pdf_P8451_hw6

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Import Data

1. Restrict the NHANES data to the list of 11 variables below. Partition the data into training and testing using a 70/30 split.

```
data(NHANES)
hw6_df = NHANES %>% select(Age, Race1, Education, HHIncome, Weight, Height, Pulse, Diabetes, BMI, PhysAc
summary(hw6_df)
```

```
hw6_df = hw6_df %>%
    janitor::clean_names() %>%
    na.omit()
```

After excluding the missing values, we have total 6356 observations with 11 variables.

```
set.seed(100)
trRow = createDataPartition(hw6_df$diabetes, p = 0.7, list = FALSE)

train_dat = hw6_df[trRow,]
```

Partitioning

```
## Warning: The ‘i‘ argument of ‘‘[‘()‘ can’t be a matrix as of tibble 3.0.0.
## Convert to a vector.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_warnings()‘ to see where this warning was generated.
```

```
test_dat = hw6_df[-trRow,]

x.train = model.matrix(diabetes~., train_dat)[,-1]
x.test = model.matrix(diabetes~., test_dat)[,-1]
```

2. Construct three prediction models to predict diabetes using the 11 features from NHANES.

3.You will optimize each model using cross-validation to choose hyperparameters in the training data and then compare performance across models.

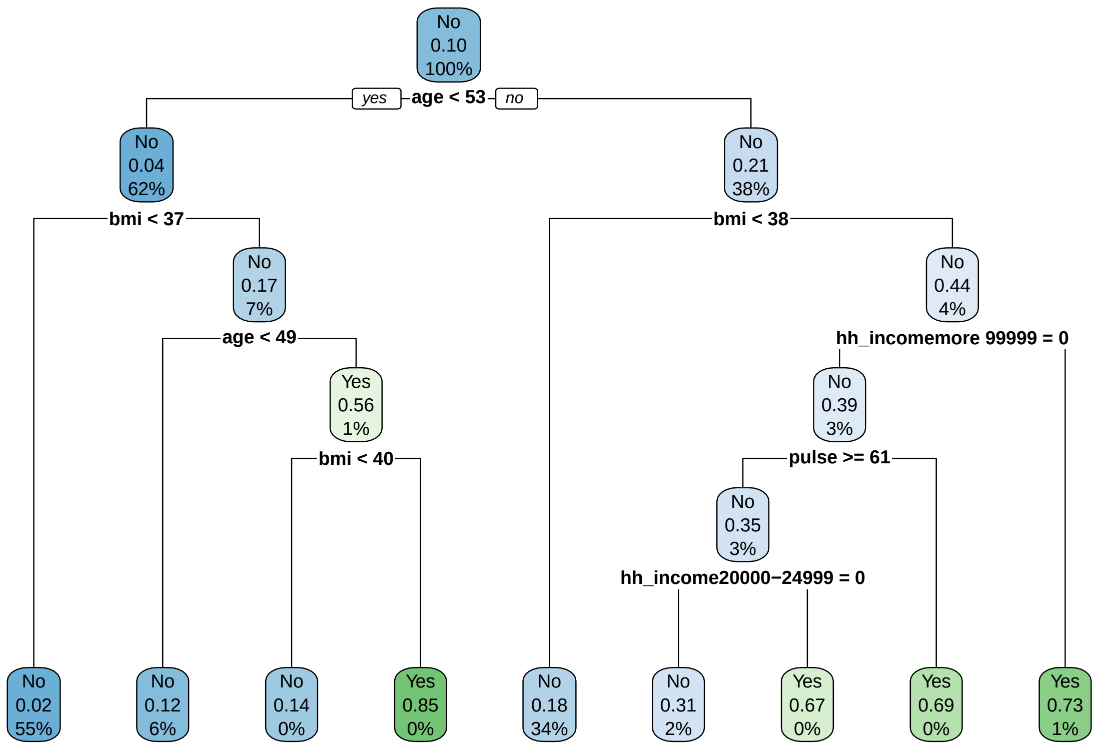
You will use the following three algorithms to create your prediction models:

a) Classification Tree

```
set.seed(100)
train_ctrl = trainControl(method = "cv", number = 10)
tree_db1 = train(diabetes~ . , data = train_dat, method = "rpart",trControl = train_ctrl)
tree_db1$bestTune
```

```
##            cp
## 2 0.008658009
```

```
rpart.plot(tree_db1$finalModel)
```



```
pred_treedb1 = tree_db1 %>% predict(newx = x.test, type = 'prob')
tree_db1_prob = ifelse(pred_treedb1$Yes > 0.5,1,0)
test_treedb1 = (as.numeric(test_dat$diabetes) - 1)
misClasificError_treedb1 = mean(tree_db1_prob != test_treedb1, na.rm = T)
```

```
## Warning in tree_db1_prob != test_treedb1: longer object length is not a multiple
## of shorter object length
```

```
print(paste('Accuracy Model Tree model 1',1 - misClasificError_treedb1))
```

```
## [1] "Accuracy Model Tree model 1 0.883820224719101"
```

