MEDI 504A: Working with Diabetes Data

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This document aims to present the general steps for analyzing binary data using machine learning methods. The data source is described in Strack B. et al. [1] link. The dataset can be downloaded from here. Below we present the codes for processing the analytic data following the guideline presented in the paper.

Data Inspection

Coding of predictors

The predictors are coded following the steps outlined in the paper.

Model specifiction

For the purpose of comparison, we select the same set of predictors and interactions as in the paper.

Model Estimation

Outcome and model specification:

```
class(diabetic.data$readmitted)
```

```
## [1] "factor"
```

```
levels(diabetic.data$readmitted)
```

```
## [1] "NO"  "YES"
```

```
model.formula <- as.formula("readmitted ~ discharge + race + source +
                                           medical_specialty +
                                           time_in_hospital + age +
                                           diag_1 + A1Cresult  +
                                           diag_1 * discharge + race * discharge +
                                           medical_specialty*discharge +
                                           discharge*time_in_hospital +
                                           time_in_hospital*medical_specialty +
                                           age * medical_specialty +
                                           time_in_hospital*diag_1 +
                                           A1Cresult* diag_1")
```

1. Fit a logistic regression model using the above formula and the analytic data `diabetic.data`.

Hint: a) The results should be comparable to the values reported in Table 4 (but may not be exactly the same). b) use `summary()` function to report the fit

```
#fit model to formula and data
fit_full = glm(model.formula, data = diabetic.data,
               family = binomial(link = "logit"))

#reporting the fit
summary(fit_full)
```

```
##
## Call:
## glm(formula = model.formula, family = binomial(link = "logit"),
##     data = diabetic.data)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9379  -0.4857  -0.3992  -0.3458   2.8224
##
## Coefficients:
##                                                  Estimate Std. Error
## (Intercept)                                     -3.173941   0.176193
## dischargeOther                                   0.292095   0.195068
## raceMissing                                     -0.316646   0.134056
## raceOther                                       -0.295328   0.104848
## raceCaucasian                                    0.015916   0.048438
## sourceOther                                     -0.123723   0.040933
## sourceReferral                                  -0.020914   0.032175
## medical_specialtyFamily/GeneralPractice          0.409992   0.184320
## medical_specialtyInternalMedicine                0.402032   0.164915
## medical_specialtyMissing or Unknown              0.422134   0.150039
## medical_specialtyOther                           0.288985   0.164017
## medical_specialtySurgery                         0.435112   0.204922
## time_in_hospital                                 0.128699   0.025829
## age< 30                                          1.492980   0.665627
## age[60, 100)                                     0.265849   0.140993
## diag_1Circulatory                                0.105830   0.105093
## diag_1Respiratory                               -0.318237   0.120590
## diag_1Digestive                                 -0.064051   0.128546
## diag_1Injury and poisoning                      -0.004056   0.145035
## diag_1Musculoskeletal                           -0.721710   0.178061
## diag_1Genitourinary                             -0.277143   0.150977
## diag_1Neoplasms                                  0.157242   0.165829
## diag_1Other                                      0.028990   0.112182
## A1Cresulthigh_ch                                -0.391866   0.140098
## A1Cresulthigh_noch                              -0.524933   0.216807
## A1CresultNormal                                  0.006444   0.150850
## dischargeOther:diag_1Circulatory                -0.026805   0.111298
## dischargeOther:diag_1Respiratory                 0.098943   0.129727
## dischargeOther:diag_1Digestive                   0.024280   0.141330
## dischargeOther:diag_1Injury and poisoning        0.278475   0.148976
```

