MATH 6350 Fall 2020 MSDS

Homework 5: Random Forest

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Introduction

In this report, we will continue to add to what we have performed in Homework 2,3, and 4 by looking into improving our data through Random Forest. A brief reminder of what was done in Homework 2,3, and 4: we selected three font data sets consisting of digitized images of typed characters and determined using the KNN function in R to predict our best K. Next we used PCA, a dimensionality reduction method that reduces the dimensionality of a large data set, by capturing as much of the data information as possible into a smaller one that contains most of the information of the large set. And lastly, K-means clustering was used to minimize the distance within a cluster all while maximizing the distance between different clusters.

The files were downloaded from a zip file from the following link: *https://archive.ics.uci.edu/ml/machine-learning-databases/00417/*

The font types that we chose were: COMIC, BOOKMAN, and MONOTYPE. Each has 412 column features along with total observed cases of 2669, 2388, and 2388 respectively. Each case describes numerically a digitized image of some specific character typed in each of the fonts. The images have 20x20 = 400 pixel sizes, each with its own “gray level” indicated by an integer value of 0 to 255. All the fonts have 412 feature columns, where 400 of them describe the 400 pixels named:

{ r0c0, r0c1,r0c2, … , r19,c17, r19c18, r19c19}

"rLcM" = gray level image intensity for pixel in position **{Row L, Column M}**.

As stated earlier, in Homework 5, we will be more focused on using the random forest to help improve our prediction outcome.

DATA Set up

A quick reminder of our data set up from Homework 2, we will briefly go over this section as a refresher. The following steps are taken to get R ready as well as organize our data for the steps that follow. Other than the 400 columns that are associated with the pixels, the data set font files each have the following 12 names:

{ font, fontVariant, m_label, strength, italic, orientation, m_top, m_left, originalH, originalW, h, w }

Of these 12 we need to discard the following 9:

{fontVariant, m_label, orientation, m_top, m_left, originalH, originalW, h, w}

And keep the following 3: ***{font, strength, italic}*** as well as the 400 pixel columns named: ***{ r0c0, r0c1,r0c2, … , r19,c17, r19c18, r19c19}*** therefore we are left with 403 columns. After these steps are completed, we define three CLASSES on images of the "normal" character were we extract all the rows in which our three fonts have both strength of 0.4 and italic of 0:

CL1 = all rows of **comic.csv** file for which {strength = 0.4 and italic=0}

CL2 = all rows of **bookman.csv** file for which {strength = 0.4 and italic=0}

CL3 = all rows of **monotype.csv** file for which {strength = 0.4 and italic=0}

And left with the following row outputs:

```
> n1 = nrow(CL1)
> n2 = nrow(CL2)
> n3 = nrow(CL3)
> N = sum(n1, n2, n3)
> n1;n2;n3;N
[1] 597
[1] 667
[1] 667
[1] 1931
```

The respected row sizes for CLASS1, CLASS2, and CLASS3 are named

n1, n2, n3 = 597, 667, 667 and there sum → N = 1931 cases

We combine them all together into a data set named DATA using the function **rbind()** and see it has dimensions of 1931 rows and 403 columns: the 403 being font,

strength, italic, +400 pixels we will call features X1, X2, … X400. Each such feature Xj is observed N times, and its N observed values are listed in the column "j" of DATA.

Once again, we make sure to standardize the 400 features. Define the ***start_col*** and ***end_col*** to be the feature X1 starts and X400 ends respectfully. Now that we have created our [1931x403] ***DATA*** set table, we observe the mean, m = mean(X1)....mean(X400), and standard deviation, s = sd(X1) ....sd(400) for each of our pixel features 1 to 400. The most important step to do before running our program is to standardize the data features in order to set everything at a mean of 0 and a standard deviation at 1. It is important to standardize because when we compare measurements they can have different units as one can observe in the table above. In the table below observe the variance of the data before and after standardization. Notice the variance of the DATA of X1 and X2 features before, and after when they all equal to 1. Variables that are measured at different scales do not contribute equally to the analysis and might end up creating a bias. We scale the data and name it SDATA. Note that X is a data frame from our DATA where we start at feature X1 and end at feature X400.

```
> var(DATA[,4]); var(DATA[,5])
[1] 7328.596
[1] 10008.27
>X = DATA[,start_col: end_col]
> SDATA = scale(X)
> var(SDATA[,4]); var(SDATA[,5])
[1] 1
[1] 1
```

Finally part of our data set up we explore our data outcome from Homework 3, PCA. Our Percentage of Variance Explained we calculated using the ***cumsum(D)/sum(D)*** functions in R, where D is defined as our eigenvalues. 95% (PVE(r) = 95%) of the variance, we identified to be r = 112 dimensions (or about 28%). Therefore, we concluded that 95% of our data falls within 1 to 112 dimensions and computed the PCA: new features also known as principal components.
Y1(n), Y2(n),.., Yr(n) for each case in n and r = 112.

```
> #transpose of the matrix W^T, ==> principal components Y1(n)...Yr(n)
> #Y1(n) = Q11 * X1(n) + Q21* X2(n) + … + Qr1 * Xr(n)
> Qt = t(eigen(R)$vector)[1:6,1:6]; Qt
             [,1]         [,2]        [,3]        [,4]        [,5]         [,6]
[1,]  0.037554270  0.042860673  0.04316449  0.04698484  0.04820854  0.052766042
[2,]  0.009644978  0.013215923  0.01723940  0.01635823  0.01393625  0.013510422
[3,] -0.044836953 -0.054798554 -0.04991597 -0.03201898 -0.01691300 -0.009282794
[4,]  0.124525697  0.136898628  0.14209661  0.14214624  0.13047797  0.102531423
[5,] -0.048293288 -0.041227763 -0.04463198 -0.05573747 -0.05368905 -0.054488360
[6,] -0.005032767 -0.003129964 -0.00605311 -0.01219605 -0.01925138 -0.017942660
```

```
> Qt = t(eigen(R)$vector)[112,1:6]; Qt
[1] -0.017344514  0.039593019 -0.002696742 -0.019101426 -0.032370772  0.035545753
```

That being said:

Y1(n) = 0.0375*F1(n) + 0.0428*F2(n) + 0.0431*F3(n) + 0.0469*F4(n) + 0.0482*F5(n) + 0.0527*F6(n)

Y2(n) = 0.0096*F1(n) + 0.0132*F2(n) + 0.0172*F3(n) + 0.0163*F4(n) + 0.0139*F5(n) + 0.01351*F6(n)

…

Y112(n) = -0.0050*F1(n) + 0.0395*F2(n) - 0.0026*F3(n) - 0.0191*F4(n) -0.0323*F5(n) - 0.0355*F6(n)

In conclusion, the goal of PCA was to find a low-dimensional representation of the observation that explains a good fraction of the variance and in Homework 3 we believe we found a reasonable value of new features r = 112 out of our 400. Compression helps eliminate unnecessary, redundant, or noisy information. Using linear compression through PCA is helpful when we have large numerical features.

