# Final Project

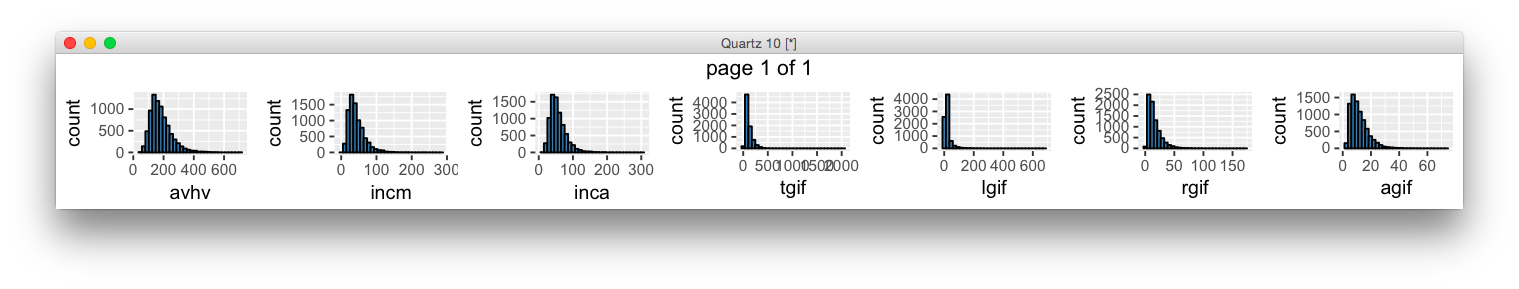
## Introduction

In this report we are developing machine-learning models to optimize a charitable organization’s direct marketing campaign. Our goal is two-fold: to identify likely donors using a classification model in order to maximize the net profit from the mailings, and to estimate the gift amounts from donors using a prediction model. We created several classification models, including logistic regression, logistic regression general additive model (GAM), Linear Discriminant Analysis (LDA), Quadratic Discriminant Analysis (QDA), k-nearest neighbors, decision tree, boosted trees, random forests, and support vector machines, in order to determine which model best identifies likely donors. We also created several prediction models, including least squares regression, best subset selection with k-fold cross-validation, principal components regression, partial least squares, ridge regression, and lasso regression in order to predict the amount of donations.

## Data Exploration

The data we are using for this report is the charity data set. This data set contains 3984 training observations, 2018 validation observations, and 2007 test observations. The data has been weighted in order to make the training and validation samples each contain roughly an equivalent number of donors and non-donors. The charity data set includes two response variables, donr (donor) and damt (donation amount), for the classification models and prediction models, respectively. It also contains 20 predictor variables, including the geographic regions of previous donors, whether the donor is a homeowner or not, the number of children the donor has, the donor’s income, the donor’s gender, the amounts of previous donations, and various other wealth, income, and donation factors that may help create strong classification and prediction machine-learning models.

Prior to developing any models, we examined our data in order to see if there were any missing values or abnormalities in the data. Although the data set did not contain any missing values, we noticed that several of the variables might benefit from transformations. We decided to apply logarithmic transformations to seven right-skewed variables: avhv, incm, inca, tgif, lgif, rgif, and agif. The top row of **Figure 1** shows the variables prior to transformation, while the bottom row shows the variables after transformation.[[1]](#footnote-1) As the figure shows, the logarithmic transformation helped normalize the distributions of these seven variables.



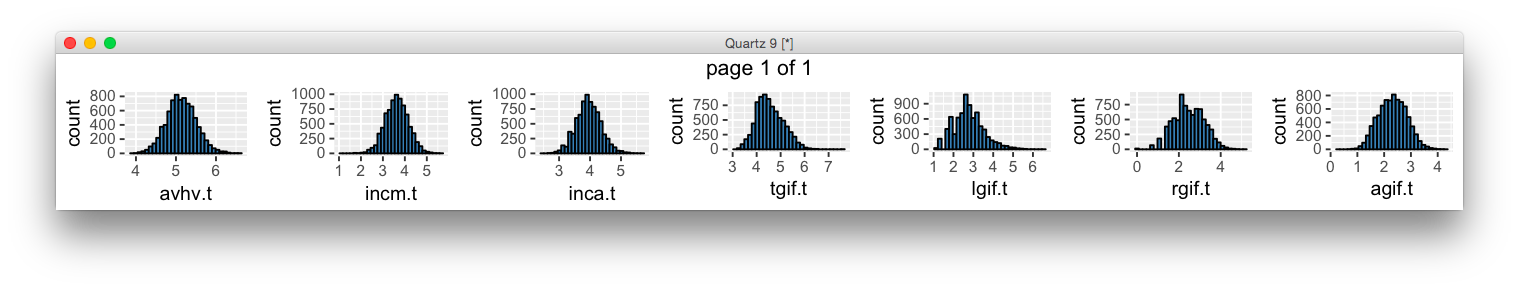


Figure : Transformation of Variables

After transforming our variables, we created a correlation matrix to gain further insight into the data. **Figure 2** shows a visualization of the correlation matrix, while **Table 1** shows the values of the most statistically significant correlations.

