Modeling

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05 December, 2018

Contents

Imports

```
library(dplyr)
library(mosaic)
library(ROCR)
library(randomForest)
library(reprtree) #devtools::install_github('araastat/reprtree')
```

Load Data

```
train <- readRDS(file = "../data/PIMA_train.Rds")
test <- readRDS(file = "../data/PIMA_test.Rds")
```

Baseline

```
tally(~ hasDiabetes, data = train)
```

```
## hasDiabetes
##   0   1
## 196  98
```

Any model we choose has to have an accuracy higher than 98/(98+196) = 33%. This is the baseline accuracy score.

Logistic Regression Classifier

Training

```
clf_LR <- glm(hasDiabetes ~ ., family = binomial(link='logit'), data = train)
summary(clf_LR)
```

```
##
## Call:
## glm(formula = hasDiabetes ~ ., family = binomial(link = "logit"),
##     data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.8732  -0.6344  -0.3526   0.5918   2.2488
##
## Coefficients:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -1.090e+01  1.516e+00  -7.190 6.48e-13 ***
## pregnancies               1.310e-01  6.738e-02   1.944  0.05192 .
## glucoseConcentration      4.080e-02  6.740e-03   6.054 1.41e-09 ***
## bloodPressure             2.284e-03  1.367e-02   0.167  0.86732
## skinThickness            -3.725e-06  2.118e-02   0.000  0.99986
## insulin                  -1.764e-03  1.544e-03  -1.142  0.25325
## bmi                       9.483e-02  3.472e-02   2.731  0.00631 **
## diabetesPedigreeFunction  1.472e+00  4.967e-01   2.963  0.00305 **
## age                       2.227e-02  2.099e-02   1.061  0.28881
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 374.27  on 293  degrees of freedom
## Residual deviance: 251.84  on 285  degrees of freedom
## AIC: 269.84
##
## Number of Fisher Scoring iterations: 5
```

```
saveRDS(clf_LR, file = "../models/LogisticRegressionClassifier_Full.Rds")
```

Model Evaluation on Train Set

```
predict_LR <- predict(clf_LR, type = 'response')

with(train,
     table(hasDiabetes, predict_LR > 0.3))
```

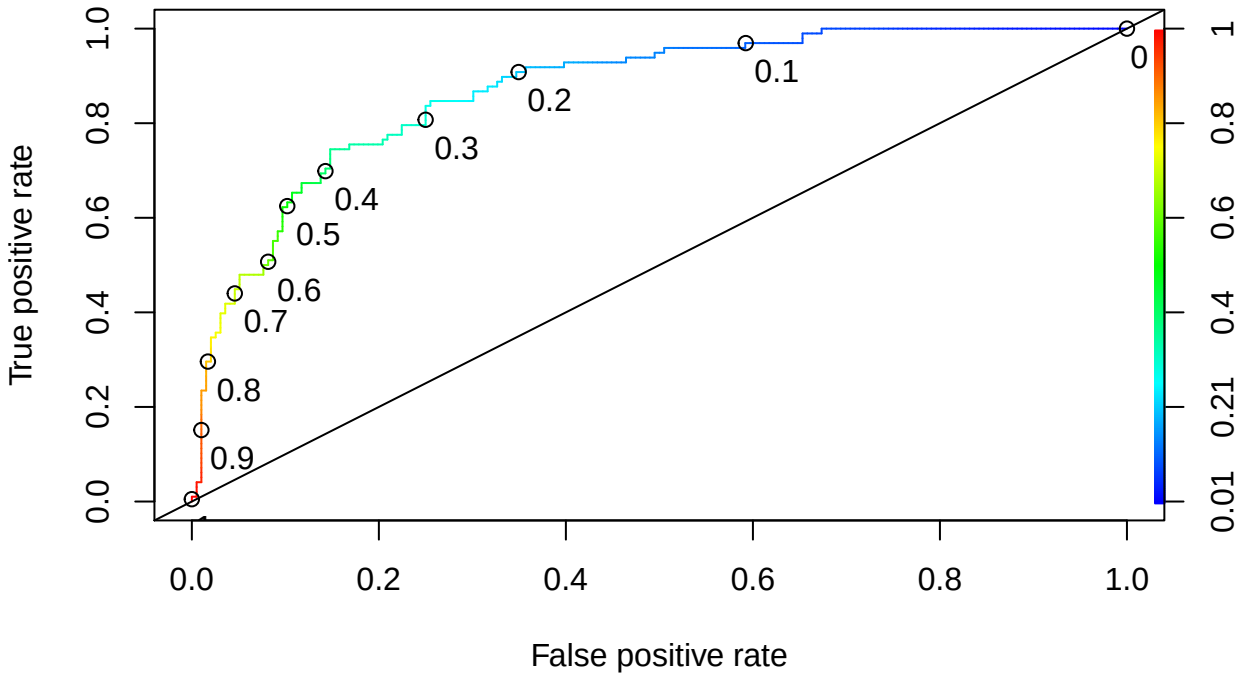
```
##
## hasDiabetes FALSE TRUE
##           0   147   49
##           1    19   79
```

