HW 7 - KELLY “SCOTT” SIMS

Code

Using the same crime data set uscrime.txt as in Questions 8.2 and 9.1, find the best model you can using (a) a regression tree model, and (b) a random forest model. In R, you can use the tree package or the rpart package, and the randomForest package. For each model, describe one or two qualitative takeaways you get from analyzing the results (i.e., don’t just stop when you have a good model, but interpret it too).

Load Libraries

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```
library(rsample)     # data splitting
library(dplyr)       # data wrangling
library(rpart)       # performing regression trees
library(rpart.plot)  # plotting regression trees
library(randomForest)
library(h2o)
library(ggplot2)
library(caTools)
library(caret)
library(pROC)
```

Load the data and inspect

Hide

```
data <- read.table('uscrime.txt', header = TRUE, stringsAsFactors = FALSE)
#Separate independent and dependent variables just in case
Y = as.data.frame((data[,16]))
X = as.data.frame(data[,1:15])
head(data)
```

	M <dbl>	So <int>	Ed <dbl>	Po1 <dbl>	Po2 <dbl>	LF <dbl>	M.F <dbl>	Pop <int>	NW <dbl>
1	15.1	1	9.1	5.8	5.6	0.510	95.0	33	30.1
2	14.3	0	11.3	10.3	9.5	0.583	101.2	13	10.2
3	14.2	1	8.9	4.5	4.4	0.533	96.9	18	21.9
4	13.6	0	12.1	14.9	14.1	0.577	99.4	157	8.0
5	14.1	0	12.1	10.9	10.1	0.591	98.5	18	3.0
6	12.1	0	11.0	11.8	11.5	0.547	96.4	25	4.4

6 rows | 1-10 of 16 columns

CART

With regressions trees, there’s no need to scale the data before constructing a model. See quote below as noted from stats.stackexchange.com

> “Standardization does not add or subtract information contained in a given variable and does not distort its relationship to a target variable. For example, if you had a variable”age" which was a predictor for “purchase car”. By changing age to (age - mean / sd) is not going to change its relationship to purchase car, it merely maps it to a new space. When CART looks for the best splits, it going to use entropy or gini to calculate information gain, this is not dependent on the scale of your predictor variable, rather on the resultant purity of the variable “purchase car”."

Build the CART model

Hide

```
cart_model <- rpart(
  formula = Crime ~ .,
  data    = data,
  method  = "anova"
  )
summary(cart_model)
```

```
Call:
rpart(formula = Crime ~ ., data = data, method = "anova")
  n= 47

          CP nsplit rel error    xerror      xstd
1 0.36296293      0 1.0000000 1.0305847 0.2597006
2 0.14814320      1 0.6370371 0.9549942 0.2291904
3 0.05173165      2 0.4888939 1.0562329 0.2361933
4 0.01000000      3 0.4371622 1.0693713 0.2362816

Variable importance
   Po1    Po2 Wealth   Ineq   Prob      M     NW    Pop   Time     Ed     LF     So
    17     17     11     11     10     10      9      5      4      4      1      1

Node number 1: 47 observations,    complexity param=0.3629629
  mean=905.0851, MSE=146402.7
  left son=2 (23 obs) right son=3 (24 obs)
  Primary splits:
      Po1    < 7.65      to the left,  improve=0.3629629, (0 missing)
      Po2    < 7.2       to the left,  improve=0.3629629, (0 missing)
      Prob   < 0.0418485 to the right, improve=0.3217700, (0 missing)
      NW     < 7.65      to the left,  improve=0.2356621, (0 missing)
      Wealth < 6240      to the left,  improve=0.2002403, (0 missing)
  Surrogate splits:
      Po2    < 7.2       to the left,  agree=1.000, adj=1.000, (0 split)
      Wealth < 5330      to the left,  agree=0.830, adj=0.652, (0 split)
      Prob   < 0.043598  to the right, agree=0.809, adj=0.609, (0 split)
      M      < 13.25     to the right, agree=0.745, adj=0.478, (0 split)
      Ineq   < 17.15     to the right, agree=0.745, adj=0.478, (0 split)

Node number 2: 23 observations,    complexity param=0.05173165
  mean=669.6087, MSE=33880.15
  left son=4 (12 obs) right son=5 (11 obs)
  Primary splits:
      Pop < 22.5      to the left,  improve=0.4568043, (0 missing)
      M   < 14.5      to the left,  improve=0.3931567, (0 missing)
      NW  < 5.4       to the left,  improve=0.3184074, (0 missing)
      Po1 < 5.75      to the left,  improve=0.2310098, (0 missing)
      U1  < 0.093     to the right, improve=0.2119062, (0 missing)
  Surrogate splits:
      NW   < 5.4       to the left,  agree=0.826, adj=0.636, (0 split)
      M    < 14.5      to the left,  agree=0.783, adj=0.545, (0 split)
      Time < 22.30055  to the left,  agree=0.783, adj=0.545, (0 split)
      So   < 0.5       to the left,  agree=0.739, adj=0.455, (0 split)
      Ed   < 10.85     to the right, agree=0.739, adj=0.455, (0 split)

Node number 3: 24 observations,    complexity param=0.1481432
  mean=1130.75, MSE=150173.4
  left son=6 (10 obs) right son=7 (14 obs)
  Primary splits:
      NW   < 7.65      to the left,  improve=0.2828293, (0 missing)
      M    < 13.05     to the left,  improve=0.2714159, (0 missing)
      Time < 21.9001   to the left,  improve=0.2060170, (0 missing)
```

```
      M.F  < 99.2      to the left,  improve=0.1703438, (0 missing)
      Po1  < 10.75     to the left,  improve=0.1659433, (0 missing)
  Surrogate splits:
      Ed   < 11.45     to the right, agree=0.750, adj=0.4, (0 split)
      Ineq < 16.25     to the left,  agree=0.750, adj=0.4, (0 split)
      Time < 21.9001   to the left,  agree=0.750, adj=0.4, (0 split)
      Pop  < 30        to the left,  agree=0.708, adj=0.3, (0 split)
      LF   < 0.5885    to the right, agree=0.667, adj=0.2, (0 split)

Node number 4: 12 observations
  mean=550.5, MSE=20317.58

Node number 5: 11 observations
  mean=799.5455, MSE=16315.52

Node number 6: 10 observations
  mean=886.9, MSE=55757.49

Node number 7: 14 observations
  mean=1304.929, MSE=144801.8
```

The summary statistic above explains steps of the splits. For example, we start with n = 47 observations at the root node (very beginning) and the first variable we split on (the first variable that optimizes a reduction in SSE) is Po1. Node #2 has 23 observations and is split on Pop. Opposite of that node is Node #3 being split on NW. We could continue to analyze these superfluous statistics, but it is much easier to just visualize the tree itself.

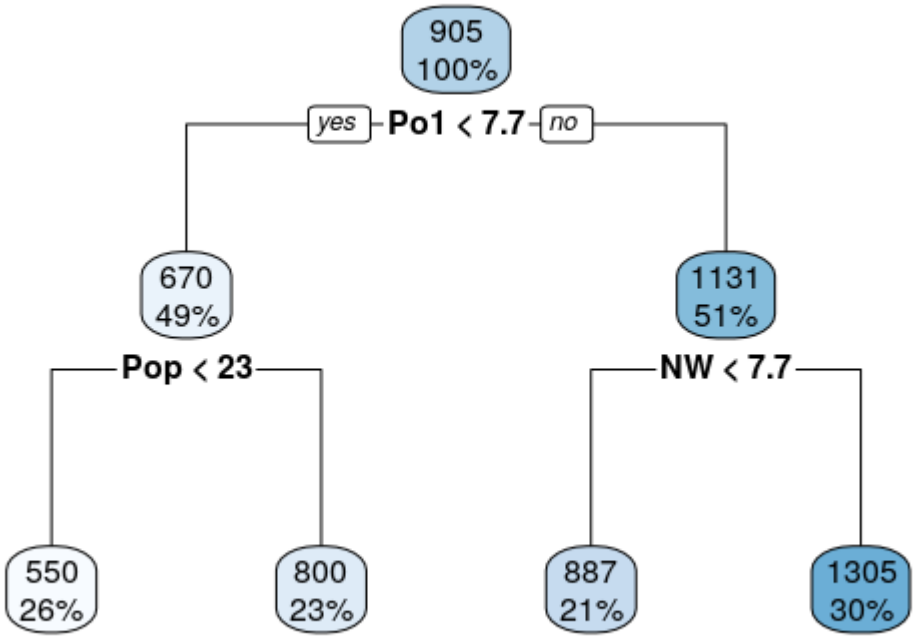
#Note:

At the very top of the summary statistics above, there is a cp table which lists the 4 nodes after 3 splits. For the 3rd split, we see the xerror term is *1.005*. This is what we will be trying to imporve upon

Plot the Regression Tree

Hide

