Assignment 6: Comparison between Classification Trees, SVM and Logistic Regression

2024-02-26

library(tidyverse)  
library(rpart)  
library(caret)  
library(rpart.plot)  
library(pROC)  
library(kernlab)  
library(e1071)

This analysis follows the methodology presented by Yu et al., which utilizes NHANES data from 1999-2004 to predict diabetes and pre-diabetes using Support Vector Machines (SVM). Our goal is to predict Diabetes using a similar set of variables but acknowledging that the available data and outcomes may differ, leading to unique insights.

### Question 1 & 2: Data Loading and Preprocessing

set.seed(123)  
library(NHANES)  
  
nhanes = NHANES %>% janitor::clean\_names()  
  
nhanes = nhanes |> select(age, race1, education, hh\_income, weight, height, pulse, diabetes, bmi, phys\_active, smoke100) |> na.omit()  
  
partition <- createDataPartition(y = nhanes$diabetes, p = 0.7, list = FALSE)  
  
# Creating training and testing sets  
train\_data <- nhanes[partition, ]  
test\_data <- nhanes[-partition, ]

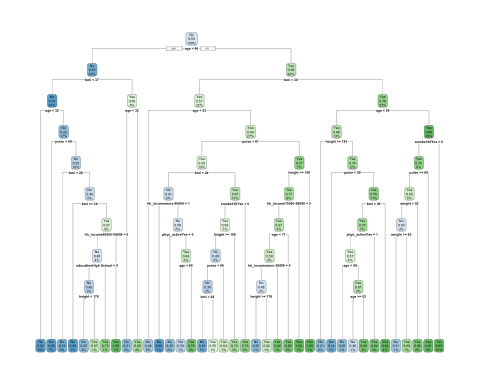
## Question 3: Model Training and Evaluation

### Classification Tree

set.seed(123)  
# Set up 10-fold cross-validation with down-sampling for imbalance   
train.control <- trainControl(method = "cv", number = 10, sampling = "down", summaryFunction = twoClassSummary, classProbs = TRUE, savePredictions = TRUE)  
  
# Create a sequence of cp values to try  
cpGrid <- expand.grid(cp = seq(0.001, 0.3, by = 0.01))  
  
# Train the model  
tree.diabetes <- train(  
 diabetes ~ .,  
 data = train\_data,  
 method = "rpart",  
 trControl = train.control,  
 tuneGrid = cpGrid,  
 metric = "ROC"  
)  
  
# Best tuning parameter  
tree.diabetes$bestTune

## cp  
## 1 0.001

# Plotting the tree  
rpart.plot(tree.diabetes$finalModel)



# Variable importance  
varImp(tree.diabetes)

## rpart variable importance  
##   
## only 20 most important variables shown (out of 35)  
##   
## Overall  
## age 100.0000  
## bmi 69.7194  
## weight 49.7904  
## height 29.0285  
## pulse 28.3578  
## educationCollege Grad 22.7297  
## phys\_activeYes 11.6649  
## hh\_incomemore 99999 11.2164  
## race1White 4.5234  
## smoke100Yes 4.4698  
## hh\_income45000-54999 4.0866  
## race1Mexican 3.7162  
## race1Hispanic 1.9055  
## educationSome College 1.8275  
## hh\_income55000-64999 1.1010  
## hh\_income65000-74999 1.0431  
## educationHigh School 0.8472  
## hh\_income75000-99999 0.7452  
## hh\_income20000-24999 0.5552  
## `hh\_income55000-64999` 0.0000