Question 1

1.1) Selecting random train and test sets for each of the three classes:

```
set.seed(123)
pd1 = sample(x = 2, size = nrow(CL1), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL1
pd2 = sample(x = 2, size = nrow(CL2), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL2
pd3 = sample(x = 2, size = nrow(CL3), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL3
trainCL1 = CL1[pd1==1, ]
testCL1 = CL1[pd1==2, ]
trainCL2 = CL2[pd2==1, ]
testCL2 = CL2[pd2==2, ]
trainCL3 = CL3[pd3==1, ]
testCL3 = CL3[pd3==2, ]

> table(DATA$font)

   COMIC BOOKMAN MONOTYPE
     597      667      667
```

As you recall from our Data Set Up we see each class has the following cases:

n1, n2, n3 = 597, 667, 667

After the train and test sets are separated by 80% and 20% respectfully for each class, we have the following cases for each class:

```
> dim(trainCL1);dim(testCL1)  # Comic
[1] 477 113
[1] 120 113
> dim(trainCL2);dim(testCL2)  # Bookman
[1] 541 113
[1] 126 113
> dim(trainCL3);dim(testCL3)  # Monotype
[1] 527 113
[1] 140 113
```

1.2) As we can see in the dimensions above, we observe trainCL1:trainCL3 with the size 477, 541, and 527 respectively (79.9%, 81.1%, and 79.0% of the train set) and testCL1: trainCL3 with the size 102, 126, and 140 respectively (17.0%, 18.9%, and 21.0% of the test set) therefore the gap between these percentage is too small to justify cloning or undersampling.

1.3) Now we have new pairs of the train and test sets. Re-define our true train/test set: ***TRAINSET_TARGET / TESTSET_TARGET*** by regrouping across classes using row combining these new pairs. The same goes for the ***TRAINSET / TESTSET:***

```
TRAINSET_TARGET = rbind(trainCL1, trainCL2, trainCL3)[,1] # true train set
TESTSET_TARGET = rbind(testCL1, testCL2, testCL3)[,1]        # true test set

TRAINSET = rbind(trainCL1, trainCL2, trainCL3)[,-1]
TESTSET = rbind(testCL1, testCL2, testCL3)[,-1]

> dim(TRAINSET); dim(TESTSET)
[1] 1545  112
[1] 386 112
```

Once again, as we can see in the dimensions above, we observe TRAINSET = 1545 cases at 80% separated and TESTSET = 386 at 20% separated, where our data sets' total number of cases is N = 1931.

Question 2

2.1) Random Forest(RF) is the combination of tree predictors where each tree depends on the values of random vectors sampled independently with the same distribution for all trees. It helps avoid overfitting and, such as our data, it can deal with a large number of features to help make predictions.

2.2) To get started in performing random forest, we first make sure to set our *TRAINSET_TARGET* into factors using as.factor(). Next using the function randomForest(), from the package: library(randomForest) in R. Defined as ***rf_CL*** we input the factored *TRAINSET_TARGET* as our model as a function of all the other remaining variables and set the data = *TRAINSET.*

```
library(randomForest)
TRAINSET_TARGET <- as.factor(TRAINSET_TARGET)
rf_CL <- randomForest(TRAINSET_TARGET~.,data=TRAINSET)
```

```
> print(rf_CL)

Call:
 randomForest(formula = TRAINSET_TARGET ~ ., data = TRAINSET)
               Type of random forest: classification
                     Number of trees: 500
No. of variables tried at each split: 10

        OOB estimate of  error rate: 22.46%
Confusion matrix:
          BOOKMAN COMIC MONOTYPE class.error
BOOKMAN       398    49       94   0.2643253
COMIC          41   407       29   0.1467505
MONOTYPE       94    40      393   0.2542694
```

From the results, we can see that we have a classification type of random forest with the default number of trees (ntree) set to 500. The number of variables tried at each split (mtry) is 10. We note that the default is sqrt(p), where p = number of features. In our case, the number of features we have in both our TRAINSET and TESTSET is based on our results from our PCA in the Data Set-Up, r = 112. (from here

and moving forward, we will note r = p = 112). Going back to our randomForest mtry = sqrt(P) = sqrt(112) ≈ 10

The Out Of Bag (OOB) estimate of error rate = 22.46% ≈ (100*(1- .2246) = 77.45% accuracy) it is a good accuracy, but could be better/improved. Looking at the confusion matrix, we see that predictions are the best when predicting for class 1, COMIC with the lowest class error of 14.7% on the train set. In the terms of predicting our other two classes, we see a higher class error with 26.4% for Bookman and 25.4% for Monotype on the train set. For the OOB accuracy of 77.45%, we need to remember that it is the data this particular tree has not seen yet, therefore the accuracy is based on the error calculation.

2.3) Using the *predict()* function we input ***rf_CL*** associated to the randomForest and train = TRAINSET. We observe the following outputs:

```
p0 <- predict(rf_CL,TRAINSET)
```

```
> head(p0)
  668   669   670   673   674   676
COMIC COMIC COMIC COMIC COMIC COMIC
Levels: BOOKMAN COMIC MONOTYPE
```

```
> p0[10:15]
    681     682     684     685     686     689
BOOKMAN BOOKMAN   COMIC   COMIC   COMIC   COMIC
Levels: BOOKMAN COMIC MONOTYPE
```

Using the *head()* function we see what is contained in the first 6 outputs of our predict function. The first 6 predictions are seen to be the class1: Comic. For curiosity, we see what the predictions are for [10:15], and for 10,11 we see it is class2: Bookman and rest are once again class1:Comic.

2.4) Using the *confutionMatrix()* function, we input our prediction ***p0*** associated to the randomForest and true train = TRAINSET_TARGET. We observe the following outputs for the table and overall accuracy:

```
> confusionMatrix(p0,TRAINSET_TARGET)$table
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN      540     8       27
  COMIC          1   469        3
  MONOTYPE       0     0      497
> confusionMatrix(p0,TRAINSET_TARGET)$overall[1]
 Accuracy
0.9747573
```

As we can see in our table, we have the reference values/ actual classes as the column and the prediction values of the three classes. We see the correct classification is observed 540 times as the font: Bookman while the model also predicted it to be Bookman. The same goes for 469 times for Comic and 497 times for Monotype to be classified as the respected fonts while actually being at the font. We can also see that there are a total of (8 + 27+1 +3) = 39 misclassifications.

As for our accuracy we see that total classified correct/ total cases in the TRAINSET = [(540+469+497) / (1545)] = [1506/1545]100% = 97.4% accuracy. (classification error is less than 1%). Unlike the OOB estimation, we have a much higher accuracy using the prediction function. This is due to the training data provided to the randomForest model based on our TRAINSET data of 1545 cases, resulting in higher accuracy.

Question 3

3.1) Fixing the number of trees (ntree) set to 100, and the number of variables tried at each split (mtry) to sqrt(p) we repeat the steps done in part 2.2) applying random forest to classify our data set into the 3 classes. Note we are using the p =112 new features we found in our PCA result.

```
> set.seed(123)
> rf = randomForest(TRAINSET_TARGET~., data = TRAINSET, ntree = 100, mtry = sqrt(p))
> print(rf)

Call:
 randomForest(formula = TRAINSET_TARGET ~ ., data = TRAINSET,
 ntree = 100, mtry = sqrt(p))
               Type of random forest: classification
                     Number of trees: 100
No. of variables tried at each split: 11

        OOB estimate of  error rate: 27.25%
Confusion matrix:
          BOOKMAN COMIC MONOTYPE class.error
BOOKMAN       382    63       96   0.2939002
COMIC          66   365       46   0.2348008
MONOTYPE      109    41      377   0.2846300
```

We observe the classification random forest, at ntree = 100 and mtry = 11. Compared to out randomForest in part 2.2) we observe a slight increase the OOB estimate of the error rate to 27.25% resulting in a slight decrease in accuracy at (1-.2725)*100% = 72.75% (whereas in part 2.2 it was 77.45%).

