

Machine Learning

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Introduction

1. Definition: It is a method of teaching computers to make predictions based on data
2. Types of machine learning:
 - Supervised learning
 - Unsupervised learning
3. Machine Learning in Everyday life:
 - Spam filtering
 - Product recommendation
 - Fraud detection

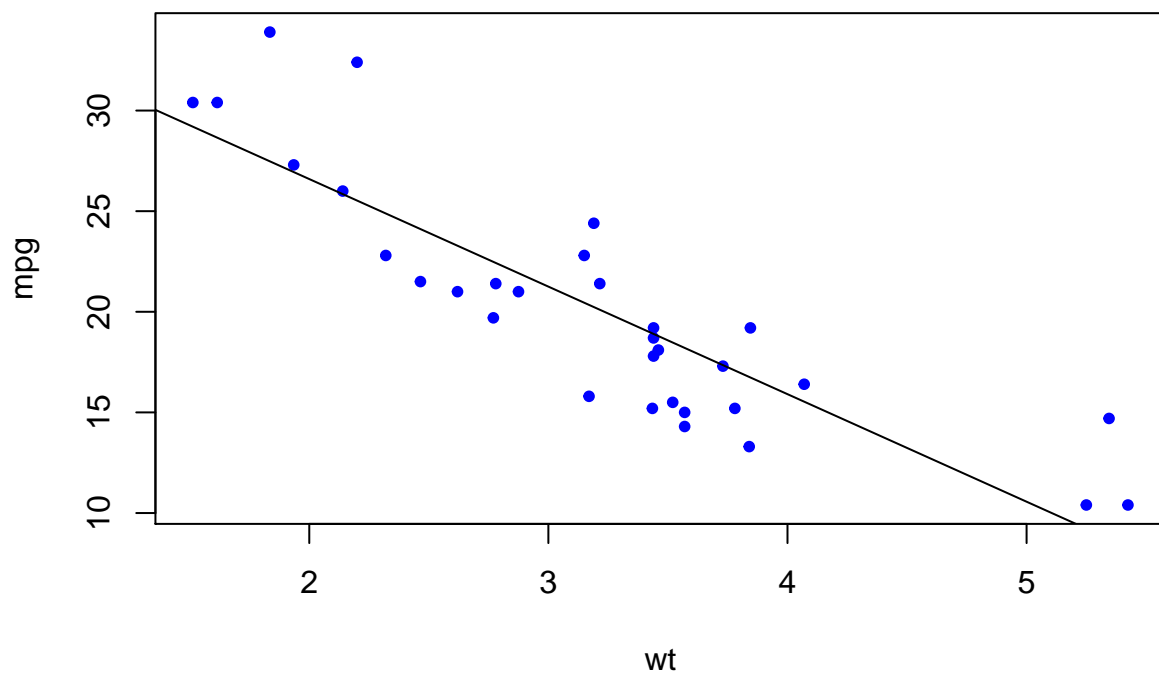
Linear Regression

Working principle

Find a straight line that best describes the relationship between the dependent and the independent variables. In order to obtain the predicted value of the dependent variable, plug in the the values of the independent variable in the equation of the line.

Example

Build a linear model to describe the relationship between mpg (miles per gallon) and wt (weight of the car) in the mtcars dataset



Codes

```
## Build the linear model object
lmModel <- lm(mpg ~ wt, data = mtcars)

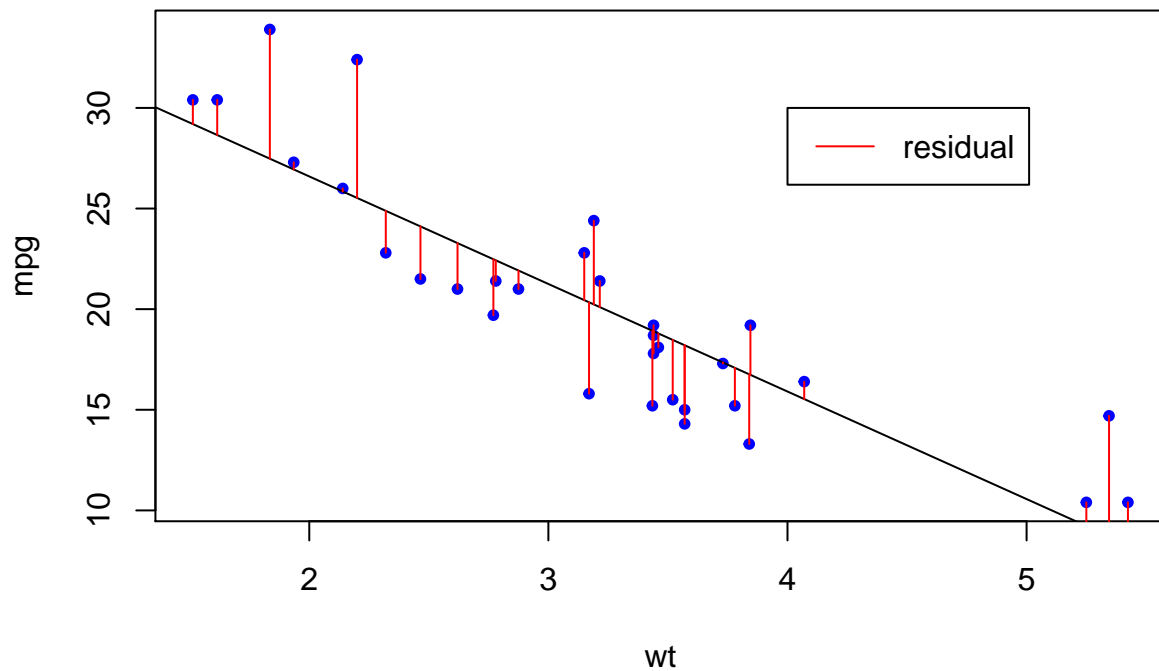
## Obtain the model parameters
sumModel <- summary(lmModel)
sumModel$coefficients

## Prediction using the model
```

```
predValue <- predict(lmModel, data.frame(wt = c(3.5, 4.2)))
predValue <- predict(lmModel, data.frame(wt = mtcars$wt))
```