|  |  |  |
| --- | --- | --- |
| var1 | var2 | corr |
| damt | donr | 0.9817018 |
| tgif | npro | 0.8734276 |
| rgif | lgif | 0.8512241 |
| inca | avhv | 0.8484572 |
| inca | incm | 0.8296747 |
| agif | lgif | 0.8294224 |
| plow | incm | -0.8120381 |
| agif | rgif | 0.7706645 |
| plow | inca | -0.7510141 |
| incm | avhv | 0.7304313 |
| plow | avhv | -0.7187952 |
| damt | chld | -0.5531045 |
| donr | chld | -0.5326077 |



Figure : Correlation Matrix Table 1: Significant Correlations

As **Figure 2** and **Table 1** reveal, certain variables have strong correlations. For instance, tgif (dollar amount of lifetime gifts to date) has a very strong positive correlation with npro (lifetime number of promotions received to date). Some variables, such as plow (percent categorized as “low income” in potential donor's neighborhood) and incm (median family income in potential donor's neighborhood in $ thousands), have a strong negative correlation. The correlations are something we bear in mind as we create our classification and prediction models.

## Classification Models and Analysis

# Model Technique 1: Logistic Regression

# Model Technique 2: Logistic General Additive Model

# Model Technique 3: Linear Discriminant Analysis

# Model Technique 4: Quadratic Discriminant Analysis

# Model Technique 5: K-Nearest Neighbor Classification

# Model Technique 6: Decision Tree

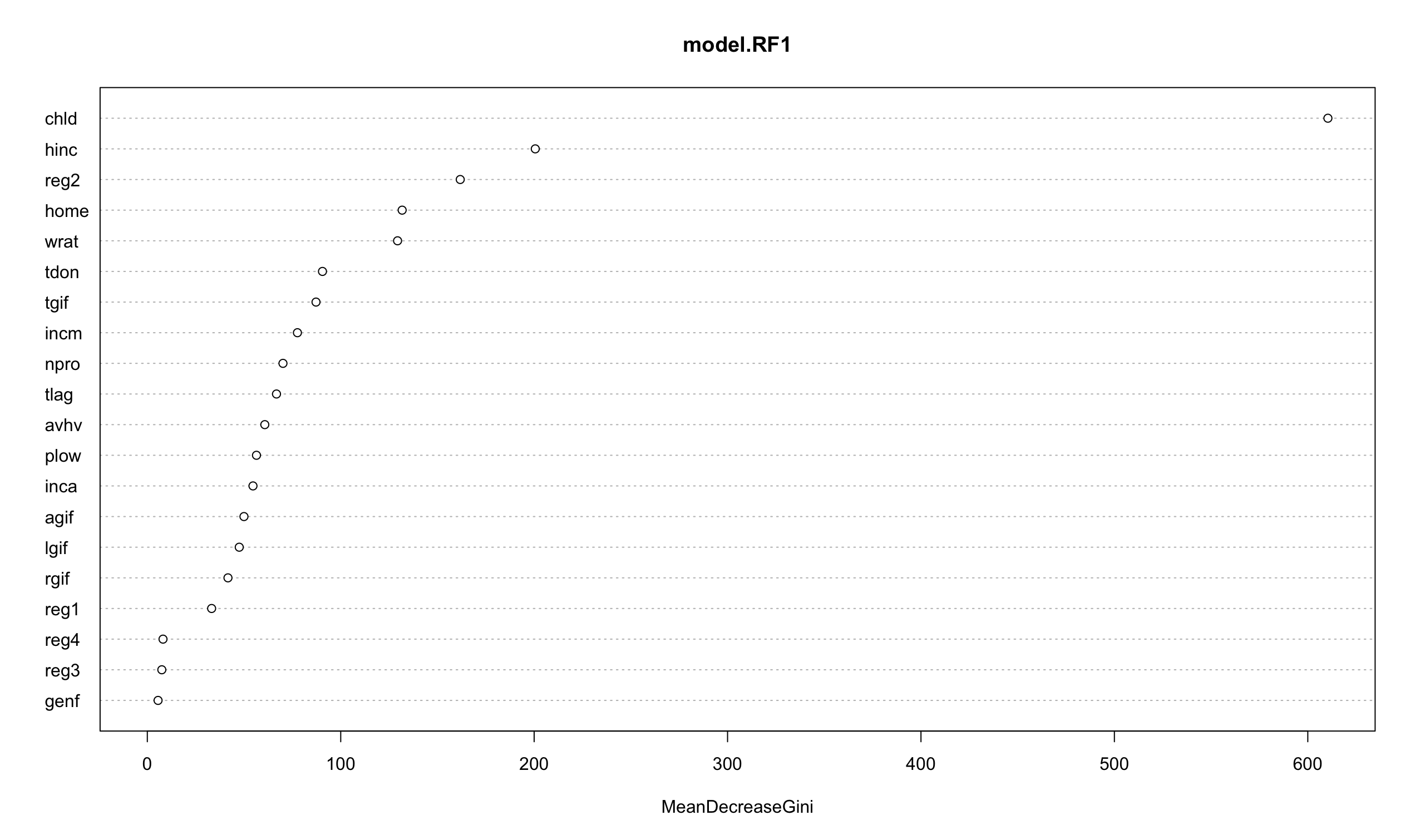
Since Tree-based methods are considered simple and useful for interpretation, a simple decision tree is considered for classifying whether or not an individual is a donor or not. Since the process of building a decision tree includes a technique for pruning the resulting tree, all 20 variables are passed in for model fitting. Although the initial decision tree fit results in 1362 mailings and a profit of $11,413.50, it is good practice to examine pruning the tree to ensure the original tree is not limited in performance due to over-fitting by the training data.