```
rpart.plot(cart_model)
```



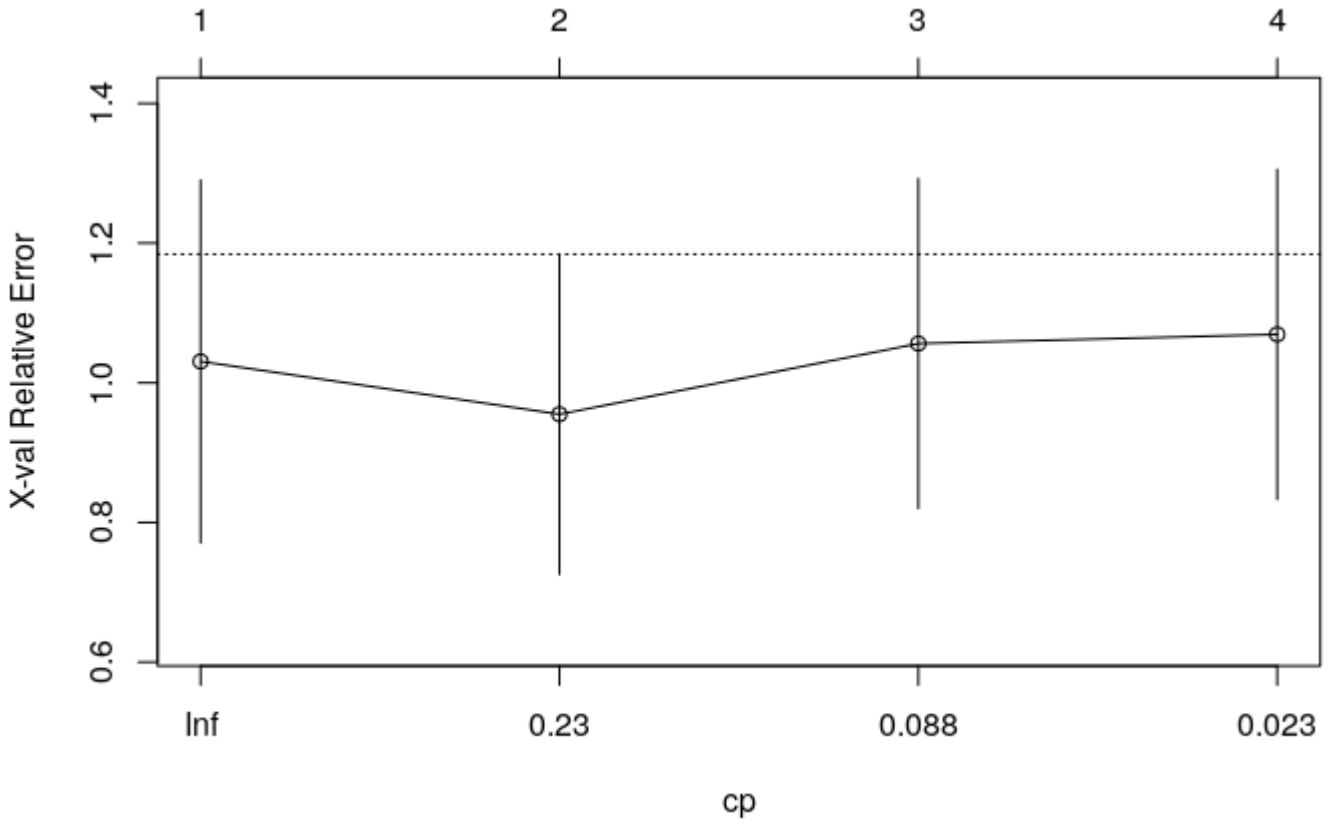
This visualization makes it easier to see that in the initial model, there were only three splits performed. These splits coincide with what was stated above, Po1 being the most important factor followed by Pop and NW respectively. But if three features are being split upon, what about the other 12 features in the model? According to the post below, rpart is doing the following behind the scenes

> Behind the scenes rpart is automatically applying a range of cost complexity (αlpha) values to prune the tree. To compare the error for each αlpha value, rpart performs a 10-fold cross validation so that the error associated with a given αlpha value is computed on the hold-out validation data.

In this example, we find diminishing returns for the 4 terminal nodes as seen blelow. The y-axis is the cross validation error. The lower x-axis is cost complexity parameter (alpha), and the upper x-axis is the number of terminal nodes. The complexity parameter (cp) is used to control the size of the decision tree and to select the optimal tree size. If the cost of adding another variable to the decision tree from the current node is above the value of cp, then tree building does not continue. We could also say that tree construction does not continue unless it would decrease the overall lack of fit by a factor of cp.

Hide

```
plotcp(cart_model)
```



Tuning the model with Gridsearch

In addition to the cost complexity parameter, it is also common to tune:

1. minsplit: the minimum number of data points required to attempt a split before it is forced to create a terminal node. The default is 20. Making this smaller allows for terminal nodes that may contain only a handful of observations to create the predicted value.
2. maxdepth: the maximum number of internal nodes between the root node and the terminal nodes. The default is 30, which is quite liberal and allows for fairly large trees to be built.

To perform a grid search we first create our hyperparameter grid. In this example, I search a range of minsplit from 1-20 and vary maxdepth from 2-15. This gives 280 different hyperparameter combinations to try.

Hide

```
hyper_grid <- expand.grid(
  minsplit = seq(1, 20, 1),
  maxdepth = seq(2, 15, 1)
)
head(hyper_grid)
```

	minsplit <dbl>	maxdepth <dbl>
1	1	2
2	2	2
3	3	2

	minsplit <dbl>	maxdepth <dbl>
4	4	2
5	5	2
6	6	2

6 rows

Hide

```
length(hyper_grid[,1])
```

```
[1] 280
```

Iterate through the hypergrid creating a model for each combination

We will store the resulting model in a list called models. We will use this list of models to extract the best one

Hide

```
models <- list()
for (i in 1:nrow(hyper_grid)) {

  # get minsplit, maxdepth values at row i
  minsplit <- hyper_grid$minsplit[i]
  maxdepth <- hyper_grid$maxdepth[i]
  # train a model and store in the list
  models[[i]] <- rpart(
    formula = Crime ~ .,
    data    = data,
    method  = "anova",
    control = list(minsplit = minsplit, maxdepth = maxdepth)
    )
}
```

Extract the best performing models, and their subsequent hyperparameters

Next, from each model, we will extract the lowest **xerror** and the lowest **cp** value for each model, and append those values to the hypergrid next to their subseqent hyperparameters. We will then sort the hypergrid by lowest error and pick the best performing model.

Hide