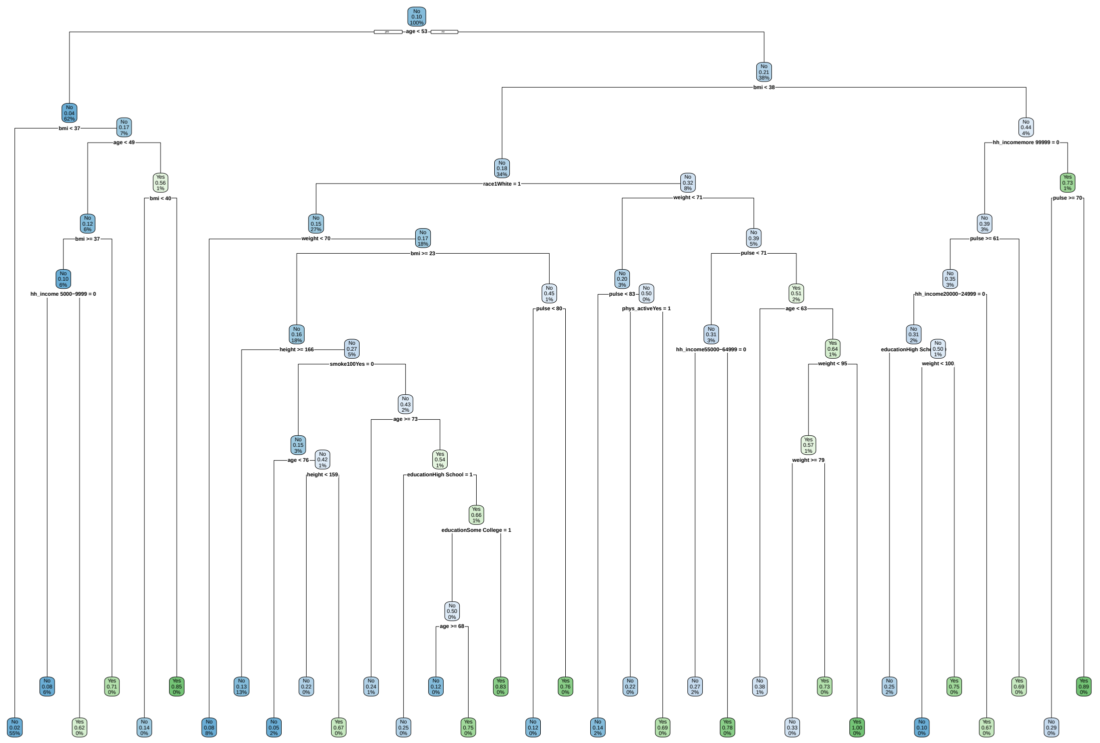
```
varImp(tree_db1)
```

```
## rpart variable importance
##
##   only 20 most important variables shown (out of 34)
##
##                            Overall
## age                        100.000
## bmi                         88.357
## weight                      58.870
## race1White                  22.478
## phys_activeYes              22.263
## pulse                       11.946
## hh_incomemore 99999         11.235
## height                      10.732
## race1Mexican                 8.144
## hh_income20000-24999         6.610
## hh_income 5000-9999          5.562
## hh_income10000-14999         2.706
## educationHigh School         2.378
## smoke100Yes                  1.797
## hh_income65000-74999         1.700
## hh_income45000-54999         1.698
## educationCollege Grad        1.152
## `hh_income10000-14999`       0.000
## `hh_incomemore 99999`        0.000
## `education9 - 11th Grade`    0.000
```

