#158

DZone Refcardz

CONTENTS INCLUDE

Big Data Machine Learning:

Patterns for Predictive Analytics

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INTRODUCTION

Predictive Analytics is about predicting future outcome based on analyzing data collected previously. It includes two phases:

1. Training phase: Learn a model from training data
2. Predicting phase: Use the model to predict the unknown or future outcome

PREDICTIVE MODELS

We can choose many models, each based on a set of different assumptions regarding the underlying distribution of data. Therefore, we are interested in two general types of problems in this discussion: 1. Classification—about predicting a category (a value that is discrete, finite with no ordering implied), and 2. Regression—about predicting a numeric quantity (a value that's continuous and infinite with ordering).

For classification problems, we use the "iris" data set and predict its "species" from its "width" and "length" measures of sepals and petals. Here is how we set up our training and testing data:

```
> summary(iris)
  Sepal.Length    Sepal.Width     Petal.Length   Petal.Width
 Min.   :4.300000   Min.   :2.000000   Min.   :1.000   Min.   :0.100000
 1st Qu.:5.100000   1st Qu.:2.800000   1st Qu.:1.600   1st Qu.:0.300000
 Median :5.800000   Median :3.000000   Median :4.350   Median :1.300000
 Mean   :5.843333   Mean   :3.057333   Mean   :3.758   Mean   :1.199333
 3rd Qu.:6.400000   3rd Qu.:3.300000   3rd Qu.:5.100   3rd Qu.:1.800000
 Max.   :7.900000   Max.   :4.400000   Max.   :6.900   Max.   :2.500000
      Species
 setosa    :50
 versicolor:50
 virginica :50

> 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
>
> # Prepare training and testing data
> testidx <- which(1:length(iris[,1])%%5 == 0)

> iristrain <- iris[-testidx,]
> iristest <- iris[testidx,]
```

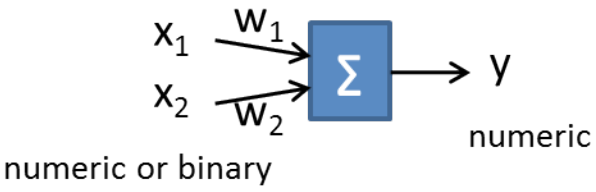
To illustrate a regression problem (where the output we predict is a numeric quantity), we'll use the "Prestige" data set imported from the "car" package to create our training and testing data.

```
> library(car)
> summary(Prestige)
   education          income            women
 Min.   : 6.38000   Min.   :  611.000   Min.   : 0.00000
 1st Qu.: 8.44500   1st Qu.: 4106.000   1st Qu.: 3.59250
 Median :10.54000   Median : 5930.500   Median :13.60000
 Mean   :10.73804   Mean   : 6797.902   Mean   :28.97902
 3rd Qu.:12.64750   3rd Qu.: 8187.250   3rd Qu.:52.20250
 Max.   :15.97000   Max.   :25879.000   Max.   :97.51000
    prestige           census          type
 Min.   :14.80000   Min.   :1113.000   bc  :44
 1st Qu.:35.22500   1st Qu.:3120.500   prof:31
 Median :43.60000   Median :5135.000   wc  :23
 Mean   :46.83333   Mean   :5401.775   NA's: 4
 3rd Qu.:59.27500   3rd Qu.:8312.500
 Max.   :87.20000   Max.   :9517.000
> head(Prestige)
                    education income women prestige census type
gov.administrators      13.11  12351 11.16     68.8   1113 prof
general.managers        12.26  25879  4.02     69.1   1130 prof
accountants             12.77   9271 15.70     63.4   1171 prof
purchasing.officers    11.42   8865  9.11     56.8   1175 prof
chemists                14.62   8403 11.68     73.5   2111 prof
physicists              15.64  11030  5.13     77.6   2113 prof
> testidx <- which(1:nrow(Prestige)%%4==0)
> prestige_train <- Prestige[-testidx,]
> prestige_test <- Prestige[testidx,]
```

LINEAR REGRESSION

Linear regression has the longest, most well-understood history in statistics, and is the most popular machine learning model. It is based on the assumption that a linear relationship exists between the input and output variables, as follows:

$$y = \Theta_0 + \Theta_1 x_1 + \Theta_2 x_2 + \ldots$$



…where y is the output numeric value, and xi is the input numeric value.

