

# Practical Machine Learning - Week3

*Saul Lugo*

*January 22, 2016*

## Predicting with Trees

The basic algorithm for predicting with trees is the following:

- 1) Start with all the variables in one group
- 2) Find the variable/split that best separates the outcomes
- 3) Divide the data into two groups (“leaves”) on that split
- 4) Within each split, find the variable that best separates the outcome
- 5) Continue until the groups are too small or sufficiently pure

## Example with the Iris dataset

```
data(iris)
library(ggplot2)
library(caret)
names(iris)
```

```
## [1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width"
## [5] "Species"
```

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

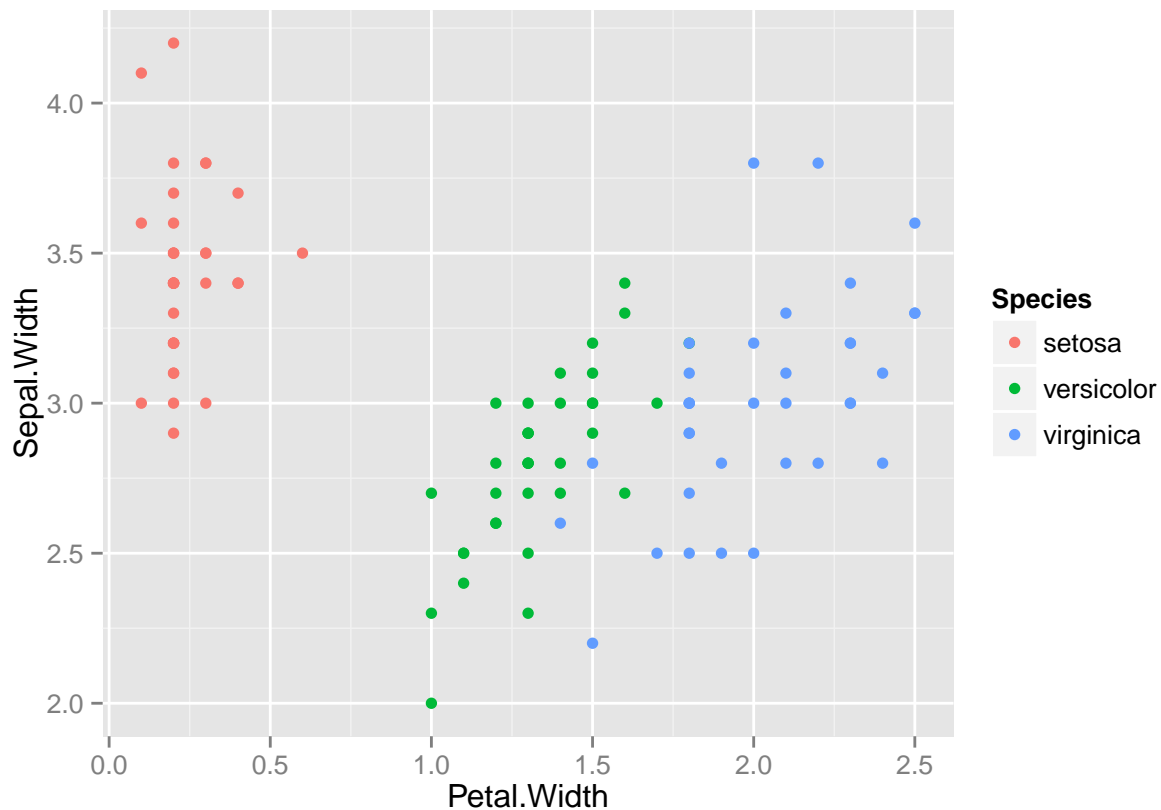
```
##
##      setosa versicolor  virginica
##         50         50         50
```

```
#Create the data partition
inTrain <- createDataPartition(y=iris$Species,p=0.7,list=FALSE)
training <- iris[inTrain,]
testing <- iris[-inTrain,]
dim(training); dim(testing)
```

```
## [1] 105  5
```

```
## [1] 45  5
```

```
#Exploring the data
qplot(Petal.Width,Sepal.Width,colour=Species,data=training)
```

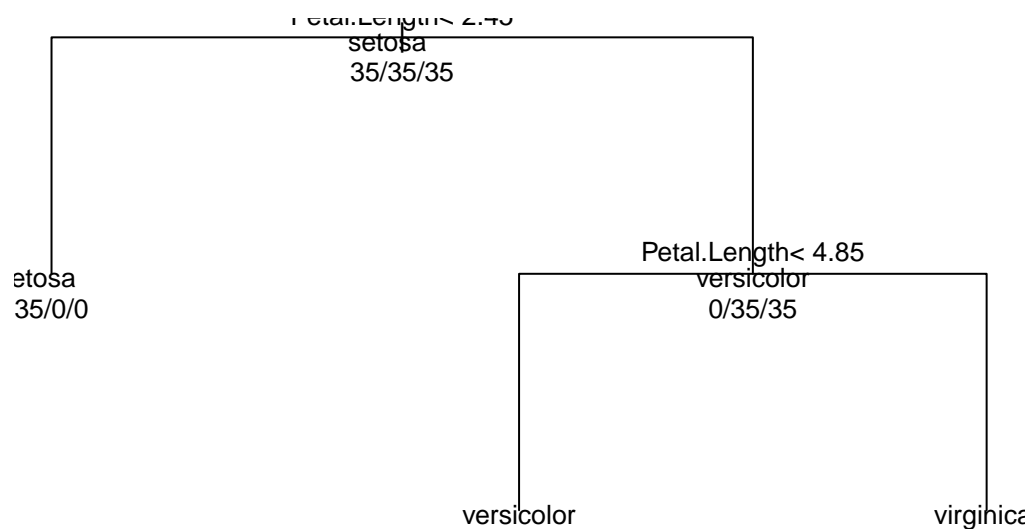


```
#Training the model (a tree model)
modFit <- train(Species ~ ., method="rpart", data = training)
modFit_PredTree <- modFit
print(modFit$finalModel)
```

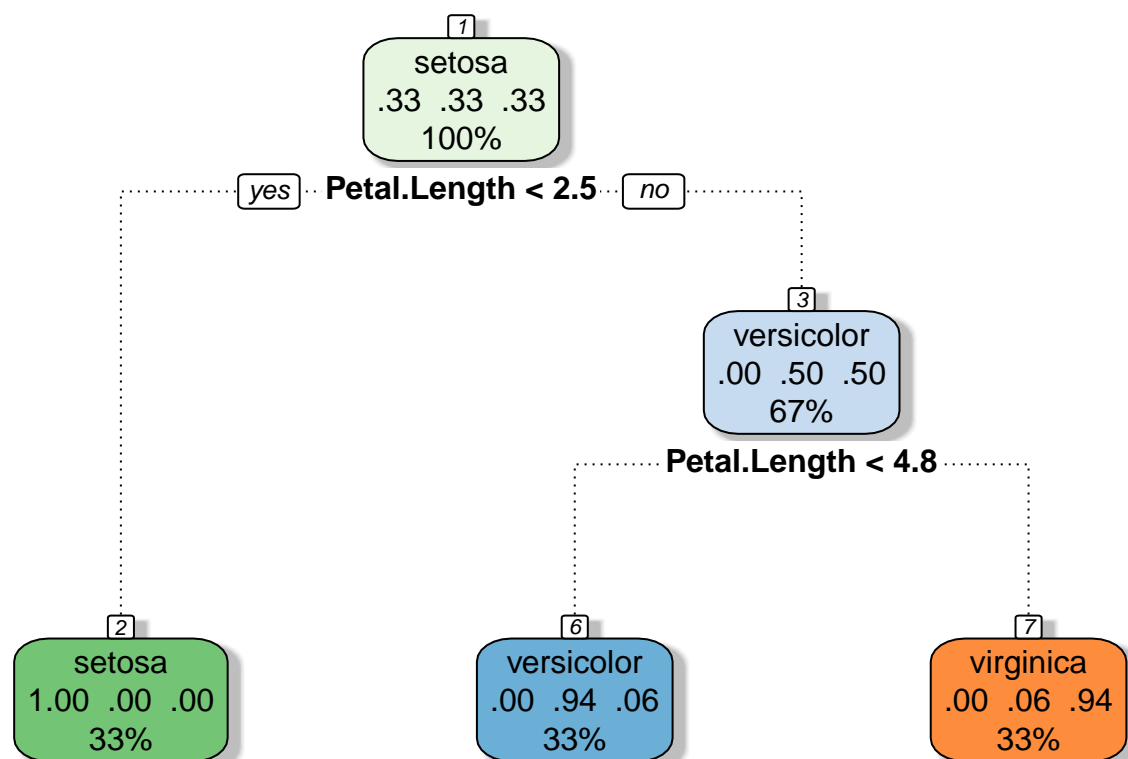
```
## n= 105
##
## node), split, n, loss, yval, (yprob)
##      * denotes terminal node
##
## 1) root 105 70 setosa (0.33333333 0.33333333 0.33333333)
##   2) Petal.Length< 2.45 35 0 setosa (1.00000000 0.00000000 0.00000000) *
##   3) Petal.Length>=2.45 70 35 versicolor (0.00000000 0.50000000 0.50000000)
##     6) Petal.Length< 4.85 35 2 versicolor (0.00000000 0.94285714 0.05714286) *
##     7) Petal.Length>=4.85 35 2 virginica (0.00000000 0.05714286 0.94285714) *
```

```
#Plotting the model
plot(modFit$finalModel, uniform=TRUE, main="Classification Tree")
text(modFit$finalModel, use.n=TRUE, all=TRUE, cex=0.8)
```