```
## dischargeOther:diag_1Musculoskeletal                          0.423824   0.175323
## dischargeOther:diag_1Genitourinary                           -0.185280   0.159566
## dischargeOther:diag_1Neoplasms                               -0.166814   0.178869
## dischargeOther:diag_1Other                                    0.198855   0.119152
## dischargeOther:raceMissing                                    0.285862   0.188412
## dischargeOther:raceOther                                      0.496983   0.150673
## dischargeOther:raceCaucasian                                  0.016840   0.071921
## dischargeOther:medical_specialtyFamily/GeneralPractice        0.318945   0.180204
## dischargeOther:medical_specialtyInternalMedicine              0.191219   0.164819
## dischargeOther:medical_specialtyMissing or Unknown            0.236041   0.154060
## dischargeOther:medical_specialtyOther                         0.374703   0.165871
## dischargeOther:medical_specialtySurgery                       0.723663   0.198158
## dischargeOther:time_in_hospital                              -0.027635   0.009256
## medical_specialtyFamily/GeneralPractice:time_in_hospital     -0.061614   0.026133
## medical_specialtyInternalMedicine:time_in_hospital           -0.036593   0.023105
## medical_specialtyMissing or Unknown:time_in_hospital         -0.057010   0.021505
## medical_specialtyOther:time_in_hospital                      -0.051532   0.023610
## medical_specialtySurgery:time_in_hospital                    -0.110316   0.029429
## medical_specialtyFamily/GeneralPractice:age< 30              -2.136860   0.844157
## medical_specialtyInternalMedicine:age< 30                    -1.660124   0.732318
## medical_specialtyMissing or Unknown:age< 30                  -1.108086   0.678110
## medical_specialtyOther:age< 30                               -2.059354   0.701992
## medical_specialtySurgery:age< 30                             -2.841808   1.216233
## medical_specialtyFamily/GeneralPractice:age[60, 100)          0.061838   0.180533
## medical_specialtyInternalMedicine:age[60, 100)               -0.015595   0.162112
## medical_specialtyMissing or Unknown:age[60, 100)             -0.096594   0.147866
## medical_specialtyOther:age[60, 100)                          -0.107182   0.159704
## medical_specialtySurgery:age[60, 100)                        -0.200098   0.196519
## time_in_hospital:diag_1Circulatory                           -0.034196   0.016936
## time_in_hospital:diag_1Respiratory                           -0.007534   0.019708
## time_in_hospital:diag_1Digestive                             -0.034019   0.021961
## time_in_hospital:diag_1Injury and poisoning                  -0.042871   0.022531
## time_in_hospital:diag_1Musculoskeletal                        0.022708   0.027858
## time_in_hospital:diag_1Genitourinary                          0.041262   0.025003
## time_in_hospital:diag_1Neoplasms                             -0.047114   0.026554
## time_in_hospital:diag_1Other                                 -0.057156   0.018053
## diag_1Circulatory:A1Cresulthigh_ch                            0.543173   0.169401
## diag_1Respiratory:A1Cresulthigh_ch                            0.323641   0.231354
## diag_1Digestive:A1Cresulthigh_ch                              0.509108   0.289201
## diag_1Injury and poisoning:A1Cresulthigh_ch                  -0.152828   0.361694
## diag_1Musculoskeletal:A1Cresulthigh_ch                        0.789333   0.361859
## diag_1Genitourinary:A1Cresulthigh_ch                          0.439763   0.307627
## diag_1Neoplasms:A1Cresulthigh_ch                             -0.109459   0.542317
## diag_1Other:A1Cresulthigh_ch                                  0.265904   0.204995
## diag_1Circulatory:A1Cresulthigh_noch                          0.516588   0.254539
## diag_1Respiratory:A1Cresulthigh_noch                          0.357910   0.335146
## diag_1Digestive:A1Cresulthigh_noch                            0.187666   0.427307
## diag_1Injury and poisoning:A1Cresulthigh_noch                 0.276748   0.485056
## diag_1Musculoskeletal:A1Cresulthigh_noch                      0.793634   0.530661
## diag_1Genitourinary:A1Cresulthigh_noch                       -0.352285   0.632472
## diag_1Neoplasms:A1Cresulthigh_noch                            0.716933   0.653358
## diag_1Other:A1Cresulthigh_noch                                0.639614   0.294052
## diag_1Circulatory:A1CresultNormal                            -0.051316   0.169459
## diag_1Respiratory:A1CresultNormal                            -0.505827   0.212218
```