The prediction and confusion matrix of the train and test set are as follow at ntree= 100 and mtry = sqrt(p):

```
> # prediction & confusion matrix - train data
> library(caret)
> pred1 = predict(rf, TRAINSET)
> trainconf = confusionMatrix(pred1, TRAINSET_TARGET)$table # or table(pred1,
 TRAINSET_TARGET)
> print(trainconf)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN      538     9       25
  COMIC          0   467        1
  MONOTYPE       3     1      501
> trainperf = confusionMatrix(pred1, TRAINSET_TARGET)$overall[1] # or sum(diag
(trainconf))/sum(trainconf)
> print(trainperf)
 Accuracy
0.9747573
```

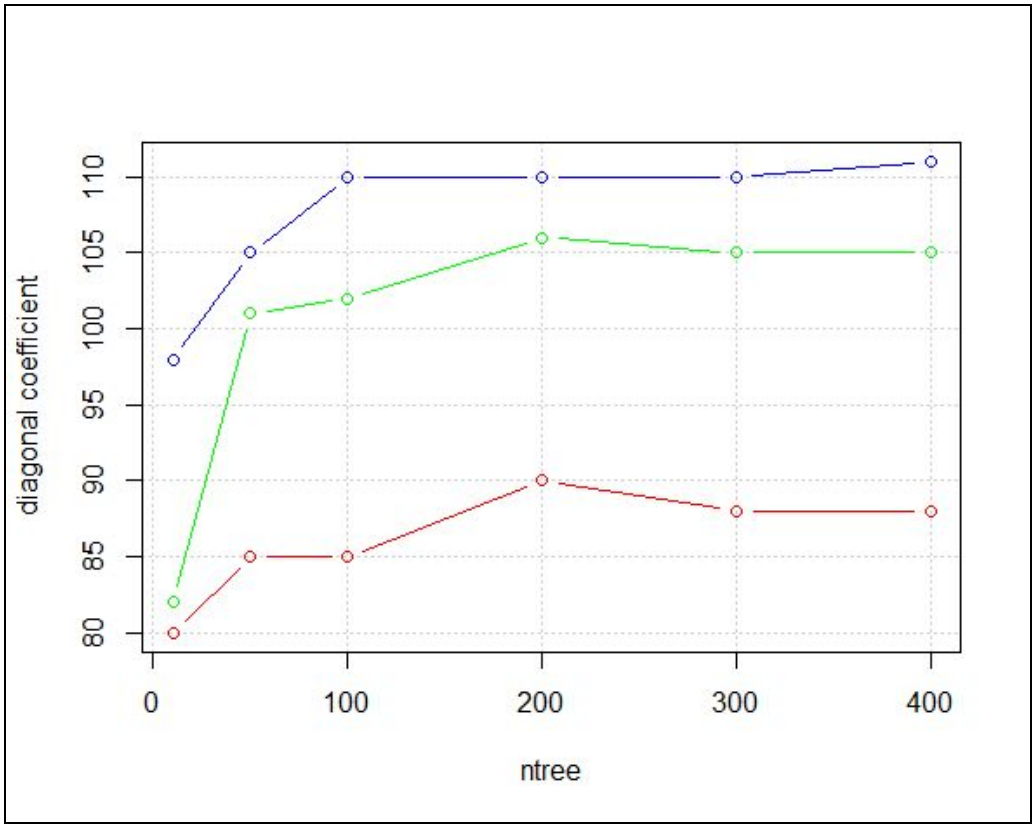
For the TRAINSET prediction, we observe the same percentage of accuracy as in our TRAINSET in part 2.3 and 2.4) at 97.4%. However that being said, we do notice a difference in the correct classification. Though slightly different, we observed 538 *(compared to 540)* times as the font: Bookman while the model also predicted it to be Bookman. The same goes for 467 *(compared to 469)* times for Comic and 501 *(compared to 497)* times for Monotype to be classified as the respected fonts while actually being at font. We can also see that there is still a total of (3+1+9+25+1) = 39 misclassifications. *(compared to (8 + 27+1 +3) = 39 in part 2.4)* therefore, we can suggest the changing from default ntree = 500, to ntree = 100 did not make much of a change.

```
> # prediction & confusion matrix - test data
> pred2 = predict(rf, TESTSET)
> testconf = confusionMatrix(pred2, TESTSET_TARGET)$table
> print(testconf)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN       86    12       25
  COMIC         17   102        5
  MONOTYPE      23     6      110
> testperf = confusionMatrix(pred2, TESTSET_TARGET)$overall[1]
> print(testperf)
 Accuracy
0.7720207
```

For the TESTSET prediction of the true test: TESTSET_TARGET, we observe the percent accuracy has decreased down to 77.2%. this testset data has not been seen by the random forest model, we can conclude this is a more accurate assessment accuracy of the model.

3.2) We will not explore the random forest at a fix ntry = sqrt(p) and explore the the testset confusion matrices along with their performance accuracy at
ntree= {10, 50, 100, 200, 300, 400}

```
> conf(1)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        80    20        30
  COMIC          20    82        12
  MONOTYPE       26    18        98
> conf(2)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        85    14        28
  COMIC          18   101         7
  MONOTYPE       23     5       105
> conf(3)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        85    12        25
  COMIC          17   102         5
  MONOTYPE       24     6       110
> conf(4)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        90    10        25
  COMIC          14   106         5
  MONOTYPE       22     4       110
> conf(5)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        88    10        27
  COMIC          15   105         3
  MONOTYPE       23     5       110
> conf(6)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        88    10        26
  COMIC          15   105         3
  MONOTYPE       23     5       111
```



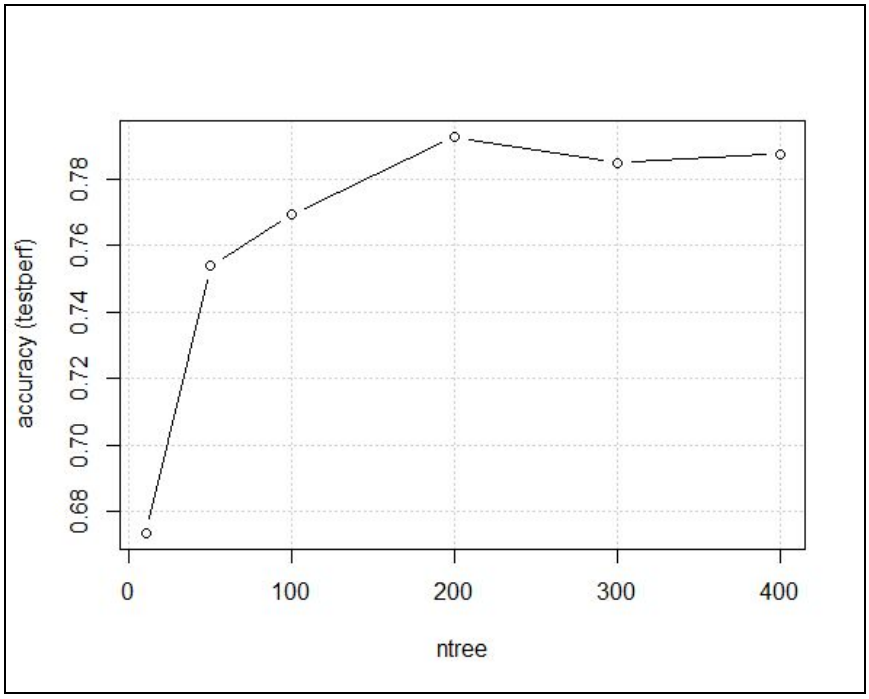
The following curve above represents the diagonal coefficients vs, the ntrees of each class. Compare it to 6 confusion matrices above, we observe

Red: The first diagonal coefficients of the 6 matrices (1,1), {80, 85, 85, 90, 88, 88}