The learning algorithm will learn the set of parameters such that the sum of square error (yactual - yestimate)2 is minimized. Here is the sample code that uses the R language to predict the output "prestige" from a set of input variables:

```
> model <- lm(prestige~., data=prestige_train)
> # Use the model to predict the output of test data
> prediction <- predict(model, newdata=prestige_test)
> # Check for the correlation with actual result
> cor(prediction, prestige_test$prestige)
[1] 0.9376719009
> summary(model)
Call:
lm(formula = prestige ~ ., data = prestige_train)
Residuals:
        Min          1Q      Median          3Q         Max
-13.9078951  -5.0335742   0.3158978   5.3830764  17.8851752
Coefficients:
                  Estimate     Std. Error  t value     Pr(>|t|)
(Intercept) -20.7073113585  11.4213272697 -1.81304    0.0743733 .
education     4.2010288017   0.8290800388  5.06710 0.0000034862 ***
income        0.0011503739   0.0003510866  3.27661    0.0016769 **
women         0.0363017610   0.0400627159  0.90612    0.3681668
census        0.0018644881   0.0009913473  1.88076    0.0644172 .
typeprof     11.3129416488   7.3932217287  1.53018    0.1307520
typewc        1.9873305448   4.9579992452  0.40083    0.6898376
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 7.41604 on 66 degrees of freedom
  (4 observations deleted due to missingness)
Multiple R-squared: 0.820444,   Adjusted R-squared: 0.8041207
F-statistic: 50.26222 on 6 and 66 DF,  p-value: < 0.000000000000000022204
```

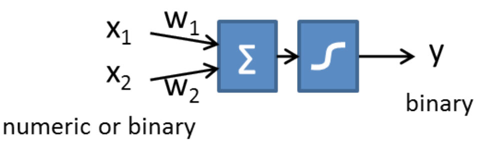
The coefficient column gives an estimation of Θ_i, and an associated p-value gives the confidence of each estimated Θ_i. For example, features not marked with at least one * can be safely ignored.

In the above model, education and income has a high influence to the prestige.

The goal of minimizing the square error makes linear regression very sensitive to outliers that greatly deviate in the output. It is a common practice to identify those outliers, remove them, and then rerun the training.

LOGISTIC REGRESSION

In a classification problem, the output is binary rather than numeric. We can imagine doing a linear regression and then compressing the numeric output into a 0..1 range using the logit function 1/(1+e-t), shown here:



$y = 1/(1 + e^{-(\Theta_0 + \Theta_1 x_1 + \Theta_2 x_2 + \ldots)})$

…where y is the 0 .. 1 value, and xi is the input numeric value.

The learning algorithm will learn the set of parameters such that the cost $(y_{actual} * \log y_{estimate} + (1 - y_{actual}) * \log(1 - y_{estimate}))$ is minimized.

Here is the sample code that uses the R language to perform a binary classification using iris data.

```
> newcol = data.frame(isSetosa=(iristrain$Species == 'setosa'))
> traindata <- cbind(iristrain, newcol)
> head(traindata)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species isSetosa
1          5.1         3.5          1.4         0.2  setosa     TRUE
2          4.9         3.0          1.4         0.2  setosa     TRUE
3          4.7         3.2          1.3         0.2  setosa     TRUE
4          4.6         3.1          1.5         0.2  setosa     TRUE
6          5.4         3.9          1.7         0.4  setosa     TRUE
7          4.6         3.4          1.4         0.3  setosa     TRUE
> formula <- isSetosa ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width
> logisticModel <- glm(formula, data=traindata, family="binomial")
Warning messages:
1: glm.fit: algorithm did not converge
2: glm.fit: fitted probabilities numerically 0 or 1 occurred
> # Predict the probability for test data
> prob <- predict(logisticModel, newdata=iristest, type='response')
> round(prob, 3)
  5  10  15  20  25  30  35  40  45  50  55  60  65  70  75  80  85  90  95 100
  1   1   1   1   1   1   1   1   1   1   0   0   0   0   0   0   0   0   0   0
105 110 115 120 125 130 135 140 145 150
  0   0   0   0   0   0   0   0   0   0
```

REGRESSION WITH REGULARIZATION

To avoid an over-fitting problem (the trained model fits too well with the training data and is not generalized enough), the regularization technique is used to shrink the magnitude of Θ_i. This is done by adding a penalty (a function of the sum of Θ_i) into the cost function.