# Printing Model   
print(tree.diabetes)

## CART   
##   
## 4450 samples  
## 10 predictor  
## 2 classes: 'No', 'Yes'   
##   
## No pre-processing  
## Resampling: Cross-Validated (10 fold)   
## Summary of sample sizes: 4005, 4005, 4004, 4005, 4005, 4006, ...   
## Addtional sampling using down-sampling  
##   
## Resampling results across tuning parameters:  
##   
## cp ROC Sens Spec   
## 0.001 0.7890664 0.6988275 0.7531452  
## 0.011 0.7569938 0.6549590 0.7924144  
## 0.021 0.7280242 0.6263807 0.7836263  
## 0.031 0.7262132 0.6050554 0.8162350  
## 0.041 0.7062907 0.5842533 0.8224329  
## 0.051 0.6887251 0.5506694 0.8267808  
## 0.061 0.6887251 0.5506694 0.8267808  
## 0.071 0.6887251 0.5506694 0.8267808  
## 0.081 0.6887251 0.5506694 0.8267808  
## 0.091 0.6887251 0.5506694 0.8267808  
## 0.101 0.6887251 0.5506694 0.8267808  
## 0.111 0.6887251 0.5506694 0.8267808  
## 0.121 0.6887251 0.5506694 0.8267808  
## 0.131 0.6887251 0.5506694 0.8267808  
## 0.141 0.6887251 0.5506694 0.8267808  
## 0.151 0.6887251 0.5506694 0.8267808  
## 0.161 0.6887251 0.5506694 0.8267808  
## 0.171 0.6887251 0.5506694 0.8267808  
## 0.181 0.6887251 0.5506694 0.8267808  
## 0.191 0.6887251 0.5506694 0.8267808  
## 0.201 0.6887251 0.5506694 0.8267808  
## 0.211 0.6887251 0.5506694 0.8267808  
## 0.221 0.6887251 0.5506694 0.8267808  
## 0.231 0.6887251 0.5506694 0.8267808  
## 0.241 0.6887251 0.5506694 0.8267808  
## 0.251 0.6887251 0.5506694 0.8267808  
## 0.261 0.6887251 0.5506694 0.8267808  
## 0.271 0.6887251 0.5506694 0.8267808  
## 0.281 0.6887251 0.5506694 0.8267808  
## 0.291 0.6887251 0.5506694 0.8267808  
##   
## ROC was used to select the optimal model using the largest value.  
## The final value used for the model was cp = 0.001.

AUC for the Classification Tree model is 0.7891.

### Support Vector Classifier (i.e. Support Vector Machine with a linear classifier)

set.seed(123)  
  
# Setting up cross-validation and specifying AUC as the metric  
trainControl <- trainControl(method = "cv",  
 number = 10,  
 summaryFunction = twoClassSummary,  
 classProbs = TRUE,   
 savePredictions = "final")  
  
# Define a tuning grid for SVM hyperparameters, focusing on 'C'  
tuningGrid <- expand.grid(C = seq(0.001, 2, length = 20))  
  
# Train the SVM model with cross-validation  
svmModel <- train(diabetes ~ .,  
 data = train\_data,  
 method = "svmLinear",  
 trControl = trainControl,  
 tuneGrid = tuningGrid,  
 metric = "ROC",  
 preProcess = c("center", "scale")) # Pre-processing steps

## maximum number of iterations reached 0.01085536 0.00980073maximum number of iterations reached 0.0105926 0.009455061maximum number of iterations reached 0.006430752 0.006051302maximum number of iterations reached 0.007632995 0.007202278maximum number of iterations reached 0.008759899 0.008002154maximum number of iterations reached 0.009586973 0.008841425maximum number of iterations reached 0.007648205 0.007093961maximum number of iterations reached 0.006859105 0.006472282maximum number of iterations reached 0.006895285 0.006482649maximum number of iterations reached 0.003274548 0.003195983maximum number of iterations reached 0.002348811 0.002296483maximum number of iterations reached 0.003629752 0.003534933maximum number of iterations reached 0.007452818 0.00700977maximum number of iterations reached 0.006690161 0.006301762maximum number of iterations reached 0.002641242 0.002593289maximum number of iterations reached 0.007056303 0.006651266maximum number of iterations reached 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0.007939136 0.007357904maximum number of iterations reached 0.01152945 0.01013226maximum number of iterations reached 0.01011191 0.009147048maximum number of iterations reached 0.01251445 0.01128809maximum number of iterations reached 0.009321572 0.008205296maximum number of iterations reached 0.009521744 0.008569203maximum number of iterations reached 0.007064436 0.006590269maximum number of iterations reached 0.006179598 0.005844302maximum number of iterations reached 0.01003708 0.00900283maximum number of iterations reached 0.009261981 0.008540321maximum number of iterations reached 0.009409718 0.008414993maximum number of iterations reached 0.01341965 0.01177212maximum number of iterations reached 0.01101157 0.009913959maximum number of iterations reached 0.009148721 0.008396371maximum number of iterations reached 0.009903562 0.008774564maximum number of iterations reached 0.009245791 0.008384683maximum number of iterations reached 0.0112127 0.01012064maximum number of iterations reached 0.01177063 0.01062817