## Classification Tree



```
##A better plot
library(rattle)
fancyRpartPlot(modFit$finalModel)
```



Rattle 2016-Jan-24 22:41:58 saul

```
#Now predicting the outcome in the testing set
prediction <- predict(modFit,newdata=testing)
prediction
```

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

```
CM_PredTree <- confusionMatrix(testing$Species,prediction)
CM_PredTree
```

```
## Confusion Matrix and Statistics
##
##              Reference
## Prediction  setosa versicolor virginica
## setosa      15          0          0
## versicolor   0         13          2
## virginica    0          1         14
##
## Overall Statistics
##
##              Accuracy : 0.9333
##              95% CI : (0.8173, 0.986)
##      No Information Rate : 0.3556
##      P-Value [Acc > NIR] : 5.426e-16
##
##              Kappa : 0.9
##  McNemar's Test P-Value : NA
##
## Statistics by Class:
##
##              Class: setosa Class: versicolor Class: virginica
## Sensitivity              1.0000              0.9286              0.8750
## Specificity              1.0000              0.9355              0.9655
## Pos Pred Value           1.0000              0.8667              0.9333
## Neg Pred Value           1.0000              0.9667              0.9333
## Prevalence               0.3333              0.3111              0.3556
## Detection Rate           0.3333              0.2889              0.3111
## Detection Prevalence     0.3333              0.3333              0.3333
## Balanced Accuracy        1.0000              0.9320              0.9203
```

## Notes on predicting with trees

- 1) Classification trees are non-linear models - They use interactions between variables - Data transformation might be less important - Trees can also be use for regression problems (continious outcome)
- 2) There are several options for building trees in R: - party, rpart in the caret package - tree, out of the carect package

## Bagging with the Caret Package

Bagging stands for **B**ootstrap **A**ggregating.

The following is an example of Bagging using the caret package:

```
library(ElemStatLearn); data(ozone,package="ElemStatLearn")
library(caret)
head(ozone)
```

```
##   ozone radiation temperature wind
## 1    41         190           67  7.4
## 2    36         118           72  8.0
## 3    12         149           74 12.6
## 4    18         313           62 11.5
## 5    23         299           65  8.6
## 6    19          99           59 13.8
```

```
predictors = data.frame(ozone=ozone$ozone)
temperature = ozone$temperature
treebag <- bag(predictors,temperature,B=10,bagControl = bagControl(fit = ctreeBag$fit, predict = ctreeB
treebag$fit
```

```
## [[1]]
## [[1]]$fit
##
##   Conditional inference tree with 3 terminal nodes
##
## Response:  y
## Input:  ozone
## Number of observations:  111
##
## 1) ozone <= 46; criterion = 1, statistic = 46.25
##   2) ozone <= 19; criterion = 0.999, statistic = 10.356
##     3)* weights = 27
##   2) ozone > 19
##     4)* weights = 47
## 1) ozone > 46
##   5)* weights = 37
##
## [[1]]$vars
## [1] 1
##
## [[1]]$oob
##      pred obs      key
## 1  76.68085  67 yjqgxyvpfd
## 2  70.14815  62 yjqgxyvpfd
## 3  70.14815  61 yjqgxyvpfd
## 4  70.14815  69 yjqgxyvpfd
## 5  70.14815  66 yjqgxyvpfd
## 6  70.14815  58 yjqgxyvpfd
## 7  76.68085  66 yjqgxyvpfd
## 8  76.68085  68 yjqgxyvpfd
```

```

## 9 76.68085 81 yjqgxyvpvd
## 10 76.68085 76 yjqgxyvpvd
## 11 87.48649 90 yjqgxyvpvd
## 12 76.68085 87 yjqgxyvpvd
## 13 76.68085 82 yjqgxyvpvd
## 14 76.68085 77 yjqgxyvpvd
## 15 76.68085 72 yjqgxyvpvd
## 16 76.68085 65 yjqgxyvpvd
## 17 70.14815 73 yjqgxyvpvd
## 18 70.14815 76 yjqgxyvpvd
## 19 87.48649 85 yjqgxyvpvd
## 20 87.48649 83 yjqgxyvpvd
## 21 87.48649 89 yjqgxyvpvd
## 22 76.68085 81 yjqgxyvpvd
## 23 87.48649 81 yjqgxyvpvd
## 24 87.48649 86 yjqgxyvpvd
## 25 87.48649 81 yjqgxyvpvd
## 26 70.14815 81 yjqgxyvpvd
## 27 70.14815 82 yjqgxyvpvd
## 28 76.68085 86 yjqgxyvpvd
## 29 87.48649 80 yjqgxyvpvd
## 30 76.68085 77 yjqgxyvpvd
## 31 70.14815 72 yjqgxyvpvd
## 32 87.48649 96 yjqgxyvpvd
## 33 87.48649 91 yjqgxyvpvd
## 34 87.48649 92 yjqgxyvpvd
## 35 87.48649 93 yjqgxyvpvd
## 36 70.14815 67 yjqgxyvpvd
## 37 70.14815 82 yjqgxyvpvd
## 38 70.14815 64 yjqgxyvpvd
## 39 76.68085 71 yjqgxyvpvd
## 40 76.68085 70 yjqgxyvpvd
## 41 70.14815 76 yjqgxyvpvd
## 42 76.68085 68 yjqgxyvpvd
##
##
## [[2]]
## [[2]]$fit
##
## Conditional inference tree with 3 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 65; criterion = 1, statistic = 70.791
## 2) ozone <= 30; criterion = 1, statistic = 25.262
## 3)* weights = 52
## 2) ozone > 30
## 4)* weights = 31
## 1) ozone > 65
## 5)* weights = 28
##
## [[2]]$vars

```

```

## [1] 1
##
## [[2]]$oob
##      pred obs      key
## 1  79.38710  72 dxfxqxycfi
## 2  71.82692  65 dxfxqxycfi
## 3  71.82692  59 dxfxqxycfi
## 4  71.82692  69 dxfxqxycfi
## 5  71.82692  68 dxfxqxycfi
## 6  71.82692  58 dxfxqxycfi
## 7  79.38710  66 dxfxqxycfi
## 8  71.82692  57 dxfxqxycfi
## 9  71.82692  62 dxfxqxycfi
## 10 90.67857  79 dxfxqxycfi
## 11 79.38710  76 dxfxqxycfi
## 12 71.82692  82 dxfxqxycfi
## 13 79.38710  85 dxfxqxycfi
## 14 79.38710  83 dxfxqxycfi
## 15 79.38710  83 dxfxqxycfi
## 16 71.82692  73 dxfxqxycfi
## 17 71.82692  81 dxfxqxycfi
## 18 79.38710  81 dxfxqxycfi
## 19 79.38710  84 dxfxqxycfi
## 20 79.38710  85 dxfxqxycfi
## 21 90.67857  86 dxfxqxycfi
## 22 90.67857  85 dxfxqxycfi
## 23 79.38710  86 dxfxqxycfi
## 24 79.38710  81 dxfxqxycfi
## 25 71.82692  81 dxfxqxycfi
## 26 71.82692  82 dxfxqxycfi
## 27 90.67857  89 dxfxqxycfi
## 28 90.67857  90 dxfxqxycfi
## 29 71.82692  82 dxfxqxycfi
## 30 71.82692  77 dxfxqxycfi
## 31 71.82692  72 dxfxqxycfi
## 32 90.67857  81 dxfxqxycfi
## 33 79.38710  87 dxfxqxycfi
## 34 71.82692  76 dxfxqxycfi
## 35 71.82692  82 dxfxqxycfi
## 36 71.82692  71 dxfxqxycfi
## 37 71.82692  63 dxfxqxycfi
## 38 71.82692  68 dxfxqxycfi
##
##
## [[3]]
## [[3]]$fit
##
## Conditional inference tree with 5 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 37; criterion = 1, statistic = 54.42