|  |  |
| --- | --- |
|  |  |

Although [Figure X] demonstrates that the best decision tree is of size 10, the resulting tree from fitting that model is the exact same as the original decision tree model fit, capping this technique off at a $11,413.50 profit.

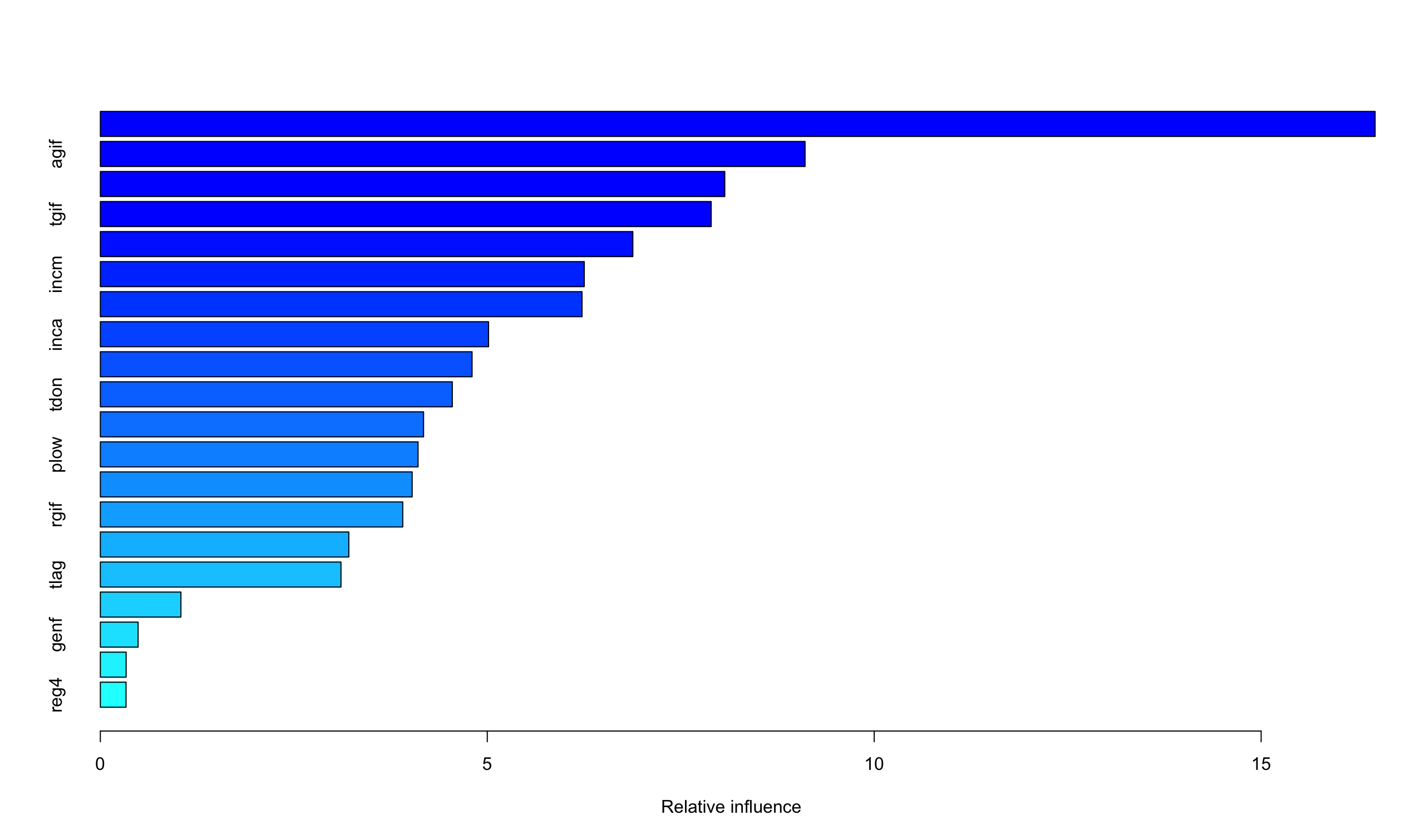
# Model Technique 7: Random Forest

Having observed that the single, pruned decision tree still hasn’t maximized profit, a logical next step would be to try a method for aggregating several decision trees to enhance the performance of a single tree. Although there are three common techniques used to achieve this (bagging, boosting and random forests), the first of two techniques to be tested for this analysis is the Random Forest modeling technique. The model fit results in only 1,055 total mailings, maxing out its profit at $11,099.50. Although this technique is demonstrating that it isn’t the best in terms of profit, the illustrating in [Figure X] below is incredibly useful in that it provide a clear visualization of the variables that are contributing the most to whether or not an individual will donate or not.



# Model Technique 8: Boosted Tree

With the resultant random forest performing so poorly in contrast to the individual decision tree, one additional attempt at a multiple tree aggregation method will be performed. This method, referred to as boosting, learns more slowly and tends to reduce the likelihood of over-fitting as well. The boosted tree results in a total of 1308 mailings, soaring the resulting profit to $11,565.00. Of all tree based classification methods built, this is by far the highest performer. In [Figure X] below, one can observe a similar visualization of the variables based on their relative influence on the classification of whether or not an individual is a donor or not. Similarly to the other two tree based models, the most important variable is how many children the potential donor has.



|  |  |
| --- | --- |
| Var | Relative Influence |
| chld | 16.4728955 |
| agif | 9.1065005 |
