Random forests

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Random forests

similar to bagging

1. Bootstrap samples
2. At each split, bootstrap variables

   at each potential split, only a subset of variables is considered.

3. Grow multiple trees and vote

   or average

Pros:

1. Accuracy

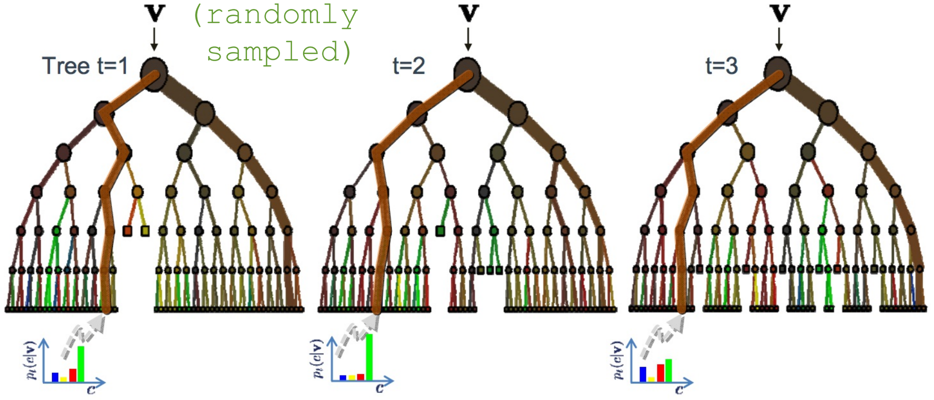
Cons:

1. Speed slow
2. Interpretability
3. Overfitting

   so it's very important to use cross validation when using random forests

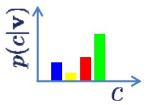
Random forests

each tree is based on a separate subset of the data (randomly sampled)



The ensemble model

Forest output probability $p(c|\mathbf{v}) = \frac{1}{T}\sum_{t}^{T} p_t(c|\mathbf{v})$



http://www.robots.ox.ac.uk/~az/lectures/ml/lect5.pdf

this link doesn't work

Iris data

```r
data(iris); library(ggplot2)
inTrain <- createDataPartition(y=iris$Species,
                              p=0.7, list=FALSE)
training <- iris[inTrain,]
testing <- iris[-inTrain,]
```

Random forests

```
library(caret)
modFit <- train(Species~ .,data=training,method="rf",prox=TRUE)
modFit                                              random forest
```

```
105 samples
  4 predictors
  3 classes: 'setosa', 'versicolor', 'virginica'

No pre-processing
Resampling: Bootstrap (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     0.9       0.9    0.03         0.04
  3     0.9       0.9    0.03         0.05
  4     0.9       0.9    0.03         0.05
```

Getting a single tree

```
getTree(modFit$finalModel,k=2)
```

get the second tree

which variable was used to split

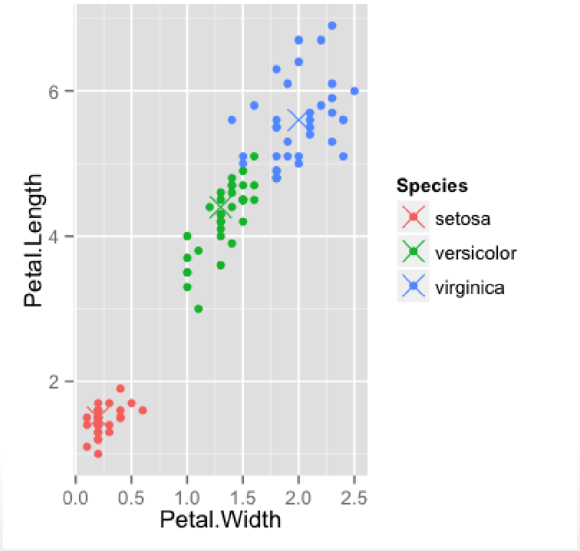
and where

```
   left daughter right daughter split var split point status prediction
1              2              3         4        0.70      1          0
2              0              0         0        0.00     -1          1
3              4              5         4        1.70      1          0
4              6              7         3        4.95      1          0
5              8              9         3        4.85      1          0
6              0              0         0        0.00     -1          2
7             10             11         4        1.55      1          0
8             12             13         1        5.95      1          0
9              0              0         0        0.00     -1          3
10             0              0         0        0.00     -1          3
11             0              0         0        0.00     -1          2
12             0              0         0        0.00     -1          2
13             0              0         0        0.00     -1          3
```

each row is 1 split

Class "centers"

```
irisP <- classCenter(training[,c(3,4)], training$Species, modFit$finalModel$prox)
irisP <- as.data.frame(irisP); irisP$Species <- rownames(irisP)
p <- qplot(Petal.Width, Petal.Length, col=Species,data=training)
p + geom_point(aes(x=Petal.Width,y=Petal.Length,col=Species),size=5,shape=4,data=irisP)
```



Predicting new values

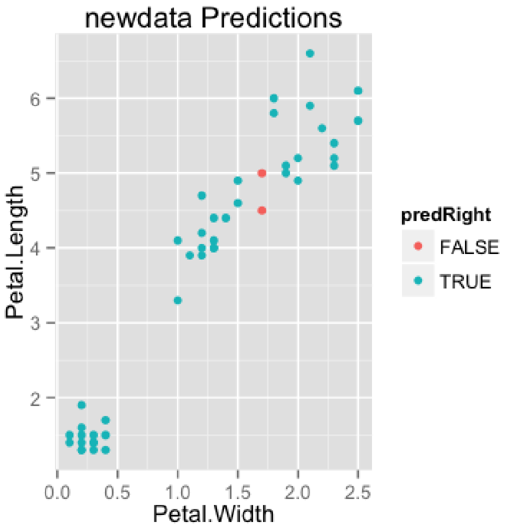
```
pred <- predict(modFit,testing); testing$predRight <- pred==testing$Species
table(pred,testing$Species)
```

```

pred         setosa versicolor virginica
  setosa         15          0         0
  versicolor      0         14         1
  virginica       0          1        14
```

Predicting new values

```
qplot(Petal.Width,Petal.Length,colour=predRight,data=testing,main="newdata Predictions")
```



Notes and further resources

Notes:

- Random forests are usually one of the two top performing algorithms along with boosting in prediction contests.
- Random forests are difficult to interpret but often very accurate.
- Care should be taken to avoid overfitting (see rfcv funtion)

Further resources:

- Random forests
- Random forest Wikipedia
- Elements of Statistical Learning