```
## diag_1Digestive:A1CresultNormal                                -0.073048   0.234012
## diag_1Injury and poisoning:A1CresultNormal                     -0.596278   0.259305
## diag_1Musculoskeletal:A1CresultNormal                          -0.096769   0.282496
## diag_1Genitourinary:A1CresultNormal                             0.219060   0.246088
## diag_1Neoplasms:A1CresultNormal                                 0.243043   0.306575
## diag_1Other:A1CresultNormal                                    -0.070059   0.185184
##                                                                z value Pr(>|z|)
## (Intercept)                                                    -18.014  < 2e-16 ***
## dischargeOther                                                   1.497 0.134289
## raceMissing                                                     -2.362 0.018175 *
## raceOther                                                       -2.817 0.004851 **
## raceCaucasian                                                    0.329 0.742471
## sourceOther                                                     -3.023 0.002506 **
## sourceReferral                                                  -0.650 0.515680
## medical_specialtyFamily/GeneralPractice                          2.224 0.026125 *
## medical_specialtyInternalMedicine                                2.438 0.014776 *
## medical_specialtyMissing or Unknown                              2.813 0.004901 **
## medical_specialtyOther                                           1.762 0.078084 .
## medical_specialtySurgery                                         2.123 0.033728 *
## time_in_hospital                                                 4.983 6.27e-07 ***
## age< 30                                                          2.243 0.024899 *
## age[60, 100)                                                     1.886 0.059355 .
## diag_1Circulatory                                                1.007 0.313927
## diag_1Respiratory                                               -2.639 0.008315 **
## diag_1Digestive                                                 -0.498 0.618292
## diag_1Injury and poisoning                                      -0.028 0.977688
## diag_1Musculoskeletal                                           -4.053 5.05e-05 ***
## diag_1Genitourinary                                             -1.836 0.066407 .
## diag_1Neoplasms                                                  0.948 0.343019
## diag_1Other                                                      0.258 0.796087
## A1Cresulthigh_ch                                                -2.797 0.005157 **
## A1Cresulthigh_noch                                              -2.421 0.015469 *
## A1CresultNormal                                                  0.043 0.965925
## dischargeOther:diag_1Circulatory                                -0.241 0.809679
## dischargeOther:diag_1Respiratory                                 0.763 0.445641
## dischargeOther:diag_1Digestive                                   0.172 0.863597
## dischargeOther:diag_1Injury and poisoning                        1.869 0.061587 .
## dischargeOther:diag_1Musculoskeletal                             2.417 0.015633 *
## dischargeOther:diag_1Genitourinary                              -1.161 0.245583
## dischargeOther:diag_1Neoplasms                                  -0.933 0.351025
## dischargeOther:diag_1Other                                       1.669 0.095133 .
## dischargeOther:raceMissing                                       1.517 0.129213
## dischargeOther:raceOther                                         3.298 0.000972 ***
## dischargeOther:raceCaucasian                                     0.234 0.814869
## dischargeOther:medical_specialtyFamily/GeneralPractice           1.770 0.076743 .