In L2 regularization (also known as Ridge regression), Θ_i^2 will be added to the cost function. In L1 regularization (also known as Lasso regression), $\Theta||\Theta_i||$ will be added to the cost function. Both L1, L2 will shrink the magnitude of **Θi**. For variables that are inter-dependent, L2 tends to spread the shrinkage such that all interdependent variables are equally influential. On the other hand, L1 tends to keep one variable and shrink all the other dependent variables to values very close to zero. In other words, L1 shrinks the variables in an uneven manner so that it can also be used to select input variables.

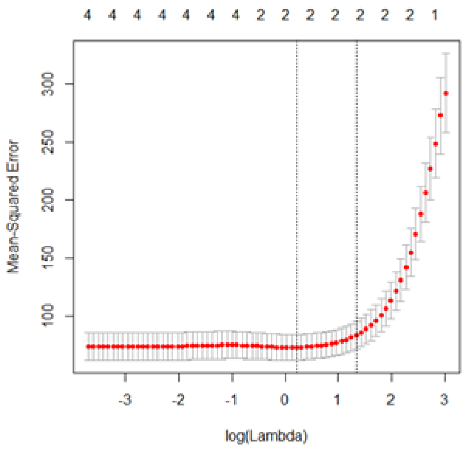
Combining L1 and L2, the general form of the cost function becomes the following:

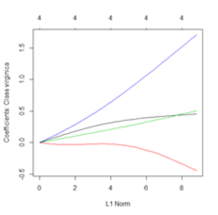
Cost == Non-regularization-cost $+ \lambda (\alpha.\Sigma ||\Theta_i|| + (1- \alpha).\Sigma \Theta_i^2)$

Notice the 2 tunable parameters, lambda, and alpha. Lambda controls the degree of regularization (0 means no regularization and infinity means ignoring all input variables because all coefficients of them will be zero). Alpha controls the degree of mix between L1 and L2 (0 means pure L2 and 1 means pure L1). Glmnet is a popular regularization package. The alpha parameter needs to be supplied based on the application's need, i.e., its need for selecting a reduced set of variables. Alpha=1 is preferred. The library provides a cross-validation test to automatically choose the better lambda value.
Let's repeat the above linear regression example and use regularization this time. We pick alpha = 0.7 to favor L1 regularization.

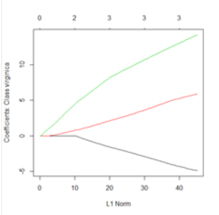
```
> library(glmnet)
> cv.fit <- cv.glmnet(as.matrix(prestige_train[,c(-4, -6)]), as.vector(prestige_
train[,4]), nlambda=100, alpha=0.7, family="gaussian")
> plot(cv.fit)
> coef(cv.fit)
5 x 1 sparse Matrix of class "dgCMatrix"
                         1
(Intercept) 6.3876684930151
education   3.2111461944976
income      0.0009473793366
women       0.0000000000000
census      0.0000000000000
> prediction <- predict(cv.fit, newx=as.matrix(prestige_test[,c(-4, -6)]))
> cor(prediction, as.vector(prestige_test[,4]))
          [,1]
1 0.9291181193
```

This is the cross-validation plot. It shows the best lambda with minimal-root,mean-square error.

