



# Predicting with trees

Jeffrey Leek

Johns Hopkins Bloomberg School of Public Health

# Key ideas

- Iteratively split variables into groups
- Evaluate "homogeneity" within each group
- Split again if necessary

## Pros:

- Easy to interpret
- Better performance in nonlinear settings

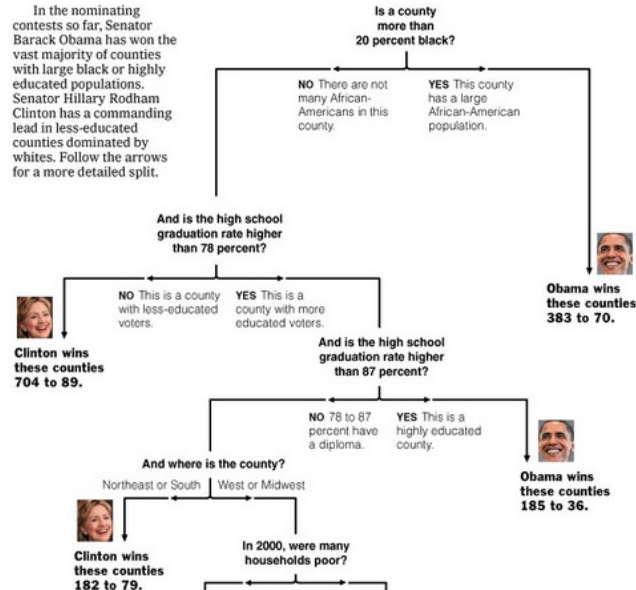
## Cons:

- Without pruning/cross-validation can lead to overfitting
- Harder to estimate uncertainty
- Results may be variable

# Example Tree

## Decision Tree: The Obama-Clinton Divide

In the nominating contests so far, Senator Barack Obama has won the vast majority of counties with large black or highly educated populations. Senator Hillary Rodham Clinton has a commanding lead in less-educated counties dominated by whites. Follow the arrows for a more detailed split.



<http://graphics8.nytimes.com/images/2008/04/16/us/0416-nat-subOBAMA.jpg>

# Basic algorithm

1. Start with all 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 ("node")
4. Within each split, find the best variable/split that separates the outcomes
5. Continue until the groups are too small or sufficiently "pure"

# Measures of impurity

$$\hat{p}_{mk} = \frac{1}{N_m} \sum_{x_i \text{ in Leaf } m} \mathbb{I}(y_i = k)$$

**Misclassification Error:**

$$1 - \hat{p}_{mk(m)}; k(m) = \text{most; common; } k$$

- 0 = perfect purity
- 0.5 = no purity

**Gini index:**

$$\sum_{k \neq k'} \hat{p}_{mk} \times \hat{p}_{mk'} = \sum_{k=1}^K \hat{p}_{mk}(1 - \hat{p}_{mk}) = 1 - \sum_{k=1}^K \hat{p}_{mk}^2$$

- 0 = perfect purity
- 0.5 = no purity

# Measures of impurity

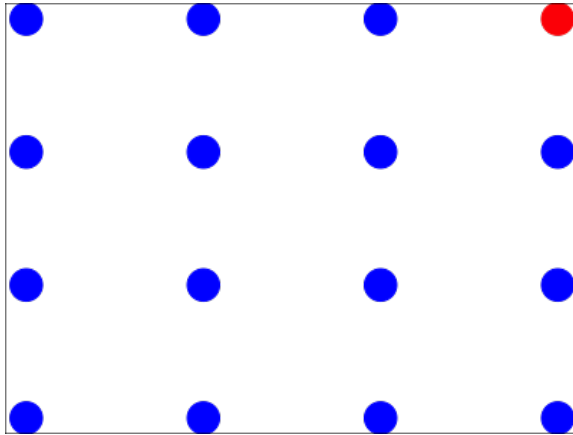
Deviance/information gain:

$$-\sum_{k=1}^K \hat{p}_{mk} \log_2 \hat{p}_{mk}$$

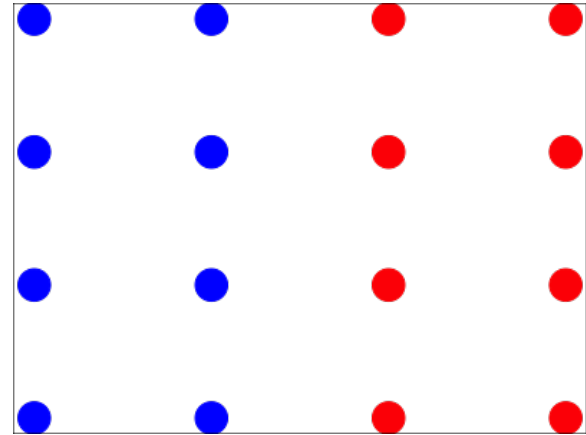
- 0 = perfect purity
- 1 = no purity

[http://en.wikipedia.org/wiki/Decision\\_tree\\_learning](http://en.wikipedia.org/wiki/Decision_tree_learning)

# Measures of impurity



- **Misclassification:**  $1/16 = 0.06$
- **Gini:**  $1 - [(1/16)^2 + (15/16)^2] = 0.12$
- **Information:**  
 $-[1/16 \times \log_2(1/16) + 15/16 \times \log_2(15/16)] = 0.34$



- **Misclassification:**  $8/16 = 0.5$
- **Gini:**  $1 - [(8/16)^2 + (8/16)^2] = 0.5$
- **Information:**  
 $-[1/16 \times \log_2(1/16) + 15/16 \times \log_2(15/16)] = 1$