## dischargeOther:medical_specialtyInternalMedicine                 1.160 0.245975
## dischargeOther:medical_specialtyMissing or Unknown               1.532 0.125488
## dischargeOther:medical_specialtyOther                            2.259 0.023883 *
## dischargeOther:medical_specialtySurgery                          3.652 0.000260 ***
## dischargeOther:time_in_hospital                                 -2.986 0.002830 **
## medical_specialtyFamily/GeneralPractice:time_in_hospital        -2.358 0.018389 *
## medical_specialtyInternalMedicine:time_in_hospital              -1.584 0.113255
## medical_specialtyMissing or Unknown:time_in_hospital            -2.651 0.008024 **
## medical_specialtyOther:time_in_hospital                         -2.183 0.029065 *
```

```
## medical_specialtySurgery:time_in_hospital                -3.749 0.000178 ***
## medical_specialtyFamily/GeneralPractice:age< 30          -2.531 0.011362 *
## medical_specialtyInternalMedicine:age< 30                -2.267 0.023394 *
## medical_specialtyMissing or Unknown:age< 30              -1.634 0.102242
## medical_specialtyOther:age< 30                           -2.934 0.003351 **
## medical_specialtySurgery:age< 30                         -2.337 0.019462 *
## medical_specialtyFamily/GeneralPractice:age[60, 100)      0.343 0.731953
## medical_specialtyInternalMedicine:age[60, 100)           -0.096 0.923362
## medical_specialtyMissing or Unknown:age[60, 100)         -0.653 0.513593
## medical_specialtyOther:age[60, 100)                      -0.671 0.502139
## medical_specialtySurgery:age[60, 100)                    -1.018 0.308577
## time_in_hospital:diag_1Circulatory                       -2.019 0.043478 *
## time_in_hospital:diag_1Respiratory                       -0.382 0.702257
## time_in_hospital:diag_1Digestive                         -1.549 0.121367
## time_in_hospital:diag_1Injury and poisoning              -1.903 0.057079 .
## time_in_hospital:diag_1Musculoskeletal                    0.815 0.415000
## time_in_hospital:diag_1Genitourinary                      1.650 0.098886 .
## time_in_hospital:diag_1Neoplasms                         -1.774 0.076010 .
## time_in_hospital:diag_1Other                             -3.166 0.001545 **
## diag_1Circulatory:A1Cresulthigh_ch                        3.206 0.001344 **
## diag_1Respiratory:A1Cresulthigh_ch                        1.399 0.161844
## diag_1Digestive:A1Cresulthigh_ch                          1.760 0.078341 .
## diag_1Injury and poisoning:A1Cresulthigh_ch              -0.423 0.672635
## diag_1Musculoskeletal:A1Cresulthigh_ch                    2.181 0.029159 *
## diag_1Genitourinary:A1Cresulthigh_ch                      1.430 0.152851
## diag_1Neoplasms:A1Cresulthigh_ch                         -0.202 0.840045
## diag_1Other:A1Cresulthigh_ch                              1.297 0.194587
## diag_1Circulatory:A1Cresulthigh_noch                      2.030 0.042407 *
## diag_1Respiratory:A1Cresulthigh_noch                      1.068 0.285556
## diag_1Digestive:A1Cresulthigh_noch                        0.439 0.660529
## diag_1Injury and poisoning:A1Cresulthigh_noch             0.571 0.568305
## diag_1Musculoskeletal:A1Cresulthigh_noch                  1.496 0.134769
## diag_1Genitourinary:A1Cresulthigh_noch                   -0.557 0.577529
## diag_1Neoplasms:A1Cresulthigh_noch                        1.097 0.272509
## diag_1Other:A1Cresulthigh_noch                            2.175 0.029617 *
## diag_1Circulatory:A1CresultNormal                        -0.303 0.762024
## diag_1Respiratory:A1CresultNormal                        -2.384 0.017148 *
## diag_1Digestive:A1CresultNormal                          -0.312 0.754924
## diag_1Injury and poisoning:A1CresultNormal               -2.300 0.021475 *
## diag_1Musculoskeletal:A1CresultNormal                    -0.343 0.731937
## diag_1Genitourinary:A1CresultNormal                       0.890 0.373376
## diag_1Neoplasms:A1CresultNormal                           0.793 0.427912
## diag_1Other:A1CresultNormal                              -0.378 0.705192
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 42244  on 69972  degrees of freedom
## Residual deviance: 41240  on 69883  degrees of freedom
## AIC: 41420
##
## Number of Fisher Scoring iterations: 6
```