```

```

## 2) ozone <= 20; criterion = 1, statistic = 15.73
## 3)* weights = 33
## 2) ozone > 20
## 4)* weights = 30
## 1) ozone > 37
## 5) ozone <= 65; criterion = 0.957, statistic = 4.077
## 6)* weights = 23
## 5) ozone > 65
## 7) ozone <= 110; criterion = 0.975, statistic = 5.046
## 8)* weights = 17
## 7) ozone > 110
## 9)* weights = 8
##
## [[3]]$vars
## [1] 1
##
## [[3]]$oob
##      pred obs      key
## 1  82.78261  67 shxfortrzy
## 2  68.90909  74 shxfortrzy
## 3  68.90909  62 shxfortrzy
## 4  68.90909  59 shxfortrzy
## 5  68.90909  61 shxfortrzy
## 6  68.90909  69 shxfortrzy
## 7  68.90909  64 shxfortrzy
## 8  76.03333  66 shxfortrzy
## 9  68.90909  57 shxfortrzy
## 10 76.03333  61 shxfortrzy
## 11 68.90909  76 shxfortrzy
## 12 76.03333  81 shxfortrzy
## 13 82.78261  83 shxfortrzy
## 14 82.78261  83 shxfortrzy
## 15 90.17647  92 shxfortrzy
## 16 68.90909  74 shxfortrzy
## 17 90.17647  85 shxfortrzy
## 18 68.90909  82 shxfortrzy
## 19 82.78261  86 shxfortrzy
## 20 82.78261  81 shxfortrzy
## 21 68.90909  82 shxfortrzy
## 22 90.17647  90 shxfortrzy
## 23 68.90909  72 shxfortrzy
## 24 90.17647  94 shxfortrzy
## 25 90.17647  91 shxfortrzy
## 26 90.17647  92 shxfortrzy
## 27 82.78261  81 shxfortrzy
## 28 76.03333  76 shxfortrzy
## 29 68.90909  67 shxfortrzy
## 30 76.03333  68 shxfortrzy
## 31 68.90909  82 shxfortrzy
## 32 68.90909  64 shxfortrzy
## 33 76.03333  71 shxfortrzy
## 34 68.90909  75 shxfortrzy
##
##

```



```

## [[4]]
## [[4]]$fit
##
## Conditional inference tree with 3 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 46; criterion = 1, statistic = 43.289
## 2) ozone <= 24; criterion = 0.996, statistic = 8.097
## 3)* weights = 50
## 2) ozone > 24
## 4)* weights = 27
## 1) ozone > 46
## 5)* weights = 34
##
## [[4]]$vars
## [1] 1
##
## [[4]]$oob
##      pred obs      key
## 1  71.16000  61 tlxnxzilmf
## 2  71.16000  66 tlxnxzilmf
## 3  71.16000  64 tlxnxzilmf
## 4  71.16000  61 tlxnxzilmf
## 5  77.22222  76 tlxnxzilmf
## 6  77.22222  82 tlxnxzilmf
## 7  71.16000  82 tlxnxzilmf
## 8  71.16000  77 tlxnxzilmf
## 9  77.22222  72 tlxnxzilmf
## 10 86.61765  85 tlxnxzilmf
## 11 86.61765  83 tlxnxzilmf
## 12 86.61765  92 tlxnxzilmf
## 13 86.61765  92 tlxnxzilmf
## 14 77.22222  82 tlxnxzilmf
## 15 86.61765  87 tlxnxzilmf
## 16 86.61765  85 tlxnxzilmf
## 17 71.16000  74 tlxnxzilmf
## 18 86.61765  86 tlxnxzilmf
## 19 71.16000  82 tlxnxzilmf
## 20 86.61765  88 tlxnxzilmf
## 21 86.61765  89 tlxnxzilmf
## 22 86.61765  90 tlxnxzilmf
## 23 77.22222  86 tlxnxzilmf
## 24 71.16000  77 tlxnxzilmf
## 25 71.16000  76 tlxnxzilmf
## 26 71.16000  77 tlxnxzilmf
## 27 71.16000  72 tlxnxzilmf
## 28 86.61765  86 tlxnxzilmf
## 29 86.61765  97 tlxnxzilmf
## 30 86.61765  92 tlxnxzilmf
## 31 86.61765  93 tlxnxzilmf
## 32 86.61765  87 tlxnxzilmf

```

```

## 33 71.16000 80 tlxnxzilmf
## 34 71.16000 78 tlxnxzilmf
## 35 71.16000 75 tlxnxzilmf
## 36 77.22222 81 tlxnxzilmf
## 37 71.16000 76 tlxnxzilmf
## 38 71.16000 71 tlxnxzilmf
## 39 77.22222 81 tlxnxzilmf
##
##
## [[5]]
## [[5]]$fit
##
## Conditional inference tree with 3 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 37; criterion = 1, statistic = 45.114
## 2) ozone <= 20; criterion = 0.964, statistic = 4.407
## 3)* weights = 35
## 2) ozone > 20
## 4)* weights = 28
## 1) ozone > 37
## 5)* weights = 48
##
## [[5]]$vars
## [1] 1
##
## [[5]]$oob
##      pred obs      key
## 1  86.35417 67 ppoxfdqegj
## 2  74.14286 72 ppoxfdqegj
## 3  68.34286 74 ppoxfdqegj
## 4  68.34286 58 ppoxfdqegj
## 5  68.34286 64 ppoxfdqegj
## 6  68.34286 57 ppoxfdqegj
## 7  68.34286 62 ppoxfdqegj
## 8  68.34286 73 ppoxfdqegj
## 9  86.35417 81 ppoxfdqegj
## 10 74.14286 76 ppoxfdqegj
## 11 86.35417 90 ppoxfdqegj
## 12 68.34286 65 ppoxfdqegj
## 13 68.34286 76 ppoxfdqegj
## 14 86.35417 81 ppoxfdqegj
## 15 74.14286 82 ppoxfdqegj
## 16 68.34286 82 ppoxfdqegj
## 17 86.35417 86 ppoxfdqegj
## 18 86.35417 86 ppoxfdqegj
## 19 86.35417 83 ppoxfdqegj
## 20 68.34286 82 ppoxfdqegj
## 21 86.35417 90 ppoxfdqegj
## 22 86.35417 86 ppoxfdqegj
## 23 86.35417 79 ppoxfdqegj

```

```

## 24 86.35417 78 ppoxfdqegj
## 25 68.34286 72 ppoxfdqegj
## 26 86.35417 86 ppoxfdqegj
## 27 86.35417 94 ppoxfdqegj
## 28 86.35417 96 ppoxfdqegj
## 29 86.35417 91 ppoxfdqegj
## 30 86.35417 92 ppoxfdqegj
## 31 74.14286 84 ppoxfdqegj
## 32 68.34286 80 ppoxfdqegj
## 33 74.14286 78 ppoxfdqegj
## 34 74.14286 73 ppoxfdqegj
## 35 86.35417 81 ppoxfdqegj
## 36 74.14286 76 ppoxfdqegj
## 37 68.34286 67 ppoxfdqegj
## 38 74.14286 68 ppoxfdqegj
## 39 68.34286 82 ppoxfdqegj
## 40 74.14286 71 ppoxfdqegj
## 41 74.14286 70 ppoxfdqegj
## 42 68.34286 76 ppoxfdqegj
##
##
## [[6]]
## [[6]]$fit
##
## Conditional inference tree with 5 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 41; criterion = 1, statistic = 58.444
## 2) ozone <= 7; criterion = 0.989, statistic = 6.472
## 3)* weights = 8
## 2) ozone > 7
## 4)* weights = 60
## 1) ozone > 41
## 5) ozone <= 64; criterion = 0.988, statistic = 6.327
## 6)* weights = 18
## 5) ozone > 64
## 7) ozone <= 89; criterion = 0.973, statistic = 4.909
## 8)* weights = 18
## 7) ozone > 89
## 9)* weights = 7
##
## [[6]]$vars
## [1] 1
##
## [[6]]$oob
## pred obs key
## 1 72.41667 61 zmikpzroyt
## 2 72.41667 66 zmikpzroyt
## 3 63.50000 57 zmikpzroyt
## 4 72.41667 73 zmikpzroyt
## 5 82.50000 81 zmikpzroyt

```

```

## 6 72.41667 87 zmikpzroyt
## 7 72.41667 77 zmikpzroyt
## 8 72.41667 72 zmikpzroyt
## 9 88.14286 84 zmikpzroyt
## 10 72.41667 81 zmikpzroyt
## 11 90.11111 88 zmikpzroyt
## 12 88.14286 92 zmikpzroyt
## 13 72.41667 73 zmikpzroyt
## 14 63.50000 80 zmikpzroyt
## 15 82.50000 81 zmikpzroyt
## 16 82.50000 84 zmikpzroyt
## 17 90.11111 87 zmikpzroyt
## 18 90.11111 86 zmikpzroyt
## 19 88.14286 85 zmikpzroyt
## 20 72.41667 82 zmikpzroyt
## 21 82.50000 86 zmikpzroyt
## 22 82.50000 83 zmikpzroyt
## 23 72.41667 81 zmikpzroyt
## 24 88.14286 90 zmikpzroyt
## 25 72.41667 82 zmikpzroyt
## 26 90.11111 80 zmikpzroyt
## 27 72.41667 77 zmikpzroyt
## 28 82.50000 79 zmikpzroyt
## 29 72.41667 76 zmikpzroyt
## 30 90.11111 97 zmikpzroyt
## 31 90.11111 92 zmikpzroyt
## 32 88.14286 93 zmikpzroyt
## 33 72.41667 84 zmikpzroyt
## 34 72.41667 78 zmikpzroyt
## 35 72.41667 73 zmikpzroyt
## 36 72.41667 77 zmikpzroyt
## 37 72.41667 71 zmikpzroyt
## 38 82.50000 78 zmikpzroyt
## 39 72.41667 67 zmikpzroyt
## 40 72.41667 68 zmikpzroyt
## 41 72.41667 71 zmikpzroyt
## 42 72.41667 81 zmikpzroyt
## 43 72.41667 63 zmikpzroyt
## 44 72.41667 75 zmikpzroyt
## 45 72.41667 76 zmikpzroyt
##
##
## [[7]]
## [[7]]$fit
##
## Conditional inference tree with 3 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 41; criterion = 1, statistic = 49.074
## 2) ozone <= 18; criterion = 0.997, statistic = 8.907
## 3)* weights = 31