```
# function to get optimal cp
get_cp <- function(x) {
  min    <- which.min(x$cptable[, "xerror"])
  cp <- x$cptable[min, "CP"]
}
# function to get minimum error
get_min_error <- function(x) {
  min    <- which.min(x$cptable[, "xerror"])
  xerror <- x$cptable[min, "xerror"]
}
hyper_grid %>%
  mutate(
    cp    = purrr::map_dbl(models, get_cp),
    error = purrr::map_dbl(models, get_min_error)
    ) %>%
  arrange(error) %>%
  top_n(-5, wt = error)
```

minsplit <dbl>	maxdepth <dbl>	cp <dbl>	error <dbl>
17	6	0.01	0.6916775
4	11	0.01	0.7063107
7	14	0.01	0.7092623
10	11	0.01	0.7202334
3	7	0.01	0.7296096

5 rows

We Can see above that the best performing model was one that has a minsplit of 8, maxdepth of 9 and a cp of 0.01. Let's build this model and visualize the resulting tree

Best Model

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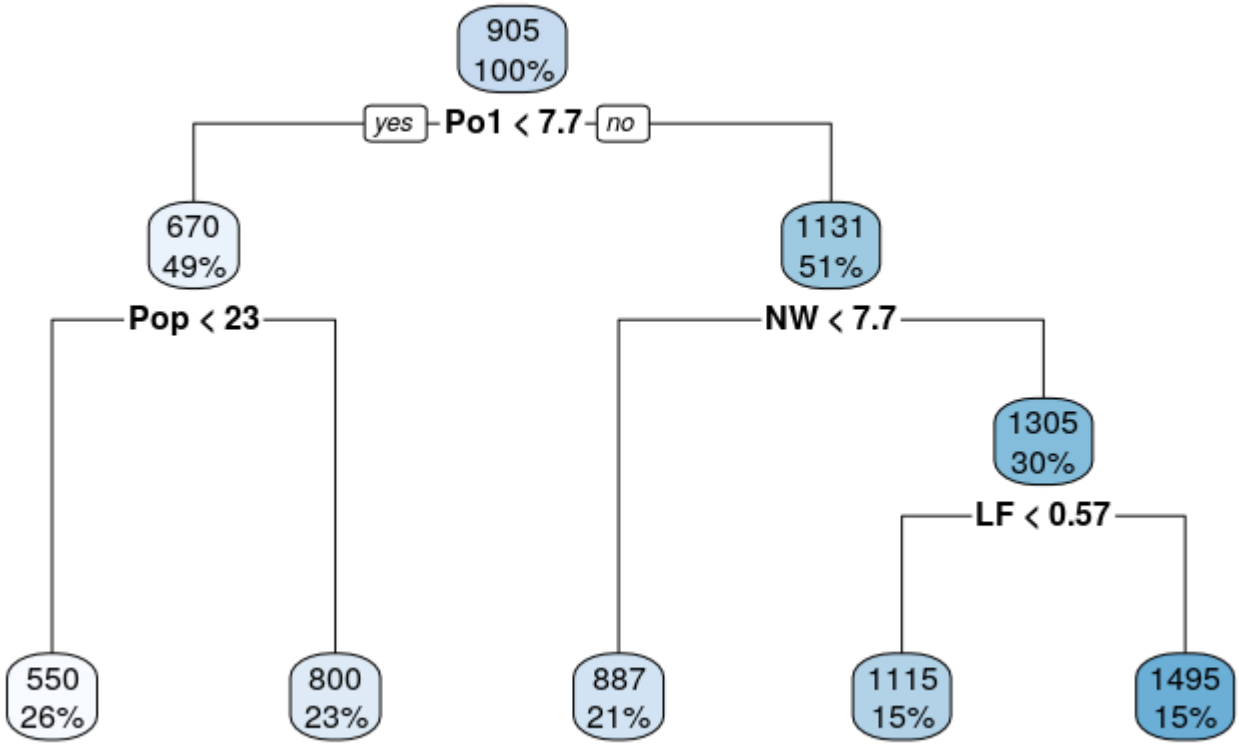
```
optimal_tree <- rpart(
    formula = Crime ~ .,
    data    = data,
    method  = "anova",
    control = list(minsplit = 8, maxdepth = 9, cp = 0.01)
    )
rpart.plot(optimal_tree)
```



So here we have the best tuned model. We can see that it just added one more split from the original model. At the leafs, we can see that there is 26% of the data at a Crime rate average of 550, 23% at a crime rate average of 800, etc etc. Let's use last weaks "new unseen data" and make a prediction with this model

Prediction

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```
new.data <- data.frame("M"= 14,
"So" = 0,
"Ed" = 10,
"Po1" = 12,
"Po2" = 15.5,
"LF" = .640,
"M.F" = 94,
"Pop" = 150,
"NW" = 1.1,
"U1" = .120,
"U2" = 3.6,
"Wealth" = 3200,
"Ineq" = 20.1,
"Prob" = .04,
"Time" = 39)
predict(optimal_tree, newdata = new.data)
```