Model Performance and Discrimination

To describe the discriminative ability of the model over different possible cutoffs, we can resort to the receiver operating characteristic (ROC) plot. The area under the ROC curve (AUC) is a popular indicator of how well the model performs with regards to discrimination.

2. Report AUC from ROC.

```
require(pROC)

obs.y2 <- diabetic.data$readmitted # Observed
pred.y2 <- predict(fit_full, type = "response") # Predicted
rocobj <- roc(obs.y2, pred.y2) #ROC
```

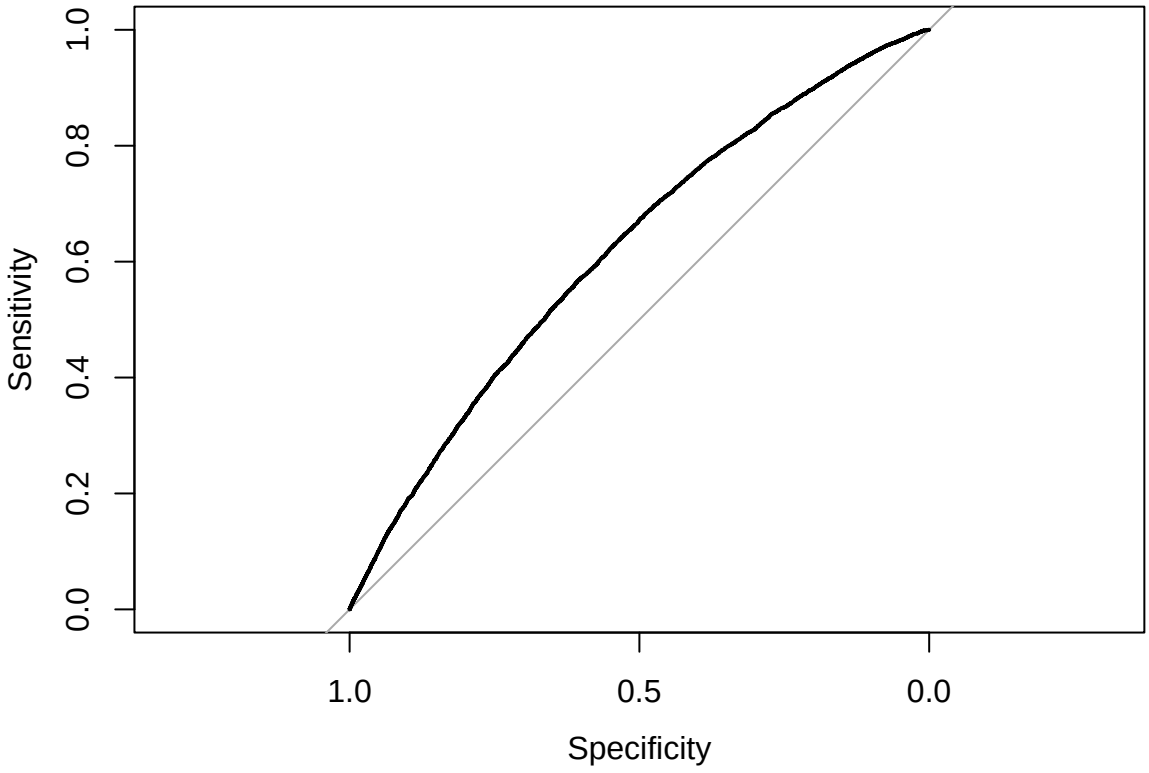
```
## Setting levels: control = NO, case = YES
```

```
## Setting direction: controls < cases
```

```
rocobj #looking at ROC object
```

```
##
## Call:
## roc.default(response = obs.y2, predictor = pred.y2)
##
## Data: pred.y2 in 63696 controls (obs.y2 NO) < 6277 cases (obs.y2 YES).
## Area under the curve: 0.6189
```

```
plot(rocobj) #ROC plot
```




```
auc(rocobj) #AUC
```

```
## Area under the curve: 0.6189
```

The AUC is 0.6189. This is not a great result (0.5 is no better than chance).

Validation

Previously, we considered measures of performance using the whole dataset, and predictions of the same observations that were used to build the model. For a more realistic assessment of the model's performance, the model should be validated, and there are a couple of options: split-sample validation and K-fold cross-validation (CV).

Cross-validation

3. Set up 5-fold cross-validation, fit logistic regression and obtain AUC from ROC from all the test datasets.

```
require(caret)

#control
trCntl <- trainControl(method = "cv", number = 5,
                       classProbs = TRUE,
```

```
                    summaryFunction = twoClassSummary)


#fit model with method glm and specify family of model to binomial()
#due to nature of outcome variable
fit_CV <- train(model.formula,
                trControl = trCntl,
                data = diabetic.data,
                method = "glm",
                family = binomial(),
                metric = "ROC")

fit_CV #look at model
```

```
## Generalized Linear Model
##
## 69973 samples
##     8 predictor
##     2 classes: 'NO', 'YES'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 55978, 55979, 55979, 55978, 55978
## Resampling results:
##
##   ROC        Sens  Spec
##   0.6091467  1     0
```

```
fit_CV$resample #look at results for each cross validation fold
```

```
##         ROC Sens Spec Resample
## 1 0.6096593    1    0    Fold1
## 2 0.6139256    1    0    Fold2
## 3 0.6017726    1    0    Fold3
## 4 0.6116908    1    0    Fold4
## 5 0.6086850    1    0    Fold5
```

```
mean(fit_CV$resample$ROC) #mean AUC for all test datasets/resamples
```

```
## [1] 0.6091467
```

Great. Above we utilize 5-fold cross-validation and fit a linear regression model. We obtain an average AUC of 0.6081 which, again, is not a great result.

Lasso, ridge or elastic net

4. Within 5 fold cross-validation, run the regularized regressions with the following parameter grids: `alpha = c(0,0.5,1), lambda = c(0.25, 0.75)`. Report the best alpha and lambda values the provides best AUC from ROC.