Specify tuneGrid so caret explores wider variety of cp-values

```
grid = expand.grid(cp = seq(0.001,0.1, by = 0.001))
tree_db2 = train(diabetes ~ ., data = train_dat, method = "rpart", trControl = train_ctrl, tuneGrid = g
rpart.plot(tree_db2$finalModel)
```

```
## Warning: labs do not fit even at cex 0.15, there may be some overplotting
```



```
tree_db2$bestTune
```

```
##      cp
## 4 0.004
```

```
pred_treedb2 = tree_db2 %>% predict(newx = x.test, type = 'prob')
tree_db2_prob = ifelse(pred_treedb2$Yes > 0.5,1,0)
test_treedb2 = (as.numeric(test_dat$diabetes) - 1)
misClasificError_treedb2 = mean(tree_db2_prob != test_treedb2, na.rm = T)
```

```
## Warning in tree_db2_prob != test_treedb2: longer object length is not a multiple
## of shorter object length
```

```
print(paste('Accuracy Model Tree model 2',1 - misClasificError_treedb2))
```

```
## [1] "Accuracy Model Tree model 2 0.857528089887641"
```

```
varImp(tree_db2)
```

```
## rpart variable importance
##
##   only 20 most important variables shown (out of 39)
##
```

```
##                          Overall
## age                      100.000
## bmi                       79.830
## weight                    70.390
## height                    43.034
## pulse                     42.267
## phys_activeYes            25.790
## race1White                24.433
## hh_incomemore 99999       14.381
## race1Mexican              13.937
## hh_income 5000-9999        9.699
## smoke100Yes                9.313
## educationHigh School       9.308
## hh_income55000-64999       8.181
## educationSome College      7.088
## hh_income20000-24999       3.914
## education9 - 11th Grade    2.984
## educationCollege Grad      2.855
## hh_income35000-44999       2.439
## hh_income10000-14999       1.602
## hh_income65000-74999       1.007
```

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

```r
set.seed(100)
linear_tune = tune.svm(diabetes ~., data = train_dat,
                        kernel = "linear",
                        range = list(cost = 10^(-3:2)))

#summary(linear_tune)
best_linear = linear_tune$best.model
tune_test = predict(best_linear, newdata = test_dat)
table(tune_test, test_dat$diabetes)
```

```
##
## tune_test   No  Yes
##       No  1709  197
##       Yes    0    0
```

```r
confusionMatrix(tune_test, test_dat$diabetes, positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   No  Yes
##        No  1709  197
##        Yes    0    0
##
##                Accuracy : 0.8966
##                  95% CI : (0.8821, 0.91)
##     No Information Rate : 0.8966
##     P-Value [Acc > NIR] : 0.519
```

```
##
##                    Kappa : 0
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.0000
##             Specificity : 1.0000
##          Pos Pred Value :    NaN
##          Neg Pred Value : 0.8966
##              Prevalence : 0.1034
##          Detection Rate : 0.0000
##    Detection Prevalence : 0.0000
##       Balanced Accuracy : 0.5000
##
##        'Positive' Class : Yes
##
```

c) Logistic regression.

- Include all features, fit manually

```r
set.seed(100)
logit_mod = glm(diabetes ~ ., family = binomial(link = 'logit'), data = train_dat)
summary(logit_mod)
```

