Random Forest

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2023-04-30

```
library(dplyr)
dat <- read.csv('brfss_final.csv')
outcome <- data.frame(dat$X,dat$MICHD,dat$CVDINFR4,dat$CVDCRHD4)
outcome %>% group_by(dat.MICHD) %>% summarise(count=n())
```

```
## # A tibble: 2 x 2
##   dat.MICHD count
##       <int> <int>
## 1         1 14580
## 2         2 14580
```

```
outcome %>% group_by(dat.CVDINFR4) %>% summarise(count=n())
```

```
## # A tibble: 4 x 2
##   dat.CVDINFR4 count
##          <int> <int>
## 1            1  9188
## 2            2 19802
## 3            7   160
## 4            9    10
```

```
outcome %>% group_by(dat.CVDCRHD4) %>% summarise(count=n())
```

```
## # A tibble: 4 x 2
##   dat.CVDCRHD4 count
##          <int> <int>
## 1            1  9729
## 2            2 18874
## 3            7   550
## 4            9     7
```

```
## remove the ones that responded don't know & not sure in CVDINFR4 & CVDCRHD4
dat <- dat[-which(dat$CVDINFR4 == 7 | dat$CVDINFR4 == 9),]
dat <- dat[-which(dat$CVDCRHD4 == 7 | dat$CVDCRHD4 == 9),]
# remove columns that has only 1 value for all rows
dat <- dat[ , -which(names(dat) %in% c("MEDSHEPB","TOLDCFS", "HAVECFS", "WORKCFS"))]
```

