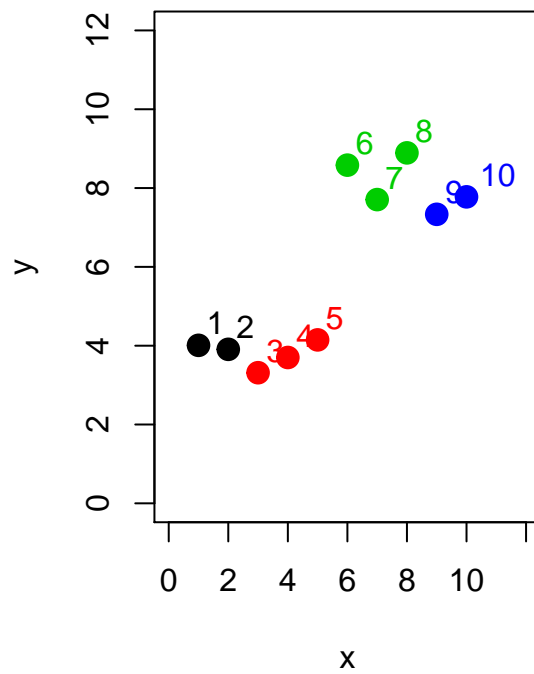
```
mem <- cutree(clusters, k =4)
data.frame(obs, cluster = mem)
```

##	x	y	cluster
## 1	1	4.009373	1
## 2	2	3.907874	1
## 3	3	3.314335	2
## 4	4	3.700416	2
## 5	5	4.147273	2
## 6	6	8.581343	3
## 7	7	7.707038	3
## 8	8	8.892733	3
## 9	9	7.333703	4
## 10	10	7.776717	4

Cluster Dendrogram



Same color points form a group



## Cross-validation

### 5 fold cross validation illustration



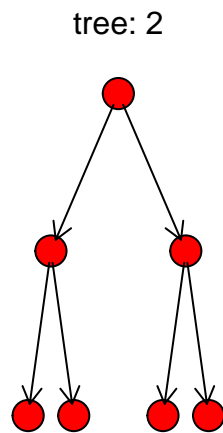
### random Forest

There are two parameters in the random forest ntree mtry

```
## [1] 2 1 1
## [1] 2 2 1
## [1] 3 1 1
## [1] 3 2 1
## [1] 3 3 2
## [1] 3 4 2
```

```
## [1] 2 1 1
## [1] 2 2 1
## [1] 3 1 1
## [1] 3 2 1
## [1] 3 3 2
## [1] 3 4 2
```

## Random Forest



```
rfModel <- randomForest(Species ~ . , data = trainData, ntree = 3)
```