```

```

## 2) ozone > 18
## 4)* weights = 38
## 1) ozone > 41
## 5)* weights = 42
##
## [[7]]$vars
## [1] 1
##
## [[7]]$oob
##      pred obs      key
## 1  75.28947  72 iogyetcrf
## 2  75.28947  59 iogyetcrf
## 3  69.58065  61 iogyetcrf
## 4  69.58065  69 iogyetcrf
## 5  69.58065  64 iogyetcrf
## 6  75.28947  68 iogyetcrf
## 7  69.58065  62 iogyetcrf
## 8  69.58065  61 iogyetcrf
## 9  87.26190  79 iogyetcrf
## 10 75.28947  82 iogyetcrf
## 11 75.28947  65 iogyetcrf
## 12 69.58065  73 iogyetcrf
## 13 75.28947  81 iogyetcrf
## 14 87.26190  83 iogyetcrf
## 15 87.26190  88 iogyetcrf
## 16 87.26190  92 iogyetcrf
## 17 69.58065  73 iogyetcrf
## 18 75.28947  81 iogyetcrf
## 19 75.28947  82 iogyetcrf
## 20 87.26190  87 iogyetcrf
## 21 87.26190  85 iogyetcrf
## 22 75.28947  82 iogyetcrf
## 23 87.26190  86 iogyetcrf
## 24 87.26190  88 iogyetcrf
## 25 87.26190  89 iogyetcrf
## 26 87.26190  90 iogyetcrf
## 27 87.26190  78 iogyetcrf
## 28 69.58065  72 iogyetcrf
## 29 87.26190  86 iogyetcrf
## 30 87.26190  97 iogyetcrf
## 31 87.26190  92 iogyetcrf
## 32 87.26190  93 iogyetcrf
## 33 75.28947  80 iogyetcrf
## 34 75.28947  73 iogyetcrf
## 35 87.26190  81 iogyetcrf
## 36 75.28947  77 iogyetcrf
## 37 69.58065  71 iogyetcrf
## 38 87.26190  78 iogyetcrf
## 39 69.58065  67 iogyetcrf
## 40 69.58065  64 iogyetcrf
## 41 75.28947  71 iogyetcrf
## 42 69.58065  69 iogyetcrf
## 43 75.28947  70 iogyetcrf
## 44 75.28947  68 iogyetcrf

```

```

##
##
## [[8]]
## [[8]]$fit
##
## Conditional inference tree with 3 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 46; criterion = 1, statistic = 47.438
## 2) ozone <= 14; criterion = 0.995, statistic = 8.039
## 3)* weights = 23
## 2) ozone > 14
## 4)* weights = 62
## 1) ozone > 46
## 5)* weights = 26
##
## [[8]]$vars
## [1] 1
##
## [[8]]$oob
##      pred obs      key
## 1  70.47826  74 ibegordtbe
## 2  75.67742  62 ibegordtbe
## 3  75.67742  58 ibegordtbe
## 4  70.47826  64 ibegordtbe
## 5  75.67742  68 ibegordtbe
## 6  70.47826  59 ibegordtbe
## 7  70.47826  73 ibegordtbe
## 8  87.50000  79 ibegordtbe
## 9  87.50000  90 ibegordtbe
## 10 75.67742  82 ibegordtbe
## 11 75.67742  77 ibegordtbe
## 12 75.67742  65 ibegordtbe
## 13 75.67742  81 ibegordtbe
## 14 87.50000  88 ibegordtbe
## 15 87.50000  92 ibegordtbe
## 16 87.50000  89 ibegordtbe
## 17 70.47826  73 ibegordtbe
## 18 87.50000  87 ibegordtbe
## 19 75.67742  74 ibegordtbe
## 20 87.50000  86 ibegordtbe
## 21 87.50000  86 ibegordtbe
## 22 87.50000  83 ibegordtbe
## 23 87.50000  81 ibegordtbe
## 24 87.50000  89 ibegordtbe
## 25 75.67742  86 ibegordtbe
## 26 75.67742  82 ibegordtbe
## 27 75.67742  78 ibegordtbe
## 28 70.47826  72 ibegordtbe
## 29 87.50000  81 ibegordtbe
## 30 87.50000  86 ibegordtbe

```

```

## 31 87.50000 94 ibegordtbe
## 32 87.50000 94 ibegordtbe
## 33 87.50000 91 ibegordtbe
## 34 87.50000 93 ibegordtbe
## 35 87.50000 87 ibegordtbe
## 36 75.67742 78 ibegordtbe
## 37 70.47826 76 ibegordtbe
## 38 75.67742 71 ibegordtbe
## 39 75.67742 81 ibegordtbe
## 40 75.67742 70 ibegordtbe
##
##
## [[9]]
## [[9]]$fit
##
## Conditional inference tree with 3 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 37; criterion = 1, statistic = 61.733
## 2)* weights = 62
## 1) ozone > 37
## 3) ozone <= 65; criterion = 1, statistic = 13.63
## 4)* weights = 26
## 3) ozone > 65
## 5)* weights = 23
##
## [[9]]$vars
## [1] 1
##
## [[9]]$oob
##      pred obs      key
## 1  82.19231 67 stpcxtuojz
## 2  70.45161 72 stpcxtuojz
## 3  70.45161 74 stpcxtuojz
## 4  70.45161 61 stpcxtuojz
## 5  70.45161 57 stpcxtuojz
## 6  70.45161 73 stpcxtuojz
## 7  70.45161 61 stpcxtuojz
## 8  89.39130 79 stpcxtuojz
## 9  70.45161 76 stpcxtuojz
## 10 89.39130 90 stpcxtuojz
## 11 82.19231 87 stpcxtuojz
## 12 70.45161 77 stpcxtuojz
## 13 70.45161 65 stpcxtuojz
## 14 70.45161 73 stpcxtuojz
## 15 70.45161 76 stpcxtuojz
## 16 82.19231 85 stpcxtuojz
## 17 70.45161 81 stpcxtuojz
## 18 89.39130 88 stpcxtuojz
## 19 89.39130 92 stpcxtuojz
## 20 70.45161 73 stpcxtuojz