Drop columns with more than 5% data missing, impute the rest using KNN

```
# convert outcome variables
dat$MICHD <- factor(2-dat$MICHD)
dat$CVDINFR4 <- factor(2-dat$CVDINFR4)
dat$CVDCRHD4 <- factor(2-dat$CVDCRHD4)
# i believe X is the index column, not needed
# remove weights
dat <- dat[, !colnames(dat) %in% c('X', 'LLCPWT2', 'LLCPWT', 'CLLCPWT','STRWT','WT2RAKE')]
dat <- dat[, !colnames(dat) %in% c('QSTVER', 'STSTR','RAWRAKE')] # remove based on knowledge
threshold <- .05
ncol(dat) # 190
```

```
## [1] 187
```

```
dat <- dat[, colMeans(is.na(dat)) <= threshold]
ncol(dat) # 52 columns left
```

```
## [1] 49
```

```
columns_to_impute <- colnames(dat)[colSums(is.na(dat)) > 0]
columns_to_impute
```

```
##  [1] "CPDEMO1B" "VETERAN3" "EMPLOY1"  "INCOME3"  "DEAF"     "BLIND"   
##  [7] "DECIDE"   "DIFFWALK" "DIFFDRES" "DIFFALON" "USENOW3"  "METSTAT" 
## [13] "URBSTAT"  "MSCODE"   "DRDXAR3" 
```

```
str(dat[,columns_to_impute])
```

```
## ’data.frame’:    28433 obs. of  15 variables:
##  $ CPDEMO1B: int  1 1 8 1 1 8 8 1 1 2 ...
##  $ VETERAN3: int  2 2 2 2 1 2 1 2 2 2 ...
##  $ EMPLOY1 : int  8 7 2 7 7 7 7 8 7 7 ...
##  $ INCOME3 : int  77 3 99 77 7 99 5 77 5 10 ...
##  $ DEAF    : int  2 2 2 2 2 2 1 2 2 2 ...
##  $ BLIND   : int  1 2 2 2 2 2 2 2 2 2 ...
##  $ DECIDE  : int  1 2 1 2 1 2 2 2 2 2 ...
##  $ DIFFWALK: int  1 2 2 2 2 1 1 1 2 2 ...
##  $ DIFFDRES: int  2 2 2 2 2 1 2 2 2 2 ...
##  $ DIFFALON: int  1 2 2 2 2 1 1 2 2 2 ...
##  $ USENOW3 : int  3 3 3 3 3 3 3 3 3 3 ...
##  $ METSTAT : int  1 1 1 1 1 2 1 2 1 1 ...
##  $ URBSTAT : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ MSCODE  : int  2 1 3 1 3 2 2 5 2 3 ...
##  $ DRDXAR3 : int  1 2 1 1 2 1 1 2 1 1 ...
```

```
complete_columns <- colnames(dat)[colSums(is.na(dat)) == 0 &
                                      !colnames(dat) %in% c('MICHD', 'CVDINFR4','CVDCRHD4')]
for (c in columns_to_impute) {
    col <- dat[[c]]
    scaled <- scale(dat[, complete_columns])
    knn <- knn(
        train = scaled[!is.na(col), complete_columns],
        test  = scaled[is.na(col), complete_columns],
        cl    = dat[!is.na(col), c]
        )

    dat[is.na(col), c] = knn
}
colSums(is.na(dat))
```

```
##  GENHLTH PHYSHLTH MENTHLTH PRIMINSR PERSDOC3 MEDCOST1 CHECKUP1 CVDINFR4
##        0        0        0        0        0        0        0        0
## CVDCRHD4 CVDSTRK3 CHCSCNCR CHCOCNCR CHCCOPD3 ADDEPEV3 CHCKDNY2 DIABETE4
##        0        0        0        0        0        0        0        0
##  MARITAL RENTHOM1 NUMHHOL3 CPDEMO1B VETERAN3  EMPLOY1  INCOME3     DEAF
##        0        0        0        0        0        0        0        0
##    BLIND   DECIDE DIFFWALK DIFFDRES DIFFALON  USENOW3  QSTLANG  METSTAT
##        0        0        0        0        0        0        0        0
##  URBSTAT   MSCODE  DUALUSE  TOTINDA  RFHYPE6  CHOLCH3    MICHD  ASTHMS1
##        0        0        0        0        0        0        0        0
##  DRDXAR3     RACE      SEX    AGE80  CHLDCNT   EDUCAG  SMOKER3  CURECI1
##        0        0        0        0        0        0        0        0
## DROCDY3_
##        0
```

```
library(caret)
```

```
## Loading required package: ggplot2

## Loading required package: lattice
```

```
library(randomForest)
```

```
## randomForest 4.7-1.1

## Type rfNews() to see new features/changes/bug fixes.

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:ggplot2':
##
##     margin

## The following object is masked from 'package:dplyr':
##
##     combine
```

```r
library(ggplot2)
library(ROCR)
set.seed(263)
train_index <- createDataPartition(dat$MICHD, p = 0.8, list = FALSE)
train <- dat[train_index, ]
test <- dat[-train_index, ]
train$weights <- ifelse(as.numeric(train$MICHD) == 1,
                        1/mean(as.numeric(train$MICHD) == 1),
                        1/(1-mean(as.numeric(train$MICHD) == 1)))
train$weights <- as.numeric(train$weights)
test$weights <- ifelse(as.numeric(test$MICHD) == 1,
                        1/mean(as.numeric(test$MICHD) == 1),
                        1/(1-mean(as.numeric(test$MICHD) == 1)))
test$weights <- as.numeric(test$weights)
index_weight <- which(names(train) == "weights")
```

Parameter Tuning

Let's tune number of trees ntrees and number of features selected to place split mtry. In the following, let's use 10-fold cross-validation.

```r
## get index of the other two outcomes

index_michd <- which(names(train) == "MICHD")
index_infr <- which(names(train) == "CVDINFR4")
index_crhd <- which(names(train) == "CVDCRHD4")
```

