plotROC Package Investigation

June 10, 2020

1 Packages

```
[2]: library(mdsr)
    library(tidyverse)
    library(rpart)
    library(randomForest)
    library(e1071)
    library(class)
    library(nnet)
    library(ROCR)
    library(plotROC)
    library(plotly)
    library(gridExtra)
```

2 Init

```
[3]: census <- read.csv(
       "http://archive.ics.uci.edu/ml/machine-learning-databases/adult/adult.data",
       header = FALSE)
     names(census) <- c("age", "workclass", "fnlwgt", "education",</pre>
                          "education.num", "marital.status", "occupation", u
      \hookrightarrow "relationship",
                          "race", "sex", "capital.gain", "capital.loss", "hours.per.
      →week",
                          "native.country", "income")
     set.seed(364)
     n <- nrow(census)</pre>
     test_idx <- sample.int(n, size = round(0.2 * n))</pre>
     train <- census[-test_idx,]</pre>
     test <- census[test_idx,]</pre>
     form <- as.formula("income ~ age + workclass + education + marital.status +</pre>
       occupation + relationship + race + sex + capital.gain + capital.loss +
       hours.per.week")
```

We will need to convert our income labels into binary to use plotROC comfortably.

```
[4]: test_income_binary <- ifelse(test$income == ' <=50K', 0, 1)
test_income_binary %>% head()
```

1. 0 2. 1 3. 0 4. 0 5. 0 6. 0

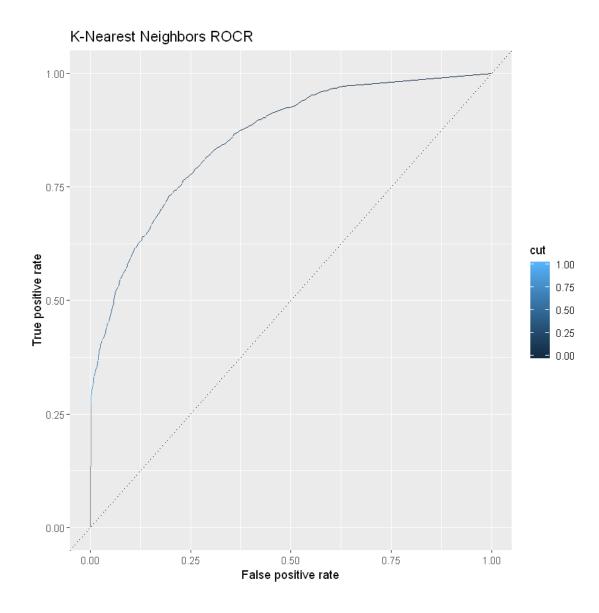
3 Models

3.1 K-Nearest Neighbors

We will need to calculate the probabilities for each model, not only for ROCR, but for plotROC as well.

$1. \ 0 \ 2. \ 0.3 \ 3. \ 0 \ 4. \ 0 \ 5. \ 0 \ 6. \ 0$

Below is the ROCR ROC curve as normal.



We can convert this ROCR implementation into plotly to become interactive. plotly currently has a bug where geom_line will not display if color is specified in the aesthetic. This is why geom_point is added.

HTML widgets cannot be represented in plain text (need html)

In order to use plotROC, you first need a data frame with a column for ground truth classifications (D) and a column for probabilities returned by your model (M). The D column should be in 0's and 1's, or else plotROC will make an educated guess as to which factor level will be mapped to 0 and which will be mapped to 1.

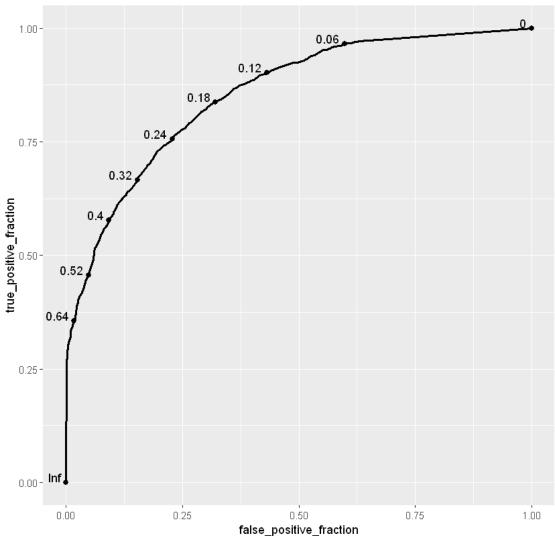
```
[9]: plotroc_knn_df <- data.frame(test_income_binary, income_knn_probs)
    names(plotroc_knn_df) <- c('D', 'M')
    plotroc_knn_df %>% head()
```