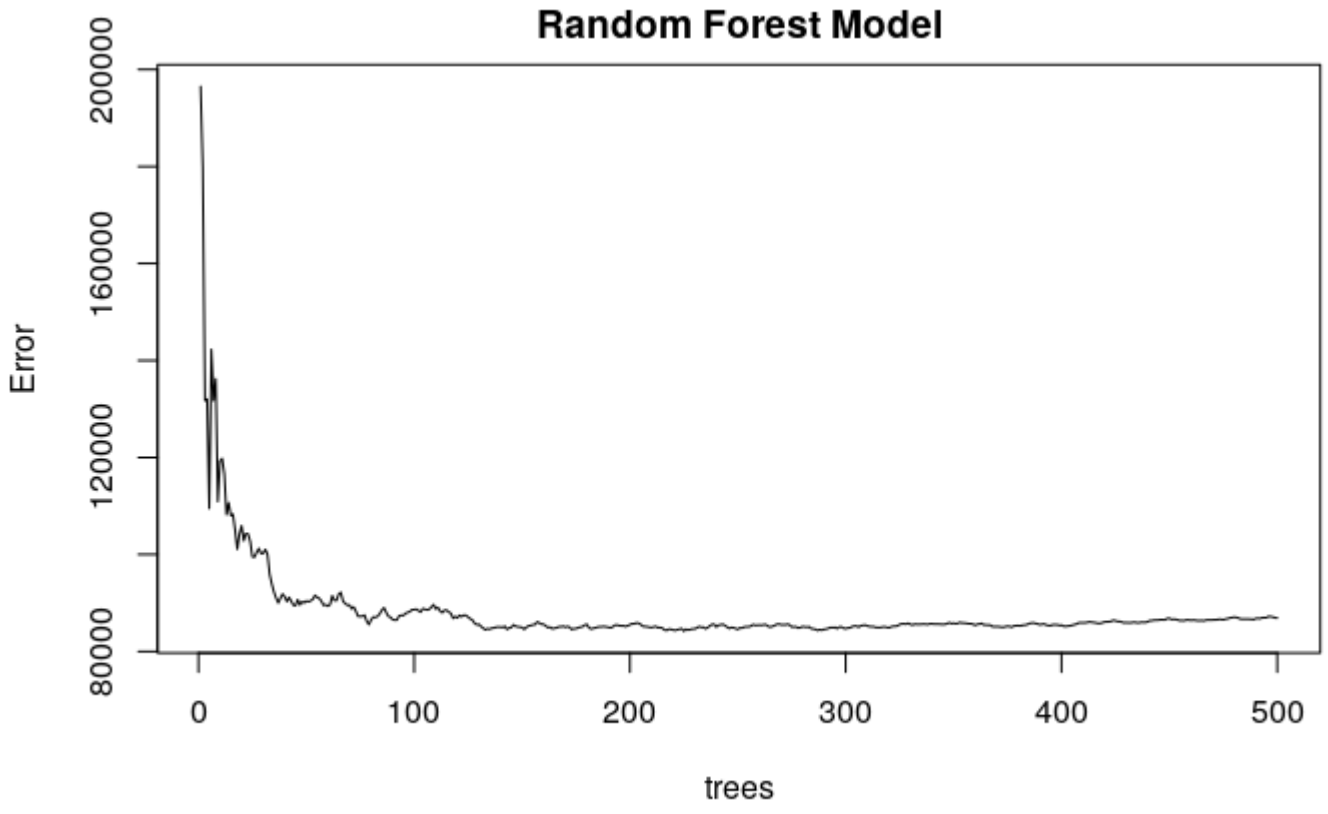
```
    1
886.9
```

*__Analysis__ We can see that the predicted crime average is 887. This seems lower than what other models had been predicting in weeks past. If you trace the regression tree, we can see exactly where the model divered from expectations. Po1 for the new data is greater than 7.7, so we go to the right side of the tree. Next, we can see that NW is less than the constraint 7.7, so this moves of to the left of that node, bringing us to 887. Had it not been for that one lower value, we can see on the right side of that split, our data is larger than 0.57 for LF, and that would have brought us around the crime average we have been seeing, 1495.

RANDOM FOREST

Hide

```
set.seed(42)
RF_model <- randomForest(
  formula = Crime ~ .,
  data    = data
)
plot(RF_model, main = 'Random Forest Model')
```



Hide

```
# number of trees with lowest MSE
which.min(RF_model$mse)
```

```
[1] 225
```

Hide

```
# RMSE of this optimal random forest
sqrt(RF_model$mse[which.min(RF_model$mse)])
```

```
[1] 290.168
```

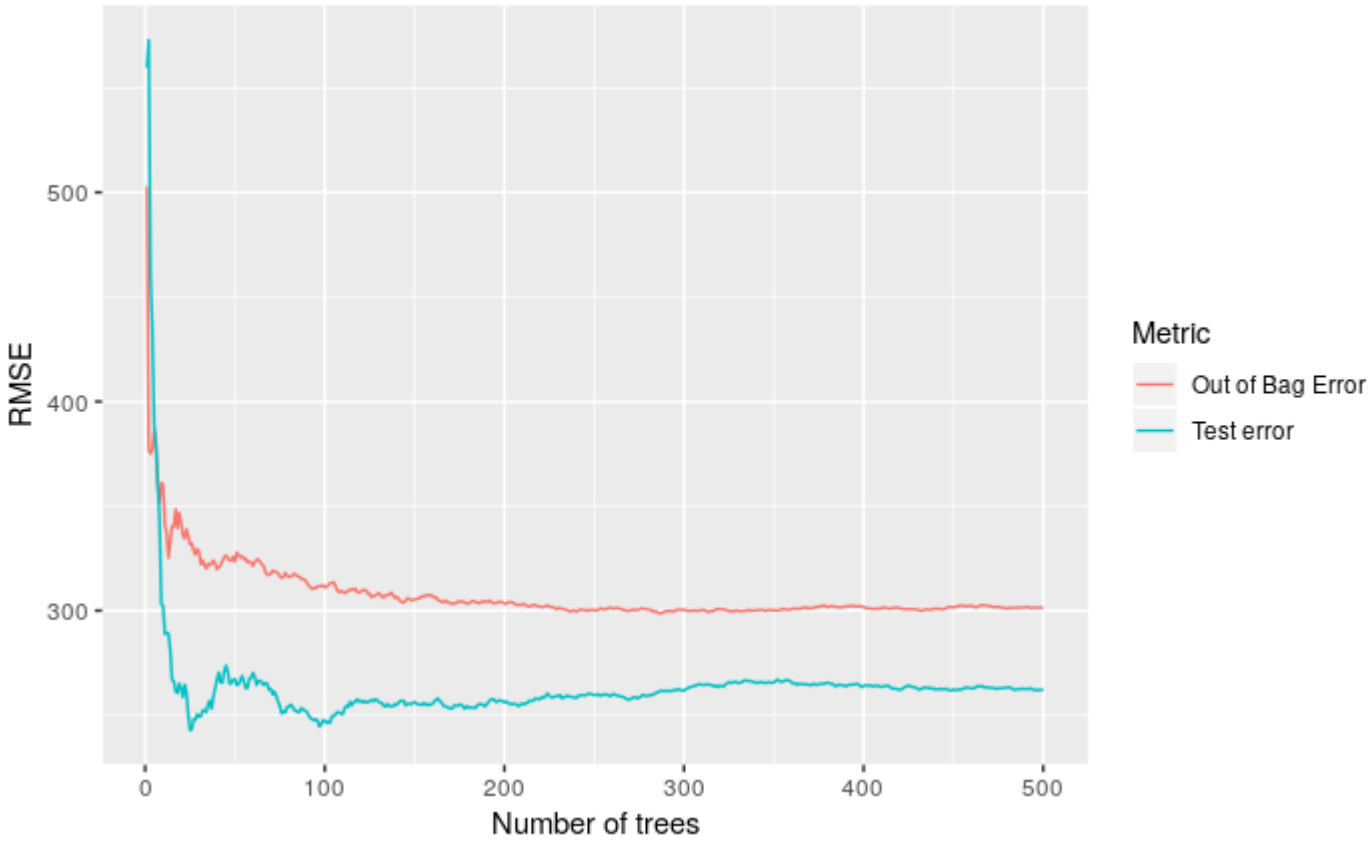
In the plot above we can see the model that produces the lowest (best) error has about 225 Trees. It's RMSE is 290. After that, the graph flattens out without much of any improvement. randomForest allows the use of crossvalidation in order to train a model as well

Cross Validation

Note - the following example is one adapted from an online source. It is not my original code

Hide

```
set.seed(24)
valid_split <- initial_split(data, .8)
# training data
train <- analysis(valid_split)
# validation data
valid <- assessment(valid_split)
x_test <- valid[setdiff(names(valid), "Crime")]
y_test <- valid$Crime
rf_oob_comp <- randomForest(
  formula = Crime ~ .,
  data    = train,
  xtest   = x_test,
  ytest   = y_test
)
# extract OOB & validation errors
oob <- sqrt(rf_oob_comp$mse)
validation <- sqrt(rf_oob_comp$test$mse)
# compare error rates
tibble::tibble(
  `Out of Bag Error` = oob,
  `Test error` = validation,
  ntrees = 1:rf_oob_comp$ntree
) %>%
  gather(Metric, RMSE, -ntrees) %>%
  ggplot(aes(ntrees, RMSE, color = Metric)) +
  geom_line() +
  scale_y_continuous() +
  xlab("Number of trees")
```



Tuning

The following is quote from source - https://uc-r.github.io/random_forests (https://uc-r.github.io/random_forests)

Random forests are fairly easy to tune since there are only a handful of tuning parameters. Typically, the primary concern when starting out is tuning the number of candidate variables to select from at each split. However, there are a few additional hyperparameters that we should be aware of. Although the argument names may differ across packages, these hyperparameters should be present: * ntree: number of trees. We want enough trees to stabalize the error but using too many trees is unncessarily inefficient, especially when using large data sets. * mtry: the number of variables to randomly sample as candidates at each split. When mtry =p the model equates to bagging. When mtry = 1 the split variable is completely random, so all variables get a chance but can lead to overly biased results. A common suggestion is to start with 5 values evenly spaced across the range from 2 to p. * sampsize: the number of samples to train on. The default value is 63.25% of the training set since this is the expected value of unique observations in the bootstrap sample. Lower sample sizes can reduce the training time but may introduce more bias than necessary. Increasing the sample size can increase performance but at the risk of overfitting because it introduces more variance. Typically, when tuning this parameter we stay near the 60-80% range. * nodesize: minimum number of samples within the terminal nodes. Controls the complexity of the trees. Smaller node size allows for deeper, more complex trees and smaller node results in shallower trees. This is another bias-variance tradeoff where deeper trees introduce more variance (risk of overfitting) and shallower trees introduce more bias (risk of not fully capturing unique patters and relatonships in the data). * maxnodes: maximum number of terminal nodes. Another way to control the complexity of the trees. More nodes equates to deeper, more complex trees and less nodes result in shallower trees.