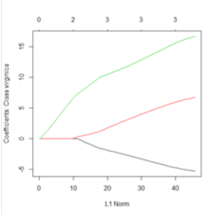




α = 0



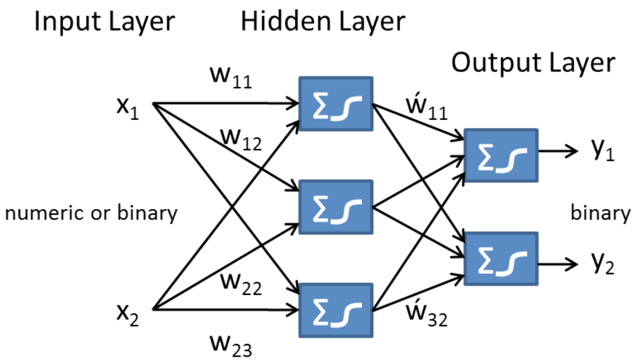
α = 0.8



α = 1

NEURAL NETWORK

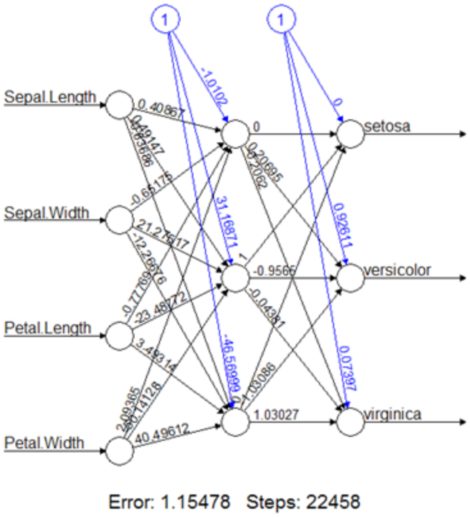
A Neural Network emulates the structure of a human brain as a network of neurons that are interconnected to each other. Each neuron is technically equivalent to a logistic regression unit.



In this setting, neurons are organized in multiple layers where every neuron at layer i connects to every neuron at layer i+1 and nothing else. The tuning parameters in a neural network include the number of hidden layers (commonly set to 1), the number of neurons in each layer (which should be same for all hidden layers and usually at 1 to 3 times the input variables), and the learning rate. On the other hand, the number of neurons at the output layer depends on how many binary outputs need to be learned. In a classification problem, this is typically the number of possible values at the output category.

The learning happens via an iterative feedback mechanism where the error of training data output is used to adjust the corresponding weights of input. This adjustment propagates to previous layers and the learning algorithm is known as "back-propagation." Here is an example:

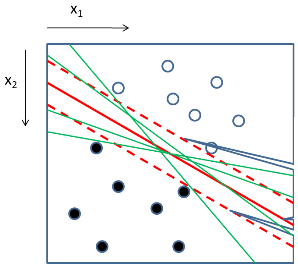
```
> library(neuralnet)
> nnet_iristrain <-iristrain
> #Binarize the categorical output
> nnet_iristrain <- cbind(nnet_iristrain, iristrain$Species == ‘setosa’)
> nnet_iristrain <- cbind(nnet_iristrain, iristrain$Species == ‘versicolor’)
> nnet_iristrain <- cbind(nnet_iristrain, iristrain$Species == ‘virginica’)
> names(nnet_iristrain)[6] <- ‘setosa’
> names(nnet_iristrain)[7] <- ‘versicolor’
> names(nnet_iristrain)[8] <- ‘virginica’
> nn <- neuralnet(setosa+versicolor+virginica ~ Sepal.Length + Sepal.Width +
Petal.Length + Petal.Width, data=nnet_iristrain, hidden=c(3))
> plot(nn)
> mypredict <- compute(nn, iristest[-5])$net.result
> # Consolidate multiple binary output back to categorical output
> maxidx <- function(arr) {
+     return(which(arr == max(arr)))
+ }
> idx <- apply(mypredict, c(1), maxidx)
> prediction <- c(‘setosa’, ‘versicolor’, ‘virginica’)[idx]
> table(prediction, iristest$Species)

prediction   setosa versicolor virginica
  setosa         10          0         0
  versicolor      0         10         3
  virginica       0          0         7
```



Neural networks are very good at learning non-linear functions. They can even learn multiple outputs simultaneously, though the training time is relatively long, which makes the network susceptible to local minimum traps. This can be mitigated by doing multiple rounds and picking the best-learned model.

SUPPORT VECTOR MACHINE

A Support Vector Machine provides a binary classification mechanism based on finding a hyperplane between a set of samples with +ve and -ve outputs. It assumes the data is linearly separable.



All green lines can separate the points
Which one is the best ?
The red line has biggest margin

The problem can be structured as a quadratic programming optimization problem that maximizes the margin subjected to a set of linear constraints (i.e., data output on one side of the line must be +ve while the other side must be -ve). This can be solved with the quadratic programming technique.