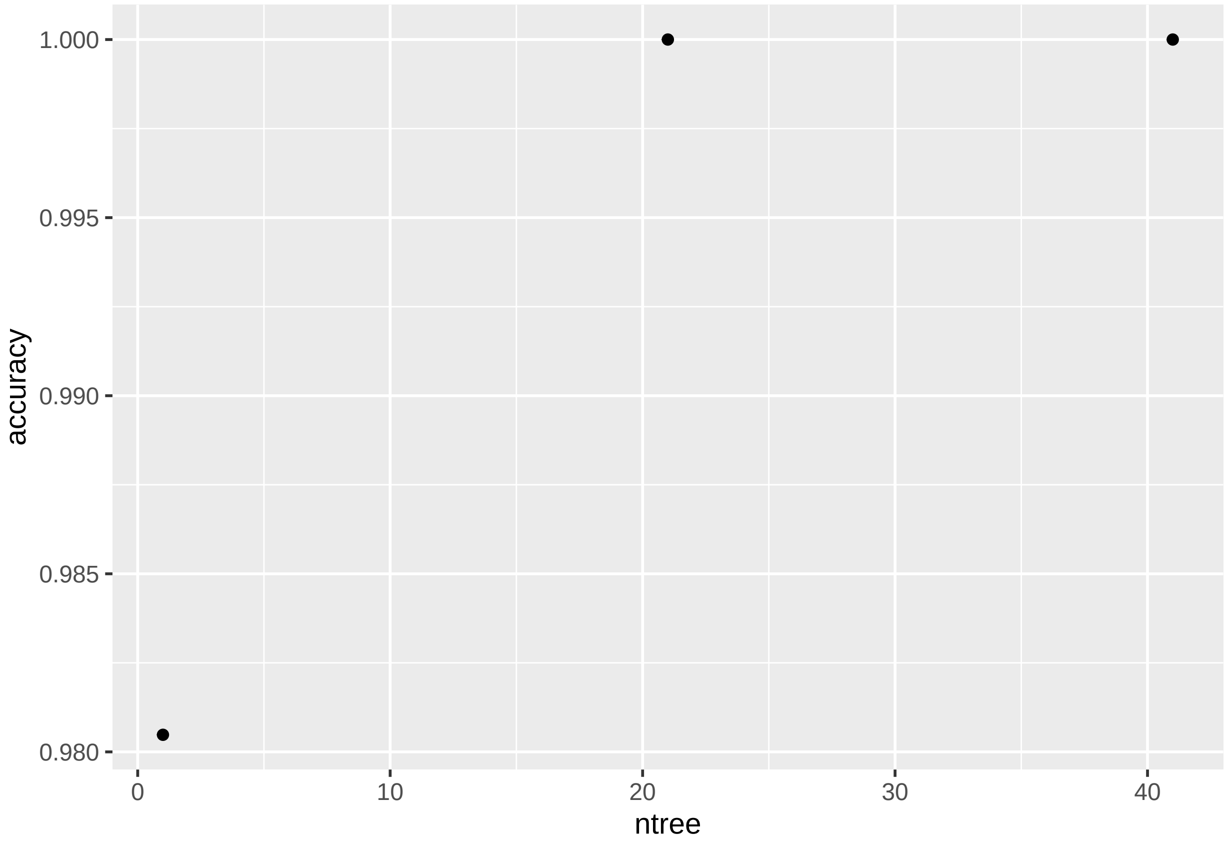
Tune number of trees

Let's set mtry = 10.

```r
ntree <- seq(1, 51, by = 20)
accuracy <- sapply(ntree, function(n){
  train(as.factor(MICHD) ~ ., method = "rf",
        data = train[, -c(index_infr, index_crhd)],
        tuneGrid = data.frame(mtry = 10),
        ntree = n, trControl = trainControl(method = "cv", number = 10))$results$Accuracy
})

qplot(ntree, accuracy)
```

```
## Warning: ‘qplot()‘ was deprecated in ggplot2 3.4.0.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_lifecycle_warnings()‘ to see where this warning was
## generated.
```