Tuning with H20

The following code is adapted from the same online source as above. It will be used to note the most optimal way (effeciency) to tune a random forest model. I'm using the code as provided by the source because i've never used the H2o library before and I am very unfamiliary with it's syntax and operations. It will be used as is in order to come back to as reference material in the future.

Start an h2o instance

Hide

```
h2o.no_progress()
h2o.init(max_mem_size = "5g")
```

```
H2O is not running yet, starting it now...

Note:  In case of errors look at the following log files:
    /tmp/RtmpGkGNvW/h2o_scott_started_from_r.out
    /tmp/RtmpGkGNvW/h2o_scott_started_from_r.err
```

```
openjdk version "1.8.0_191"
OpenJDK Runtime Environment (build 1.8.0_191-8u191-b12-2ubuntu0.18.04.1-b12)
OpenJDK 64-Bit Server VM (build 25.191-b12, mixed mode)
```

```
Starting H2O JVM and connecting: . Connection successful!

R is connected to the H2O cluster:
    H2O cluster uptime:         1 seconds 97 milliseconds
    H2O cluster timezone:       America/Denver
    H2O data parsing timezone:  UTC
    H2O cluster version:        3.22.1.1
    H2O cluster version age:    1 month and 28 days
    H2O cluster name:           H2O_started_from_R_scott_eky936
    H2O cluster total nodes:    1
    H2O cluster total memory:   4.44 GB
    H2O cluster total cores:    8
    H2O cluster allowed cores:  8
    H2O cluster healthy:        TRUE
    H2O Connection ip:          localhost
    H2O Connection port:        54321
    H2O Connection proxy:       NA
    H2O Internal Security:      FALSE
    H2O API Extensions:         XGBoost, Algos, AutoML, Core V3, Core V4
    R Version:                  R version 3.4.4 (2018-03-15)
```

Hide

```
# create feature names
y <- "Crime"
x <- setdiff(names(data), y)
# turn training set into h2o object
train.h2o <- as.h2o(data)
# hyperparameter grid
hyper_grid.h2o <- list(
  ntrees      = seq(100, 400, by = 100),
  mtries      = seq(2, 10, by = 2),
  max_depth   = seq(5, 10, by = 5),
  min_rows    = seq(1, 5, by = 1),
  nbins       = seq(2, 10, by = 2),
  sample_rate = c(.55, .632, .75)
)
# random grid search criteria
search_criteria <- list(
  strategy = "RandomDiscrete",
  stopping_metric = "mse",
  stopping_tolerance = 0.005,
  stopping_rounds = 10,
  max_runtime_secs = 15*60
  )
# build grid search
random_grid <- h2o.grid(
  algorithm = "randomForest",
  grid_id = "rf_grid2",
  x = x,
  y = y,
  training_frame = train.h2o,
  hyper_params = hyper_grid.h2o,
  search_criteria = search_criteria
  )
# collect the results and sort by our model performance metric of choice
grid_perf2 <- h2o.getGrid(
  grid_id = "rf_grid2",
  sort_by = "mse",
  decreasing = FALSE
  )
print(grid_perf2)
```

```
H2O Grid Details
================

Grid ID: rf_grid2
Used hyper parameters:
  -  max_depth
  -  min_rows
  -  mtries
  -  nbins
  -  ntrees
  -  sample_rate
Number of models: 1615
Number of failed models: 0

Hyper-Parameter Search Summary: ordered by increasing mse
  max_depth min_rows mtries nbins ntrees sample_rate           model_ids               m
se
1         5      1.0      2     6    100       0.632 rf_grid2_model_1244 59004.748514740
89
2         5      2.0      2     4    100        0.75 rf_grid2_model_1498 62320.184884909
32
3         5      1.0      4     2    300        0.75 rf_grid2_model_1455 62591.536607509
01
4        10      2.0      2     4    100        0.75  rf_grid2_model_342 62822.858219060
99
5        10      2.0      4    10    100        0.75  rf_grid2_model_372 62869.192932444
99

---
     max_depth min_rows mtries nbins ntrees sample_rate           model_ids
mse
1610        10      2.0      8     8    100        0.75 rf_grid2_model_1276 102407.55645
595942
1611        10      1.0     10     8    100        0.75  rf_grid2_model_361 102636.99566
886043
1612        10      4.0     10     2    100        0.75 rf_grid2_model_1149 103720.44807
938437
1613         5      3.0     10     2    200        0.75  rf_grid2_model_101 104725.55961
112442
1614         5      1.0     10     6    100        0.75  rf_grid2_model_401 107590.72059
492703
1615        10      2.0     10     4    100        0.75  rf_grid2_model_642 108064.80649
182363
```

As we can see above, we ran through 1615 different models to arrive at the best one. Let's extract the best model using h2o's API, and compare its RMSE to the original models RMSE of 290.168, at the top of this section

Hide

```
# Grab the model_id for the top model, chosen by validation error
best_model_id <- grid_perf2@model_ids[[1]]
best_model <- h2o.getModel(best_model_id)
# RMSE of best model
h2o.mse(best_model) %>% sqrt()
```

```
[1] 242.9089
```

Hide

```
## [1] 23104.67
```

With an RMSE of 242.90, this model is performing better than the non tuned model. Let's use this model to predict on the new unseen data. We will compare its results to those of the CART model in the first section.

Hide

```
pred_h2o <- predict(best_model, as.h2o(new.data))
head(pred_h2o)
```

	predict <dbl>
1	1172.36

1 row

*__Analysis__ The Random Forest model predcited a value of 1172. This is more along the lines of the values we had been seing in the other models. Remember that the CART model predict 872. There was a gross estimation in contrast to all the other models, leading us to the obvious conlcusion that the Rnadom Forest model is much better than the simpler CART model

Always shutdown your h2o instances when done

Hide

```
h2o.shutdown(prompt = TRUE)
y
```

```
[1] TRUE
```

Question 10.2 Describe a situation or problem from your job, everyday life, current events, etc., for which a logistic regression model would be appropriate. List some (up to 5) predictors that you might use.

> Logistic Regression models are used today in the medical field in order to determine if a patient's tumor is benign or malignant. Various features can be used in the model to predict one of the binary classes. Such as: 1. Age of patient 2. Gender 3. Family history with cancer 4. Length of tumor 5. Width of tumor 6. Any image indicators from CT and/or Sonograph

Using the GermanCredit data set germancredit.txt from http://archive.ics.uci.edu/ml/machine-learning-databases/statlog/german (http://archive.ics.uci.edu/ml/machine-learning-databases/statlog/german) / (description at http://archive.ics.uci.edu/ml/datasets/Statlog+%28German+Credit+Data%29 (http://archive.ics.uci.edu/ml/datasets/Statlog+%28German+Credit+Data%29)), use logistic regression to find a good predictive model for whether credit applicants are good credit risks or not. Show your model (factors used and their coefficients), the software output, and the quality of fit. You can use the glm function in R. To get a logistic regression (logit) model on data where the response is either zero or one, use family=binomial(link="logit") in your glm function call.