```

```

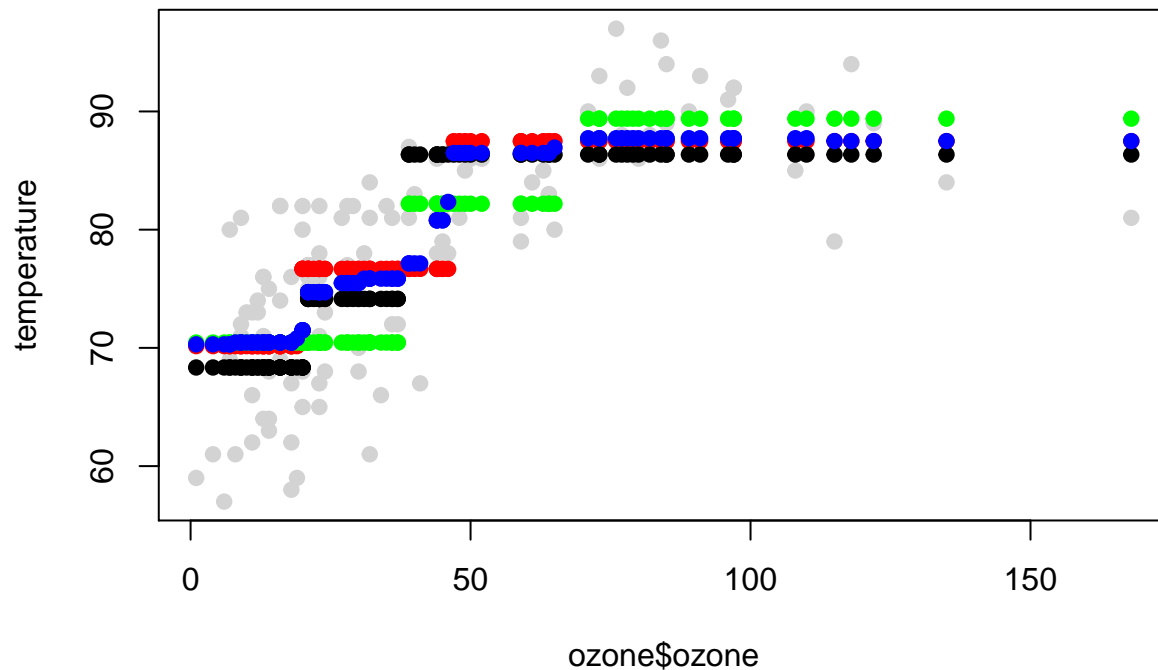
## 21 70.45161 81 stpcxtuojz
## 22 70.45161 80 stpcxtuojz
## 23 70.45161 82 stpcxtuojz
## 24 70.45161 82 stpcxtuojz
## 25 82.19231 86 stpcxtuojz
## 26 82.19231 81 stpcxtuojz
## 27 70.45161 82 stpcxtuojz
## 28 89.39130 89 stpcxtuojz
## 29 70.45161 82 stpcxtuojz
## 30 70.45161 72 stpcxtuojz
## 31 89.39130 81 stpcxtuojz
## 32 89.39130 96 stpcxtuojz
## 33 89.39130 94 stpcxtuojz
## 34 89.39130 91 stpcxtuojz
## 35 70.45161 76 stpcxtuojz
## 36 70.45161 77 stpcxtuojz
## 37 70.45161 71 stpcxtuojz
## 38 70.45161 82 stpcxtuojz
## 39 70.45161 71 stpcxtuojz
## 40 70.45161 81 stpcxtuojz
## 41 70.45161 68 stpcxtuojz
##
##
## [[10]]
## [[10]]$fit
##
## Conditional inference tree with 3 terminal nodes
##
## Response: y
## Input: ozone
## Number of observations: 111
##
## 1) ozone <= 45; criterion = 1, statistic = 48.188
## 2) ozone <= 20; criterion = 0.993, statistic = 7.307
## 3)* weights = 35
## 2) ozone > 20
## 4)* weights = 43
## 1) ozone > 45
## 5)* weights = 33
##
## [[10]]$vars
## [1] 1
##
## [[10]]$oob
##      pred obs      key
## 1  77.06977 72 grucogev
## 2  70.45714 74 grucogev
## 3  77.06977 65 grucogev
## 4  70.45714 61 grucogev
## 5  70.45714 68 grucogev
## 6  70.45714 57 grucogev
## 7  70.45714 62 grucogev
## 8  70.45714 59 grucogev
## 9  77.06977 67 grucogev

```



```
## 10 77.06977 81 grucogevch
## 11 87.96970 90 grucogevch
## 12 77.06977 87 grucogevch
## 13 87.96970 83 grucogevch
## 14 77.06977 83 grucogevch
## 15 87.96970 89 grucogevch
## 16 87.96970 81 grucogevch
## 17 77.06977 82 grucogevch
## 18 87.96970 84 grucogevch
## 19 87.96970 87 grucogevch
## 20 87.96970 86 grucogevch
## 21 70.45714 82 grucogevch
## 22 87.96970 86 grucogevch
## 23 87.96970 88 grucogevch
## 24 70.45714 82 grucogevch
## 25 87.96970 89 grucogevch
## 26 87.96970 90 grucogevch
## 27 77.06977 86 grucogevch
## 28 77.06977 76 grucogevch
## 29 77.06977 78 grucogevch
## 30 70.45714 72 grucogevch
## 31 87.96970 86 grucogevch
## 32 87.96970 94 grucogevch
## 33 77.06977 78 grucogevch
## 34 77.06977 81 grucogevch
## 35 87.96970 78 grucogevch
## 36 77.06977 71 grucogevch
## 37 77.06977 81 grucogevch
## 38 70.45714 69 grucogevch
## 39 70.45714 63 grucogevch
## 40 77.06977 70 grucogevch
## 41 70.45714 75 grucogevch
## 42 70.45714 76 grucogevch
```

```
plot(ozone$ozone, temperature, col="lightgrey", pch=19)
#Plotting the prediction 1 of the treebag
points(ozone$ozone, predict(treebag$fits[[1]]$fit,predictors),pch=19,col="red")
#Plotting the prediction 9 of the treebag
points(ozone$ozone, predict(treebag$fits[[9]]$fit,predictors),pch=19,col="green")
#Plotting the prediction 5 of the treebag
points(ozone$ozone, predict(treebag$fits[[5]]$fit,predictors),pch=19,col="black")
#Plotting the aggregated predictions of the treebag
points(ozone$ozone, predict(treebag,predictors),pch=19, col="blue")
```



We can see that the aggregated prediction (the blue dots in the plot) is the closest to the real values of temperature.

Also we can verify that the aggregated prediction has the lowest **RSME** (Root Mean Squared Error):

```
#The following is the RSME of the aggregated prediction:
sqrt(sum((ozone$temperature-predict(treebag,predictors))^2)/111)
```

```
## [1] 6.004662
```

```
#The next 10 are the RSME of each of the fitted predictions. One can see that the lowest one is the RSM
sqrt(sum((ozone$temperature-predict(treebag$fits[[1]]$fit,predictors))^2)/111)
```

```
## [1] 6.213156
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[2]]$fit,predictors))^2)/111)
```

```
## [1] 6.380369
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[3]]$fit,predictors))^2)/111)
```

```
## [1] 5.882444
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[4]]$fit,predictors))^2)/111)
```

```
## [1] 6.283436
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[5]]$fit,predictors))^2)/111)
```

```
## [1] 6.456446
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[6]]$fit,predictors))^2)/111)
```

```
## [1] 6.219213
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[7]]$fit,predictors))^2)/111)
```

```
## [1] 6.395468
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[8]]$fit,predictors))^2)/111)
```

```
## [1] 6.43415
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[9]]$fit,predictors))^2)/111)
```

```
## [1] 6.351157
```

```
sqrt(sum((ozone$temperature-predict(treebag$fits[[10]]$fit,predictors))^2)/111)
```

```
## [1] 6.325346
```

## Random Forrest

The **Random Forrest** algorithm is similar to bagging. It bootstraps samples of the data and built a tree. At each split of the tree it bootstrap a set of the variables (of the predictors). Then, the algorithm also creates many trees following the same logic.

For the prediction, each set of predictors is passed through each tree and then the final answer is the average of all the answers from each tree.

RF is a highly accurate algorithm, however it can lead to overfitting. Therefore, cross-validation must be used in order to detect the overfitting.

The following is an example of RF algorithm in R:

```
data(iris); library(ggplot2)
library(caret)
inTrain <- createDataPartition(y=iris$Species,p=0.7, list=FALSE)
training <- iris[inTrain,]
testing <- iris[-inTrain,]
modFit_RF <- train(Species ~ .,data=training,method="rf",prox=TRUE)
modFit_RF
```

```
## Random Forest
##
## 105 samples
## 4 predictor
## 3 classes: 'setosa', 'versicolor', 'virginica'
##
## No pre-processing
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 105, 105, 105, 105, 105, 105, ...
## Resampling results across tuning parameters:
##
## mtry Accuracy Kappa Accuracy SD Kappa SD
## 2 0.9490312 0.9221163 0.03738606 0.05756782
## 3 0.9521264 0.9269105 0.03618188 0.05549883
## 4 0.9522851 0.9271339 0.03604642 0.05530885
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 4.
```

```
#Comparing the RF model with the Prediction Tree Model
modFit_PredTree
```

```
## CART
##
## 105 samples
## 4 predictor
## 3 classes: 'setosa', 'versicolor', 'virginica'
##
## No pre-processing
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 105, 105, 105, 105, 105, 105, ...
## Resampling results across tuning parameters:
##
## cp Accuracy Kappa Accuracy SD Kappa SD
## 0.0000000 0.9370643 0.9043921 0.02805579 0.04254972
## 0.4428571 0.7500694 0.6348239 0.17135543 0.24405380
## 0.5000000 0.5339367 0.3305523 0.14747235 0.19752127
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was cp = 0.
```

```
#I can check one of the specific trees:
getTree(modFit_RF$finalModel,k=2)
```

```
## left daughter right daughter split var split point status prediction
## 1 2 3 3 2.45 1 0
## 2 0 0 0 0.00 -1 1
## 3 4 5 4 1.65 1 0
## 4 0 0 0 0.00 -1 2
## 5 6 7 3 5.05 1 0
## 6 8 9 2 2.90 1 0
## 7 0 0 0 0.00 -1 3
## 8 0 0 0 0.00 -1 3
## 9 0 0 0 0.00 -1 2
```

```
#Predicting over the testing set:
pred <- predict(modFit_RF,testing)
confusionMatrix(testing$Species,pred)
```

```
## Confusion Matrix and Statistics
##
##              Reference
## Prediction  setosa versicolor virginica
##   setosa      15         0         0
##   versicolor   0        14         1
##   virginica    0         0        15
##
## Overall Statistics
##
##              Accuracy : 0.9778
##              95% CI : (0.8823, 0.9994)
##   No Information Rate : 0.3556
##   P-Value [Acc > NIR] : < 2.2e-16
##
##              Kappa : 0.9667
##   Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##              Class: setosa Class: versicolor Class: virginica
## Sensitivity              1.0000              1.0000              0.9375
## Specificity              1.0000              0.9677              1.0000
## Pos Pred Value           1.0000              0.9333              1.0000
## Neg Pred Value           1.0000              1.0000              0.9667
## Prevalence               0.3333              0.3111              0.3556
## Detection Rate           0.3333              0.3111              0.3333
## Detection Prevalence     0.3333              0.3333              0.3333
## Balanced Accuracy        1.0000              0.9839              0.9688
```

```
#Comparing the confusion Matrices of RF model and the pred tree model:
```

```
CM_PredTree
```

```
## Confusion Matrix and Statistics
##
##              Reference
## Prediction  setosa versicolor virginica
##   setosa      15         0         0
##   versicolor   0        13         2
##   virginica    0         1        14
##
## Overall Statistics
##
##              Accuracy : 0.9333
##              95% CI : (0.8173, 0.986)
##   No Information Rate : 0.3556
##   P-Value [Acc > NIR] : 5.426e-16
##
```

```
##                Kappa : 0.9
## McNemar's Test P-Value : NA
##
## Statistics by Class:
##
##                Class: setosa Class: versicolor Class: virginica
## Sensitivity          1.0000          0.9286          0.8750
## Specificity          1.0000          0.9355          0.9655
## Pos Pred Value       1.0000          0.8667          0.9333
## Neg Pred Value       1.0000          0.9667          0.9333
## Prevalence           0.3333          0.3111          0.3556
## Detection Rate       0.3333          0.2889          0.3111
## Detection Prevalence 0.3333          0.3333          0.3333
## Balanced Accuracy    1.0000          0.9320          0.9203
```