D	Μ
0	0.0
1	0.3
0	0.0
0	0.0
0	0.0
0	0.0

Once you have this data frame, you use ggplot with d equal to the D column and m equal to the M column in the initial aesthetic. Then you add a geom_roc label.

```
[10]: plotroc_knn <- plotroc_knn_df %>% ggplot(aes(d = D, m = M)) +
    geom_roc(labelround = 2) + ggtitle("K-Nearest Neighbors plotROC")
plotroc_knn
```

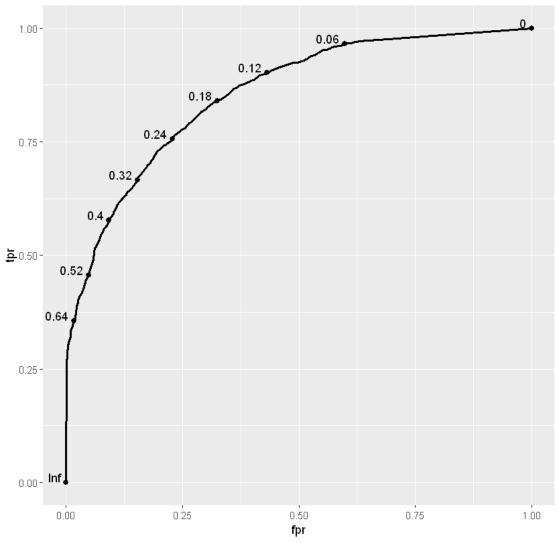
K-Nearest Neighbors plotROC



Alternatively, you could simply use the fpr, tpr, and cut returned from the ROCR::performance function. Just set x = fpr, y = tpr, and label = cut. Then add a geom_roc layer with stat = "identity" inside.

```
[11]: plotroc_knn_alt <- perf_knn_df %>% ggplot(aes(x = fpr, y = tpr, label = cut)) + geom_roc(stat = "identity", labelround = 2) + ggtitle("K-Nearest Neighbors_u \( \to \plotroc_knn_alt \) plotroc_knn_alt
```





The first plotROC ROC curve can be made into an interactive plot easily.

However, the second curve cannot currently be made into an interactive plot.

```
Error in `[.data.frame`(ggroc_p$data, , Mran.name): undefined columns⊔

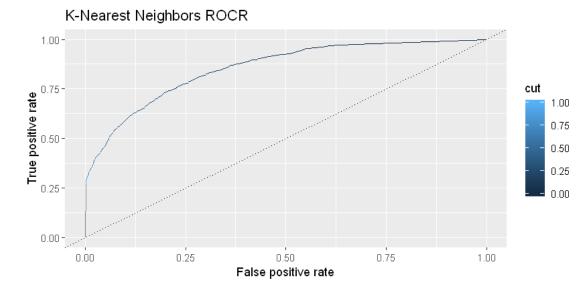
⇒selected

Traceback:
```

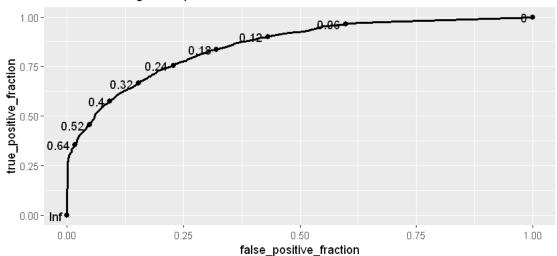
```
1. plotroc_knn_alt %>% plot_interactive_roc()
2. withVisible(eval(quote(`_fseq`(`_lhs`)), env, env))
3. eval(quote(`_fseq`(`_lhs`)), env, env)
4. eval(quote(`_fseq`(`_lhs`)), env, env)
5. `_fseq`(`_lhs`)
6. freduce(value, `_function_list`)
7. withVisible(function_list[[k]](value))
8. function_list[[k]](value)
9. plot_interactive_roc(.)
10. export_interactive_roc(ggroc, ...)
11. ggroc_p$data[, Mran.name]
12. `[.data.frame`(ggroc_p$data, , Mran.name)
13. stop("undefined columns selected")
```

Here is a look at the differences between the ROCR ROC curve and the plotROC ROC curve.

```
[14]: grid.arrange(rocr_knn, plotroc_knn)
```