# Print Model  
print(svmModel)

## Support Vector Machines with Linear Kernel   
##   
## 4450 samples  
## 10 predictor  
## 2 classes: 'No', 'Yes'   
##   
## Pre-processing: centered (26), scaled (26)   
## Resampling: Cross-Validated (10 fold)   
## Summary of sample sizes: 4005, 4005, 4004, 4005, 4005, 4006, ...   
## Resampling results across tuning parameters:  
##   
## C ROC Sens Spec  
## 0.0010000 0.6306119 1 0   
## 0.1062105 0.5847105 1 0   
## 0.2114211 0.6380646 1 0   
## 0.3166316 0.5998203 1 0   
## 0.4218421 0.6055757 1 0   
## 0.5270526 0.6163412 1 0   
## 0.6322632 0.6125682 1 0   
## 0.7374737 0.6077398 1 0   
## 0.8426842 0.6227003 1 0   
## 0.9478947 0.6276718 1 0   
## 1.0531053 0.5807192 1 0   
## 1.1583158 0.6220556 1 0   
## 1.2635263 0.6065399 1 0   
## 1.3687368 0.5887346 1 0   
## 1.4739474 0.5973733 1 0   
## 1.5791579 0.6238115 1 0   
## 1.6843684 0.5954001 1 0   
## 1.7895789 0.6258926 1 0   
## 1.8947895 0.6168653 1 0   
## 2.0000000 0.6266020 1 0   
##   
## ROC was used to select the optimal model using the largest value.  
## The final value used for the model was C = 0.2114211.

AUC for the SVM model is 0.6378.

### Logistic regression

set.seed(123)  
  
# Set up cross-validation with down-sampling for imbalance handling  
train.control <- trainControl(method = "cv", number = 10, summaryFunction = twoClassSummary, classProbs = TRUE, savePredictions = TRUE, sampling = "down")  
  
# Train the logistic regression model  
logistic.diabetes <- train(  
 diabetes ~ .,  
 data = train\_data,  
 method = "glm",  
 family = "binomial",  
 trControl = train.control,  
 metric = "ROC"  
)  
  
# Display the model  
print(logistic.diabetes)

## Generalized Linear Model   
##   
## 4450 samples  
## 10 predictor  
## 2 classes: 'No', 'Yes'   
##   
## No pre-processing  
## Resampling: Cross-Validated (10 fold)   
## Summary of sample sizes: 4005, 4005, 4004, 4005, 4005, 4006, ...   
## Addtional sampling using down-sampling  
##   
## Resampling results:  
##   
## ROC Sens Spec   
## 0.8116997 0.7098695 0.7574468

# model coefficients as an indication of importance  
coef(logistic.diabetes$finalModel)

## (Intercept) age race1Hispanic   
## -17.75238906 0.08363345 0.00587355   
## race1Mexican race1White race1Other   
## -0.33996094 -0.31476772 0.38709174   
## `education9 - 11th Grade` `educationHigh School` `educationSome College`   
## -0.59279910 -0.12930804 -0.18752616   
## `educationCollege Grad` `hh\_income 5000-9999` `hh\_income10000-14999`   
## -0.74332582 -0.43085274 -0.97167538   
## `hh\_income15000-19999` `hh\_income20000-24999` `hh\_income25000-34999`   
## -0.90323120 -0.95586731 -1.01499637   
## `hh\_income35000-44999` `hh\_income45000-54999` `hh\_income55000-64999`   
## -0.74797103 -0.90332763 -1.03173653   
## `hh\_income65000-74999` `hh\_income75000-99999` `hh\_incomemore 99999`   
## -1.19233954 -0.79696627 -1.21677931   
## weight height pulse   
## -0.04819816 0.05690495 0.01670732   
## bmi phys\_activeYes smoke100Yes   
## 0.25677116 0.35976558 0.53279940

AUC for the logistic regression model is 0.8117.

