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Course: CS185C
Date: 12/1/2019

Comparison of Malware Detection Technique of HMM, PCA, and MLP

Abstract

In this project, we used different machine learning techniques to train on some Malware files to gain models. Then, we used the models to score on the Malware files and benign files to gain some scores. Using these scores, we then did some analysis and comparisons. Specifically, we used two features of Malware files. One is sequence of the Opcode, another is the frequency of the registers. In the HMM process, we used Opcode to train and score. In then PCA process, we trained and scored on the frequencies of the registers. Then, we calculate the True Positive Rate (TPR), False Positive Rate (FPR) to obtain ROC curve and PR curve. Basing on the curves, we found the thresholds and train the multilayer perceptron to classify the malware and benign files on the HMM scores and PCA scores. At the end, we concluded that PCA technique with frequencies of the registers had a effective way to detect Malware while HMM didn't show an ideal accuracy on the detection. In addition, with an accurate threshold, the MLP can yield a better classification.

1. Introduction

Signature detection to malware is simplest and lowest-cost technology. When it detect on some simple malware, it yields a low FPR. However, the viruses we might experience now are no more simple. They already evolved to some metamorphic viruses. At this point, signature detection has no longer advantages. Meanwhile, some machine learning techniques will yield a better result than signature because those techniques can make computer become smarter. Basing on the data we offer, those techniques can train a model to identify the other data belonging to the same or close kind of data that we offered.

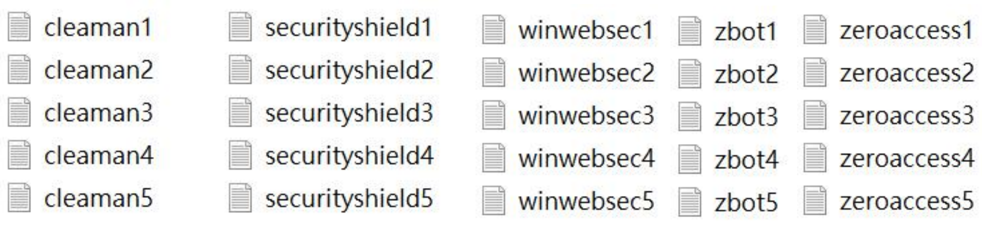
Informally, the machines can learn the important information from the Malware features and use that information to help us classify the Malware and benign files.

2. Methods

2.1 Cross Validation

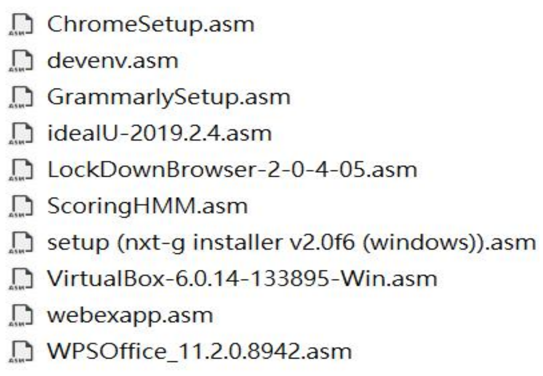
We used 5 cross validation to train and score the data sets. First we asked Professor Fabio to get the Malware files. We choose 5 families and 5 files for each Family. We also downloaded 10 benign files as our test set. In each fold, we chose 20 Malware files from those 5 families to train a model, then used the model to score on the rest 5 Malware files and those 10 benign files. That is, in each fold, we obtained 5 Malware scores and 10 benign scores. After 5 folds, we got 25 Malware scores and 50 benign scores. Then, we calculate the average scores with the 50 benign scores since they were repeated.

For every Malware files, we released it in virtual box, and extracted the ASM file. Then using program to read the Opcode sequence and count the register frequency. For convenience, we rename all the Malware files as "family name+ number".



cleaman1	securityshield1	winwebsec1	zbot1	zeroaccess1
cleaman2	securityshield2	winwebsec2	zbot2	zeroaccess2
cleaman3	securityshield3	winwebsec3	zbot3	zeroaccess3
cleaman4	securityshield4	winwebsec4	zbot4	zeroaccess4
cleaman5	securityshield5	winwebsec5	zbot5	zeroaccess5

Figure 1 : name of Malware files



ChromeSetup.asm
devenv.asm
GrammarlySetup.asm
idealU-2019.2.4.asm
LockDownBrowser-2-0-4-05.asm
ScoringHMM.asm
setup (nxt-g installer v2.0f6 (windows)).asm
VirtualBox-6.0.14-133895-Win.asm
webexapp.asm
WPSOffice_11.2.0.8942.asm

Figure 2: name of benign files

2.2 HMM with Opcode Sequence

In HMM, we used forward and backward algorithm to get the probability at time t while the observation is O_t and the state is q_i. We also used Baum-Welch algorithm to re-estimate the model. In our project, we use 200 iterations for each re-estimate. And we used 2 hidden states, 54 observations and 100 random restart. Then, we use forward algorithm to score on the test set. The normalizing Log probability represented the score.