Model Assessment

1. Visual Inspection



2. R-squared value

```
sumModel <- summary(lmModel)
sumModel$r.squared
```

```
## [1] 0.7528328
```

3. F-statistics

```
sumModel$fstatistic
```

```
##      value      numdf      dendif
## 91.37533    1.00000   30.00000
```

Extension of linear model

```
## More than one predictors
lmModel2 <- lm(mpg ~ wt+hp+disp, data = mtcars) # wt, hp, and disp will be used as predictor
lmModel3 <- lm(mpg ~ ., data = mtcars) # All the variable will be used

## subset selection: 1) Identify the best model that contains a given number of predictors
## 2) Identify the overall best model

library(leaps) # subset selection library
fwdSelection <- regsubsets(mpg ~ ., data = mtcars, method = "forward")
sumFwdSel <- summary(fwdSelection)
sumFwdSel$outmat # 1) Included predictor in the Best Model when the number of predictors is fixed
which.max(sumFwdSel$adjr2) # 2) overall best model has the highest adjusted r-squared value
```

Output

1. Included predictors in the best model when the number of predictors are fixed

```
sumFwdSel$outmat
```

```
##      cyl disp hp drat wt  qsec vs  am  gear carb
## 1 ( 1 ) " " " " " " " " " " " " " " " "
## 2 ( 1 ) "*" " " " " " " "*" " " " " " " " "
## 3 ( 1 ) "*" " " "*" " " "*" " " " " " " " "
## 4 ( 1 ) "*" " " "*" " " "*" " " " " "*" " " "
## 5 ( 1 ) "*" " " "*" " " "*" "*" " " "*" " " "
## 6 ( 1 ) "*" "*" "*" " " "*" "*" " " "*" " " "
## 7 ( 1 ) "*" "*" "*" "*" "*" "*" " " "*" " " "
## 8 ( 1 ) "*" "*" "*" "*" "*" "*" " " "*" "*" " "
```

2. Overall best model

```
n <- which.max(sumFwdSel$adjr2)
coef(fwdSelection, n)
```

```
## (Intercept)      cyl      disp      hp      wt      qsec
## 20.05169952 -0.50206577  0.01396099 -0.01956054 -3.99773180  0.81017782
##      am
## 2.94074955
```