Load the data

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```
gc_data <- read.table('germancredit.txt', header = FALSE, stringsAsFactors = TRUE)
gc_data$V21 <- as.factor(gc_data$V21)
head(gc_data)
```

	V1 <fctr>	V2 <int>	V3 <fctr>	V4 <fctr>	V5 <int>	V6 <fctr>	V7 <fctr>	V8 <int>	V9 <fctr>
1	A11	6	A34	A43	1169	A65	A75	4	A93
2	A12	48	A32	A43	5951	A61	A73	2	A92
3	A14	12	A34	A46	2096	A61	A74	2	A93
4	A11	42	A32	A42	7882	A61	A74	2	A93
5	A11	24	A33	A40	4870	A61	A73	3	A93
6	A14	36	A32	A46	9055	A65	A73	2	A93

6 rows | 1-10 of 21 columns

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```
summary(gc_data)
```

```
  V1            V2         V3            V4            V5
A11:274   Min.   : 4.0   A30: 40   A43    :280   Min.   :  250
A12:269   1st Qu.:12.0   A31: 49   A40    :234   1st Qu.: 1366
A13: 63   Median :18.0   A32:530   A42    :181   Median : 2320
A14:394   Mean   :20.9   A33: 88   A41    :103   Mean   : 3271
          3rd Qu.:24.0   A34:293   A49    : 97   3rd Qu.: 3972
          Max.   :72.0             A46    : 50   Max.   :18424
                                   (Other): 55
  V6        V7            V8          V9        V10
A61:603   A71: 62   Min.   :1.000   A91: 50   A101:907
A62:103   A72:172   1st Qu.:2.000   A92:310   A102: 41
A63: 63   A73:339   Median :3.000   A93:548   A103: 52
A64: 48   A74:174   Mean   :2.973   A94: 92
A65:183   A75:253   3rd Qu.:4.000
                    Max.   :4.000

     V11          V12           V13          V14        V15
Min.   :1.000   A121:282   Min.   :19.00   A141:139   A151:179

1st Qu.:2.000   A122:232   1st Qu.:27.00   A142: 47   A152:713
Median :3.000   A123:332   Median :33.00   A143:814   A153:108
Mean   :2.845   A124:154   Mean   :35.55
3rd Qu.:4.000              3rd Qu.:42.00
Max.   :4.000              Max.   :75.00

     V16          V17           V18          V19        V20
Min.   :1.000   A171: 22   Min.   :1.000   A191:596   A201:963
1st Qu.:1.000   A172:200   1st Qu.:1.000   A192:404   A202: 37
Median :1.000   A173:630   Median :1.000
Mean   :1.407   A174:148   Mean   :1.155
3rd Qu.:2.000              3rd Qu.:1.000
Max.   :4.000              Max.   :2.000

V21
1:700
2:300
```

Looking at the summary of the data, we can see that there is a mix between numerical columns and categorical columns. We set the “stringAsFacotrs” as TRUE. This is R’s way of converting string columns into categorical variables to be handled in the model. For instances, we can see how R is going to categorize the first column

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```
contrasts(gc_data$V1)
```

```
    A12 A13 A14
A11   0   0   0
A12   1   0   0
A13   0   1   0
A14   0   0   1
```

We can see that entries of A11 will be encoded as (0,0,0), A12 will be encoded as (1,0,0), A13 will be encoded as (0,1,0) etc.

Train / Test Split of data

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```
set.seed(42)
sample = sample.split(gc_data, SplitRatio = .8)
train = subset(gc_data, sample == TRUE)
test = subset(gc_data, sample == FALSE)
```

Fit the Model

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```
gc_model <- glm(V21 ~., family = binomial(link='logit'), data = train)
summary(gc_model)
```

```
Call:
glm(formula = V21 ~ ., family = binomial(link = "logit"), data = train)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.4184  -0.6750  -0.3459   0.6592   2.5177

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.006e+00  1.259e+00   1.593 0.111148
V1A12       -2.226e-01  2.583e-01  -0.862 0.388776
V1A13       -1.029e+00  4.404e-01  -2.336 0.019480 *
V1A14       -1.583e+00  2.750e-01  -5.758 8.49e-09 ***
V2           3.344e-02  1.105e-02   3.025 0.002485 **
V3A31       -5.816e-01  6.683e-01  -0.870 0.384150
V3A32       -1.367e+00  5.352e-01  -2.555 0.010618 *
V3A33       -1.544e+00  5.816e-01  -2.655 0.007934 **
V3A34       -2.114e+00  5.486e-01  -3.853 0.000117 ***
V4A41       -1.812e+00  4.401e-01  -4.118 3.83e-05 ***
V4A410      -2.171e+00  1.030e+00  -2.107 0.035102 *
V4A42       -9.321e-01  3.041e-01  -3.064 0.002180 **
V4A43       -1.196e+00  2.971e-01  -4.028 5.63e-05 ***
V4A44       -1.494e+01  5.668e+02  -0.026 0.978970
V4A45       -2.916e-01  6.728e-01  -0.433 0.664735
V4A46       -3.416e-01  4.360e-01  -0.784 0.433248
V4A48       -2.032e+00  1.291e+00  -1.574 0.115486
V4A49       -1.356e+00  4.025e-01  -3.368 0.000756 ***
V5           1.277e-04  5.152e-05   2.478 0.013195 *
V6A62       -3.780e-01  3.427e-01  -1.103 0.269987
V6A63       -2.668e-01  4.490e-01  -0.594 0.552370
V6A64       -1.626e+00  6.391e-01  -2.544 0.010954 *
V6A65       -1.024e+00  3.075e-01  -3.330 0.000870 ***
V7A72        1.769e-01  5.172e-01   0.342 0.732308
V7A73       -3.159e-01  4.989e-01  -0.633 0.526604
V7A74       -6.559e-01  5.264e-01  -1.246 0.212760
V7A75       -2.303e-02  5.013e-01  -0.046 0.963362
V8           2.814e-01  1.025e-01   2.747 0.006018 **
V9A92       -1.561e-01  4.534e-01  -0.344 0.730539
V9A93       -9.241e-01  4.508e-01  -2.050 0.040378 *
V9A94       -3.761e-01  5.426e-01  -0.693 0.488209
V10A102      4.432e-01  4.788e-01   0.926 0.354555
V10A103     -8.265e-01  4.975e-01  -1.661 0.096674 .
V11         -3.812e-02  1.028e-01  -0.371 0.710886
V12A122      4.635e-02  2.961e-01   0.157 0.875608
V12A123     -2.953e-02  2.816e-01  -0.105 0.916496
V12A124      6.496e-01  4.957e-01   1.311 0.189962
V13         -1.439e-02  1.088e-02  -1.323 0.185806
V14A142      1.574e-01  4.757e-01   0.331 0.740787
V14A143     -7.768e-01  2.854e-01  -2.722 0.006490 **
V15A152     -5.517e-01  2.773e-01  -1.989 0.046654 *
V15A153     -6.840e-01  5.489e-01  -1.246 0.212714
V16          1.479e-01  2.221e-01   0.666 0.505403
```

```
V17A172      5.989e-03  8.008e-01   0.007 0.994033
V17A173      8.804e-02  7.682e-01   0.115 0.908756
V17A174      1.377e-01  7.722e-01   0.178 0.858504
V18          4.943e-01  2.865e-01   1.725 0.084542 .
V19A192     -4.104e-01  2.385e-01  -1.720 0.085348 .
V20A202     -2.381e+00  1.079e+00  -2.207 0.027345 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 926.51  on 761  degrees of freedom
Residual deviance: 655.17  on 713  degrees of freedom
AIC: 753.17