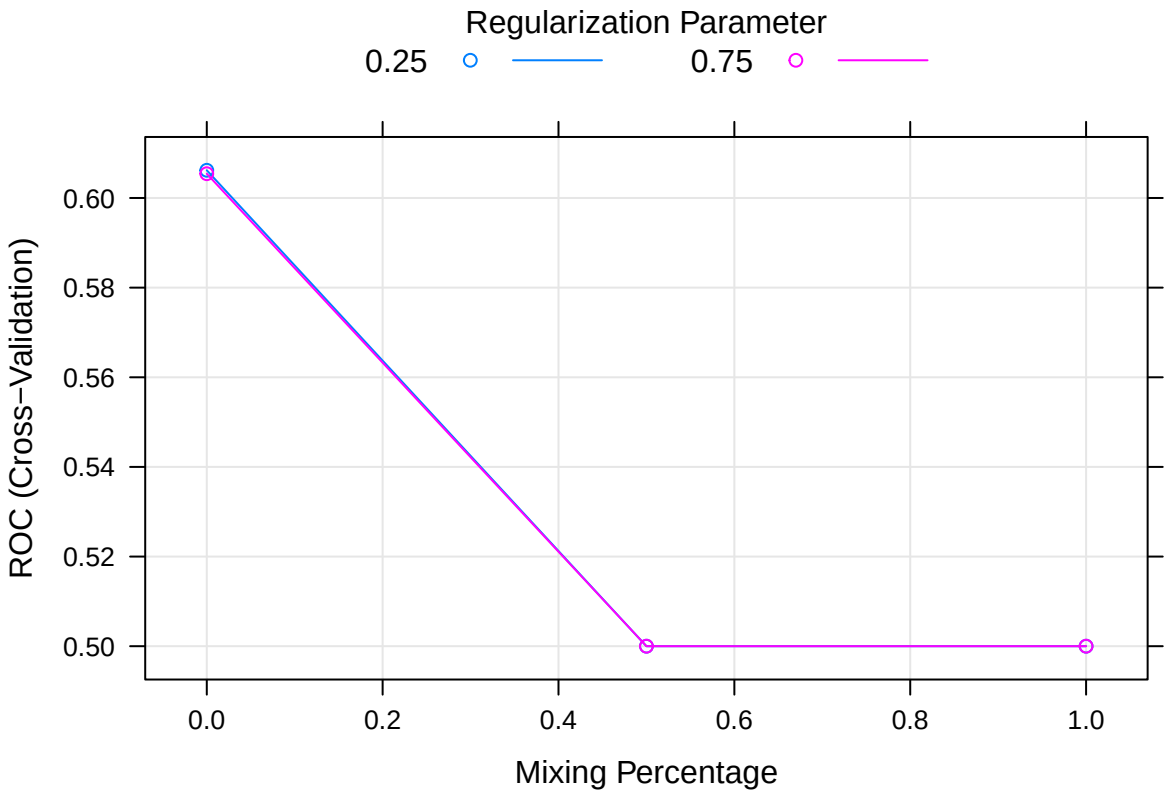
```
require(glmnet)

ctrl4 <- trainControl(method = "cv", number = 5,
                      classProbs = TRUE,
                      summaryFunction = twoClassSummary)

fit.cv.bin4 <- train(model.formula,
                     trControl = ctrl4,
                     data = diabetic.data,
                     method = "glmnet",
                     tuneGrid = expand.grid(alpha = c(0,0.5,1),
                                            lambda = c(0.25, 0.75)),
                     verbose = FALSE,
                     metric="ROC")

fit.cv.bin4 #look at the train object
```

```
## glmnet
##
## 69973 samples
##     8 predictor
##     2 classes: 'NO', 'YES'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 55979, 55978, 55979, 55978, 55978
## Resampling results across tuning parameters:
##
##   alpha  lambda  ROC        Sens  Spec
##   0.0    0.25    0.6061850  1     0
##   0.0    0.75    0.6054191  1     0
##   0.5    0.25    0.5000000  1     0
##   0.5    0.75    0.5000000  1     0
##   1.0    0.25    0.5000000  1     0
##   1.0    0.75    0.5000000  1     0
##
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were alpha = 0 and lambda = 0.25.
```

The largest ROC value (0.6070) is provided when alpha is 0 (ridge method) and lambda is 0.25.