Challenge

Use backward selection model to find the best model for mpg

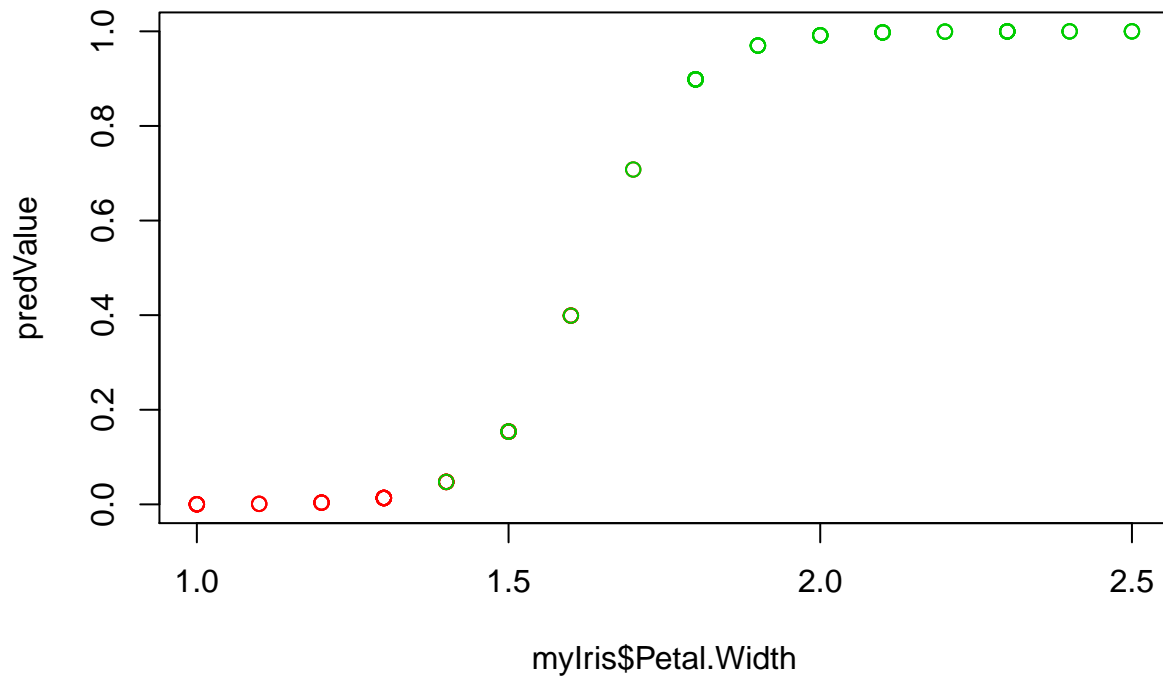
logistic regression

Codes

```

inSetosa <- iris$Species == "setosa"
myIris <- iris[!inSetosa,]
head(myIris)
glmModel <- glm(Species~Petal.Width, data = myIris, family = binomial(link="logit"))
predValue <- predict(glmModel, myIris, type = "response")
predValue
plot(myIris$Petal.Width,predValue, col = myIris$Species)

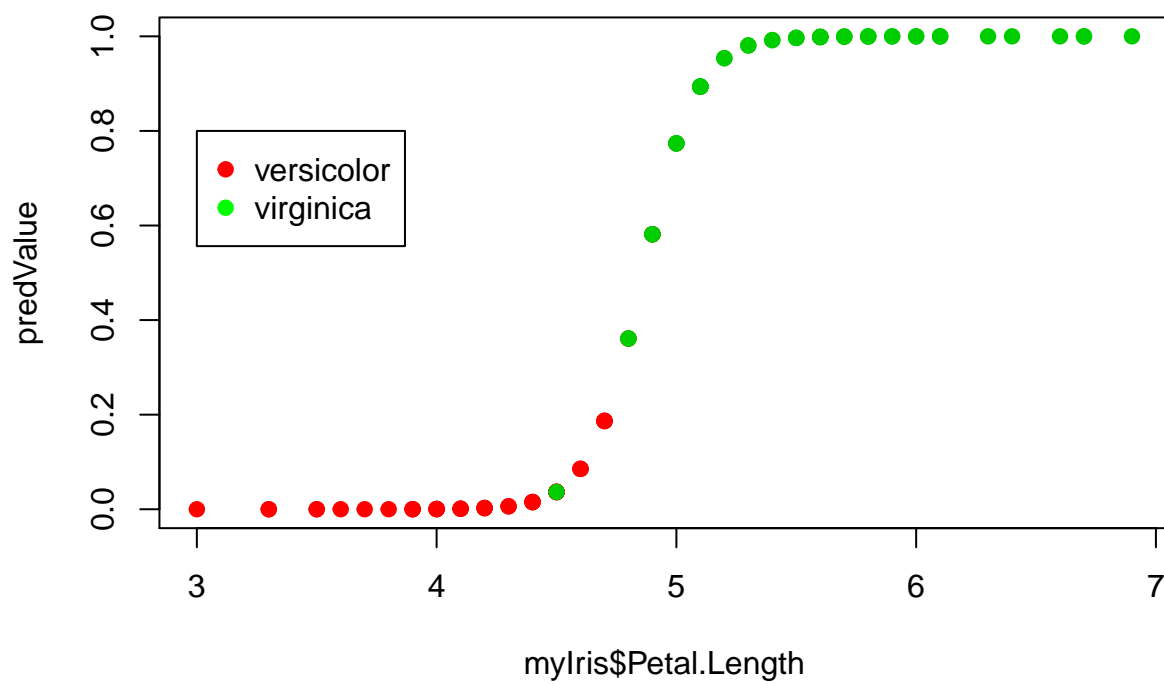
```



```

glmModel <- glm(Species ~ Petal.Length, data = myIris, family = binomial(link="logit"))
predValue <- predict(glmModel, myIris, type = "response")
predValue
plot(myIris$Petal.Length,predValue, col = myIris$Species, pch = 19)
legend(x=3, y = 0.8, legend = c("versicolor", "virginica"), pch = 19, col=c("red", "green"))

```



Tree based algorithm

Used both for classification and regression

Working principle

Divide the data set into several small regions such that the response variables are (nearly) homogeneous in those regions. The predicted value of a new observation is the most dominant class of the region to which the observation belongs.

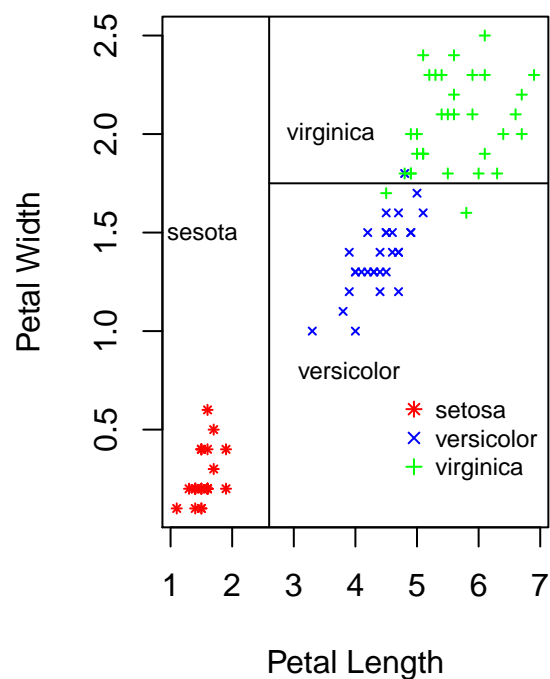
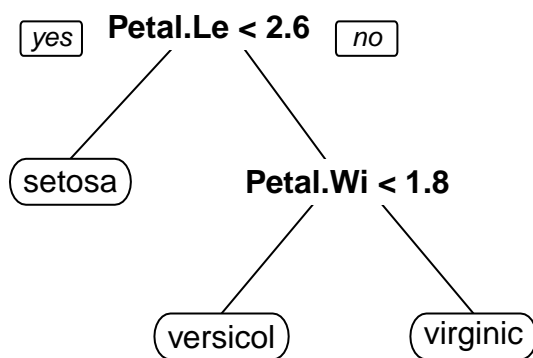
Example