## Question 4: Optimal Model Selection

The optimal model that I have chosen is the *logistic regression* due to its higher AUC value, indicating it has the best overall ability to distinguish between the classes across all thresholds. It also has slightly higher sensitivity, meaning it’s marginally better at identifying true positives and slightly higher specificity, indicating a marginally better performance at identifying true negatives.

# Prediction and Evaluation on the Testing Set  
  
# Create predictions on the test set  
pred.diabetes <- predict(logistic.diabetes, newdata = test\_data)  
  
# Evaluation results on the test set  
eval.results <- confusionMatrix(pred.diabetes, test\_data$diabetes, positive = "Yes")  
print(eval.results)

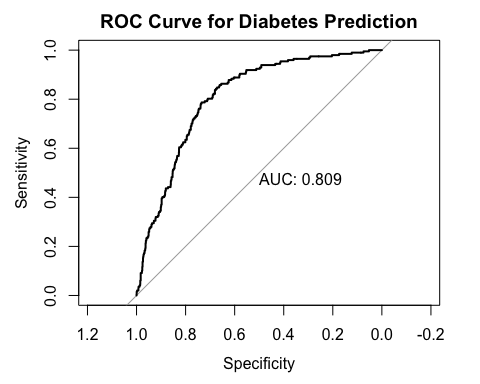
## Confusion Matrix and Statistics  
##   
## Reference  
## Prediction No Yes  
## No 1194 39  
## Yes 515 158  
##   
## Accuracy : 0.7093   
## 95% CI : (0.6884, 0.7297)  
## No Information Rate : 0.8966   
## P-Value [Acc > NIR] : 1   
##   
## Kappa : 0.242   
##   
## Mcnemar's Test P-Value : <2e-16   
##   
## Sensitivity : 0.8020   
## Specificity : 0.6987   
## Pos Pred Value : 0.2348   
## Neg Pred Value : 0.9684   
## Prevalence : 0.1034   
## Detection Rate : 0.0829   
## Detection Prevalence : 0.3531   
## Balanced Accuracy : 0.7503   
##   
## 'Positive' Class : Yes   
##

# Predictions as probabilities on the test set  
pred.diabetes.prob <- predict(logistic.diabetes, newdata = test\_data, type = "prob")  
  
# ROC analysis  
roc.analysis.2 <- roc(response = as.numeric(test\_data$diabetes), predictor = pred.diabetes.prob[,2])

## Setting levels: control = 1, case = 2

## Setting direction: controls < cases

plot(roc.analysis.2, print.auc = TRUE, main = "ROC Curve for Diabetes Prediction")



**Model Performance Overview** \* The model demonstrates fair ability to identify positive cases but struggles with a high false positive rate, as indicated by the low PPV. \* The high NPV and sensitivity suggest the model is quite conservative, effectively identifying negative cases but at the cost of missing or incorrectly predicting a significant portion of positive cases.

## Question 5: Ethical Considerations of Using Race in Predictive Modeling

Including race in disease prediction models is a complex issue with important ethical considerations. On one side, using race can help address health inequalities by recognizing that different racial groups often face different health challenges due to factors like socioeconomic status and access to healthcare. This means that including race could make predictions more accurate for everyone, potentially leading to better health care for underserved groups.

However, there are significant concerns about the negative effects of including race. It can reinforce harmful stereotypes and suggest that there are biological differences between races, which is not accurate. This could lead to unfair treatment in healthcare, where people of different races receive different levels of care even if they have the same health conditions. There’s also a worry that using race in this way could make health disparities worse, not better. While including race in prediction models might aim to make healthcare more fair and accurate, it’s crucial to ensure that it doesn’t accidentally cause more harm than good. The challenge is to use this information wisely to improve health outcomes for everyone without reinforcing biases or inequalities.