Green: The second diagonal coefficients of the 6 matrices (2,2),{82,101,102,106,105,105}

Blue: The third diagonal coefficient of the 6 matrices (3,3), {98,105,110,110,110,111}. Once again, these coefficients represent the times a font is correct while the model also predicted it to be that specific font.

```
> testperf(ntrees = 10)
 Accuracy
0.6735751
> testperf(50)
Accuracy
0.753886
> testperf(100)
 Accuracy
0.7694301
> testperf(200)
 Accuracy
0.7927461
> testperf(300)
 Accuracy
0.7849741
> testperf(400)
 Accuracy
0.7875648
```



The following curve above is the test set accuracy vs ntrees. This time we are looking at our accuracy of (total classified correct) / (total cases in the TESTSET) , where the TESTSET= 386 cases. As we can see, it appears the highest testset accuracy is at when ntrees= 200 with an accuracy of 79.27%

Therefore, we select the best ntree value, bntr = 200

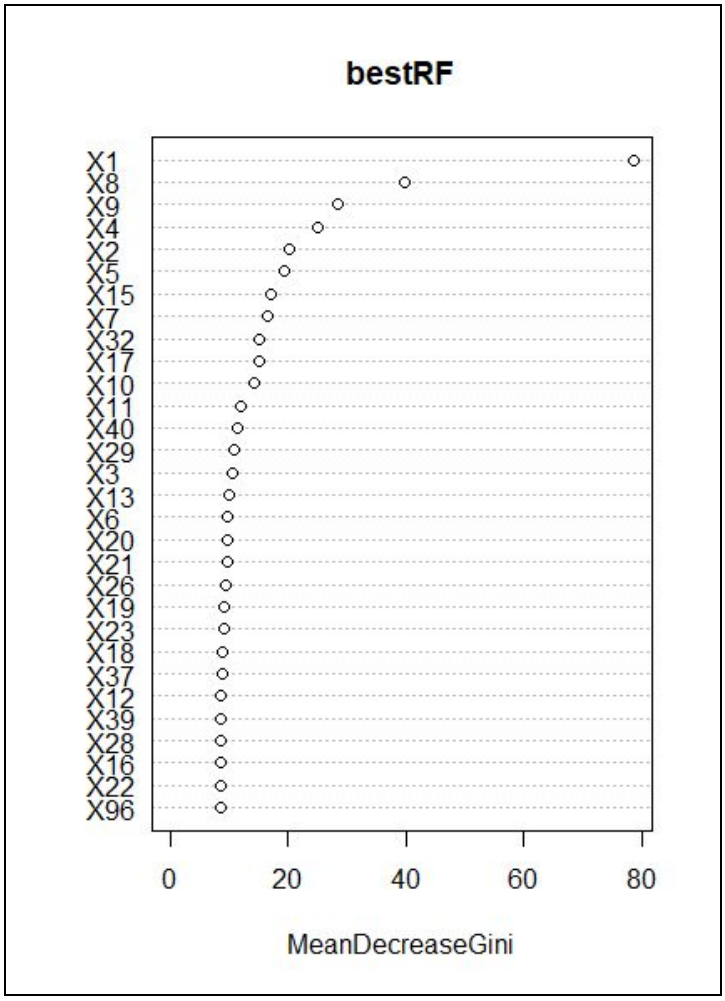
Question 4

4.1) Setting our best ntree value, bntr = 200 and number of variables to split the tree, mtry = sqrt(p) where p =112 , we define ***bestRF*** as our randomForest importance IM1...IMp of our 112 features as seen below. We observe the OOB estimate of error rate to be 24.85% (with an accuracy of (1-.2485)*100%=75.15%). We also observe that once again class font Comic displays the lowest class error at 19.7% while Bookman and Monotype are followed behind with 28.1% and 26.2%. Compared to our results from 2.2) our data has slightly decreased in accuracy.

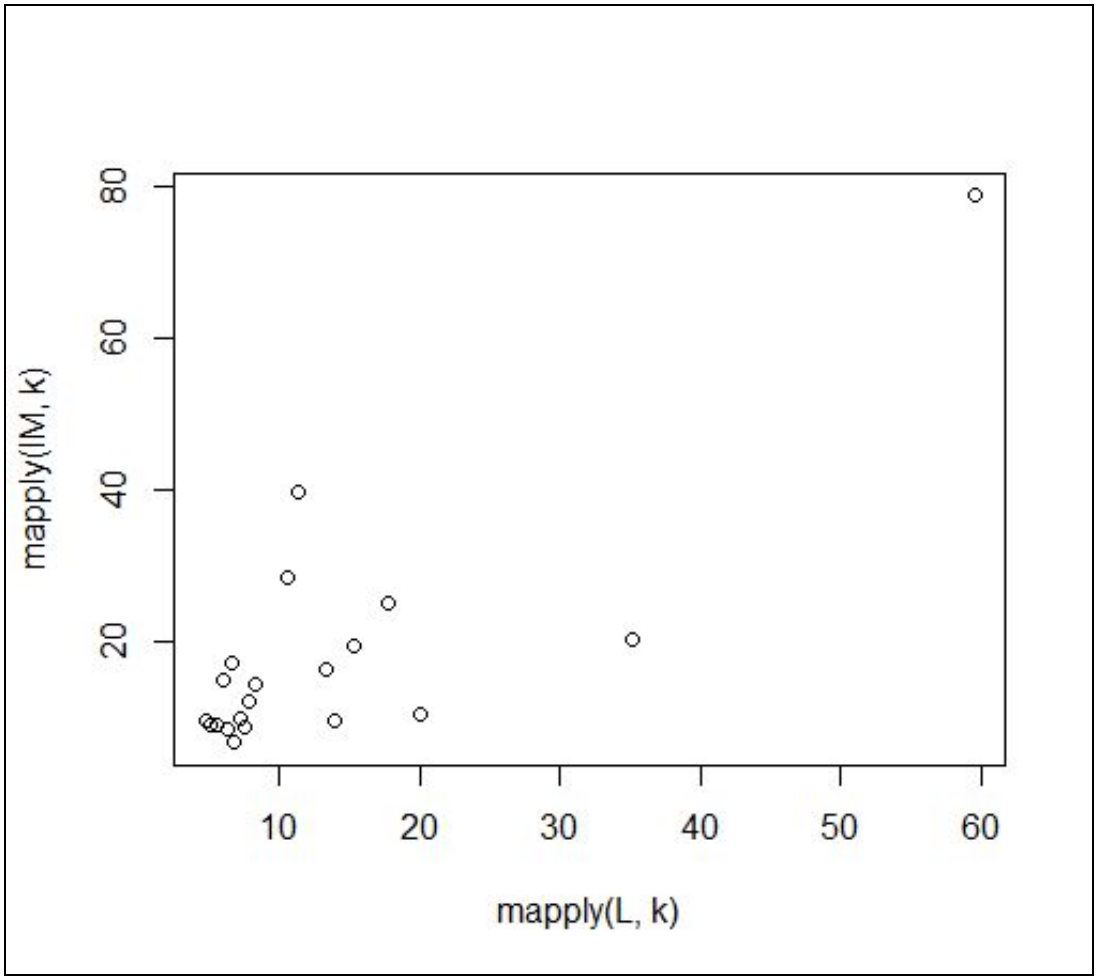
```
> set.seed(123)
> bestRF = randomForest(TRAINSET_TARGET~., data = TRAINSET, ntree = bntr, mtry = sqrt(p))
> print(bestRF)

Call:
 randomForest(formula = TRAINSET_TARGET ~ ., data = TRAINSET,
  ntree = bntr, mtry = sqrt(p))
               Type of random forest: classification
                     Number of trees: 200
No. of variables tried at each split: 11

        OOB estimate of  error rate: 24.85%
Confusion matrix:
          BOOKMAN COMIC MONOTYPE class.error
BOOKMAN       389    60       92   0.2809612
COMIC          63   383       31   0.1970650
MONOTYPE      103    35      389   0.2618596
```