Find the decision rule to predict the species of iris dataset based on Sepal.Length, Sepal.Width, Petal.Length, and Petal.Width

```
iris[c(1,100,150),]
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 100	5.7	2.8	4.1	1.3	versicolor
## 150	5.9	3.0	5.1	1.8	virginica

Decision Tree visualization



Codes

```
## Load the required libraries
library(rpart)
library(rpart.plot) # For decision tree visualization

## create the data partition
set.seed(1)
inTrain <- sample(c(TRUE, FALSE), size = nrow(iris), replace = TRUE, prob = c(0.6,0.4))
trainData <- iris[inTrain,]
testData <- iris[!inTrain,1:4]
testClass <- iris[!inTrain,5]

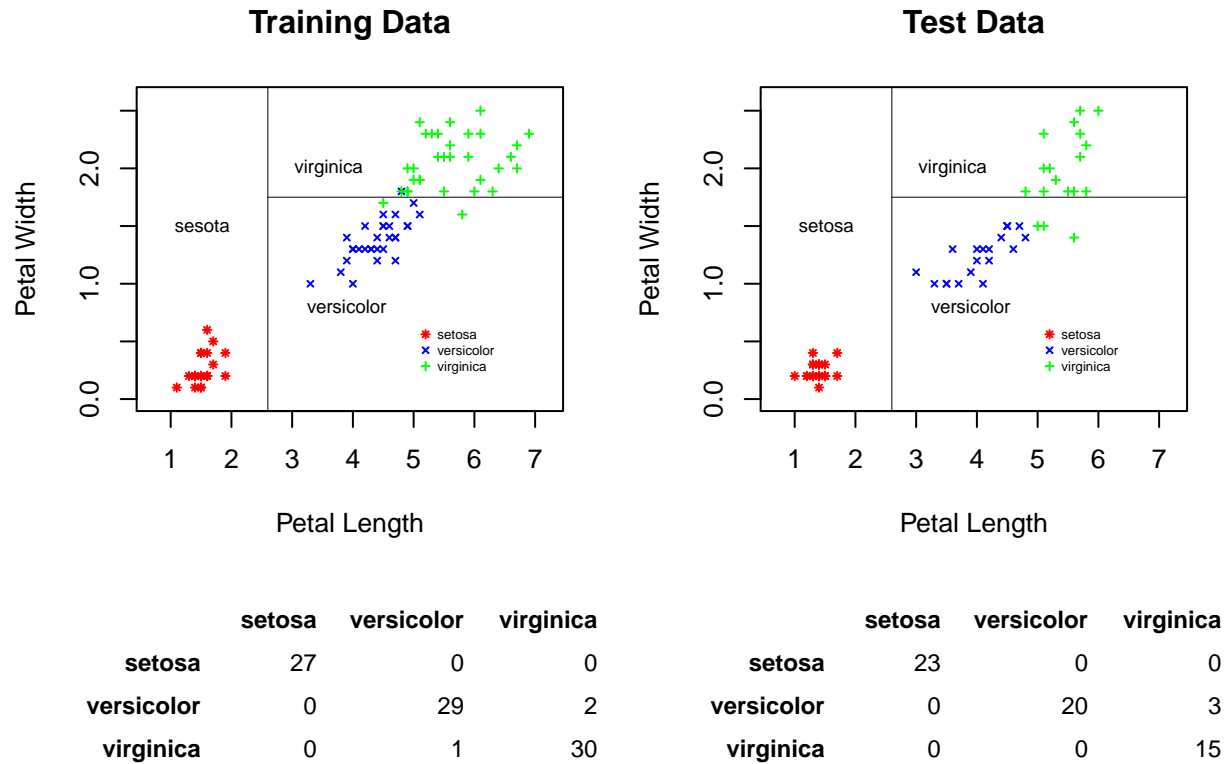
## Create the tree model
treeModel <- rpart(Species ~ ., data = trainData)

## Use the tree model to predict the class of the test data
predTrainClass <- predict(treeModel, newdata = trainData, type = "class")
predTestClass <- predict(treeModel, newdata = testData, type = "class")

## Find out the performance of the decision tree
table(predTrainClass, trainData$Species) # Confusion Matrix
mean(predTrainClass == trainData$Species) # Prediction Accuracy