K-Nearest Neighbors plotROC



3.2 Decision Tree

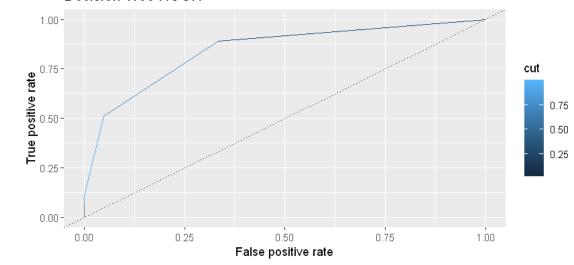
```
rocr_tree <- perf_tree_df %>% ggplot(aes(x = fpr, y = tpr, color = cut)) +
    geom_line() + geom_abline(intercept = 0, slope = 1, lty = 3) +
    ylab(perf_tree@y.name) + xlab(perf_tree@x.name) + ggtitle("Decision Tree_
    →ROCR")

plotroc_tree_df <- data.frame(test_income_binary, income_tree_probs)
names(plotroc_tree_df) <- c('D', 'M')

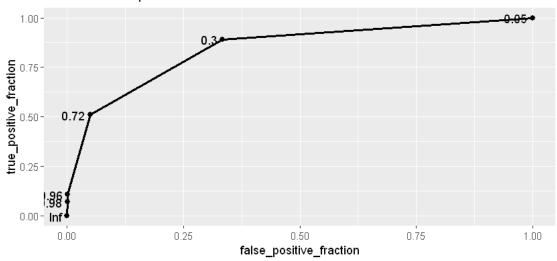
plotroc_tree <- plotroc_tree_df %>% ggplot(aes(d = D, m = M)) +
    geom_roc(labelround = 2) + ggtitle("Decision Tree plotROC")

grid.arrange(rocr_tree, plotroc_tree)
```

Decision Tree ROCR

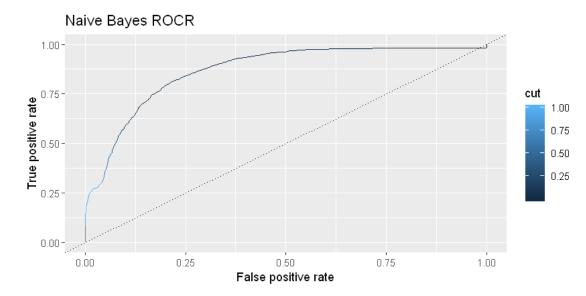


Decision Tree plotROC

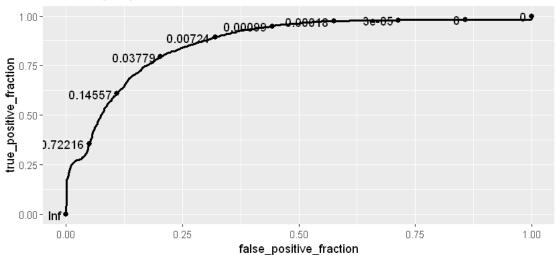


3.3 Naive Bayes

```
[16]: mod_nb <- naiveBayes(form, data = train)</pre>
      income_nb_probs <- mod_nb %>%
        predict(newdata = test, type = "raw")
      income_nb_probs <- income_nb_probs[, ' >50K']
      pred_nb <- ROCR::prediction(income_nb_probs, test$income)</pre>
      perf_nb <- ROCR::performance(pred_nb, 'tpr', 'fpr')</pre>
      perf_nb_df <- data.frame(perf_nb@x.values, perf_nb@y.values, perf_nb@alpha.</pre>
       →values)
      names(perf_nb_df) <- c("fpr", "tpr", "cut")</pre>
      rocr_nb <- perf_nb_df %>% ggplot(aes(x = fpr, y = tpr, color = cut)) +
        geom_line() + geom_abline(intercept = 0, slope = 1, lty = 3) +
        ylab(perf_nb@y.name) + xlab(perf_nb@x.name) + ggtitle("Naive Bayes ROCR")
      plotroc_nb_df <- data.frame(test_income_binary, income_nb_probs)</pre>
      names(plotroc_nb_df) <- c('D', 'M')</pre>
      plotroc_nb <- plotroc_nb_df %>% ggplot(aes(d = D, m = M)) +
        geom_roc(labelround = 5) + ggtitle("Naive Bayes plotROC")
      grid.arrange(rocr_nb, plotroc_nb)
```