2.3 PCA with Register Frequency

In PCA, we used 16 registers frequency as our measurements/features, used 20 Malware files as our experiments. So, we constructed a 16*20 matrix called B matrix. Then, we subtract the mean for each row to get A matrix. We used inner product to produce the covariance matrix and calculate the eigenvalue and eigenvector space called U. Then, we discarded the less significant eigenvector with small eigenvalue. We projected the A matrix onto U to gain scored matrix. Finally, we projected the test vector on to U and calculate the Euclidean Distance between the result and each column of the score matrix. The smallest distance was the preferred score.

2.4 Analysis with TPR, FPR, ROC and PR

In this process, our main goal was determining the threshold where we can classify Malware and benign with better accuracy and sensitivity. Therefore, we made the ROC and PR graph on both HMM and PCA scores.

2.5 MLP with HMM and PCA Scores

We then use threshold we just determined from last step to choose samples as the MLP training samples. Then we scored on all the samples to to classify them as 1 or 0. We use these classification to calculate the accuracy.

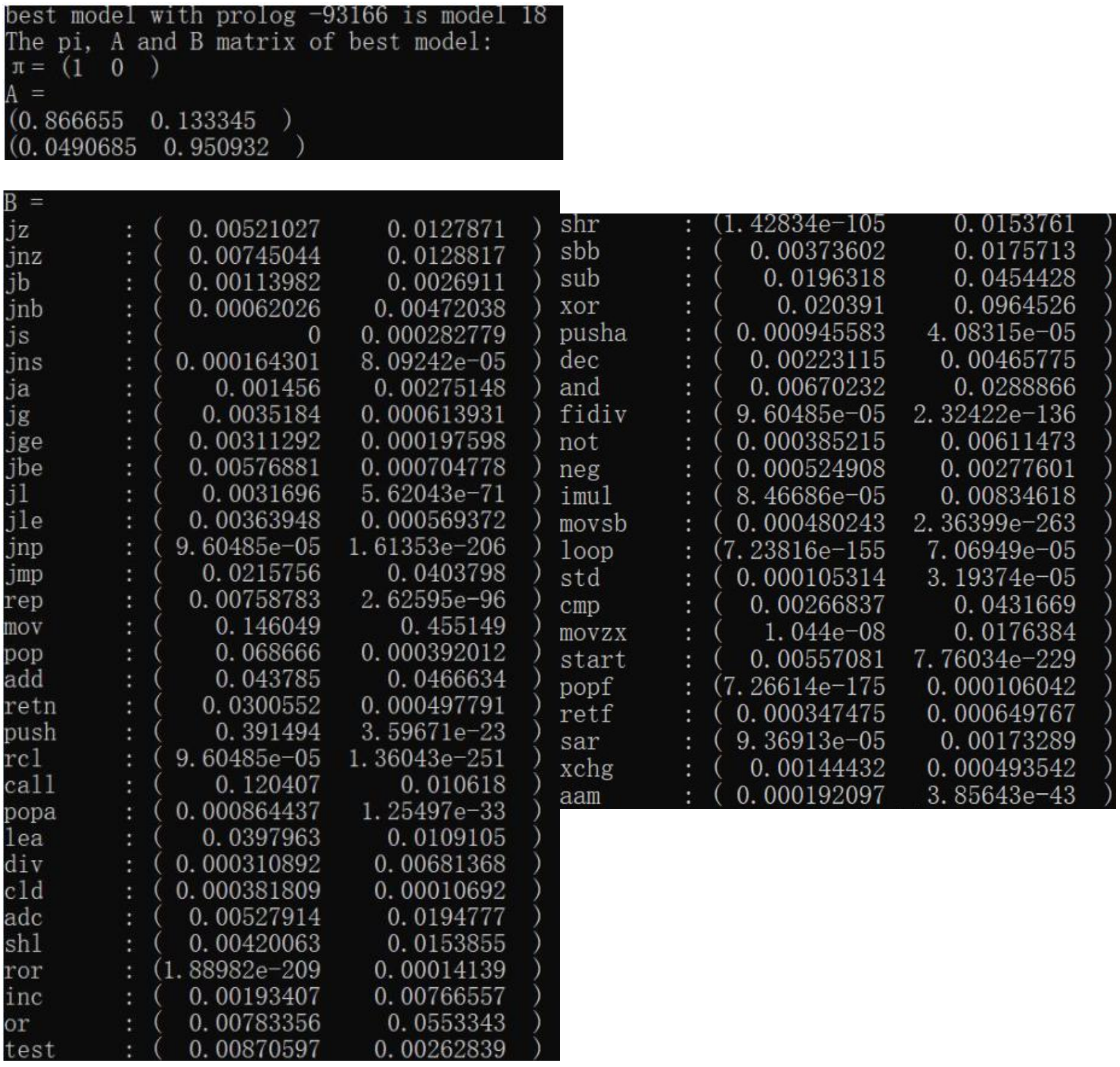
In this process, we used $f(s,t) = \frac{1}{1+e^{-(s+t)}}$ and $g(s,t) = s + t$ to construct the layers.