Using the *importance()* function, we can view the importance of each variable. We get the measure of the total decrease in node impurity that results for splits over that feature, averaged over all trees. In our plot ***varImpPlot(bestRF)*** we can clearly see how pure the nodes are at the end of the tree without each variable and feature X1 stands out the most out of all the features with the highest mean gini decrease. In the output above the bestFR plot, we displayed the values of the top 10 highest Mean Gini Decreases. We notice that X1 = 78.70, while the next highest is X8 = 39.77.

```
> bestRF$importance[c(1,8,9,4,2,5,15,7,32,17),]
       X1        X8        X9        X4        X2
78.70201 39.77565 28.55033 25.15356 20.20513
       X5       X15        X7       X32       X17
19.35398 17.06720 16.45548 15.14708 14.93685
```



The scatter plot (eigenvalues vs the RF variable importance) shows that our first eigenvalue in our data is the most important than the previous eigenvalues and that the rest of the eigenvalues are not as important. We can clearly see that the one point in the top right corner is our first/highest eigenvalue D[1] = 59.507, and bestRF$importance[1] = 78.702


mapply(lM, k)
20
40
60
80
10
20
30
40
50
60
mapply(L, k)

4.2) In this section we will select a new random train and test set by setseed() different from part 1.1). We will also set the mtry = sqrt(p), ntree=bntr. So we do not mix up our randomly selected data from part 1.1) we apply the randomForest() on the new train set defined as TRAINSET_new, and new test set TESTSET_new, along with their new train and test sets: TRAINSET_TARGET_new, TESTSET_TARGET_new.

```
> set.seed(111)
> bestRF_new = randomForest(TRAINSET_TARGET_new~., data = TRAINSET_new,
 ntree = bntr, mtry = sqrt(p))
> print(bestRF_new)

Call:
 randomForest(formula = TRAINSET_TARGET_new ~ ., data = TRAINSET_new,
    ntree = bntr, mtry = sqrt(p))
               Type of random forest: classification
                     Number of trees: 200
No. of variables tried at each split: 11

        OOB estimate of  error rate: 23.81%
Confusion matrix:
          BOOKMAN COMIC MONOTYPE class.error
BOOKMAN       409    65       82   0.2643885
COMIC          58   398       24   0.1708333
MONOTYPE       98    44      380   0.2720307
> set.seed(111)
> pred2_new = predict(bestRF_new, TESTSET_new)
> testconf_new = confusionMatrix(pred2_new, TESTSET_TARGET_new)$table
> testperf_new = confusionMatrix(pred2_new, TESTSET_TARGET_new)$overall
[1]
> print(testconf_new)
           Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        82     7       31
  COMIC          14   104       11
  MONOTYPE       15     6      103
> print(testperf_new)
 Accuracy
0.7747989
```

At ntree = bntr = 200, and mtry = sqrt(112) = 11, we get the test performance accuracy of our new randomly selected data to be *testperf_new* = *77.47%*.

Comparing the test set accuracy and confusion matrix of our past random sample (bestRF) to our new random sample (newRF) we see that our accuracy has decreased only slightly. Based on a 95% confidence interval, we compare the percentages we observe that the *testpref_b* of the **bestRF** confidence interval is narrower compared to the *testpref_new* **newRF** by only [(0.8171899 - 0.7324080) - (0.8331825 - 0.7523097)] = 0.0039091 ⇒ ***0.39%***. It is a small change and therefore not much of a difference between the two randomly selected samples.

```
> CI(p = testperf_b, n = nrow(TESTSET))
[1] 0.7523097 0.8331825
> CI(p = testperf_new, n = nrow(TESTSET_new))
[1] 0.7324080 0.8171899
>
> print(testconf_b)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        90    10       25
  COMIC          14   106        5
  MONOTYPE       22     4      110
> print(testconf_new)
          Reference
Prediction BOOKMAN COMIC MONOTYPE
  BOOKMAN        82     7       31
  COMIC          14   104       11
  MONOTYPE       15     6      103
```

Question 5

5.1) Once again, we set the ntree = bntr = 200, and mtry = sqrt(112) = 11; however, this time, we will apply the RF function to 3 problems:

D1 = CL1 vs **D0** = {CL2 and CL3}

E1 = CL2 vs **E0** = {CL1 and CL3}

F1 = CL3 vs **F0** = {CL1 and CL2}

According to the case numbers of the new two classes (**D1** vs **D0**, or **E1** vs **E0**, or **F1** vs **F0**) of all three problems, there is a serious issue regarding strong imbalances that will lead to the skewed or biased prediction. As demonstrated in the table below, **D0**, **E0**, and **F0** are twice the case size of **D1**, **E1**, and **F1**.

```
> nrow(D1);nrow(D0)
[1] 597
[1] 1334
> nrow(E1);nrow(E0)
[1] 667
[1] 1264
> nrow(F1);nrow(F0)
[1] 667
[1] 1264
```

To combat the imbalanced classes, we clone to increase the number of cases in the smaller class until the case numbers of the training set and the test set between both classes respectively match.

So, here is how it works. For the training set of the smaller class (**D1** or **E1** or **F1**), we randomly select 80% of the cases as its training set at first. Then, we clone each case of its training set n times, where “n” is the ceiling value of the training set’s size ratio of bigger class to smaller class. Basically, the number of “n” is either 2 or 3 in all three questions here. Now, the modified training set of the smaller class definitely has a larger size than the intact training set of the bigger class (**D0** or **E0** or **F0**) does. To reach a balanced state between both classes’ training sets, we randomly select “m” quantities of only cloned cases in the modified training set of the smaller class to

remove out, where “m” is the size difference between the modified training set of smaller class and the intact training set of the bigger class.

For the test set of the smaller class, because we selected the training set in the original data set just now, the rest of 20% of the cases are automatically classified as its test set. Then the next procedures are all the same as how we did in the training set just now.

```
> print(RF1)

Call:
 randomForest(formula = as.factor(trainset_target_D) ~ ., data = trainset_D,
    ntree = bntr, mtry = sqrt(p))
               Type of random forest: classification
                     Number of trees: 200
No. of variables tried at each split: 11

        OOB estimate of  error rate: 15.32%
Confusion matrix:
    D1   D0 class.error
D1 279  258  0.48044693
D0  69 1528  0.04320601
> print(RF2)

Call:
 randomForest(formula = as.factor(trainset_target_E) ~ ., data = trainset_E,
    ntree = bntr, mtry = sqrt(p))
               Type of random forest: classification
                     Number of trees: 200
No. of variables tried at each split: 11

        OOB estimate of  error rate: 10.88%
Confusion matrix:
     E0  E1 class.error
E0 1533  16  0.01032924
E1  204 269  0.43128964
> print(RF3)

Call:
 randomForest(formula = as.factor(trainset_target_F) ~ ., data = trainset_F,
    ntree = bntr, mtry = sqrt(p))
               Type of random forest: classification
                     Number of trees: 200
No. of variables tried at each split: 11

        OOB estimate of  error rate: 6.43%
Confusion matrix:
    F0  F1 class.error
F0 918  93  0.09198813
F1  37 974  0.03659743
>
```