table(predTestClass, testClass) # Confusion Matrix
mean(predTestClass == testClass) # Prediction Accuracy
```


Decision tree prediction visualization



Add some challenge

Advantages of decision tree

Easy to interpret

Problem with the decision tree

Lower prediction accuracy

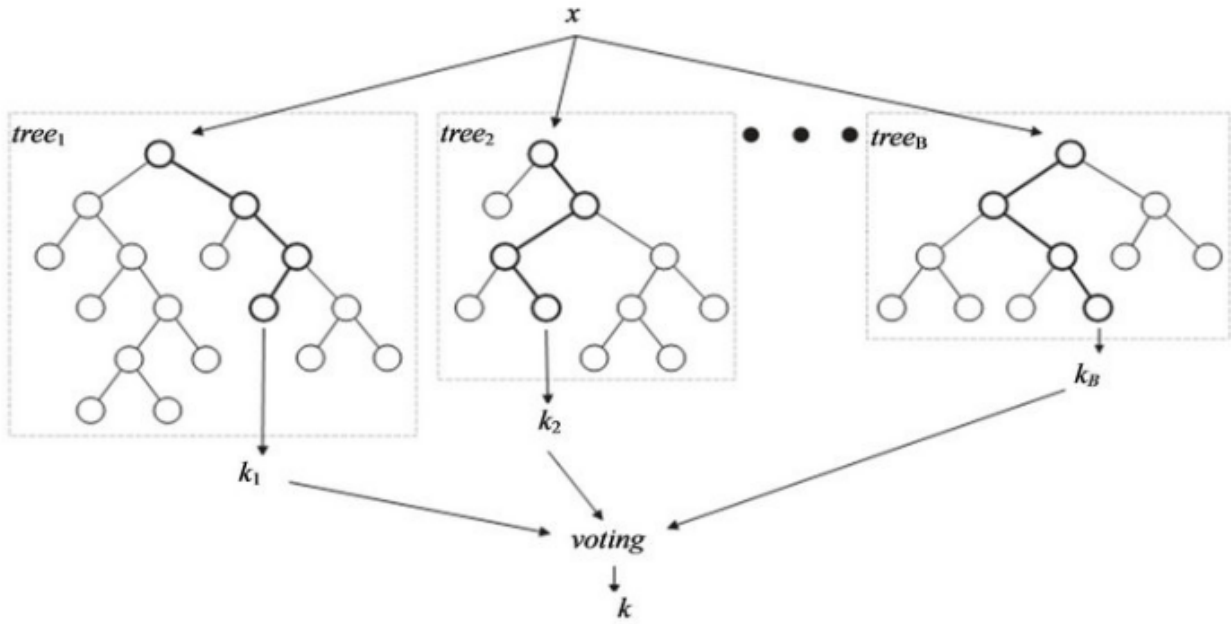
Solution

Aggregate many decision trees (bagging, random forest, boosting)

random Forest

Need to decorrelate the trees. Making it more accurate

ntree

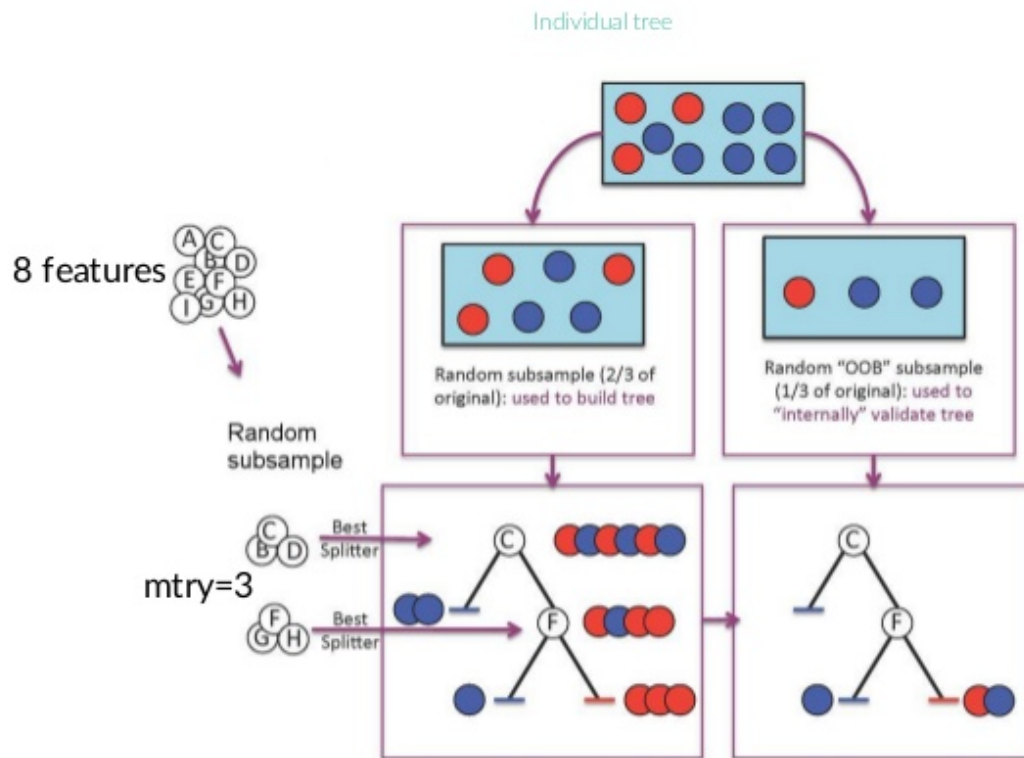


mtry

Decorrelate the trees a random sample of m predictors is chosen as split candidates from the full set of p predictors.

Random Forest classifier

16

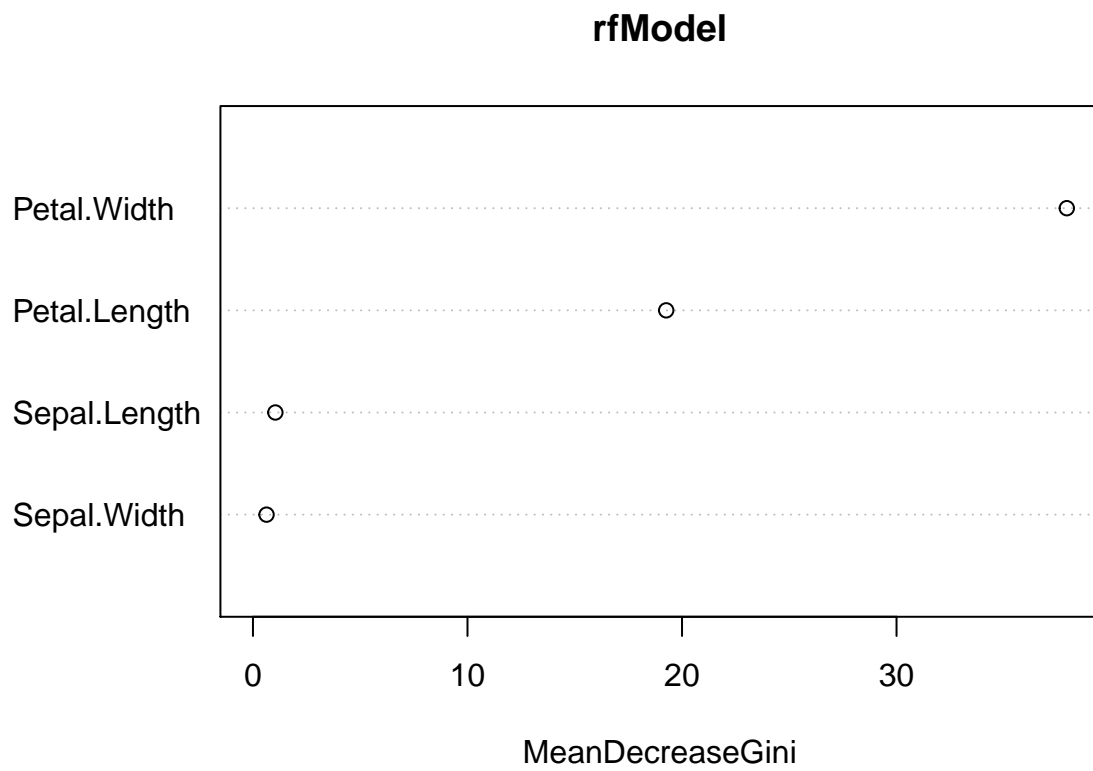


random forest example