Naive Bayes plotROC



3.4 Neural Network

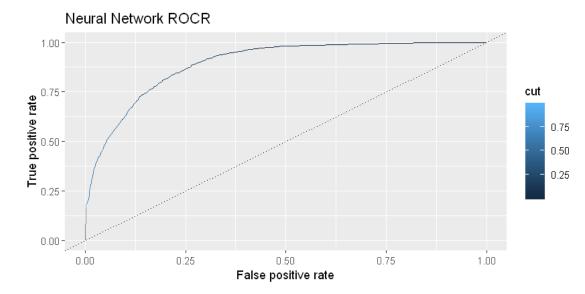
```
rocr_nn <- perf_nn_df %>% ggplot(aes(x = fpr, y = tpr, color = cut)) +
    geom_line() + geom_abline(intercept = 0, slope = 1, lty = 3) +
    ylab(perf_nn@y.name) + xlab(perf_nn@x.name) + ggtitle("Neural Network ROCR")

plotroc_nn_df <- data.frame(test_income_binary, income_nn_probs)
names(plotroc_nn_df) <- c('D', 'M')

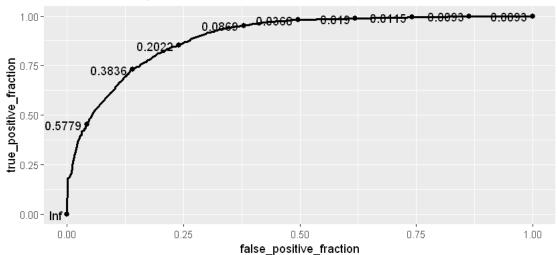
plotroc_nn <- plotroc_nn_df %>% ggplot(aes(d = D, m = M)) +
    geom_roc(labelround = 4) + ggtitle("Neural Network plotROC")

grid.arrange(rocr_nn, plotroc_nn)
```

```
# weights: 296
initial value 18084.849266
iter 10 value 13245.725269
iter 20 value 12943.091588
iter 30 value 12441.781618
iter 40 value 11682.237535
iter 50 value 10105.808035
iter 60 value 9145.121687
iter 70 value 8924.892976
iter 80 value 8785.947300
iter 90 value 8641.198852
iter 100 value 8537.477736
final value 8537.477736
stopped after 100 iterations
```

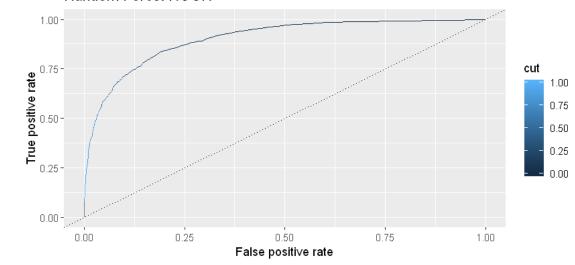


Neural Network plotROC

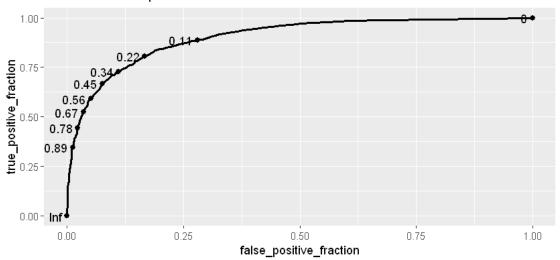


3.5 Random Forest

Random Forest ROCR



Random Forest plotROC



4 Comparing All Models

plotROC can easily calculate AUC of any plotROC ROC curve using calc_auc.

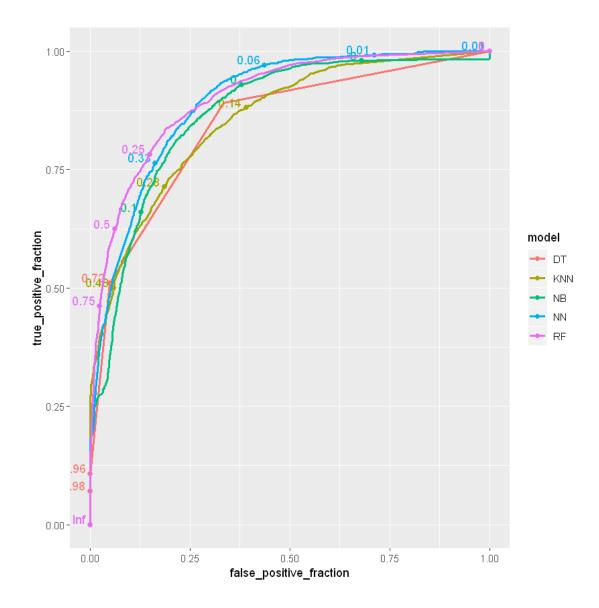
```
[19]: mod_names <- c("RF", "KNN", "NB", "NN", "DT")
plotroc_all_list <- list(plotroc_forest, plotroc_knn, plotroc_nb, plotroc_nn,

→plotroc_tree)
auc_df <- sapply(plotroc_all_list, calc_auc) %>% as.data.frame()
names(auc_df) <- mod_names
auc_df["AUC", ]
```

```
        RF
        KNN
        NB
        NN
        DT

        AUC
        0.9025387
        0.8547584
        0.8674455
        0.8933798
        0.844216
```