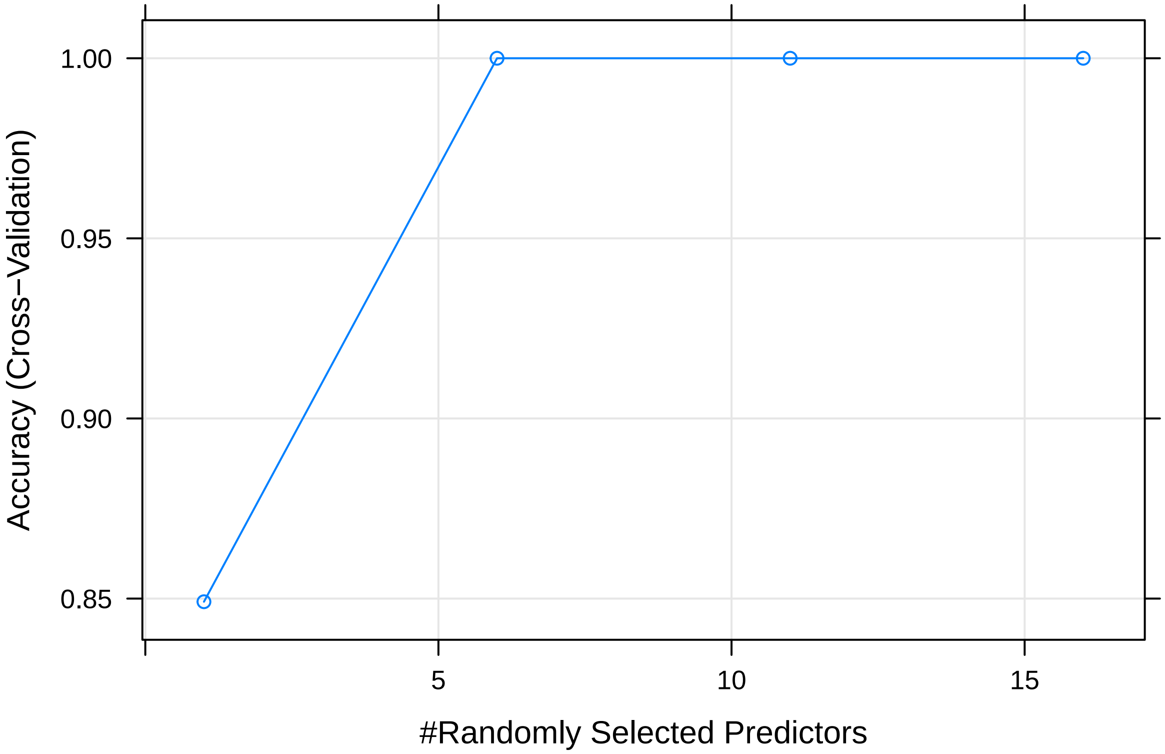
```
best_ntree <- ntree[which(accuracy == max(accuracy))]
best_ntree <- min(best_ntree)
print(paste("The best ntree is", best_ntree))
```

```
## [1] "The best ntree is 21"
```

Tune mtry

```
train_rf <- train(as.factor(MICHD) ~ ., method = "rf",
                  data = train[, -c(index_infr, index_crhd)],
                  tuneGrid = data.frame(mtry = seq(1, 20, by = 5)),
                  ntree = best_ntree,
                  nodesize = 10, trControl = trainControl(method = "cv", number = 10))

plot(train_rf)
```



```
best_mtry <- train_rf$bestTune

result_cv <- train_rf$results

print(paste("The best mtry is ", best_mtry))
```

```
## [1] "The best mtry is  6"
```

Use the best model to train random forest

The below is the confusion matrix on the test set.

```
rf_best <- randomForest(as.factor(MICHD) ~.,
                        data = train[, -c(index_infr, index_crhd)],
                        mtry = best_mtry[[1]], ntree = best_ntree, nodesize = 10,
                        weights = train[, index_weight])

pred_test <- predict(rf_best, newdata = test)
cm_test <- confusionMatrix(pred_test, as.factor(test$MICHD))

cm_test
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##          0 2916    0
##          1    0 2770
##                                           
##                Accuracy : 1          
##                  95% CI : (0.9994, 1)
##     No Information Rate : 0.5128     
##     P-Value [Acc > NIR] : < 2.2e-16  
##                                      
##                   Kappa : 1          
##                                      
##  Mcnemar’s Test P-Value : NA         
##                                      
##             Sensitivity : 1.0000     
##             Specificity : 1.0000     
##          Pos Pred Value : 1.0000     
##          Neg Pred Value : 1.0000     
##              Prevalence : 0.5128     
##          Detection Rate : 0.5128     
##    Detection Prevalence : 0.5128     
##       Balanced Accuracy : 1.0000     
##                                      
##        ’Positive’ Class : 0          
##
```

```
metric_test <- c(cm_test$overall[["Accuracy"]],
                 cm_test$byClass[c("Sensitivity","Specificity")])

cat(paste("The overall accuracy using the best tuned random forest model is",
      metric_test[1], "\n",
      "Sensitivity is", metric_test[2], "\n",
      "Specificity is", metric_test[3]))
```

```
## The overall accuracy using the best tuned random forest model is 1
##  Sensitivity is 1
##  Specificity is 1
```