After appything our random forest to the three classifiers: RF1, RF2, and RF3, we observe that RF3 generated the lowest OOB error rate at 6.43 while RF1 had the highest at 15.32%.

```
>
> print(A1)
 Accuracy
0.8483146
> print(A2)
 Accuracy
0.8616601
> print(A3)
 Accuracy
0.8003953
>
```

```
> print(M1)
          Reference
Prediction  D1  D0
        D1  69  20
        D0  61 384
> print(M2)
          Reference
Prediction  E0  E1
        E0 365  53
        E1  17  71
> print(M3)
          Reference
Prediction  F0  F1
        F0 223  71
        F1  30 182
```

For our testset confusion matrix M1 of **D0** vs **D1**, we observe it to have an accuracy of 84.8%. For the other two confusion matrix of **E1** vs **E0**, and **F1** vs **F0**, we observe prediction accuracies of 86.1% and 80.0%

5.2) Now, applying separately the predictor bestRF already computed to the classify, CL1 vs {CL2 and CL3}, CL2 vs {CL1 and CL3}, CL3 vs {CL1 and CL2}, we yield accuracies B1,B2,and B3 along with their testset confusion matrices BM1, BM2, and BM3.

```
>
>
> print(B1)
 Accuracy
0.9400749
> print(B2)
 Accuracy
0.9743083
> print(B3)
 Accuracy
0.9367589
>
```

```
> print(BM1)
          Reference
Prediction  D1  D0
        D1 122  24
        D0   8 380
> print(BM2)
          Reference
Prediction  E0  E1
        E0 372   3
        E1  10 121
> print(BM3)
          Reference
Prediction  F0  F1
        F0 249  28
        F1   4 225
```

Compared to our results of question 5.1), our accuracy all increased for each classifier, specifically as below:

- The accuracy B1 increases 9.2% if compared to the accuracy A1 (B1 is 94% and A1 is 84.8%)
- The accuracy B2 increases 11.2% if compared to the accuracy A2 (B2 is 97.4% and A2 is 86.2%)
- The accuracy B3 increases 13.7% if compared to the accuracy A3 (B3 is 93.7% and A3 is 80.0%)

  All in all, we get fairly better results for all 3 accuracies B1, B2, B3 in question 5.2) if compared to the accuracies A1, A2, A3 in question 5.1). Again, we believe our results can still be improved further in the future given that we explore and apply different approaches.

R Codes

```
rm(list=ls()) # to remove all objects from a specified environment
cat("\f") # to clean console

# Data Setup
library(readr)
setwd("~/Library/Mobile Documents/com~apple~CloudDocs/Study Files (Graduate)/MATH
6350/Homework/HW03/fonts/")

# We selected COMIC.csv, BOOKMAN.csv, MONOTYPE.csv.
COMIC <- data.frame(read_csv("COMIC.csv"))
BOOKMAN <- data.frame(read_csv("BOOKMAN.csv"))
MONOTYPE <- data.frame(read_csv("MONOTYPE.csv"))

c.names = names(COMIC) # All three font files shares same categories of columns

c.discard = match(c("fontVariant", "m_label", "orientation", "m_top", "m_left", "originalH",
                    "originalW", "h", "w"),c.names) # discard 9 columns listed
# na.omit() function is to omit all rows that contain NA values
comic = na.omit(COMIC[,-c.discard])
bookman = na.omit(BOOKMAN[,-c.discard])
monotype = na.omit(MONOTYPE[,-c.discard])

CL1 = bookman[bookman[,match("strength", names(bookman))] == 0.4 &
              bookman[,match("italic", names(bookman))] == 0,]
CL2 = comic[comic[,match("strength", names(comic))] == 0.4 &
            comic[,match("italic", names(comic))] == 0,]
CL3 = monotype[monotype[,match("strength", names(monotype))] == 0.4 &
               monotype[,match("italic", names(monotype))] == 0,]
DATA = rbind(CL1, CL2, CL3)
str(DATA)

# Standardization
true_set = as.factor(DATA[,1])
start_col = match("r0c0",names(DATA))
end_col = ncol(DATA)
X = DATA[,start_col: end_col]
m = sapply(X, mean) # same as apply(X, MARGIN = 2, mean)
s = sapply(X, sd)
SDATA = scale(X)

# Correlation Matrix Computation
R = cor(X)
# sigma = cov(X) # variance-covariance matrix "sigma"
# R=cov2cor(sigma) # either way to find correlation matrix
# all.equal(cor(X), cov2cor(sigma))

# Eigenvalues and Eigenvectors
D = eigen(R)$values
# or D = (summary(pca)$sdev)^2
Q = eigen(R)$vectors


p = order(abs(cumsum(D)/sum(D) - 0.95), decreasing = FALSE)[1]
V = Q[, 1:p]
```

```
X = as.matrix(scale(X))
Y = data.frame(true_set, X%*%V)
CL2 = Y[Y[,match("true_set", names(Y))] == "COMIC",]
CL1 = Y[Y[,match("true_set", names(Y))] == "BOOKMAN",]
CL3 = Y[Y[,match("true_set", names(Y))] == "MONOTYPE",]

n1 = nrow(CL1)
n2 = nrow(CL2)
n3 = nrow(CL3)
N = sum(n1, n2, n3)

N == nrow(DATA) # verification

SX = Y[,-1]

# Question 1
set.seed(123)
pd1 = sample(x = 2, size = nrow(CL1), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL1
pd2 = sample(x = 2, size = nrow(CL2), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL2
pd3 = sample(x = 2, size = nrow(CL3), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL3

trainCL1 = CL1[pd1==1, ]
testCL1 = CL1[pd1==2, ]
trainCL2 = CL2[pd2==1, ]
testCL2 = CL2[pd2==2, ]
trainCL3 = CL3[pd3==1, ]
testCL3 = CL3[pd3==2, ]

TRAINSET_TARGET = rbind(trainCL1, trainCL2, trainCL3)[,1] # true train set
TESTSET_TARGET = rbind(testCL1, testCL2, testCL3)[,1] # true test set

TRAINSET = rbind(trainCL1, trainCL2, trainCL3)[,-1]
TESTSET = rbind(testCL1, testCL2, testCL3)[,-1]


# Question 2: Random Forest(RF)
# reference: https://www.youtube.com/watch?v=dJclNIN-TPo
library(randomForest)
?randomForest
# convert to factors
# TRAINSET_TARGET <- as.factor(TRAINSET_TARGET)
# TESTSET_TARGET <- as.factor(TESTSET_TARGET)
rf_CL <- randomForest(TRAINSET_TARGET~.,data=TRAINSET)
print(rf_CL)
attributes(rf_CL)
rf_CL$confusion
# predication
confusionMatrix(p0,TRAINSET_TARGET)$table
confusionMatrix(p0,TRAINSET_TARGET)$overall[1]

p00 <- predict(rf_CL,TESTSET)
head(p00)
confusionMatrix(p00,TESTSET_TARGET)$table
confusionMatrix(p00,TESTSET_TARGET)$overall[1]
```

 # Question 3.1

```
set.seed(123)
rf = randomForest(TRAINSET_TARGET~., data = TRAINSET, ntree = 100, mtry = sqrt(p))
print(rf)
attributes(rf)
rf$confusion # the confusion matrix of the prediction (based on Out-of-Bag data)

# prediction & confusion matrix - train data
library(caret)
pred1 = predict(rf, TRAINSET)
trainconf = confusionMatrix(pred1, TRAINSET_TARGET)$table # or table(pred1, TRAINSET_TARGET)
print(trainconf)
trainperf = confusionMatrix(pred1, TRAINSET_TARGET)$overall[1] # or sum(diag(trainconf))/sum(trainconf)
print(trainperf)

# prediction & confusion matrix - test data
pred2 = predict(rf, TESTSET)
testconf = confusionMatrix(pred2, TESTSET_TARGET)$table
print(testconf)
testperf = confusionMatrix(pred2, TESTSET_TARGET)$overall[1]
print(testperf)
```