If the data is not linearly separable due to noise (the majority is still linearly separable), then an error term will be added to penalize the optimization.
If the data distribution is fundamentally non-linear, the trick is to transform the data to a higher dimension so the data will be linearly separable.The optimization term turns out to be a dot product of the transformed points in the high-dimension space, which is found to be equivalent to performing a kernel function in the original (before transformation) space.

The kernel function provides a cheap way to equivalently transform the original point to a high dimension (since we don't actually transform it) and perform the quadratic optimization in that high-dimension space.

There are a couple of tuning parameters (e.g., penalty and cost), so transformation is usually conducted in 2 steps—finding the optimal parameter and then training the SVM model using that parameter. Here are some example codes in R:

```
> library(e1071)
> tune <- tune.svm(Species~., data=iristrain, gamma=10^(-6:-1), cost=10^(1:4))
> summary(tune)
Parameter tuning of 'svm':
- sampling method: 10-fold cross validation
- best parameters:
 gamma  cost
 0.001 10000
- best performance: 0.03333333
> model <- svm(Species~., data=iristrain, method="C-classification",
kernel="radial", probability=T, gamma=0.001, cost=10000)
> prediction <- predict(model, iristest, probability=T)
> table(iristest$Species, prediction)
            prediction
             setosa versicolor virginica
  setosa         10          0         0
  versicolor      0         10         0
  virginica       0          3         7
>
```

SVM with a Kernel function is a highly effective model and works well across a wide range of problem sets. Although it is a binary classifier, it can be easily extended to a multi-class classification by training a group of binary classifiers and using "one vs all" or "one vs one" as predictors.

SVM predicts the output based on the distance to the dividing hyperplane. This doesn't directly estimate the probability of the prediction. We therefore use the calibration technique to find a logistic regression model between the distance of the hyperplane and the binary output. Using that regression model, we then get our estimation.

BAYESIAN NETWORK AND NAÏVE BAYES

From a probabilistic viewpoint, the predictive problem can be viewed as a conditional probability estimation; trying to find Y where P(Y | X) is maximized.

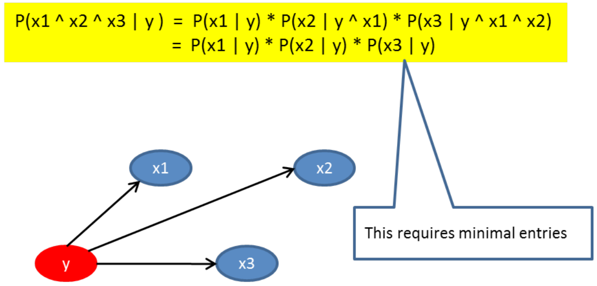
From the Bayesian rule, P(Y | X) == P(X | Y) * P(Y) / P(X)

This is equivalent to finding Y where P(X | Y) * P(Y) is maximized. Let's say the input X contains 3 categorical features— X1, X2, X3. In the general case, we assume each variable can potentially influence any other variable. Therefore the joint distribution becomes:

P(X | Y) = P(X1 | Y) * P(X2 | X1, Y) * P(X3 | X1, X2, Y)

Notice how in the last term of the above equation, the number of entries is exponentially proportional to the number of input variables.

Naïve Bayes network (complete independence assumption)


P(x1 ^ x2 ^ x3 | y) = P(x1 | y) * P(x2 | y ^ x1) * P(x3 | y ^ x1 ^ x2)
= P(x1 | y) * P(x2 | y) * P(x3 | y)
x1
x2
y
x3
This requires minimal entries

Since P(X | Y) == P(X1 | Y) * P(X2 | Y) * P(X3 | Y), we need to find the Y that maximizes P(X1 | Y) * P(X2 | Y) * P(X3 | Y) * P(Y)

Each term on the right hand side can be learned by counting the training data. Therefore we can estimate P(Y | X) and pick Y to maximize its value.

But it is possible that some patterns never show up in training data, e.g., P(X1=a | Y=y) is 0. To deal with this situation, we pretend to have seen the data of each possible value one more time than we actually have.

P(X1=a | Y=y) == (count(a, y) + 1) / (count(y) + m)

…where m is the number of possible values in X1.

When the input features are numeric, say a = 2.75, we can assume X1 is the normal distribution. Find out the mean and standard deviation of X1 and then estimate P(X1=a) using the normal distribution function.