```
library(randomForest)
rfModel <- randomForest(Species ~ ., data=trainData, mtry=3, ntree=15)
predClass <- predict(rfModel, newdata = testData)
table(predClass, testClass)
```

```
##          testClass
## predClass  setosa versicolor virginica
##  setosa      23         0         0
## versicolor   0        20         3
## virginica    0         0        15
```

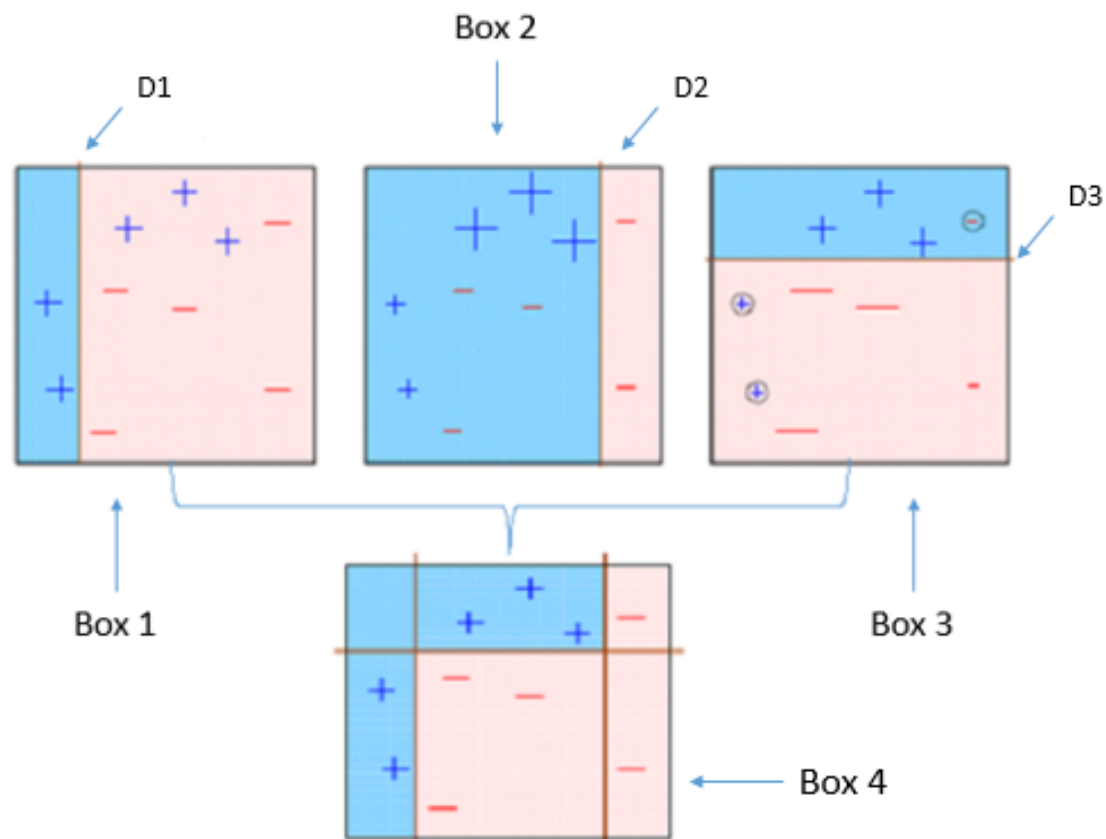
```
varImpPlot(rfModel)
```



Add some challenge

Boosting

Illustration



example

```
#gbmModel <- gbm(Species ~ ., data = trainData, distribution = "multinomial",  
#               n.trees = 20)  
#predict(gbmModel, newdata = testData, single.tree = TRUE, n.trees = 20, type = "response")  
  