Comparing the confusion matrix of the random forest algorithm over the testing set with that of the prediction tree, we can see that the RF is more accurate.

## Boosting

Boosting algorithm takes several classifiers weights and averages them in order to obtain a better one. It can use trees, glms, RF trees, etc. In R, in the **caret** packages, there are several options for boosting:

- **gbm** - boosting with trees
- **mboost** - model based boosting
- **ada** - statistical boosting based on additive logistic regression
- **gamBoost** - for boosting generalized additive models

In the next example we will use boosting prediction in the same problem of predicting the flower Species:

```
data(iris); library(ggplot2)
library(caret)
inTrain <- createDataPartition(y=iris$Species,p=0.7, list=FALSE)
training <- iris[inTrain,]
testing <- iris[-inTrain,]
MF_Boosting <- train(Species ~ .,method="gbm",data=training,verbose=FALSE)
pred <- predict(MF_Boosting,testing)
confusionMatrix(testing$Species,pred)
```

```
## Confusion Matrix and Statistics
##
##                Reference
## Prediction  setosa versicolor virginica
##   setosa      15           0           0
##   versicolor   0          14           1
##   virginica    0           1          14
##
## Overall Statistics
##
##                Accuracy : 0.9556
##                95% CI : (0.8485, 0.9946)
```

```
##      No Information Rate : 0.3333
##      P-Value [Acc > NIR] : < 2.2e-16
##
##              Kappa : 0.9333
##      McNemar's Test P-Value : NA
##
## Statistics by Class:
##
##              Class: setosa Class: versicolor Class: virginica
## Sensitivity              1.0000              0.9333              0.9333
## Specificity              1.0000              0.9667              0.9667
## Pos Pred Value           1.0000              0.9333              0.9333
## Neg Pred Value           1.0000              0.9667              0.9667
## Prevalence               0.3333              0.3333              0.3333
## Detection Rate           0.3333              0.3111              0.3111
## Detection Prevalence     0.3333              0.3333              0.3333
## Balanced Accuracy        1.0000              0.9500              0.9500
```

## Model Based Prediction

The basic ideas of model based prediction are:

- Assume that data follow a probabilistic model
- Use Bayes's theorem to identify optimal classifiers

There are several algorithms for Model Based Prediction:

- **Linear Discriminant Analysis - lda:** the discrimination function is a multivariate Gaussian with the same covariances
- **Quadratic Discriminant Analysis - qda:** the discrimination function is multivariate Gaussian with different covariances
- **Model Based Prediction:** assumes more complicated versions of the covariance matrix
- **Naive Bayes - nb:** assumes independence between features model building

In the following example we compare the Linear Discriminant Analysis algorithm with the Naive Bayes:

```
modlda <- train(Species ~ .,data=training,method="lda")
modnb <- train(Species ~ .,data=training,method="nb")
plda <- predict(modlda,testing)
pnb <- predict(modnb,testing)
confusionMatrix(testing$Species,plda)
```

```
## Confusion Matrix and Statistics
##
##              Reference
## Prediction  setosa versicolor virginica
##   setosa      15          0          0
## versicolor    0          15          0
##   virginica    0          0          15
##
```

```
## Overall Statistics
##
##           Accuracy : 1
##           95% CI : (0.9213, 1)
##       No Information Rate : 0.3333
##       P-Value [Acc > NIR] : < 2.2e-16
##
##           Kappa : 1
##   McNemar's Test P-Value : NA
##
## Statistics by Class:
##
##           Class: setosa Class: versicolor Class: virginica
## Sensitivity           1.0000           1.0000           1.0000
## Specificity           1.0000           1.0000           1.0000
## Pos Pred Value        1.0000           1.0000           1.0000
## Neg Pred Value        1.0000           1.0000           1.0000
## Prevalence            0.3333           0.3333           0.3333
## Detection Rate        0.3333           0.3333           0.3333
## Detection Prevalence  0.3333           0.3333           0.3333
## Balanced Accuracy      1.0000           1.0000           1.0000
```

```
confusionMatrix(testing$Species,pnb)
```

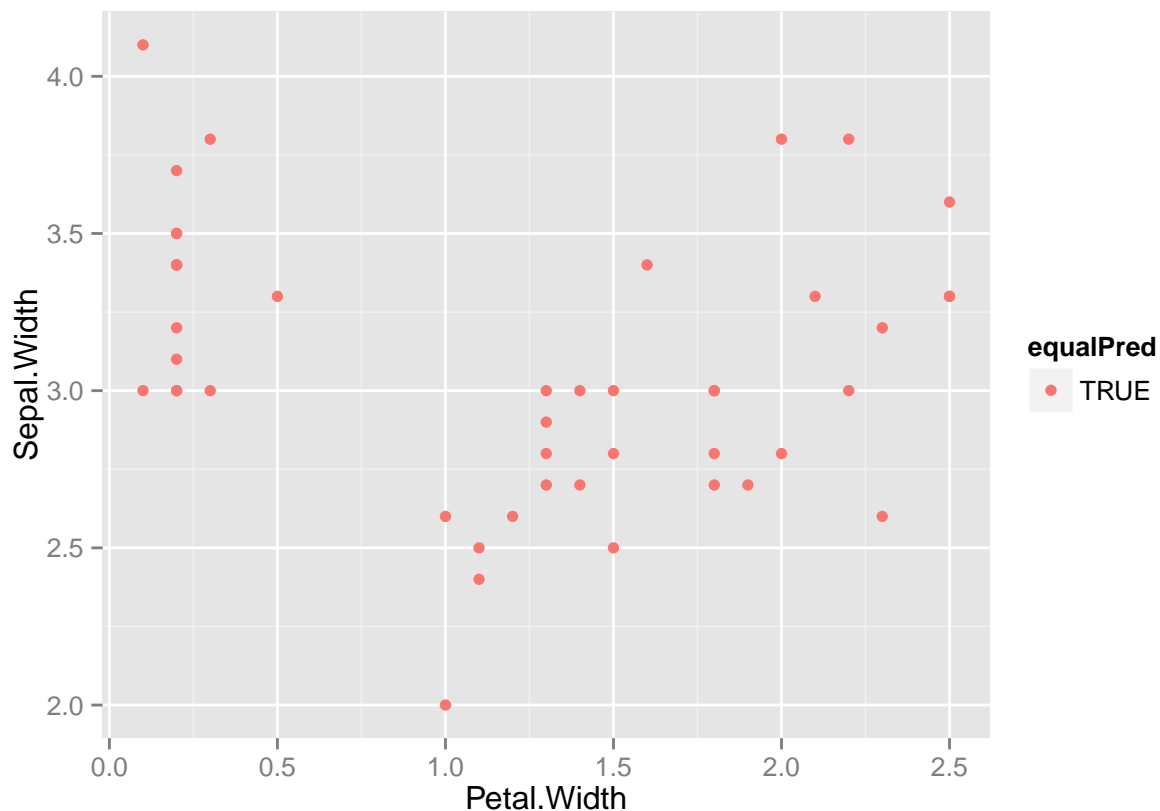
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  setosa versicolor virginica
##   setosa      15          0          0
##   versicolor   0         15          0
##   virginica    0          0         15
##
## Overall Statistics
##
##           Accuracy : 1
##           95% CI : (0.9213, 1)
##       No Information Rate : 0.3333
##       P-Value [Acc > NIR] : < 2.2e-16
##
##           Kappa : 1
##   McNemar's Test P-Value : NA
##
## Statistics by Class:
##
##           Class: setosa Class: versicolor Class: virginica
## Sensitivity           1.0000           1.0000           1.0000
## Specificity           1.0000           1.0000           1.0000
## Pos Pred Value        1.0000           1.0000           1.0000
## Neg Pred Value        1.0000           1.0000           1.0000
## Prevalence            0.3333           0.3333           0.3333
## Detection Rate        0.3333           0.3333           0.3333
## Detection Prevalence  0.3333           0.3333           0.3333
## Balanced Accuracy      1.0000           1.0000           1.0000
```