We can see in the confusion matrix that our accuracy is $(79 + 147)/(147 + 49 + 19 + 79) = 0.7687$. This is with a cutoff of 0.3.

```
ROCRpred_LR <- with(train,
                prediction(predict_LR, hasDiabetes))
```

```
ROCRperf_LR <- performance(ROCRpred_LR, 'tpr','fpr')

plot(ROCRperf_LR, colorize = TRUE, print.cutoffs.at = seq(0,1,0.1), text.adj = c(-0.2,1.7)); abline(0,1
```



In the ROC curve we can see that our model is good (the curve is away from the diagonal). Since we care about not predicting a negative result for someone that is actually positive for diabetes (false negative rate), we want to have a larger true positive rate (1 - TPR = FNR). This means that we choose a cutoff near the blue part of the curve, the lower the cutoff the more cautious our model and the less accurate.

Random Forest Classifier

Training

```
clf_RF <- randomForest(hasDiabetes ~ ., data = train)
saveRDS(clf_RF, file = "../models/RandomForestClassifier_Full.Rds")
```

Model Evaluation on the Train Set

```
predict_RF <- predict(clf_RF, type = 'prob')

with(train,
     table(hasDiabetes, predict_RF %>% as_tibble() %>% select(`1`) > 0.3))
```

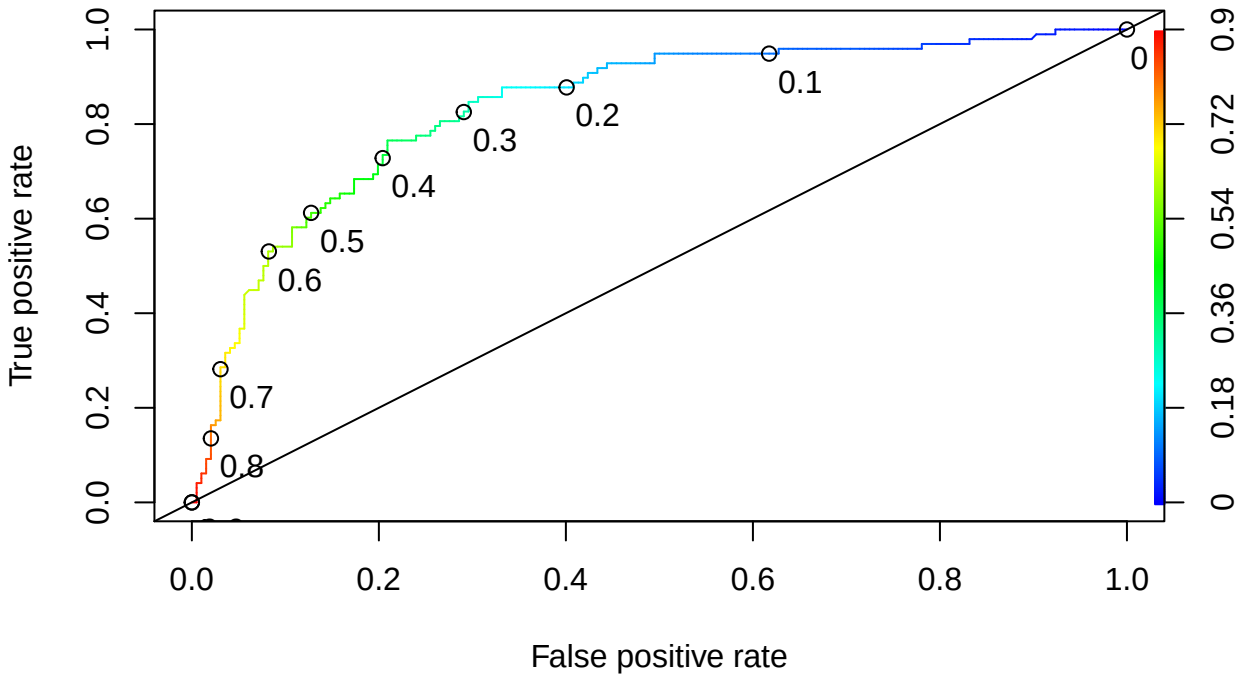
```
##
## hasDiabetes FALSE TRUE
##           0   139   57
##           1    18   80
```

We can see in the confusion matrix that our accuracy is $(140 + 83)/(140 + 56 + 15 + 83) = 0.7585$. The accuracy is slightly lower than the logistic regression model.

```
ROCRpred_RF <- with(train,
                 prediction(predict_RF %>% as_tibble() %>% select(`1`), hasDiabetes))

ROCRperf_RF <- performance(ROCRpred_RF, 'tpr','fpr')

plot(ROCRperf_RF, colorize = TRUE, print.cutoffs.at = seq(0,1,0.1), text.adj = c(-0.2,1.7)); abline(0,1
```




```
# plot only part of the representative tree
#reprtree:::plot.getTree(clf_RF, depth = 5)
```

The random forest ROC curve is less steep than the logisti regression roc curve. We still want to choose a low cutoff like 0.3 if we use this model.