| avhv | 8.0688407 |
| tgif | 7.893357 |
| hinc | 6.8809433 |
| incm | 6.2528839 |
| npro | 6.224251 |
| inca | 5.0164309 |
| wrat | 4.8032304 |
| tdon | 4.5479742 |
| lgif | 4.1767537 |
| plow | 4.1053603 |
| reg2 | 4.0291227 |

# Model Technique 9: Support Vector Machine

The last but certainly not least classifier to be tested on this data is the Support Vector Machine, first: without any tuning utilizing a linear kernel and second: utilizing cross validation to determine optimal parameters as well as utilizing a more likely applicable radial kernel. As expected, the first model tanks in comparison to all previously fit classification models with a maximal profit of $10,534, mostly due to suggesting far too many mailings at 1,925. The tuned model, utilizing the radial kernel performs substantially better, raking in a potential profit of $11,336.50 on the validation data through only 1,444 mailings.

## Results

|  |  |  |
| --- | --- | --- |
| Model | Test MSE | Standard Error of Test MSE |
| 1 | 3111.265 | 361.0908 |
| 2 | 3095.483 | 369.7526 |
| 3 | 3095.483 | 369.7526 |
| 4 | 3070.870 | 350.5467 |
| 5 | 2920.041 | 346.2248 |

Model 1 (least squares regression containing all ten predictors) resulted in the worst test MSE, although its test MSE standard error was slightly better than the test MSE standard error for Models 2 and 3. As mentioned earlier, Model 2 (best subset selection using BIC) and Model 3 (best subset selection using 10-fold cross-validation) resulted in the same six-variable model with identical coefficient estimates and test errors. Model 4 (ridge regression using 10-fold cross-validation) performed slightly better than Models 1, 2, and 3. It, however, is a more complex model than Models 2 and 3 because it uses all ten predictors rather than just six. Model 5 (lasso using 10-fold cross-validation) resulted in the smallest test MSE and test MSE standard error of all the models. It contains only six predictors. Because of its small test errors and relative simplicity, Model 5 can be considered the best model.