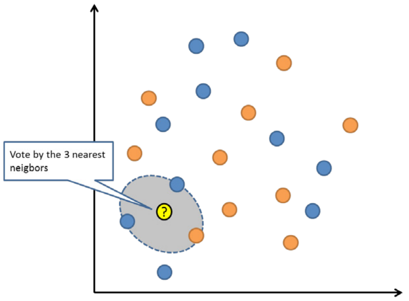
Here is how we use Naïve Bayes in R:

```
> library(e1071)
> # Can handle both categorical and numeric input variables, but output must be
categorical
> model <- naiveBayes(Species~., data=iristrain)
> prediction <- predict(model, iristest[,-5])
> table(prediction, iristest[,5])

prediction   setosa versicolor virginica
  setosa         10          0         0
  versicolor      0         10         2
  virginica       0          0         8
```

Notice the independence assumption is not true in most cases.Nevertheless, the system still performs incredibly well. Onestrength of Naïve Bayes is that it is highly scalable and can learn incrementally—all we have to do is count the observed variables and update the probability distribution.

K-NEAREST NEIGHBORS

A contrast to model-based learning is K-Nearest neighbor. This is also called instance-based learning because it doesn't even learn a single model. The training process involves memorizing all the training data. To predict a new data point, we found the closest K (a tunable parameter) neighbors from the training set and let them vote for the final prediction.



To determine the "nearest neighbors," a distance function needs to be defined (e.g., a Euclidean distance function is a common one for numeric input variables). The voting can also be weighted among the K-neighbors based on their distance from the new data point.

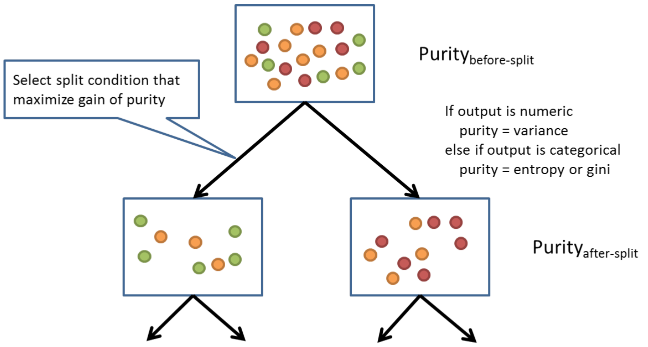
Here is the R code using K-nearest neighbor for classification.

```
> library(class)
> train_input <- as.matrix(iristrain[,-5])
> train_output <- as.vector(iristrain[,5])
> test_input <- as.matrix(iristest[,-5])
> prediction <- knn(train_input, test_input, train_output, k=5)
> table(prediction, iristest$Species)

prediction   setosa versicolor virginica
  setosa         10          0         0
  versicolor      0         10         1
  virginica       0          0         9
>
```

The strength of K-nearest neighbor is its simplicity. No model needs to be trained. Incremental learning is automatic when more data arrives (and old data can be deleted as well). The weakness of KNN, however, is that it doesn't handle high numbers of dimensions well.

DECISION TREE

Based on a tree of decision nodes, the learning approach is to recursively divide the training data into buckets of homogeneous members through the most discriminative dividing criteria possible. The measurement of "homogeneity" is based on the output label; when it is a numeric value, the measurement will be the variance of the bucket; when it is a category, the measurement will be the entropy, or "gini index," of the bucket.


Select split condition that maximize gain of purity
$\text{Purity}_{\text{before-split}}$
If output is numeric
purity = variance
else if output is categorical
purity = entropy or gini
$\text{Purity}_{\text{after-split}}$

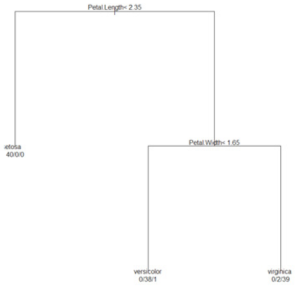
During the training, various dividing criteria based on the input will be tried (and used in a greedy manner); when the input is a category (Mon, Tue, Wed, etc.), it will first be turned into binary (isMon, isTue, isWed, etc.,) and then it will use true/false as a decision boundary to evaluate homogeneity; when the input is a numeric or ordinal value, the lessThan/greaterThan at each training-data input value will serve as the decision boundary.