 # Question 3.2

```
rf = function(ntrees) {
  set.seed(123)
  rf = randomForest(TRAINSET_TARGET~., data = TRAINSET, ntree = ntrees, mtry = sqrt(p))
  return(rf)
}
testconf = function(ntrees) {
  pred2 = predict(rf(ntrees), TESTSET)
  testconf = confusionMatrix(pred2, TESTSET_TARGET)$table
  return(testconf)
}
n = c(10, 50, 100, 200, 300, 400)
conf = function(x) {
  n = n[x]
  conf = testconf(n)
  return(conf)
}
testperf = function(ntrees) { # accuracy
  pred2 = predict(rf(ntrees), TESTSET)
  testperf = confusionMatrix(pred2, TESTSET_TARGET)$overall[1]
  return(testperf)
}
conf(1)
conf(2)
conf(3)
conf(4)
conf(5)
conf(6)

testperf(ntrees = 10)
testperf(50)
testperf(100)
testperf(200)
```

```
testperf(300)
testperf(400)

plot(n, mapply(testperf, n), type = "b",
     panel.first=grid(),
     xlab = "ntree", ylab = "accuracy (testperf)")

coeff = function(k) {
  coeff = NULL
  for (i in c(1:6)) {
    coeff[i] = diag(matrix(mapply(conf, i), 3))[k]
  }
  return(coeff)
}
plot(n, coeff(1), type = "b", col = "red", ylim = c(80, 111),
     panel.first=grid(), xlab = "ntree", ylab = "diagonal coefficient")
lines(n, coeff(2), type = "b", col = "green")
lines(n, coeff(3), type = "b", col = "blue")

bntr = 200

# Question 4.1
set.seed(111)
bestRF = randomForest(TRAINSET_TARGET~., data = TRAINSET, ntree = bntr, mtry = sqrt(p))
print(bestRF)

# prediction & confusion matrix - test data (for bestRF)
pred2_b = predict(bestRF, TESTSET)
testconf_b = confusionMatrix(pred2_b, TESTSET_TARGET)$table
testperf_b = confusionMatrix(pred2_b, TESTSET_TARGET)$overall[1]


IM = function(k) {
  IM = bestRF$importance[k]
  return(IM)
}
L = function(k) {
  L = D[k]
  return(L)
}
k = 1:p
mapply(IM, k) # IM_1, IM_2, ..., IM_p
plot(mapply(L, k), mapply(IM, k), xlab = "eigenvalue: L_k", ylab = "bestRF's Importance: IM_k")

# Question 4.2
set.seed(111) # not set.seed(123), bc we need a different starting number used to generate a sequence of random
numbers
pd1_new = sample(x = 2, size = nrow(CL1), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL1
pd2_new = sample(x = 2, size = nrow(CL2), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL2
pd3_new = sample(x = 2, size = nrow(CL3), replace = TRUE, prob = c(0.8, 0.2)) # partition data of CL3

trainCL1_new = CL1[pd1_new==1, ]
testCL1_new = CL1[pd1_new==2, ]
trainCL2_new = CL2[pd2_new==1, ]
testCL2_new = CL2[pd2_new==2, ]
trainCL3_new = CL3[pd3_new==1, ]
```

```
testCL3_new = CL3[pd3_new==2, ]

TRAINSET_TARGET_new = rbind(trainCL1_new, trainCL2_new, trainCL3_new)[,1] # true train set
TESTSET_TARGET_new = rbind(testCL1_new, testCL2_new, testCL3_new)[,1] # true test set

TRAINSET_new = rbind(trainCL1_new, trainCL2_new, trainCL3_new)[,-1]
TESTSET_new = rbind(testCL1_new, testCL2_new, testCL3_new)[,-1]

bestRF_new = randomForest(TRAINSET_TARGET_new~., data = TRAINSET_new, ntree = bntr, mtry = sqrt(p))
print(bestRF_new)

## prediction & confusion matrix - train data (new)
#library(caret)
#pred1_new = predict(bestRF_new, TRAINSET_new)
#trainconf_new = confusionMatrix(pred1_new, TRAINSET_TARGET_new)$table # or table(pred1,
TRAINSET_TARGET)
#print(trainconf_new)
#trainperf_new = confusionMatrix(pred1_new, TRAINSET_TARGET_new)$overall[1] # or
sum(diag(trainconf))/sum(trainconf)
#print(trainperf_new)

# prediction & confusion matrix - test data (new)
pred2_new = predict(bestRF_new, TESTSET_new)
testconf_new = confusionMatrix(pred2_new, TESTSET_TARGET_new)$table
testperf_new = confusionMatrix(pred2_new, TESTSET_TARGET_new)$overall[1]


CI = function(p, CL = 0.95, n) {
  ci = p + c(-1, 1)*qnorm(1-(1-CL)/2)*sqrt(p*(1-p)/n)
  return(ci)
}

print(testperf_b)
print(testperf_new)

CI(p = testperf_b, n = nrow(TESTSET))
CI(p = testperf_new, n = nrow(TESTSET_new))

print(testconf_b)
print(testconf_new)


# Question 5.1
# CL1 versus {CL2+CL3}
D1 = CL1
D0 = rbind(CL2, CL3)

set.seed(123)
x = sample(x = nrow(D1), size = as.integer(0.8*nrow(D1)), replace = FALSE)
time1 = ceiling(as.integer(0.8*nrow(D0))/length(x))
i = sample(x = setdiff(c(1:(length(x)*time1)), seq(1, length(x)*time1, time1)),
           size = length(x)*time1 - as.integer(0.8*nrow(D0)),
           replace = FALSE)
pd_D1train = rep(x, each = time1)[-i]
setdiff(x, pd_D1train) # verification for all the original 80% of cases are not missed, so we expect the output be
integer(0)
```

```
# setdiff(x, y) is the material that is in x, that is not in y

y = setdiff(c(1:nrow(D1)), x)
TIME1 = ceiling((nrow(D0) - as.integer(0.8*nrow(D0)))/length(y))
j = sample(x = setdiff(c(1:(length(y)*TIME1)), seq(1, (length(y)*TIME1), TIME1)),
          size = length(y)*TIME1 - (nrow(D0) - as.integer(0.8*nrow(D0))),
          replace = FALSE)
pd_D1test = rep(y, each = TIME1)[-j]
setdiff(y, pd_D1test) # verification for all the original 20% of cases are not missed, so we expect the output be
integer(0)

intersect(pd_D1train, pd_D1test) # verification for test set and training set do not intersect

trainD1 = D1[pd_D1train,]
testD1 = D1[pd_D1test,]

pd_D0train = sample(x = nrow(D0), size = round(0.8*nrow(D0)), replace = FALSE)
trainD0 = D0[pd_D0train,]
testD0 = D0[-pd_D0train,]

trainset_D = rbind(trainD1, trainD0)[,-1]
testset_D = rbind(testD1, testD0)[,-1]

trainset_target_D = as.factor(rbind(trainD1, trainD0)[,1])
testset_target_D = as.factor(rbind(testD1, testD0)[,1])

library(plyr) # for mapvalues() function
trainset_target_D = mapvalues(trainset_target_D, c("BOOKMAN", "COMIC", "MONOTYPE"), c("D1", "D0",
"D0"))
testset_target_D = mapvalues(testset_target_D, c("BOOKMAN", "COMIC", "MONOTYPE"), c("D1", "D0", "D0"))