# Example: Iris Data

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

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

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

setosa	versicolor	virginica
50	50	50



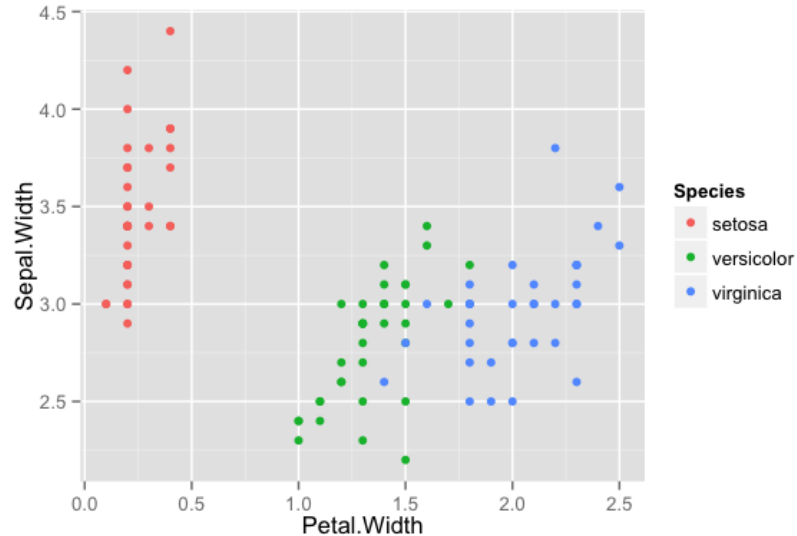
# Create training and test sets

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

```
[1] 45 5
```

# Iris petal widths/sepal width

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



# Iris petal widths/sepal width

```
library(caret)
modFit <- train(Species ~ .,method="rpart",data=training)
print(modFit$finalModel)
```

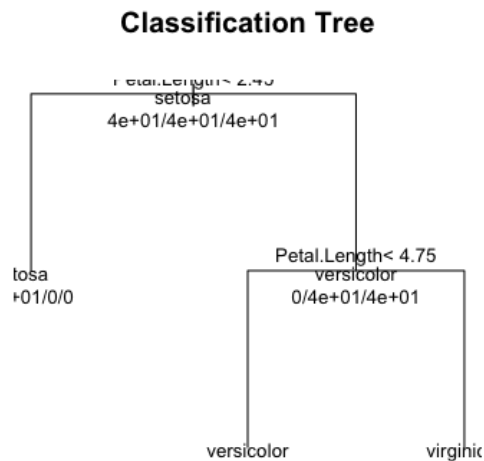
```
n= 105
```

```
node), split, n, loss, yval, (yprob)
    * denotes terminal node
```

```
1) root 105 70 setosa (0.3333 0.3333 0.3333)
  2) Petal.Length< 2.45 35 0 setosa (1.0000 0.0000 0.0000) *
  3) Petal.Length>=2.45 70 35 versicolor (0.0000 0.5000 0.5000)
    6) Petal.Length< 4.75 31 0 versicolor (0.0000 1.0000 0.0000) *
    7) Petal.Length>=4.75 39 4 virginica (0.0000 0.1026 0.8974) *
```

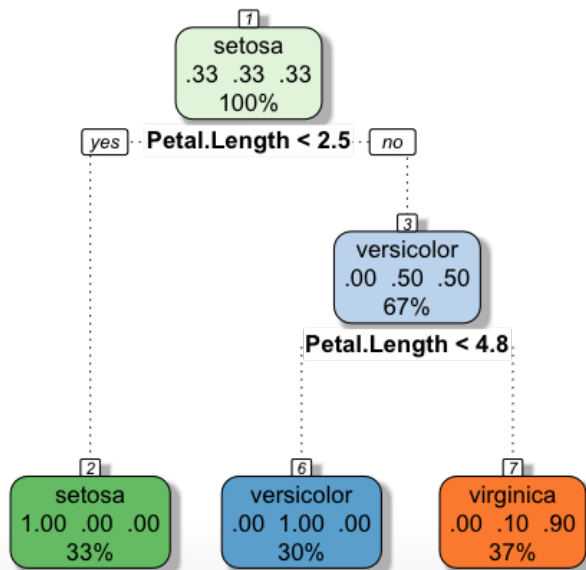
# Plot tree

```
plot(modFit$finalModel, uniform=TRUE,  
     main="Classification Tree")  
text(modFit$finalModel, use.n=TRUE, all=TRUE, cex=.8)
```



# Prettier plots

```
library(rattle)
fancyRpartPlot(modFit$finalModel)
```



Rattle 2014-May-04 07:08:33 jtleeek

# Predicting new values

```
predict(modFit,newdata=testing)
```

```
[1] setosa      setosa      setosa      setosa      setosa      setosa      setosa      setosa
[9] setosa      setosa      setosa      setosa      setosa      setosa      setosa      versicolor
[17] versicolor  versicolor  versicolor  versicolor  versicolor  versicolor  versicolor  versicolor
[25] virginica   versicolor  virginica   versicolor  versicolor  versicolor  virginica   virginica
[33] virginica   versicolor  virginica   virginica   virginica   virginica   virginica   virginica
[41] virginica   virginica   virginica   virginica   virginica
Levels: setosa versicolor virginica
```

# Notes and further resources

- Classification trees are non-linear models
  - They use interactions between variables
  - Data transformations may be less important (monotone transformations)
  - Trees can also be used for regression problems (continuous outcome)
- Note that there are multiple tree building options in R both in the caret package - [party](#), [rpart](#) and out of the caret package - [tree](#)
- [Introduction to statistical learning](#)
- [Elements of Statistical Learning](#)
- [Classification and regression trees](#)