# boost.boston=gbm(medu~.,data=Boston[train,],distribution= # #"gaussian",n.trees=5000,interaction.depth=
```

The argument `n.trees = 5000` indicates that we want 5000 trees, and the option `interaction.depth = 4` limits the depth of each tree

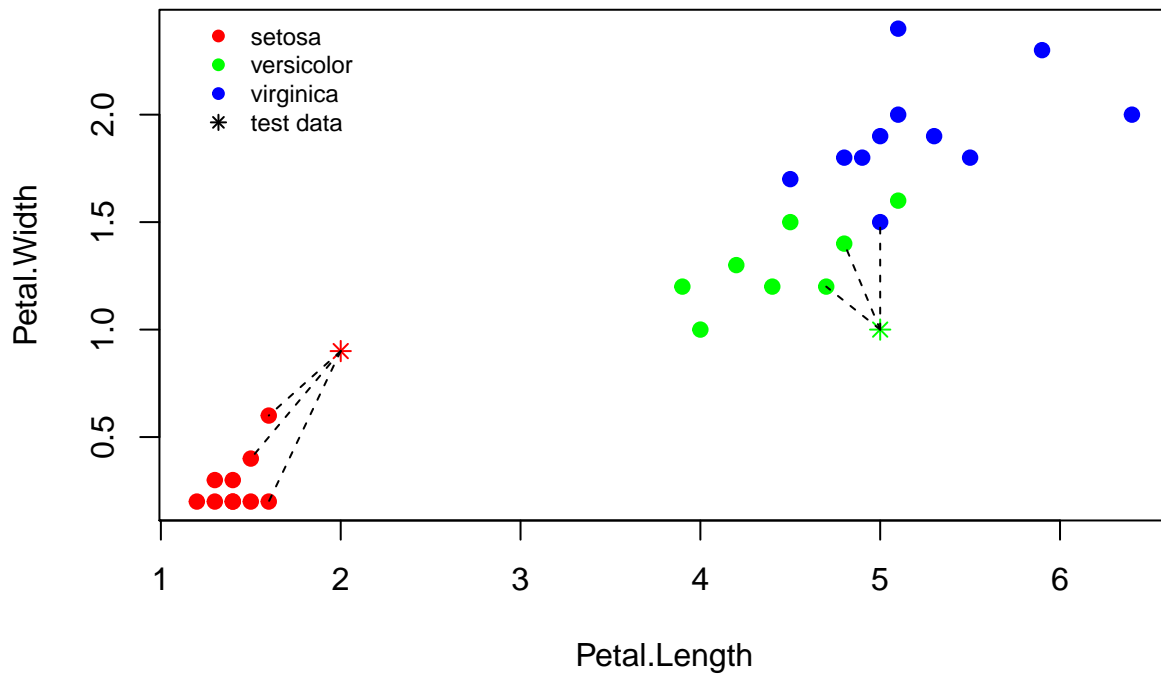
knn

make sure, you scale the data and also with an example tell why it is important to scale the data

Working principle

It assumes that the members of a given class have similar characteristics. So, a given observation is assigned the class of its nearest neighbours (number of nearest neighbour to be decided by the user)

Example



codes

```
library(class)
myIris <- iris[,3:5]

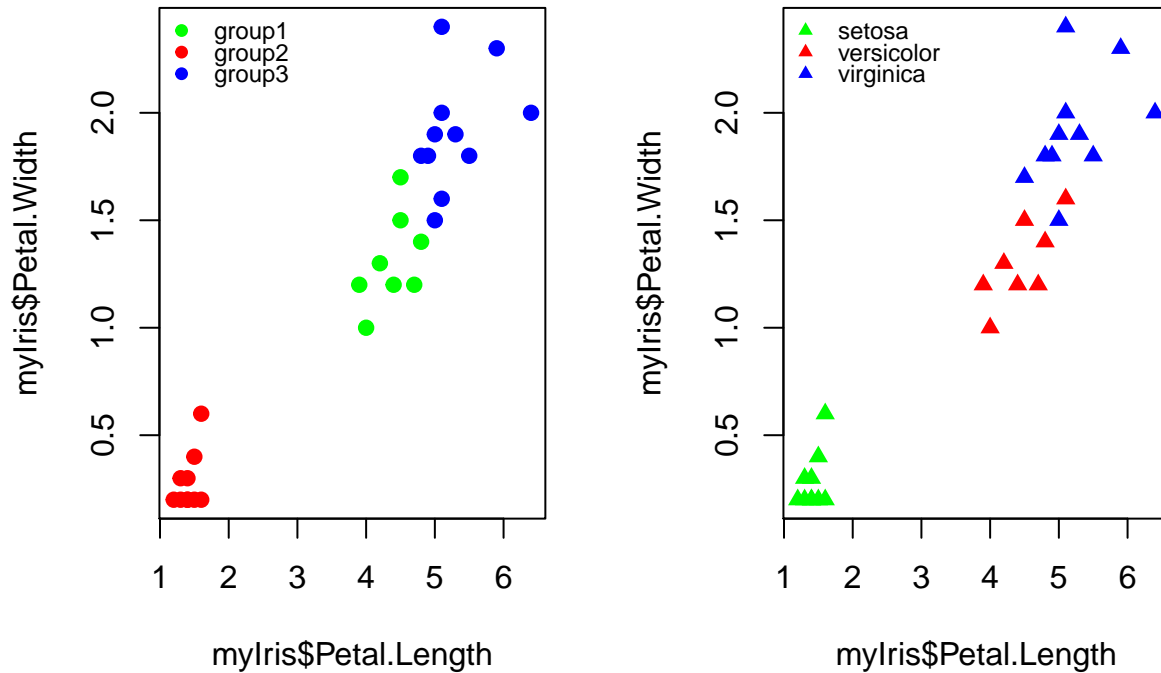
set.seed(100)
inTrain <- sample(c(TRUE, FALSE), size = nrow(myIris), replace = TRUE, prob = c(0.2,0.8))
trainData <- myIris[inTrain,1:2]
trainClass <- myIris[inTrain,3]
testData <- myIris[!inTrain,1:2]
testClass <- myIris[!inTrain,3]
```