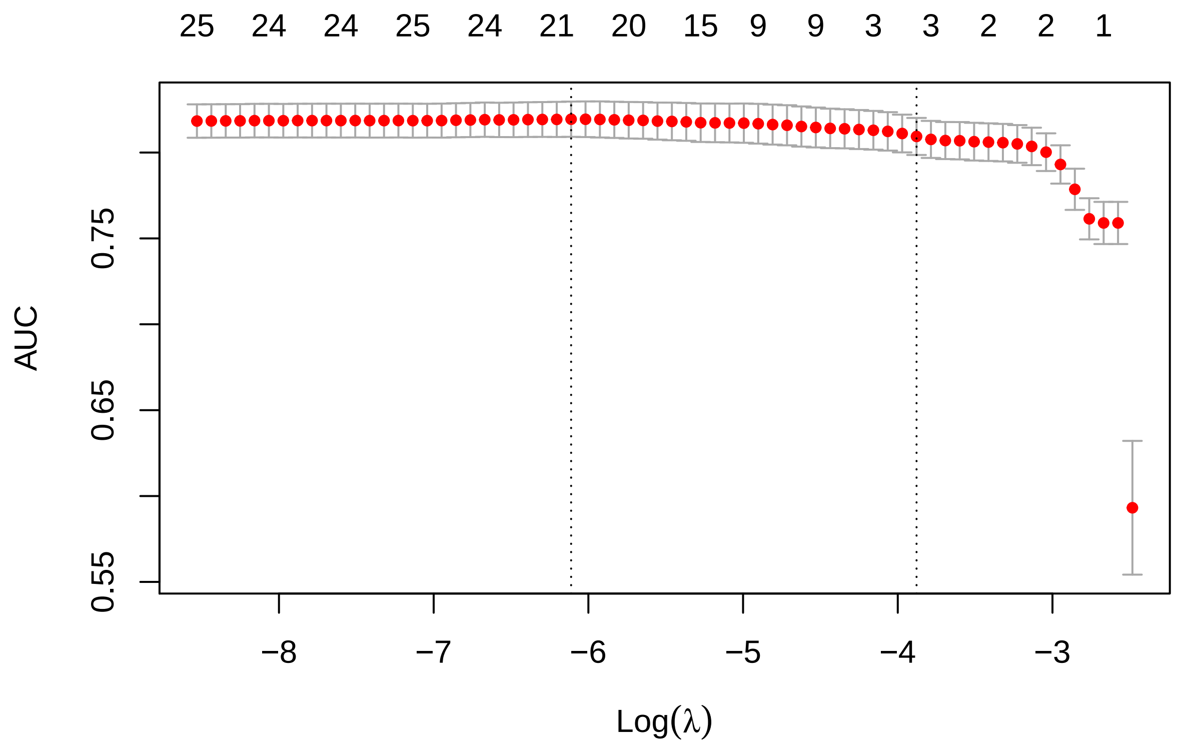
```r
fit_lm = predict(logit_mod, test_dat, type = "response")
lm_prob = ifelse(fit_lm > 0.5,1,0)
test_lm = (as.numeric(test_dat$diabetes) - 1)
misClasificError_lm = mean(lm_prob != test_lm, na.rm = T)
print(paste('Accuracy Model Logistic Model',1-misClasificError_lm))
```

```
## [1] "Accuracy Model Logistic Model 0.892444910807975"
```

Fit via cross-validation.

```r
set.seed(100)
logistic_fit = cv.glmnet(x.train, train_dat$diabetes, family = "binomial", type.measure = "auc", nfolds

plot(logistic_fit)
```



```r
logistic_fit$lambda.1se
```

```
## [1] 0.02067932
```

```r
logistic_fit$lambda.min
```

```
## [1] 0.002217376
```

```r
coef(logistic_fit, s = "lambda.1se")
```

```
## 27 x 1 sparse Matrix of class "dgCMatrix"
##                                   1
## (Intercept)              -6.12616892
## age                       0.04280580
## race1Hispanic             .
## race1Mexican              .
## race1White               -0.07562313
## race1Other                .
## education9 - 11th Grade   .
## educationHigh School      .
## educationSome College     .
## educationCollege Grad     .
## hh_income 5000-9999       .
## hh_income10000-14999      .
## hh_income15000-19999     .
## hh_income20000-24999     .
## hh_income25000-34999     .
## hh_income35000-44999     .
## hh_income45000-54999     .
## hh_income55000-64999     .
## hh_income65000-74999     .
## hh_income75000-99999     .
## hh_incomemore 99999      .
## weight                   .
## height                   .
## pulse                    .
## bmi                      0.06053640
## phys_activeYes           .
## smoke100Yes              .
```

```
pred_logistic = predict(logistic_fit, newx = x.test,
                  s = "lambda.1se",
                  type = "response")
logistic_prob = ifelse(pred_logistic > 0.5, 1, 0)
test_lm = (as.numeric(test_dat$diabetes) - 1)
misClasificError_lm = mean(logistic_prob  != test_lm, na.rm = T)
print(paste('Accuracy Model Logistic Model',1 - misClasificError_lm))
```

```
## [1] "Accuracy Model Logistic Model 0.896117523609654"
```

Compared to the accuracy of the two logistic regression, I decide to use logistic regression with cross-validation to further compare with the other two models because of higher accuracy.

4. Calculate final accuracy in a test set for the model you determine to be the most appropriate model.

From the above calculation, SVM has the highest accuracy compared to the other two models, with logistic regression coming as next and classification tree as last. I will choose SVM as the most appropriate model based on the accuracy in a test set.

5. List and describe at least two limitations of the model generated by this analysis. Limitations can be analytical or they can be regarding how the model would be used in practice.

One limitations in the practice is that, since the support vector classifier works by putting data points, above and below the classifying hyperplane there is no probabilistic explanation for the classification.

Another limitation is that SVM will underperform in a large-p-small-n scenario.