Number of Fisher Scoring iterations: 14
```

From the summary above, we can see there are not a lot of features that are statistically significant. You will also notice that in the data, there were only 20 features, but in the summary above, there is way more than 20. This is because the summary function is analyzing every category for each feature. column V1 had 3 specific categories, and they’re broken out into V1A12, V1A13, V1A14. Also note that the AIC value is 753.17. Our goal would be to lower this number while improving the model. A lower value means a better fit. One last note before we continue on, notice that a lot of the coeffecients are negative. If we look at a statistically significant value like V1A14 (no checking account), if you didn’t have a checking account, this would reduce your creditworthiness risk log odds by 1.58

ANOVA CHI SQUARED TEST

Next we will compare our model to the “NULL MODEL” (intercept only model). By using a chi squared test, we want to see how the deviance in residuals change as we add each feature one by one. We want to see an increase in difference between our model and the “NULL MODEL”

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```
anova(gc_model, test = "Chisq")
```

```
Analysis of Deviance Table

Model: binomial, link: logit

Response: V21

Terms added sequentially (first to last)

     Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                  761     926.51
V1    3   97.426       758     829.08 < 2.2e-16 ***
V2    1   26.138       757     802.94 3.179e-07 ***
V3    4   26.406       753     776.54 2.621e-05 ***
V4    9   30.846       744     745.69 0.0003146 ***
V5    1    0.914       743     744.78 0.3390073
V6    4   17.667       739     727.11 0.0014336 **
V7    4   15.419       735     711.69 0.0039061 **
V8    1    4.732       734     706.96 0.0296098 *
V9    3   12.828       731     694.13 0.0050234 **
V10   2    4.746       729     689.39 0.0932197 .
V11   1    0.020       728     689.37 0.8874504
V12   3    2.048       725     687.32 0.5625475
V13   1    2.648       724     684.67 0.1036970
V14   2   10.605       722     674.07 0.0049787 **
V15   2    3.926       720     670.14 0.1404427
V16   1    0.593       719     669.55 0.4414465
V17   3    0.190       716     669.36 0.9791643
V18   1    3.153       715     666.21 0.0757922 .
V19   1    2.497       714     663.71 0.1140365
V20   1    8.539       713     655.17 0.0034755 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

From the Chi Squared Test, we can see that adding the features V1, V2, V3, and V4 significantly reduced the Residual Deviance in comparison to the NULL model, 735 and 926.51 respectively. Adding more features definetly widens the gap between the NULL model and our model, but the gap slows down in velocity around V10.

Model Accuracy

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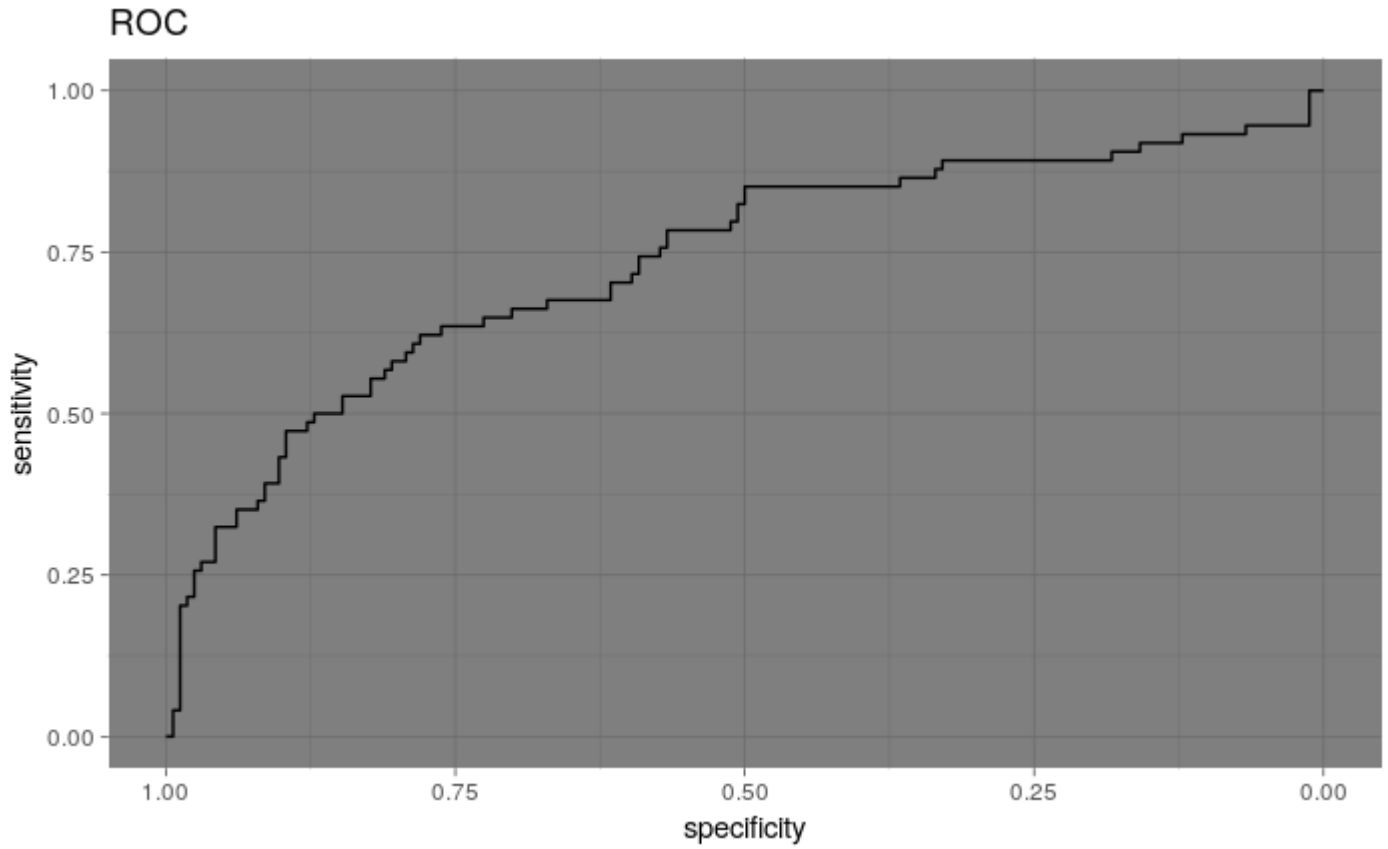
```
test_predict <- predict(gc_model, newdata = test[,1:20], type ='response')
ROC <- roc(test$V21, test_predict)
ggroc(ROC) + theme_dark() + ggtitle('ROC')
```



Hide

```
print(paste('AUC: ', auc(ROC)))
```

```
[1] "AUC:  0.734426499670402"
```

Hide

```
test_predict <- ifelse(test_predict > 0.20, 2, 1)
confusionMatrix(as.factor(test_predict), as.factor(test$V21), positive = '2')
```

```
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 99 22
         2 65 52

               Accuracy : 0.6345
                 95% CI : (0.5698, 0.6957)
    No Information Rate : 0.6891
    P-Value [Acc > NIR] : 0.9693

                  Kappa : 0.2642
 Mcnemar's Test P-Value : 6.704e-06

            Sensitivity : 0.7027
            Specificity : 0.6037
         Pos Pred Value : 0.4444
         Neg Pred Value : 0.8182
             Prevalence : 0.3109
         Detection Rate : 0.2185
   Detection Prevalence : 0.4916
      Balanced Accuracy : 0.6532