## Conclusion

After fitting various machine learning modeling techniques, including least squares regression, best subset selection using BIC, best subset selection using 10-fold cross validation, ridge regression using 10-fold cross validation, and lasso using 10-fold cross validation, I discovered that the lasso model using 10-fold cross validation performed best in predicting the progression of diabetes one year after baseline. This model contained the predictor variables sex, bmi, map, hdl, ltg, and glu. Before deploying the model, I recommend further model testing and consulting a diabetes expert to determine if the predictors included in the model make medical sense. If the model performs well in additional tests and receives the approval of a medical expert, it should be safe to deploy the model on new data.

## Appendix A: R Code

# Individual Project 1

# Andrea Bruckner

# Predict 422, Sec 56

# Load the diabetes data

install.packages("lars")

library(lars)

data(diabetes)

data.all <- data.frame(cbind(diabetes$x, y = diabetes$y))

# Get overview of data

summary(data.all) # no missing data

str(data.all) # all numeric

head(data.all)

class(data.all) # data.frame

names(data.all)

nrow(data.all) # 442 rows

ncol(data.all) # 11 variables

# Partition the patients into two groups: training (75%) and test (25%)

n <- dim(data.all)[1] # sample size = 442

set.seed(1306) # set random number generator seed to enable

# repeatability of results

test <- sample(n, round(n/4)) # randomly sample 25% test

data.train <- data.all[-test,]

data.test <- data.all[test,]

# (Use these starting in Models 3-5)

x <- model.matrix(y ~ ., data = data.all)[,-1] # define predictor matrix

# excl intercept col of 1s

x.train <- x[-test,] # define training predictor matrix

x.test <- x[test,] # define test predictor matrix

y <- data.all$y # define response variable

y.train <- y[-test] # define training response variable

y.test <- y[test] # define test response variable

n.train <- dim(data.train)[1] # training sample size = 332

n.test <- dim(data.test)[1] # test sample size = 110

# 1.) Least squares regression model using all ten predictors (R function lm).

lm.fit <- lm(y~., data = data.train)

summary(lm.fit)

par(mfrow = c(2, 2))

plot(lm.fit)

# Coefficient Estimates

coef(lm.fit)

# Calculate MSE == 3111.265

mean((data.test$y - predict(lm.fit, data.test))^2) # 3111.265

lm.pred <- predict(lm.fit, data.test)

mean((data.test$y - lm.pred)^2)

# SE of MSE == 361.0908

sd((lm.pred - data.test$y)^2)/sqrt(length((lm.pred - data.test$y)^2)) # 361.0908

# 2.) Apply best subset selection using BIC to select the number of predictors (R function regsubsets in package leaps).

# applying best subset using either 8 or 10 variables results in the same best model

library(leaps)

fit.bestsub <- regsubsets(y ~ ., data = data.train, nvmax=10) # fit the model

fit.bestsub.sum <- summary(fit.bestsub)

names(fit.bestsub.sum)

fit.bestsub.sum$bic # -201.1269 is lowest BIC, M6

summary(fit.bestsub)

plot(fit.bestsub)

which.min(fit.bestsub.sum$bic) # 6

# resets plots window

par(mfrow = c(1, 1))

plot(fit.bestsub.sum$bic,xlab="Number of Variables",ylab="BIC",type="l")

points (6, fit.bestsub.sum$bic [6], col = "red",cex = 2, pch = 20)

# Coefficient Estimates

coef(fit.bestsub,6) # plot bottoms out at 6/has smallest BIC at 6 variables

# Calculate MSE == 3095.483

predict.regsubsets = function (object, newdata, id ,...){

form = as.formula(object$call[[2]])

mat = model.matrix(form, newdata)

coefi = coef(object, id=id)

xvars = names(coefi )

mat[,xvars]%\*% coefi

}

bestsub.pred <- predict(fit.bestsub,data.test,id=6)

mean((data.test$y-bestsub.pred)^2) # 3095.483

# I think I can also use y.test instead of data.test$y

# SE of MSE == 369.7526

sd((bestsub.pred - data.test$y)^2)/sqrt(length((bestsub.pred - data.test$y)^2)) # 369.7526

sd((bestsub.pred - data.test$y)^2)/sqrt(n.test) # 369.7526

# 3.) Apply best subset selection using 10-fold cross-validation to select the number of predictors (R function regsubsets in package leaps). [Use a random number seed of 1306 before entering the command: folds <- sample(1:k, nrow(data.train), replace = TRUE).]