We also tried single layer with $f(s,t)=\frac{1}{1+e^{-(s+t)}}$ to make a single layer perceptron.

3. Result

3.1 HMM result and Analysis

After we trained on the 1st fold, it yielded a π, A, and B matrix as figures 3. We did see some Opcodes have near 0 probability on the side of B matrix, such as js, jns, jl, rep, and so on. That means these Opcodes barely show up in one of those two states.



```
best model with prolog -93166 is model 18
The pi, A and B matrix of best model:
 π = (1  0  )
A =
(0.866655   0.133345  )
(0.0490685   0.950932  )
```

```
B =
jz          : (   0.00521027       0.0127871   )
jnz         : (   0.00745044       0.0128817   )
jb          : (   0.00113982       0.0026911   )
jnb         : (   0.00062026      0.00472038   )
js          : (            0     0.000282779   )
jns         : ( 0.000164301      8.09242e-05   )
ja          : (     0.001456      0.00275148   )
jg          : (    0.0035184     0.000613931   )
jge         : (   0.00311292     0.000197598   )
jbe         : (   0.00576881     0.000704778   )
jl          : (    0.0031696     5.62043e-71   )
jle         : (   0.00363948     0.000569372   )
jnp         : ( 9.60485e-05    1.61353e-206   )
jmp         : (    0.0215756       0.0403798   )
rep         : (   0.00758783     2.62595e-96   )
mov         : (     0.146049        0.455149   )
pop         : (     0.068666     0.000392012   )
add         : (     0.043785       0.0466634   )
retn        : (    0.0300552     0.000497791   )
push        : (     0.391494     3.59671e-23   )
rcl         : ( 9.60485e-05    1.36043e-251   )
call        : (     0.120407        0.010618   )
popa        : ( 0.000864437      1.25497e-33   )
lea         : (    0.0397963       0.0109105   )
div         : ( 0.000310892       0.00681368   )
cld         : ( 0.000381809       0.00010692   )
adc         : (   0.00527914       0.0194777   )
shl         : (   0.00420063       0.0153855   )
ror         : (1.88982e-209       0.00014139   )
inc         : (   0.00193407      0.00766557   )
or          : (   0.00783356       0.0553343   )
test        : (   0.00870597      0.00262839   )
```

```
shr         : (1.42834e-105        0.0153761   )
sbb         : (   0.00373602        0.0175713   )
sub         : (    0.0196318        0.0454428   )
xor         : (     0.020391        0.0964526   )
pusha       : ( 0.000945583      4.08315e-05   )
dec         : (   0.00223115       0.00465775   )
and         : (   0.00670232        0.0288866   )
fidiv       : ( 9.60485e-05     2.32422e-136   )
not         : ( 0.000385215       0.00611473   )
neg         : ( 0.000524908       0.00277601   )
imul        : ( 8.46686e-05       0.00834618   )
movsb       : ( 0.000480243     2.36399e-263   )
loop        : (7.23816e-155      7.06949e-05   )
std         : ( 0.000105314      3.19374e-05   )
cmp         : (   0.00266837        0.0431669   )
movzx       : (     1.044e-08        0.0176384   )
start       : (   0.00557081     7.76034e-229   )
popf        : (7.26614e-175      0.000106042   )
retf        : ( 0.000347475      0.000649767   )
sar         : ( 9.36913e-05       0.00173289   )
xchg        : (   0.00144432      0.000493542   )
aam         : ( 0.000192097      3.85643e-43   )
```

Figure 3: HMM model of 1st fold

After we trained and score for 5 folds, we obtained the scores for 25 Malware and benign Opcodes as figure 4 and figure 5 shown below.