You can also plot several ROC curves on top of each other by combining them into a single data frame and labelling each case with its model. Then, when making the plotROC ROC curve, you specify color to equal the model in the ggplot aesthetic.

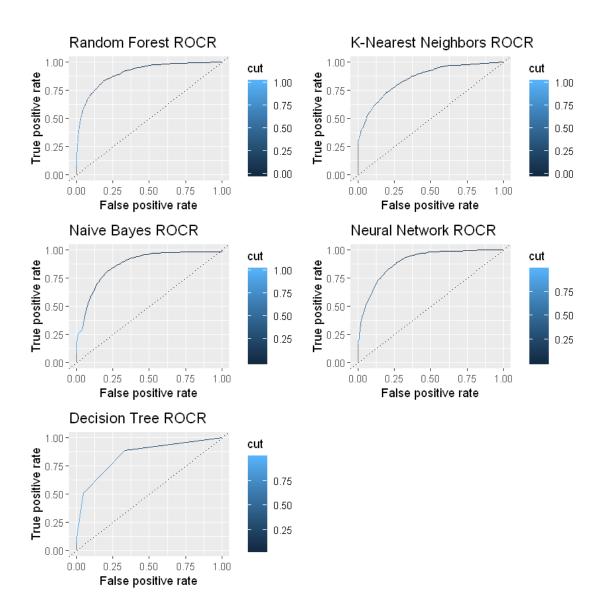


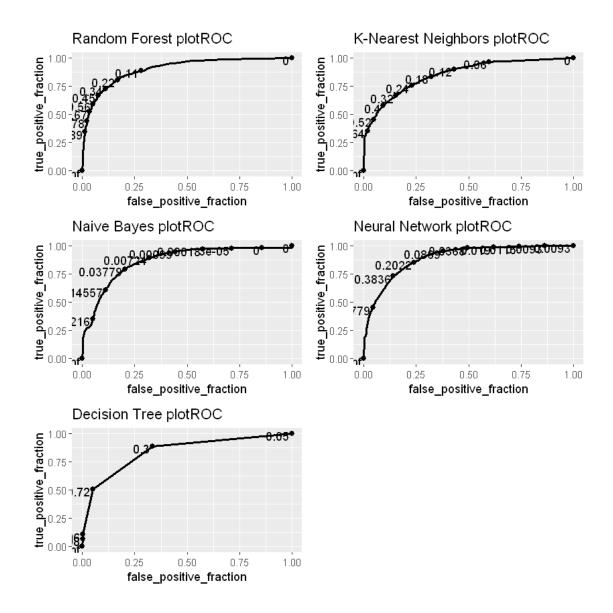
This combined form can also be turned into an interactive graph.

```
[21]: plotroc_all %>% plot_interactive_roc(labelround = 2)
```

When arranging them on a grid, the labels can get quite crammed, but you can still discern where on the curve the points are concentrated. Compare this to a grid of ROCR ROC curves.

```
[22]: grid.arrange(rocr_forest, rocr_knn, rocr_nb, rocr_nn, rocr_tree) grid.arrange(plotroc_forest, plotroc_knn, plotroc_nb, plotroc_nn, plotroc_tree)
```





Finally, compare the ROCR ROC curve overlay from before with the plotROC ROC curve overlay.

```
[23]: rocr_all <- ggplot() +
    geom_line(data = perf_tree_df, aes(x = fpr, y = tpr), color = "red") +
    geom_line(data = perf_knn_df, aes(x = fpr, y = tpr), color = "orange") +
    geom_line(data = perf_nb_df, aes(x = fpr, y = tpr), color = "green") +
    geom_line(data = perf_nn_df, aes(x = fpr, y = tpr), color = "blue") +
    geom_line(data = perf_forest_df, aes(x = fpr, y = tpr), color = "purple")

grid.arrange(rocr_all, plotroc_all)</pre>
```