k=10

set.seed(1306)

folds <- sample(1:k, nrow(data.train), replace = TRUE)

cv.errors<-matrix (NA,k,10, dimnames=list(NULL, paste(1:10)))

for(j in 1:k){

cv10.fit<-regsubsets(y ~ ., data = data.train[folds !=j,],

nvmax =10)

for(i in 1:10) {

pred=predict(cv10.fit, data.train[folds==j,], id=i)

cv.errors[j,i]=mean((data.train$y[folds==j]-pred)^2)

}

}

mean.cv.errors=apply(cv.errors, 2, mean)

mean.cv.errors # M6 has smallest error

par(mfrow =c(1,1))

plot(mean.cv.errors, type='b') # 6 variable model is best

cv10.best <- regsubsets(y ~ ., data = data.train, nvmax=10)

# Coefficient Estimates

coef(cv10.best, 6)

#coef(cv10.best, 10)

# Calculate MSE == 3095.483 --- same as # 2 MSE

cv10.pred <- predict(cv10.best, data.test, id=6)

mean((cv10.pred-y.test)^2)

mean((cv10.pred-data.test$y)^2)

# SE of MSE == 369.7526 --- same as # 2 MSE

sd((cv10.pred-data.test$y)^2)/sqrt(n.test) # 369.7526

# 4.) Ridge regression modeling using 10-fold cross-validation to select the largest value of λ such that the cross-validation error is within 1 standard error of the minimum (R functions glmnet and cv.glmnet in package glmnet). [Use a random number seed of 1306 immediately before entering the command: cv.out <- cv.glmnet(x.train, y.train, alpha = 0).]

# pages 266-269

grid = 10^seq(10,-2, length = 100)

ridge.fit0 = glmnet(x.train, y.train, alpha = 0, lambda = grid)

plot(ridge.fit0,xvar="lambda",label=T)

# is grid even necessary? -- not when you use cv.glmnet

library (glmnet)

k=10

set.seed(1306)

cv.out <- cv.glmnet(x.train, y.train, alpha = 0)

names(cv.out)

plot(cv.out)

#plot(cv.out, sign.lambda = -1)

# example of how to interpret this plot: http://gerardnico.com/wiki/r/ridge\_lasso

#plot(cv.out$glmnet.fit) # not sure what to make of this...

names(cv.out)

largelam <- cv.out$lambda.1se

largelam # lambda = 41.67209

ridge.fit <- glmnet(x.train,y.train,alpha=0,lambda=41.67209)

#plot(ridge.fit, xvar="lambda", label=T)

# the plot does not look right...

# Coefficient Estimates

coef(ridge.fit)

ridge.pred <- predict(ridge.fit,newx = x.test)

# Calculate MSE == 3070.87

mean((ridge.pred-y.test)^2) # 3070.87

# SE of MSE == 350.5467

sd((ridge.pred-y.test)^2)/sqrt(n.test) # 350.5467

# 5.) Lasso model using 10-fold cross-validation to select the largest value of λ such that the cross-validation error is within 1 standard error of the minimum (R functions glmnet and cv.glmnet in package glmnet). [Use a random number seed of 1306 immediately before entering the command: cv.out <- cv.glmnet(x.train, y.train, alpha = 1).]

library (glmnet)

k=10

set.seed(1306)

cv.out <- cv.glmnet(x.train, y.train, alpha = 1)

plot(cv.out)

names(cv.out)

largelam.lasso <- cv.out$lambda.1se

largelam.lasso # 4.791278

lasso.fit <- glmnet(x.train,y.train,alpha=1,lambda=4.791278)

#plot(lasso.fit) # doesn't look right...

# Coefficient Estimates

coef(lasso.fit)

# Calculate MSE == 2920.041

lasso.pred <- predict(lasso.fit,newx=x.test)

mean((lasso.pred-y.test)^2) # 2920.041

# SE of MSE == 346.2248

sd((lasso.pred-y.test)^2)/sqrt(n.test) # 346.2248

1. Please note: we kept the transformed variable names the same as the original variable names for our models, but we added a “.t” to the end of each variable name in Figure 1 to clearly distinguish between the original and transformed variables. [↑](#footnote-ref-1)