ROC curve

```
library(pROC)
```

```
## Type ’citation("pROC")’ for a citation.
```

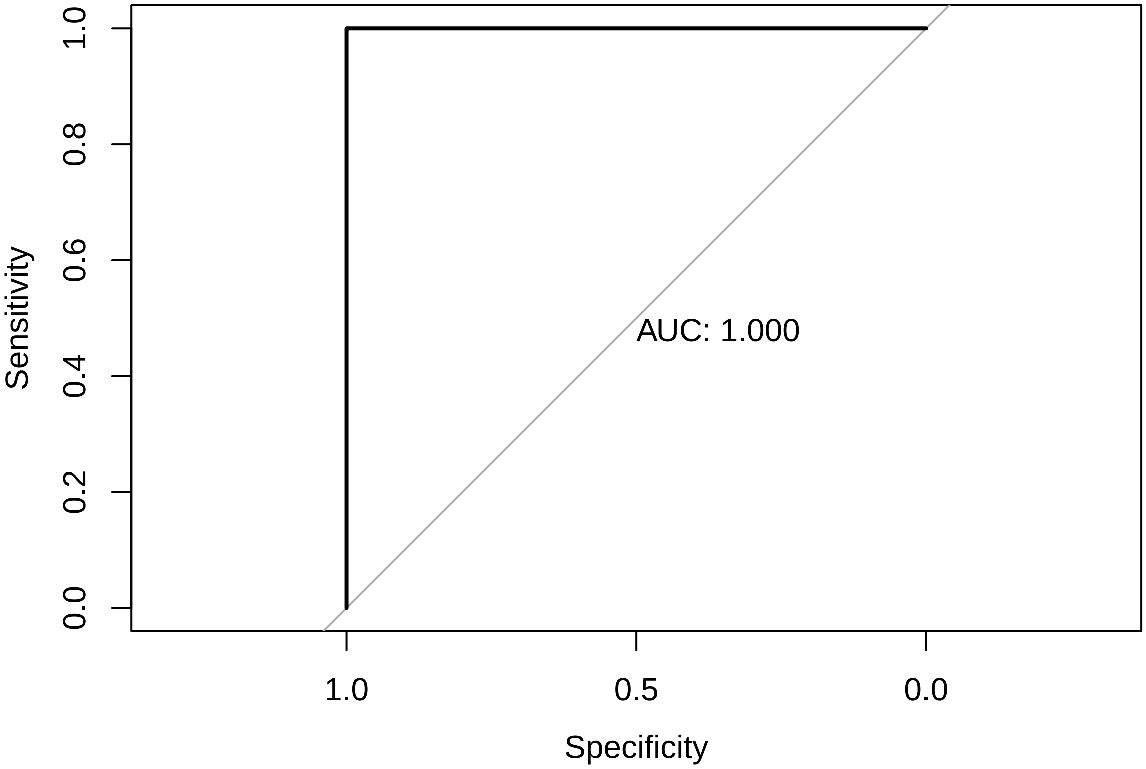
```
##
## Attaching package: ’pROC’
```

```
## The following objects are masked from ’package:stats’:
##
##     cov, smooth, var
```

```
roc_rf <- roc(as.numeric(test$MICHD) ~ as.numeric(pred_test),
              plot = TRUE, print.auc = TRUE)
```

