Combining predictors

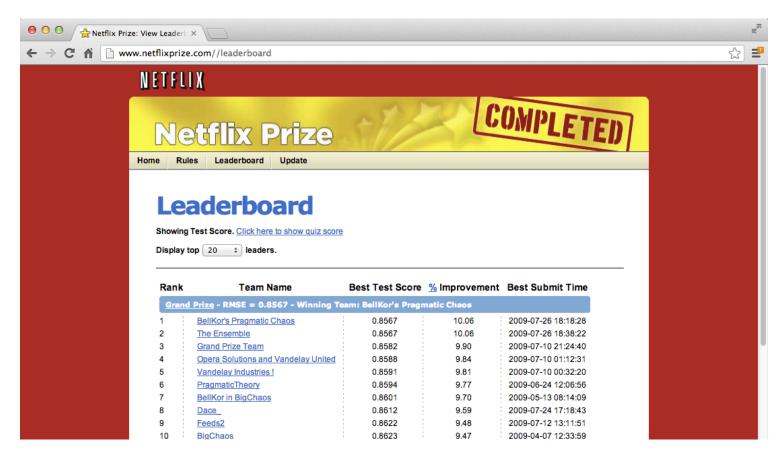
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Key ideas

- You can combine classifiers by averaging/voting
- Combining classifiers improves accuracy
- · Combining classifiers reduces interpretability

Netflix prize

BellKor = Combination of 107 predictors



http://www.netflixprize.com//leaderboard

Heritage health prize - Progress Prize 1

2. Predictive Modelling

Predictive models were built utilising the data sets created in Step 1. Numerous mathematical techniques were used to generate a set of candidate solutions.

3. Ensembling

The individual solutions produced in Step 2 were combined to create a single solution that was more accurate than any of its components.

Market Makers

1 Introduction

My milestone 1 solution to the Heritage Health Prize with a RM SLE score of 0.457239 on the leaderboard consists of a linear blend of 21 result. These are mostly generated by relatively simple models which are all trained using stochastic gradient descent. First in section 2 I provide a description of the way the data is organized and the features that were used. Then in section 3 the training method and the post-processing steps are described. In section 4 each individual model is briefly described, all the relevant meta-parameter settings can be found in appendix Parameter settings. Finally the weights in the final blend are given in section 5.

Mestrom

Basic intuition - majority vote

Suppose we have 5 completely independent classifiers

If accuracy is 70% for each:

- $10 \times (0.7)^3 (0.3)^2 + 5 \times (0.7)^4 (0.3)^2 + (0.7)^5$
- 83.7% majority vote accuracy

With 101 independent classifiers

• 99.9% majority vote accuracy

Approaches for combining classifiers

- 1. Bagging (see previous lecture)
- 2. Boosting
- 3. Combining different classifiers

Example

```
#library(devtools)
#install_github("medley", "mewo2")
library(medley)
set.seed(453234)
y <- rnorm(1000)
x1 <- (y > 0); x2 <- y*rnorm(1000)
x3 <- rnorm(1000, mean=y, sd=1); x4 <- (y > 0) & (y < 3)
x5 <- rbinom(1000, size=4, prob=exp(y)/(1+exp(y)))
x6 <- (y < -2) | (y > 2)
data <- data.frame(y=y,x1=x1,x2=x2,x3=x3,x4=x4,x5=x5,x6=x6)
train <- sample(1:1000,size=500)
trainData <- data[train,]; testData <- data[-train,]</pre>
```

Basic models

```
library(tree)
lm1 <- lm(y ~.,data=trainData)
rmse(predict(lm1,data=testData),testData$y)</pre>
```

```
[1] 1.294
```

```
tree1 <- tree(y ~.,data=trainData)
rmse(predict(tree1,data=testData),testData$y)</pre>
```

```
[1] 1.299
```

```
tree2 <- tree(y~.,data=trainData[sample(1:dim(trainData)[1]),])</pre>
```

Combining models

```
combine1 <- predict(lm1,data=testData)/2 + predict(tree1,data=testData)/2
rmse(combine1,testData$y)</pre>
```

```
[1] 1.281
```

```
[1] 1.175
```

Medley package

```
#library(devtools)
#install_github("medley", "mewo2")
library(medley)
library(e1071)
library(randomForests)
x <- trainData[,-1]
y <- trainData$\frac{1}{2}$
newx <- testData[,-1]</pre>
```

http://www.kaggle.com/users/10748/martin-o-leary

Blending models (part 1)

```
m <- create.medley(x, y, errfunc=rmse);
for (g in 1:10) {
  m <- add.medley(m, svm, list(gamma=1e-3 * g));
}</pre>
```

```
CV model 1 svm (gamma = 0.001) time: 0.362 error: 0.5557

CV model 2 svm (gamma = 0.002) time: 0.373 error: 0.5367

CV model 3 svm (gamma = 0.003) time: 0.38 error: 0.5345

CV model 4 svm (gamma = 0.004) time: 0.376 error: 0.5333

CV model 5 svm (gamma = 0.005) time: 0.364 error: 0.5301

CV model 6 svm (gamma = 0.006) time: 0.355 error: 0.5265

CV model 7 svm (gamma = 0.007) time: 0.365 error: 0.5197

CV model 8 svm (gamma = 0.008) time: 0.359 error: 0.5115

CV model 9 svm (gamma = 0.009) time: 0.369 error: 0.5026

CV model 10 svm (gamma = 0.01) time: 0.355 error: 0.4946
```

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Blending models (part 2)

```
for (mt in 1:2) {
  m <- add.medley(m, randomForest, list(mtry=mt));
}</pre>
```

```
CV model 11 randomForest (mtry = 1) time: 2.015 error: 0.4668
CV model 12 randomForest (mtry = 2) time: 3.532 error: 0.4135
```

```
m <- prune.medley(m, 0.8);
rmse(predict(m,newx),testData$y)</pre>
```

```
Sampled... 96.00 %: 3 svm (gamma = 0.01)

1.00 %: 4 svm (gamma = 0.009)

1.00 %: 5 svm (gamma = 0.008)

1.00 %: 6 svm (gamma = 0.007)

1.00 %: 7 svm (gamma = 0.006)

CV error: 0.4953
```

Notes and further resources

Notes:

- Even simple blending can be useful
- Majority vote is typical model for binary/multiclass data
- Makes models hard to interpret

Further resources:

- Bayesian model averaging
- Heritage health prize
- · Netflix model blending