       'Positive' Class : 2
```

From our “all features” model, we can see that we got about 76% Accuracy using a 50% logit prediction model (meaning if a prediction was greater than 0.5, then 2, if it is 0.5 or less, then 1). Let’s now try to tune our model and also tune the prediction threshold.

Tuning

From our Chi Square test results, let’s use the most statitically significant features from that test.

1. V1 - Status of existing checking
2. V2 - Duration in month
3. V3 - Credit History
4. V4 - Purpose
5. V6 - Savings Account balance
6. V7 - Present Employment
7. V9 - Personal Status and Sex
8. V14 - Other installment plans
9. V20 - Foreign Worker

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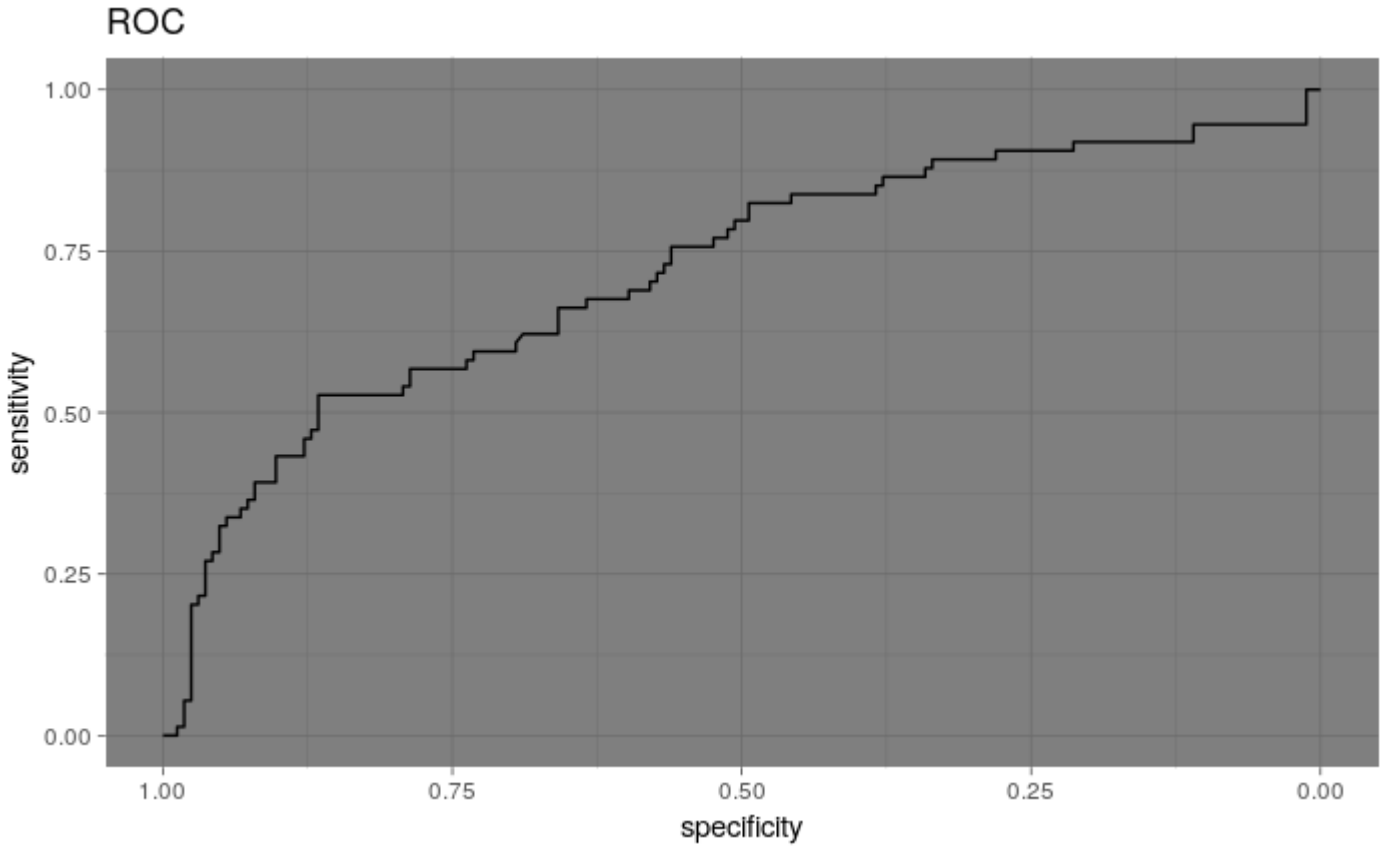
```
train_final <- train[, c(1,2,3,4,6,7,9,14,20,21)]
test_final <- test[, c(1,2,3,4,6,7,9,14,20,21)]
final_model <- glm(V21 ~., family = binomial(link='logit'), data = train_final)
final_predict <- predict(final_model, newdata = test_final, type ='response')
final_ROC <- roc(test_final$V21, final_predict)
ggroc(final_ROC) + theme_dark() + ggtitle('ROC')
```



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```
print(paste('AUC: ', auc(ROC)))
```

```
[1] "AUC:  0.734426499670402"
```

Hide

```
final_predict <- ifelse(final_predict > 0.15, 2, 1)
confusionMatrix(as.factor(final_predict), as.factor(test_final$V21), positive = '2')
```

```
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 85 17
         2 79 57

               Accuracy : 0.5966
                 95% CI : (0.5313, 0.6595)
    No Information Rate : 0.6891
    P-Value [Acc > NIR] : 0.999

                  Kappa : 0.2346
 Mcnemar's Test P-Value : 4.791e-10

            Sensitivity : 0.7703
            Specificity : 0.5183
         Pos Pred Value : 0.4191
         Neg Pred Value : 0.8333
             Prevalence : 0.3109
         Detection Rate : 0.2395
   Detection Prevalence : 0.5714
      Balanced Accuracy : 0.6443

       'Positive' Class : 2
```

Conclusion: After playing around with several probability thresholds, with the “tuned” model, it still couldn’t quite get to the results of the all variables model. Therefore, we will express the answer in terms of the all variables model

Model Coeficients

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```
coef = as.matrix(gc_model$coefficients)
coef
```

```
                    [,1]
(Intercept)  2.005960e+00
V1A12       -2.226314e-01
V1A13       -1.028931e+00
V1A14       -1.583297e+00
V2           3.343583e-02
V3A31       -5.816336e-01
V3A32       -1.367420e+00
V3A33       -1.544016e+00
V3A34       -2.113856e+00
V4A41       -1.811993e+00
V4A410      -2.171294e+00
V4A42       -9.320606e-01
V4A43       -1.196399e+00
V4A44       -1.494222e+01
V4A45       -2.916034e-01
V4A46       -3.416328e-01
V4A48       -2.031583e+00
V4A49       -1.355907e+00
V5           1.276948e-04
V6A62       -3.779772e-01
V6A63       -2.667757e-01
V6A64       -1.626021e+00
V6A65       -1.023886e+00
V7A72        1.768956e-01
V7A73       -3.159155e-01
V7A74       -6.558751e-01
V7A75       -2.302906e-02
V8           2.814237e-01
V9A92       -1.561413e-01
V9A93       -9.240783e-01
V9A94       -3.760751e-01
V10A102      4.432319e-01
V10A103     -8.264608e-01
V11         -3.811712e-02
V12A122      4.634545e-02
V12A123     -2.952799e-02
V12A124      6.496454e-01
V13         -1.439163e-02
V14A142      1.573682e-01
V14A143     -7.768228e-01
V15A152     -5.517392e-01
V15A153     -6.840414e-01
V16          1.479307e-01
V17A172      5.988959e-03
V17A173      8.804191e-02
V17A174      1.376658e-01
V18          4.942606e-01
V19A192     -4.103831e-01
V20A202     -2.380572e+00
```

Probablility Threshold

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```
cm <- confusionMatrix(as.factor(test_predict), as.factor(test$V21), positive = '2')
cm$table
```

```
          Reference
Prediction  1  2
         1 99 22
         2 65 52
```

A threshold of 20% gave the best results of limiting the 5x damage of incorrectly predicting a “bad credit risk”