```
table(plda,pnb)
```

```
##           pnb
## plda      setosa versicolor virginica
## setosa      15         0         0
## versicolor   0        15         0
## virginica    0         0        15
```

```
equalPred <- plda==pnb
qplot(Petal.Width,Sepal.Width,colour=equalPred,data=testing)
```



In the plot we can see that the values in which the predictions disagree are in the boundary between two classes.

## Quiz-3

### Question-1:

Load the cell segmentation data from the AppliedPredictiveModeling package using the commands:

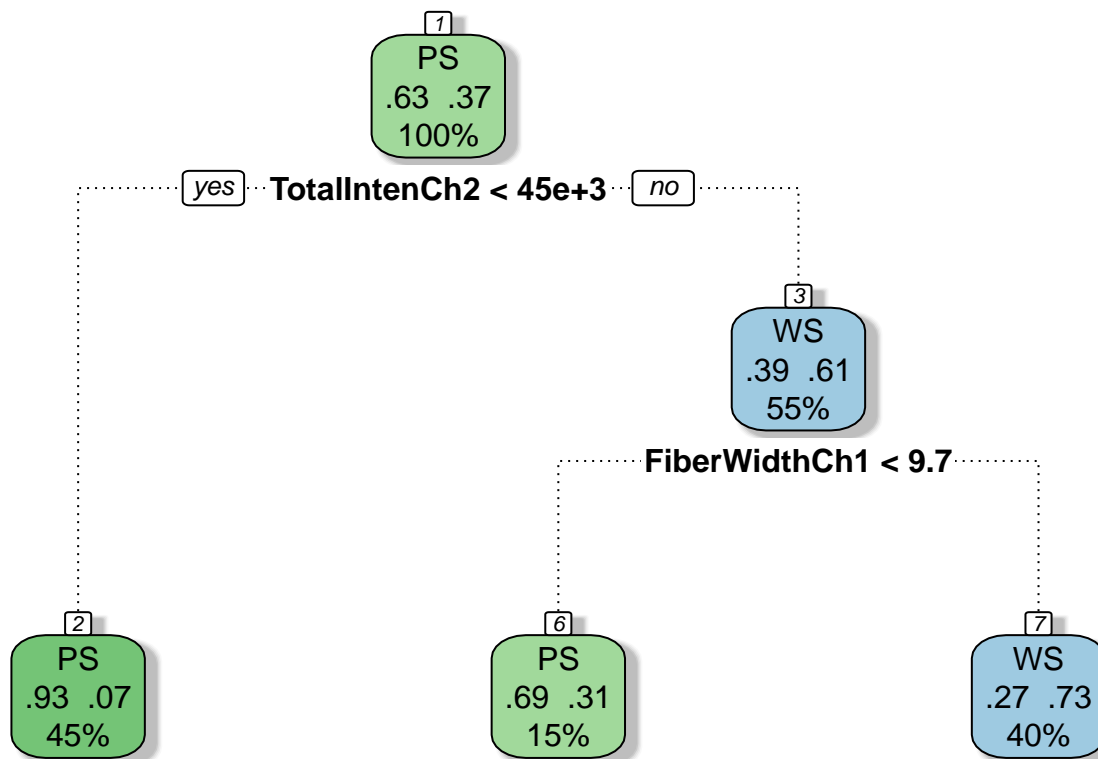
```
library(AppliedPredictiveModeling) data(segmentationOriginal) library(caret) 1. Subset the data to a training set and testing set based on the Case variable in the data set.
```

2. Set the seed to 125 and fit a CART model with the rpart method using all predictor variables and default caret settings.

3. In the final model what would be the final model prediction for cases with the following variable values:

- TotalIntench2 = 23,000; FiberWidthCh1 = 10; PerimStatusCh1=2
- TotalIntench2 = 50,000; FiberWidthCh1 = 10;VarIntenCh4 = 100
- TotalIntench2 = 57,000; FiberWidthCh1 = 8;VarIntenCh4 = 100
- FiberWidthCh1 = 8;VarIntenCh4 = 100; PerimStatusCh1=2

```
library(AppliedPredictiveModeling)
data(segmentationOriginal)
library(caret)
training <- subset(segmentationOriginal,Case=="Train")
testing <- subset(segmentationOriginal,Case=="Test")
set.seed(125)
model_CART <- train(Class ~.,data=training,method="rpart")
library(rattle)
fancyRpartPlot(model_CART$finalModel)
```



Rattle 2016-Jan-24 22:42:31 saul

Analyzing the Plot of the tree growth by the CART model we can see that the answer must be:

a.- PS b.- WS c.- PS d.- Not possible to predict

## Question-2

If K is small in a K-fold cross validation is the bias in the estimate of out-of-sample (test set) accuracy smaller or bigger? If K is small is the variance in the estimate of out-of-sample (test set) accuracy smaller or bigger. Is K large or small in leave one out cross validation?

The bias is smaller and the variance is smaller. Under leave one out cross validation K is equal to one.

The bias is larger and the variance is smaller. Under leave one out cross validation K is equal to the sample size.

The bias is larger and the variance is smaller. Under leave one out cross validation K is equal to two.

The bias is smaller and the variance is bigger. Under leave one out cross validation K is equal to one.

As a reference for this question I read the following link [Cross-validation in Wikipedia] [https://en.wikipedia.org/wiki/Cross-validation\\_\(statistics\)](https://en.wikipedia.org/wiki/Cross-validation_(statistics))

When  $k=n$  (the sample size) k-fold cross-validation is the same as leave-one-out cross-validation.

Also, the  $k$  is small you get more bias and less variance, so the answer is:

**The bias is larger and the variance is smaller. Under leave one out cross validation K is equal to the sample size.**

## Question-3

Load the olive oil data using the commands:

```
library(pgmm) data(olive) olive = olive[,-1] (NOTE: If you have trouble installing the pgmm package, you can download the -code-olive-/code- dataset here: olive_data.zip. After unzipping the archive, you can load the file using the -code-load()-/code- function in R.)
```

These data contain information on 572 different Italian olive oils from multiple regions in Italy. Fit a classification tree where Area is the outcome variable. Then predict the value of area for the following data frame using the tree command with all defaults

```
newdata = as.data.frame(t(colMeans(olive)))
```

 What is the resulting prediction? Is the resulting prediction strange? Why or why not?

2.783. There is no reason why this result is strange.

4.59965. There is no reason why the result is strange.

0.005291005 0 0.994709 0 0 0 0 0. The result is strange because Area is a numeric variable and we should get the average within each leaf.

2.783. It is strange because Area should be a qualitative variable - but tree is reporting the average value of Area as a numeric variable in the leaf predicted for newdata

```
library(pgmm)
data(olive)
olive = olive[,-1]
head(olive)
```

```
##      Area Palmitic Palmitoleic Stearic Oleic Linoleic Linolenic Arachidic
## 1      1      1075           75     226  7823      672        36         60
## 2      1      1088           73     224  7709      781        31         61
## 3      1       911           54     246  8113      549        31         63
## 4      1       966           57     240  7952      619        50         78
## 5      1      1051           67     259  7771      672        50         80
## 6      1       911           49     268  7924      678        51         70
##      Eicosenoic
## 1             29
## 2             29
```