```
predClass <- knn(trainData, testData, cl = trainClass, k = 3)
table(predClass, testClass)
```

```
##           testClass
## predClass  setosa versicolor virginica
##   setosa      40         0         0
## versicolor   0         40         1
##  virginica   0          2        38
```

clustering example

kmeans clustering

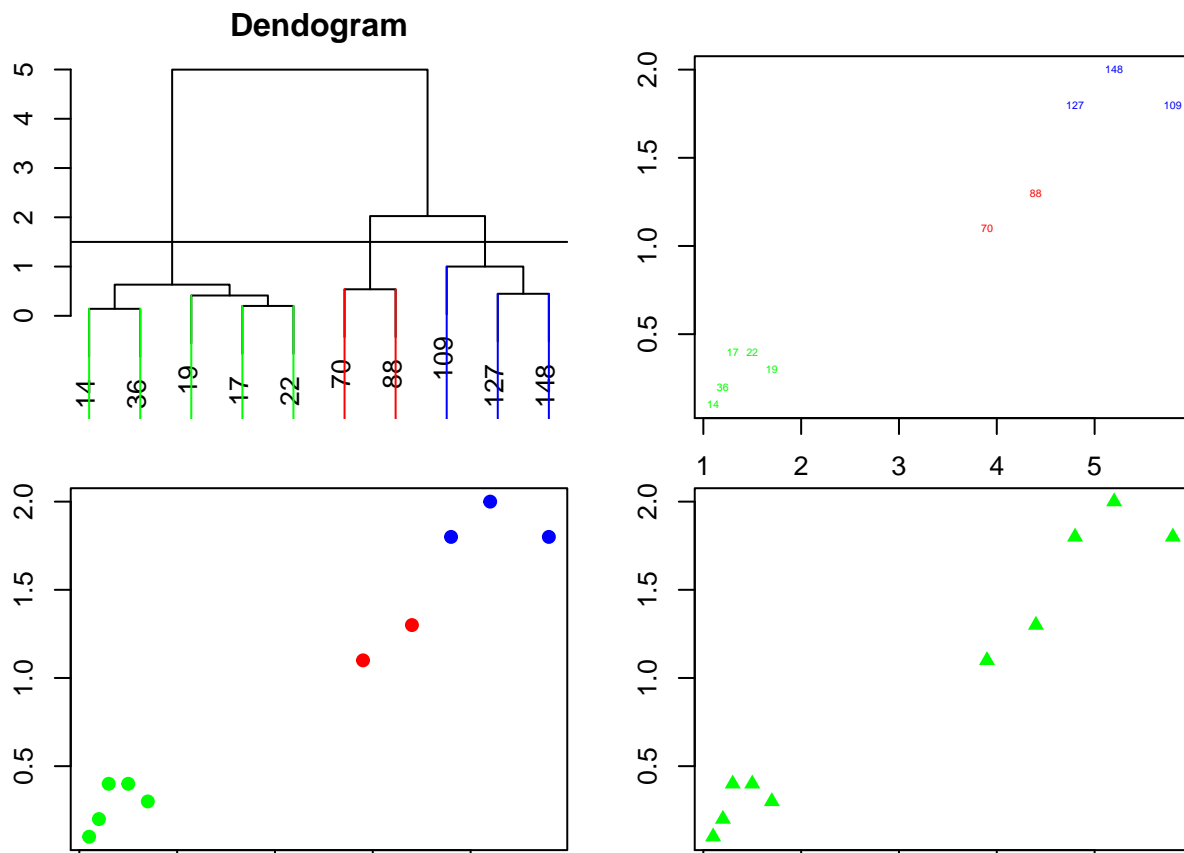


Codes

```
set.seed(100)
index <- sample(c(TRUE, FALSE), nrow(iris), p = c(0.2, 0.8), replace = TRUE)
myIris <- iris[index,3:4]
group <- iris$Species[index]
set.seed(100)
predGroup <- kmeans(myIris, centers = 3, nstart = 10)
predGroupC <- ifelse(predGroup$cluster==1, "setosa", ifelse(predGroup$cluster==2,
                                                           "versicolor", "virginica"))
predGroupC <- factor(predGroupC)
table(predGroupC, group)
```

```
##           group
## predGroupC  setosa versicolor virginica
##   setosa      0         7         1
##   versicolor  10         0         0
##   virginica   0         1        10
```


Hierarchical Clustering



```
set.seed(4)
index <- sample(c(TRUE, FALSE), nrow(iris), p = c(0.05, 0.95), replace = TRUE)
myIris <- iris[index,3:4]
disM <- dist(myIris)
irisClust <- hclust(disM)
clusters <- cutree(irisClust, k = 3)
```

Codes

Cross-validation

5 fold cross validation illustration



baye's theorem

```
#head(Titanic)
```

svm

```
#svmModel <- svm()
```