The training process stops when there is no significant gain in homogeneity after further splitting the Tree. The members of the bucket represented at leaf node will vote for the prediction; the majority wins when the output is a category. The member's average is taken when the output is a numeric.

Here is an example in R:

```
> library(rpart)
> #Train the decision tree
> treemodel <- rpart(Species~., data=iristrain)
> plot(treemodel)
> text(treemodel, use.n=T)
> #Predict using the decision tree
> prediction <- predict(treemodel, newdata=iristest, type='class')
> #Use contingency table to see how accurate it is
> table(prediction, iristest$Species)
prediction   setosa versicolor virginica
  setosa         10          0         0
  versicolor      0         10         3
  virginica       0          0         7
> names(nnet_iristrain)[8] <- 'virginica'
```

Here is the Tree model that has been learned:



The good part of the Tree is that it can take different data types of input and output variables that can be categorical, binary and numeric values. It can handle missing attributes and outliers well. Decision Tree is also good in explaining reasoning for its prediction and therefore gives good insight about the underlying data.

The limitation of Decision Tree is that each decision boundary at each split point is a concrete binary decision. Also, the decision criteria considers only one input attribute at a time, not a combination of multiple input variables. Another weakness of Decision Tree is that once learned it cannot be updated incrementally. When new training data arrives, you have to throw away the old tree and retrain all data from scratch. In practice, standalone decision trees are rarely used because their accuracy ispredictive and relatively low . Tree ensembles (described below) are the common way to use decision trees.

TREE ENSEMBLES

Instead of picking a single model, Ensemble Method combines multiple models in a certain way to fit the training data. Here are the two primary ways: "bagging" and "boosting." In "bagging", we take a subset of training data (pick n random sample out of N training data, with replacement) to train up each model. After multiple models are trained, we use a voting scheme to predict future data.

Random Forest is one of the most popular bagging models; in addition to selecting n training data out of N at each decision node of the tree, it randomly selects m input features from the total M input features (m ~ M^0.5). Then it learns a decision tree from that. Finally, each tree in the forest votes for the result.

Here is the R code to use Random Forest:

```
> library(randomForest)
#Train 100 trees, random selected attributes
> model <- randomForest(Species~., data=iristrain, nTree=500)
#Predict using the forest
> prediction <- predict(model, newdata=iristest, type='class')
> table(prediction, iristest$Species)
> importance(model)
             MeanDecreaseGini
Sepal.Length         7.807602
Sepal.Width          1.677239
Petal.Length        31.145822
Petal.Width         38.617223
```

"Boosting" is another approach in Ensemble Method. Instead of sampling the input features, it samples the training data records. It puts more emphasis, though, on the training data that is wrongly predicted in previous iterations. Initially, each training data is equally weighted. At each iteration, the data that is wrongly classified will have its weight increased.

Gradient Boosting Method is one of the most popular boosting methods. It is based on incrementally adding a function that fits the residuals.

Set i = 0 at the beginning, and repeat until convergence.

- Learn a function $F_i(X)$ to predict Y. Basically, find F that minimizes the expected(L(F(X) – Y)), where L is the lost function of the residual
- Learning another function $g_i(X)$ to predict the gradient of the above function

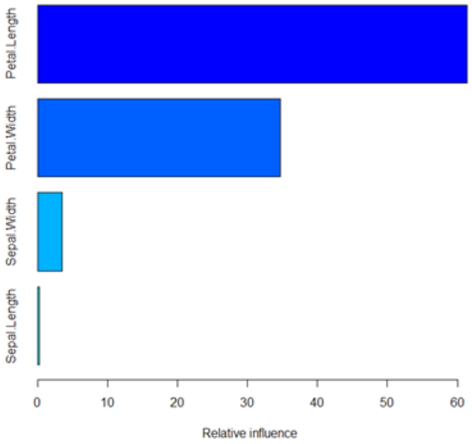
- Update $F_{i+1} = F_i + a.g_i(X)$, where a is the learning rate