```
## 3      29
## 4      35
## 5      46
## 6      44
```

```
system.time(modFit <- train(Area ~., data=olive, method="rpart"))
```

```
##      user system elapsed
##    1.427   0.006   1.447
```

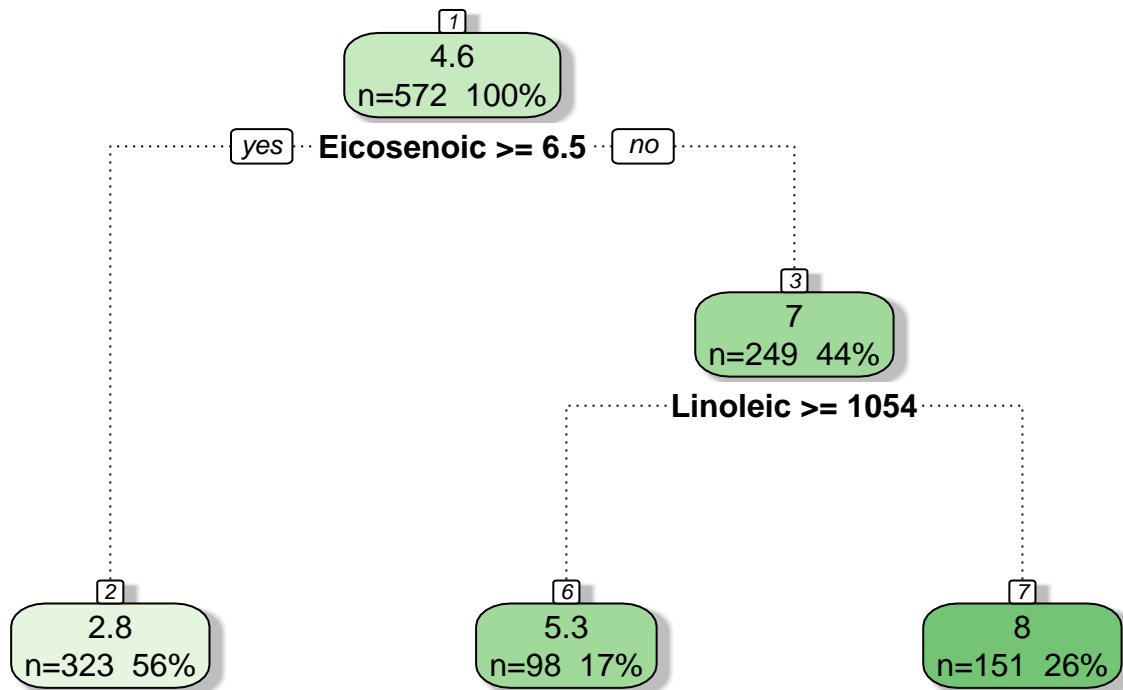
```
newdata = as.data.frame(t(colMeans(olive)))
newdata
```

```
##      Area Palmitic Palmitoleic Stearic   Oleic Linoleic Linolenic
## 1 4.59965 1231.741   126.0944 228.8654 7311.748  980.528  31.88811
##  Arachidic Eicosenoic
## 1   58.0979   16.28147
```

```
predict(modFit,newdata)
```

```
##      1
## 2.783282
```

```
fancyRpartPlot(modFit$finalModel)
```



Rattle 2016-Jan-24 22:42:34 saul

```
summary(olive$Area)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##       1.0      3.0      3.0     4.6     7.0     9.0
```

Examining the tree model plot we can see that the prediction is correct (2.783). In my opinion the result is not extrange because in the dataset “Area” is not a qualitative variable but a quantitative one.

## Question-4

Load the South Africa Heart Disease Data and create training and test sets with the following code:

library(ElemStatLearn) data(SAheart) set.seed(8484) train = sample(1:dim(SAheart)[1],size=dim(SAheart)[1]/2,replace=F)  
trainSA = SAheart[train,] testSA = SAheart[-train,] Then set the seed to 13234 and fit a logistic regression model (method=“glm”, be sure to specify family=“binomial”) with Coronary Heart Disease (chd) as the outcome and age at onset, current alcohol consumption, obesity levels, cumulative tabacco, type-A behavior, and low density lipoprotein cholesterol as predictors. Calculate the misclassification rate for your model using this function and a prediction on the “response” scale:

missClass = function(values,prediction){sum(((prediction > 0.5)\*1) != values)/length(values)} What is the misclassification rate on the training set? What is the misclassification rate on the test set?

```
library(ElemStatLearn)
data(SAheart)
set.seed(8484)
train = sample(1:dim(SAheart)[1],size=dim(SAheart)[1]/2,replace=F)
trainSA = SAheart[train,]
testSA = SAheart[-train,]
set.seed(13234)
head(trainSA)
```

```
##      sbp tobacco  ldl adiposity famhist typea obesity alcohol age chd
## 238 176      5.76 4.89    26.10 Present   46   27.30   19.44  57   0
## 114 174      0.00 8.46    35.10 Present   35   25.27    0.00  61   1
## 312 174      3.50 5.26    21.97 Present   36   22.04    8.33  59   1
## 301 166      4.10 4.00    34.30 Present   32   29.51    8.23  53   0
## 311 130      0.05 2.44    28.25 Present   67   30.86   40.32  34   0
## 179 128      0.04 8.22    28.17 Absent    65   26.24   11.73  24   0
```

```
modFit <- train(chd ~ age + alcohol + obesity + tobacco + typea + ldl,data=trainSA,method="glm",family=
missClass = function(values,prediction){sum(((prediction > 0.5)*1) != values)/length(values)}
missClass(trainSA$chd,predict(modFit,trainSA))
```

```
## [1] 0.2727273
```

```
missClass(testSA$chd,predict(modFit,testSA))
```

```
## [1] 0.3116883
```

Therefore, the misclassification error on the training set is 0.27 and on the test set is 0.31

## Question-5

Load the vowel.train and vowel.test data sets:

library(ElemStatLearn) data(vowel.train) data(vowel.test) Set the variable y to be a factor variable in both the training and test set. Then set the seed to 33833. Fit a random forest predictor relating the factor variable y to the remaining variables. Read about variable importance in random forests here: [http://www.stat.berkeley.edu/~breiman/RandomForests/cc\\_home.htm#ooberr](http://www.stat.berkeley.edu/~breiman/RandomForests/cc_home.htm#ooberr) The caret package uses by default the Gini importance.

Calculate the variable importance using the varImp function in the caret package. What is the order of variable importance?

The order of the variables is:

x.10, x.7, x.9, x.5, x.8, x.4, x.6, x.3, x.1,x.2

The order of the variables is:

x.1, x.2, x.3, x.8, x.6, x.4, x.5, x.9, x.7,x.10

The order of the variables is:

x.10, x.7, x.5, x.6, x.8, x.4, x.9, x.3, x.1,x.2

The order of the variables is:

x.2, x.1, x.5, x.6, x.8, x.4, x.9, x.3, x.7,x.10

```
library(ElemStatLearn)
data(vowel.train)
data(vowel.test)
summary(vowel.train)
```

```
##           y           x.1           x.2           x.3
## Min.      : 1   Min.    :-5.211   Min.    :-1.2740   Min.    :-2.48700
## 1st Qu.: 3   1st Qu.: -3.923   1st Qu.: 0.9167   1st Qu.: -0.94550
## Median : 6   Median : -3.097   Median : 1.7330   Median : -0.50250
## Mean      : 6   Mean      : -3.167   Mean      : 1.7353   Mean      : -0.44800
## 3rd Qu.: 9   3rd Qu.: -2.512   3rd Qu.: 2.4038   3rd Qu.: 0.04925
## Max.      :11   Max.      : -0.941   Max.      : 5.0740   Max.      : 1.41300
##           x.4           x.5           x.6           x.7
## Min.      : -1.4090   Min.      : -2.1270   Min.      : -0.8360   Min.      : -1.53700
## 1st Qu.: -0.0835   1st Qu.: -0.9307   1st Qu.: 0.1085   1st Qu.: -0.29700
## Median : 0.4565   Median : -0.4170   Median : 0.5275   Median : 0.04000
## Mean      : 0.5250   Mean      : -0.3893   Mean      : 0.5850   Mean      : 0.01748
## 3rd Qu.: 1.1640   3rd Qu.: 0.1155   3rd Qu.: 1.0097   3rd Qu.: 0.34800
## Max.      : 2.1910   Max.      : 1.8310   Max.      : 2.3270   Max.      : 1.40300
##           x.8           x.9           x.10
## Min.      : -1.29300   Min.      : -1.6130   Min.      : -1.68000
## 1st Qu.: -0.01825   1st Qu.: -0.6737   1st Qu.: -0.50700
## Median : 0.47700   Median : -0.2550   Median : -0.08250
## Mean      : 0.41739   Mean      : -0.2681   Mean      : -0.08457
## 3rd Qu.: 0.86125   3rd Qu.: 0.1375   3rd Qu.: 0.30100
## Max.      : 1.67300   Max.      : 1.3090   Max.      : 1.39600
```

```
vowel.train$y <- as.factor(vowel.train$y)
vowel.test$y <- as.factor(vowel.test$y)
set.seed(33833)
library(caret)
modFit <- train(y ~., data=vowel.train,method="rf")
modFit
```

```
## Random Forest
##
## 528 samples
## 10 predictor
## 11 classes: '1', '2', '3', '4', '5', '6', '7', '8', '9', '10', '11'
##
## No pre-processing
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 528, 528, 528, 528, 528, 528, ...
## Resampling results across tuning parameters:
##
##  mtry  Accuracy   Kappa      Accuracy SD  Kappa SD
##    2    0.9348086  0.9281044  0.01989488   0.02191478
##    6    0.9084462  0.8990394  0.02196780   0.02423451
##   10    0.8769423  0.8643308  0.02686962   0.02962649
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

```
varImp(modFit)
```

```
## rf variable importance
##
##      Overall
## x.1 100.000
## x.2  93.548
## x.5  41.699
## x.6  27.438
## x.8  18.965
## x.4   9.033
## x.3   6.735
## x.9   4.706
## x.7   1.903
## x.10  0.000
```