5. Plot the AUC from ROCs for all combinations of parameter grids used in the previous analysis.

```
plot(fit.cv.bin4)
```



Decision Trees

In addition to regression methods, the data can be explored with decision trees (specification of interaction not necessary).

6. Within 5 fold cross-validation, run the regression trees.

```
require(caret)

#new model formula
model.formula0 <- as.formula("readmitted ~ discharge + race + source +
                             medical_specialty + time_in_hospital +
                             age + diag_1 + A1Cresult  +  time_in_hospital")

#control
ctrl6<-trainControl(method = "cv", number = 5,
                    classProbs = TRUE,
                    summaryFunction = twoClassSummary)

# fit the model with formula model.formula0
fit.cv.bin6<-train(model.formula0,
                   data = diabetic.data,
                   trControl = ctrl6,
                   method = "rpart",
                   metric="ROC")
```

```
fit.cv.bin6 #look at trained model object
```

```
## CART
##
## 69973 samples
##     8 predictor
##     2 classes: 'NO', 'YES'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 55978, 55979, 55978, 55979, 55978
## Resampling results across tuning parameters:
##
##   cp            ROC        Sens       Spec
##   1.448289e-05  0.5868245  0.9993092  0.0007966859
##   1.770131e-05  0.5664721  0.9994505  0.0007966859
##   3.186235e-05  0.5342055  0.9998430  0.0000000000
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was cp = 1.448289e-05.
```

Variable importance: Report the 5 most important predictor categories.

```
caret::varImp(fit.cv.bin6, scale = FALSE)
```

```
## rpart variable importance
##
##   only 20 most important variables shown (out of 30)
##
##                                        Overall
## dischargeOther                          99.145
## time_in_hospital                        70.355
## age[60, 100)                            46.844
## diag_1Respiratory                       19.249
## diag_1Musculoskeletal                   16.106
## diag_1Circulatory                       12.166
## medical_specialtyInternalMedicine        9.803
## diag_1Injury and poisoning               8.648
## medical_specialtySurgery                 8.204
## sourceReferral                           7.390
## medical_specialtyFamily/GeneralPractice  5.421
## A1CresultNormal                          4.655
## sourceOther                              4.536
## diag_1Other                              4.406
## A1Cresulthigh_noch                       3.815
## medical_specialtyMissing or Unknown      3.077
## raceOther                                3.065
## diag_1Neoplasms                          3.026
## raceMissing                              2.966
## raceCaucasian                            2.352
```

```
caret::varImp(fit.cv.bin6, scale = TRUE) #importance values scaled between 0 and 100
```

```
## rpart variable importance
##
##   only 20 most important variables shown (out of 30)
##
##                                        Overall
## dischargeOther                         100.000
## time_in_hospital                        70.961
## age[60, 100)                            47.248
## diag_1Respiratory                       19.415
## diag_1Musculoskeletal                   16.245
## diag_1Circulatory                       12.271
## medical_specialtyInternalMedicine        9.888
## diag_1Injury and poisoning               8.723
## medical_specialtySurgery                 8.275
## sourceReferral                           7.453
## medical_specialtyFamily/GeneralPractice  5.467
## A1CresultNormal                          4.696
## sourceOther                              4.575
## diag_1Other                              4.444
## A1Cresulthigh_noch                       3.848
## medical_specialtyMissing or Unknown      3.104
## raceOther                                3.091
## diag_1Neoplasms                          3.052
## raceMissing                              2.991
## raceCaucasian                            2.372
```

The 5 most important predictor categoreis are `dischargeOther`, `time_in_hopsital`, `age[60,100)`, `diag_1Respiratory` and `diag1_Musculoskeletal`.

Bagging

7. Within 5 fold cross-validation, run the bagging method.

```
ctrl7 <- trainControl(method = "cv", number = 5,
                      classProbs = TRUE,
                      summaryFunction = twoClassSummary)

fit.cv.bin7 <- train(model.formula0,
                     data = diabetic.data,
                     trControl = ctrl7,
                     method = "bag",
                     bagControl = bagControl(fit = ldaBag$fit,
                                             predict = ldaBag$pred,
                                             aggregate = ldaBag$aggregate),
                     metric="ROC")
```

```
## Warning: executing %dopar% sequentially: no parallel backend registered
```

```
fit.cv.bin7
```

```
## Bagged Model
##
## 69973 samples
##     8 predictor
##     2 classes: 'NO', 'YES'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 55978, 55978, 55979, 55978, 55979
## Resampling results:
##
##   ROC        Sens  Spec
##   0.6061965  1     0
##
## Tuning parameter 'vars' was held constant at a value of 25
```