RF1 = randomForest(as.factor(trainset_target_D)~., data = trainset_D, ntree = bntr, mtry = sqrt(p))

pred_D = predict(RF1, testset_D)
testconf_D = confusionMatrix(pred_D, as.factor(testset_target_D))$table
M1 = testconf_D
testperf_D = confusionMatrix(pred_D, as.factor(testset_target_D))$overall[1]
A1 = testperf_D


# CL2 versus {CL1+CL3}
E1 = CL2
E0 = rbind(CL1, CL3)

set.seed(123)
x2 = sample(x = nrow(E1), size = as.integer(0.8*nrow(E1)), replace = FALSE)
time2 = ceiling(as.integer(0.8*nrow(E0))/length(x2))
i2 = sample(x = setdiff(c(1:(length(x2)*time2)), seq(1, length(x2)*time2, time2)),
          size = length(x2)*time2 - as.integer(0.8*nrow(E0)),
          replace = FALSE)
pd_E1train = rep(x2, each = time2)[-i2]
setdiff(x2, pd_E1train) # verification for all the original 80% of cases are not missed, so we expect the output be
integer(0)

y2 = setdiff(c(1:nrow(E1)), x2)
```

```
TIME2 = ceiling((nrow(E0) - as.integer(0.8*nrow(E0)))/length(y2))
j2 = sample(x = setdiff(c(1:(length(y2)*TIME2)), seq(1, (length(y2)*TIME2), TIME2)),
        size = length(y2)*TIME2 - (nrow(E0) - as.integer(0.8*nrow(E0))),
        replace = FALSE)
pd_E1test = rep(y2, each = TIME2)[-j2]
setdiff(y2, pd_E1test) # verification for all the original 20% of cases are not missed, so we expect the output be
integer(0)

intersect(pd_E1train, pd_E1test) # verification for test set and training set do not intersect


trainE1 = E1[pd_E1train,]
testE1 = E1[pd_E1test,]

pd_E0train = sample(x = nrow(E0), size = round(0.8*nrow(E0)), replace = FALSE)
trainE0 = E0[pd_E0train,]
testE0 = E0[-pd_E0train,]

trainset_E = rbind(trainE1, trainE0)[,-1]
testset_E = rbind(testE1, testE0)[,-1]

trainset_target_E = as.factor(rbind(trainE1, trainE0)[,1])
testset_target_E = as.factor(rbind(testE1, testE0)[,1])

trainset_target_E = mapvalues(trainset_target_E, c("BOOKMAN", "COMIC", "MONOTYPE"), c("E0", "E1",
"E0"))
testset_target_E = mapvalues(testset_target_E, c("BOOKMAN", "COMIC", "MONOTYPE"), c("E0", "E1", "E0"))


RF2 = randomForest(as.factor(trainset_target_E)~., data = trainset_E, ntree = bntr, mtry = sqrt(p))

pred_E = predict(RF2, testset_E)
testconf_E = confusionMatrix(pred_E, as.factor(testset_target_E))$table
M2 = testconf_E
testperf_E = confusionMatrix(pred_E, as.factor(testset_target_E))$overall[1]
A2 = testperf_E


# CL3 versus {CL1+CL2}
F1 = CL3
F0 = rbind(CL1, CL2)

set.seed(123)
x3 = sample(x = nrow(F1), size = as.integer(0.8*nrow(F1)), replace = FALSE)
time3 = ceiling(as.integer(0.8*nrow(F0))/length(x3))
i3 = sample(x = setdiff(c(1:(length(x3)*time3)), seq(1, length(x3)*time3, time3)),
        size = length(x3)*time3 - as.integer(0.8*nrow(F0)),
        replace = FALSE)
pd_F1train = rep(x3, each = time3)[-i3]
setdiff(x3, pd_F1train) # verification for all the original 80% of cases are not missed, so we expect the output be
integer(0)

y3 = setdiff(c(1:nrow(F1)), x3)
TIME3 = ceiling((nrow(F0) - as.integer(0.8*nrow(F0)))/length(y3))
j3 = sample(x = setdiff(c(1:(length(y3)*TIME3)), seq(1, (length(y3)*TIME3), TIME3)),
        size = length(y3)*TIME3 - (nrow(F0) - as.integer(0.8*nrow(F0))),
```

```
        replace = FALSE)
pd_F1test = rep(y3, each = TIME3)[-j3]
setdiff(y3, pd_F1test) # verification for all the original 20% of cases are not missed, so we expect the output be integer(0)

intersect(pd_F1train, pd_F1test) # verification for test set and training set do not intersect


trainF1 = F1[pd_F1train,]
testF1 = F1[pd_F1test,]

pd_F0train = sample(x = nrow(F0), size = round(0.8*nrow(F0)), replace = FALSE)
trainF0 = F0[pd_F0train,]
testF0 = F0[-pd_F0train,]

trainset_F = rbind(trainF1, trainF0)[,-1]
testset_F = rbind(testF1, testF0)[,-1]

trainset_target_F = as.factor(rbind(trainF1, trainF0)[,1])
testset_target_F = as.factor(rbind(testF1, testF0)[,1])

trainset_target_F = mapvalues(trainset_target_F, c("BOOKMAN", "COMIC", "MONOTYPE"), c("F0", "F0", "F1"))
testset_target_F = mapvalues(testset_target_F, c("BOOKMAN", "COMIC", "MONOTYPE"), c("F0", "F0", "F1"))

RF3 = randomForest(as.factor(trainset_target_F)~., data = trainset_F, ntree = bntr, mtry = sqrt(p))

pred_F = predict(RF3, testset_F)
testconf_F = confusionMatrix(pred_F, as.factor(testset_target_F))$table
M3 = testconf_F
testperf_F = confusionMatrix(pred_F, as.factor(testset_target_F))$overall[1]
A3 = testperf_F


print(RF1)
print(RF2)
print(RF3)

print(A1)
print(A2)
print(A3)

print(M1)
print(M2)
print(M3)


# Question 5.2
B1 = confusionMatrix(mapvalues(predict(bestRF, testset_D), c("BOOKMAN", "COMIC", "MONOTYPE"), c("D1", "D0", "D0")),
                     as.factor(testset_target_D))$overall[1]
B2 = confusionMatrix(mapvalues(predict(bestRF, testset_E), c("BOOKMAN", "COMIC", "MONOTYPE"), c("E0", "E1", "E0")),
                     as.factor(testset_target_E))$overall[1]
B3 = confusionMatrix(mapvalues(predict(bestRF, testset_F), c("BOOKMAN", "COMIC", "MONOTYPE"), c("F0", "F0", "F1")),
```

```
                as.factor(testset_target_F))$overall[1]

BM1 = confusionMatrix(mapvalues(predict(bestRF, testset_D), c("BOOKMAN", "COMIC", "MONOTYPE"),
c("D1", "D0", "D0")),
                 as.factor(testset_target_D))$table
BM2 = confusionMatrix(mapvalues(predict(bestRF, testset_E), c("BOOKMAN", "COMIC", "MONOTYPE"),
c("E0", "E1", "E0")),
                 as.factor(testset_target_E))$table
BM3 = confusionMatrix(mapvalues(predict(bestRF, testset_F), c("BOOKMAN", "COMIC", "MONOTYPE"),
c("F0", "F0", "F1")),
                 as.factor(testset_target_F))$table


print(B1)
print(B2)
print(B3)

print(BM1)
print(BM2)
print(BM3)
```