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

## Setting direction: controls < cases
```



```
print(paste("AUC is", as.numeric(roc_rf$auc)))
```

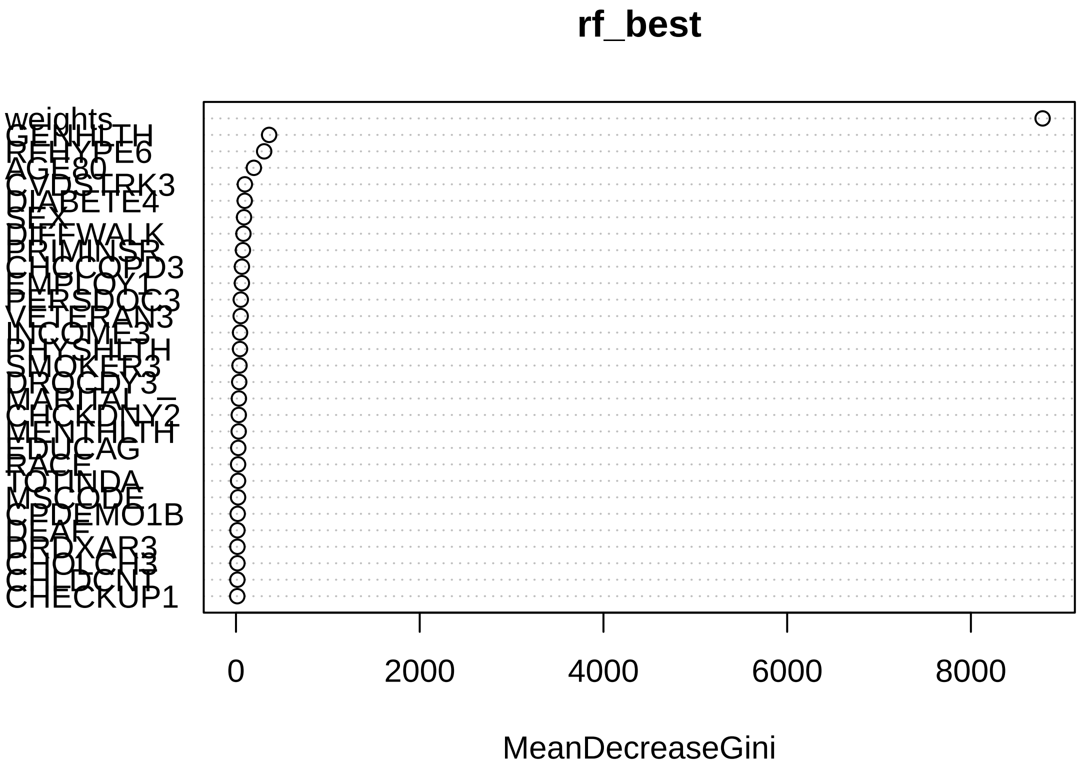
```
## [1] "AUC is 1"
```

Importance Features

```
importance(rf_best)
```

```
##          MeanDecreaseGini
## GENHLTH        360.720462
## PHYSHLTH        43.739617
## MENTHLTH        29.481553
## PRIMINSR        75.467046
## PERSDOC3        52.246191
## MEDCOST1         5.284555
## CHECKUP1        13.956534
## CVDSTRK3        96.536046
## CHCSCNCR        12.910459
## CHCOCNCR        12.117497
## CHCCOPD3        64.222906
## ADDEPEV3         9.708542
## CHCKDNY2        30.446637
## DIABETE4        95.214158
## MARITAL         31.696165
## RENTHOM1        10.207899
## NUMHHOL3        11.784564
## CPDEMO1B        18.481098
## VETERAN3        51.136403
## EMPLOY1         64.174316
## INCOME3         43.994866
## DEAF            15.830642
## BLIND            9.694895
## DECIDE          12.299206
## DIFFWALK        80.982118
## DIFFDRES         6.013997
## DIFFALON        12.001085
## USENOW3          7.430666
## QSTLANG          1.421211
## METSTAT          6.495710
## URBSTAT          8.018690
## MSCODE          22.443519
## DUALUSE          6.289627
## TOTINDA         22.608564
## RFHYPE6        306.700294
## CHOLCH3         15.485804
## ASTHMS1         12.242061
## DRDXAR3         15.631956
## RACE            22.757610
## SEX             87.361339
## AGE80          194.670975
## CHLDCNT         15.164496
## EDUCAG          24.949759
## SMOKER3         38.365643
## CURECI1          6.300702
## DROCDY3_        35.322971
## weights       8780.709056
```

```
varImpPlot(rf_best)
```


rf_best
weights
GENHLTH
RFHYPE6
AGE80
CVDSTRK3
DIABETE4
SEX
DIFFWALK
PRIMINSR
CHCCOPD3
EMPLOY1
PERSDOC3
VETERAN3
INCOME3
PHYSHLTH
SMOKER3
DROCDY3_
MARITAL
CHCKDNY2
MENTHLTH
EDUCAG
RACE
TOTINDA
MSCODE
CPDEMO1B
DEAF
DRDXAR3
CHOLCHK3
CHLDCNT
CHECKUP1
0
2000
4000
6000
8000
MeanDecreaseGini