Below is Gradient-Boosted Tree using the decision tree as the learning model F. Here is the sample code in R:

```
> library(gbm)
> iris2 <- iris
> newcol = data.frame(isVersicolor=(iris2$Species=='versicolor'))
> iris2 <- cbind(iris2, newcol)
> iris2[45:55,]
   Sepal.Length Sepal.Width Petal.Length Petal.Width    Species isVersicolor
45          5.1         3.8          1.9         0.4     setosa        FALSE
46          4.8         3.0          1.4         0.3     setosa        FALSE
47          5.1         3.8          1.6         0.2     setosa        FALSE
48          4.6         3.2          1.4         0.2     setosa        FALSE
49          5.3         3.7          1.5         0.2     setosa        FALSE
50          5.0         3.3          1.4         0.2     setosa        FALSE
51          7.0         3.2          4.7         1.4 versicolor         TRUE
52          6.4         3.2          4.5         1.5 versicolor         TRUE
53          6.9         3.1          4.9         1.5 versicolor         TRUE
54          5.5         2.3          4.0         1.3 versicolor         TRUE
55          6.5         2.8          4.6         1.5 versicolor         TRUE
> formula <- isVersicolor ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.
Width
> model <- gbm(formula, data=iris2, n.trees=1000, interaction.depth=2,
distribution="bernoulli")
Iter   TrainDeviance   ValidDeviance   StepSize   Improve
     1        1.2714         -1.#IND     0.0010    0.0008
     2        1.2705         -1.#IND     0.0010    0.0004
     3        1.2688         -1.#IND     0.0010    0.0007
     4        1.2671         -1.#IND     0.0010    0.0008
     5        1.2655         -1.#IND     0.0010    0.0008
     6        1.2639         -1.#IND     0.0010    0.0007
     7        1.2621         -1.#IND     0.0010    0.0008
     8        1.2614         -1.#IND     0.0010    0.0003
     9        1.2597         -1.#IND     0.0010    0.0008
    10        1.2580         -1.#IND     0.0010    0.0008
   100        1.1295         -1.#IND     0.0010    0.0008
   200        1.0090         -1.#IND     0.0010    0.0005
   300        0.9089         -1.#IND     0.0010    0.0005
   400        0.8241         -1.#IND     0.0010    0.0004
   500        0.7513         -1.#IND     0.0010    0.0004
   600        0.6853         -1.#IND     0.0010    0.0003
   700        0.6266         -1.#IND     0.0010    0.0003
   800        0.5755         -1.#IND     0.0010    0.0002
   900        0.5302         -1.#IND     0.0010    0.0002
  1000        0.4901         -1.#IND     0.0010    0.0002
```

```
> prediction <- predict.gbm(model, iris2[45:55,], type="response", n.trees=1000)
> round(prediction, 3)
 [1] 0.127 0.131 0.127 0.127 0.127 0.127 0.687 0.688 0.572 0.734 0.722
> summary(model)
           var       rel.inf
1 Petal.Length 61.4203761582
2  Petal.Width 34.7557511871
3  Sepal.Width  3.5407662531
4 Sepal.Length  0.2831064016
```

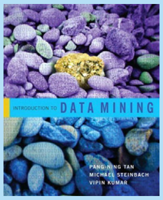
The GBM R package also gave the relative importance of the input features, as shown in the bar graph.



ABOUT THE AUTHOR

Ricky has spent the last 20 years developing and designing large scale software systems including software gateways, fraud detection, cloud computing, web analytics, and online advertising. He has played different roles from architect to developer and consultant in helping companies to apply statistics, machine learning, and optimization techniques to extract useful insight from their raw data, and also predict business trends. Ricky has 9 patents in the areas of distributed systems, cloud computing and real-time analytics. He is very passionate about algorithms and problem solving. He is an active blogger and maintains a technical blog to share his ideas at http://horicky.blogspot.com

RECOMMENDED BOOK



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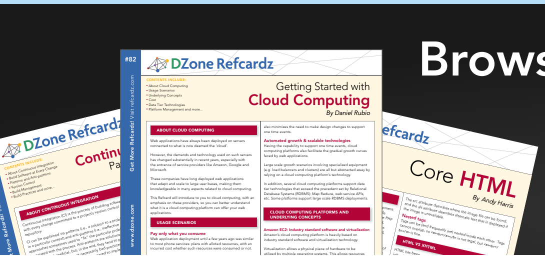

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