Variable importance: Report the 5 most important predictor categories.

```
caret::varImp(fit.cv.bin7, scale = FALSE)
```

```
## ROC curve variable importance
##
##                   Importance
## discharge             0.5785
## time_in_hospital      0.5599
## age                   0.5379
## medical_specialty     0.5096
## source                0.5094
## race                  0.5088
## A1Cresult             0.5064
## diag_1                0.5055
```

```
caret::varImp(fit.cv.bin7, scale = TRUE) # Scaled between 0 and 100
```

```
## ROC curve variable importance
##
##                   Importance
## discharge            100.000
## time_in_hospital      74.523
## age                   44.357
## medical_specialty      5.584
## source                 5.301
## race                   4.463
## A1Cresult              1.175
## diag_1                 0.000
```

The 5 most important predictor categories when using the bagging method are: `discharge`, `time_in_hospital`, `age`, `medical_speciality` and `source`. Slightly different than the results of the CART/Decision Tree.

Boosting

8. Within 5 fold cross-validation, run the boosting method.

```
ctrl8 <- trainControl(method = "cv", number = 5,
                      classProbs = TRUE,
                      summaryFunction = twoClassSummary)

fit.cv.bin8 <- train(model.formula0,
                data = diabetic.data,
                trControl = ctrl8,
                method = "gbm",
                verbose = FALSE,
                metric="ROC")
```

Variable importance: Report the 5 most important predictor categories.

```
caret::varImp(fit.cv.bin8, scale = FALSE)
```

```
## gbm variable importance
##
##   only 20 most important variables shown (out of 25)
##
##                                        Overall
## dischargeOther                         138.315
## time_in_hospital                        68.774
## age[60, 100)                            17.293
## diag_1Circulatory                       12.248
## diag_1Respiratory                       11.614
## medical_specialtyInternalMedicine       10.160
## sourceReferral                           9.088
## sourceOther                              8.964
## diag_1Genitourinary                      8.387
## diag_1Musculoskeletal                    6.772
## medical_specialtySurgery                 6.272
## raceMissing                              5.936
## diag_1Other                              5.812
## medical_specialtyFamily/GeneralPractice  5.779
## diag_1Injury and poisoning               5.689
## medical_specialtyMissing or Unknown      4.436
## raceOther                                4.310
## medical_specialtyOther                   3.856
## diag_1Neoplasms                          3.720
## A1CresultNormal                          3.545
```

```
caret::varImp(fit.cv.bin8, scale = TRUE) # Scaled between 0 and 100
```

```
## gbm variable importance
##
##   only 20 most important variables shown (out of 25)
##
##                                        Overall
```

```
## dischargeOther                           100.000
## time_in_hospital                          49.617
## age[60, 100)                              12.318
## diag_1Circulatory                          8.663
## diag_1Respiratory                          8.203
## medical_specialtyInternalMedicine          7.150
## sourceReferral                             6.373
## sourceOther                                6.283
## diag_1Genitourinary                        5.866
## diag_1Musculoskeletal                      4.695
## medical_specialtySurgery                   4.333
## raceMissing                                4.089
## diag_1Other                                4.000
## medical_specialtyFamily/GeneralPractice    3.975
## diag_1Injury and poisoning                 3.911
## medical_specialtyMissing or Unknown        3.003
## raceOther                                  2.912
## medical_specialtyOther                     2.583
## diag_1Neoplasms                            2.484
## A1CresultNormal                            2.357
```

The 5 most important predictor categories when using the boosting method are: `dischargeOther`, `time_in_hospital`, `age[60, 100)`, `diag_1Circulatory` and `medical_specialtyInternalMedicine`. Slightly different than the results than both the CART/Decision Tree and the bagging method.

Relevant Paper: [1] Beata Strack, Jonathan P. DeShazo, Chris Gennings, Juan L. Olmo, Sebastian Ventura, Krzysztof J. Cios, John N. Clore, "Impact of HbA1c Measurement on Hospital Readmission Rates: Analysis of 70,000 Clinical Database Patient Records", BioMed Research International, vol. 2014, Article ID 781670, 11 pages, 2014. https://doi.org/10.1155/2014/781670