	HMM on Opcode
Cleaman1	-2.022
Cleaman2	-2.020
Cleaman3	-2.010
Cleaman4	-2.014
Cleaman5	-2.174
Securityshield1	-2.929
Securityshield2	-2.780
Securityshield3	-2.684
Securityshield4	-2.740
Securityshield5	-2.595
Winwebsec1	-2.695
Winwebsec2	-2.742
Winwebsec3	-2.665
Winwebsec4	-2.677
Winwebsec5	-2.233
Zbot1	-2.938
Zbot2	-2.072
Zbot3	-2.840
Zbot4	-2.952
Zbot5	-2.744
Zeroaccess1	-2.364
Zeroaccess2	-2.375
Zeroaccess3	-2.376
Zeroaccess4	-2.302
Zeroaccess5	-2.411

Figure 4: HMM scores of Malware Opcodes

	HMM on Opcode
ChromeSetup	-2.924
Devenv	-2.702
GrammarlySetup	-2.837
IdealU	-2.724
LockDownBrowser	-2.861
ScoringHMM	-2.446
Setup (nxt-g installer v2.0f6 (windows))	-2.536
VirtualBox-6.0.14-133895-Win	-3.036
Webexapp	-2.279
WPSOffice	-2.718

Figure 5: HMM scores of benign Opcodes

For the Malware from Cleaman and Zeroaccess family, the scores are generally lower than the scores of the benign files, but most of the scores from Securityshield and Zbot are pretty close to the scores of the benign. These two figures show us using HMM on Securityshield, Zbot and even Winwebsec is not so ideal. However, we had an assumption that the benign files we downloaded might show the function as a malware in some ways. That might explain why the scores don't much separation.

Now, we drew the scores on the graph with circles meaning malware scores and triangle meaning benign scores.

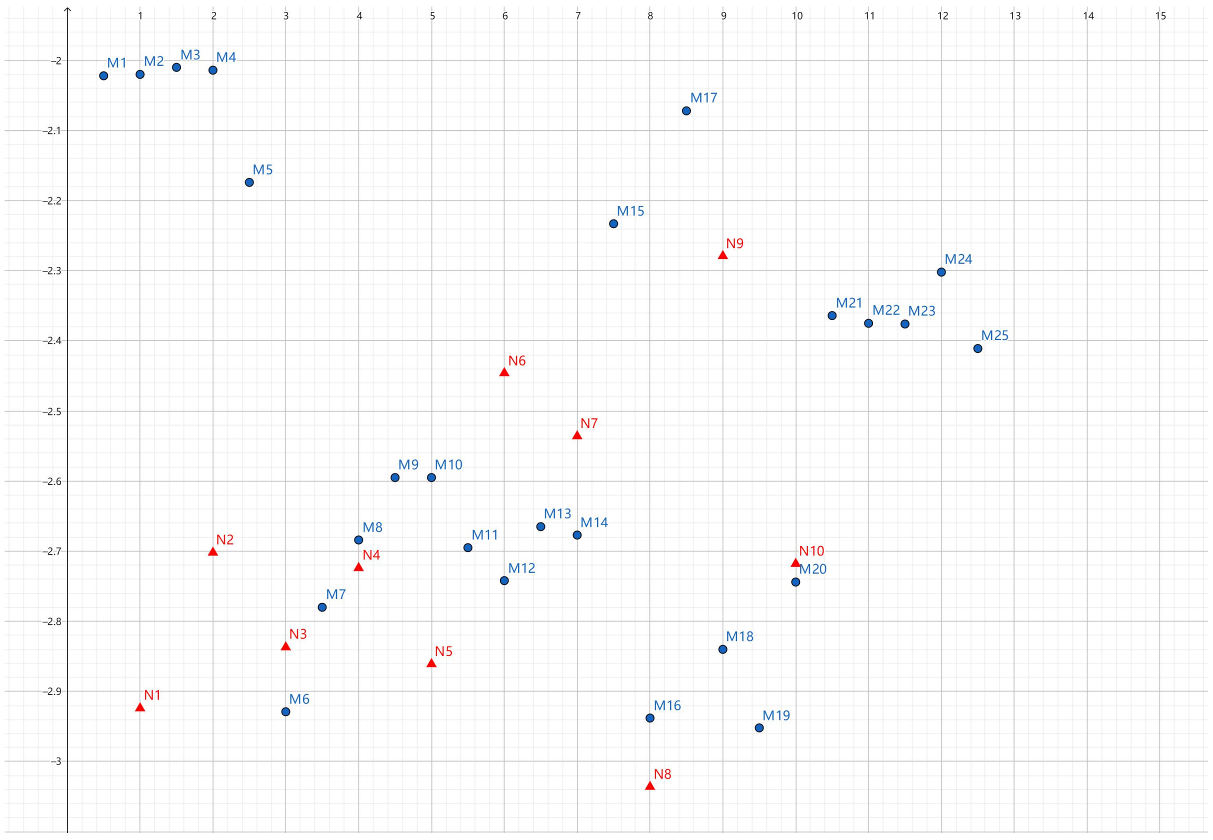


Figure 6: HMM scores of Malware and Benign

From this figure, we can see that , most of the Malware points are mixing with benign points, except Cleaman1~Cleaman5 (M1~M5) and Zeroaccess1~Zeroaccess5 (M21~M25).

Then, we drew the ROC curve and PR curve as figure 7 and 8 to see if there was a threshold that can help us to yield a better accuracy and sensitivity.

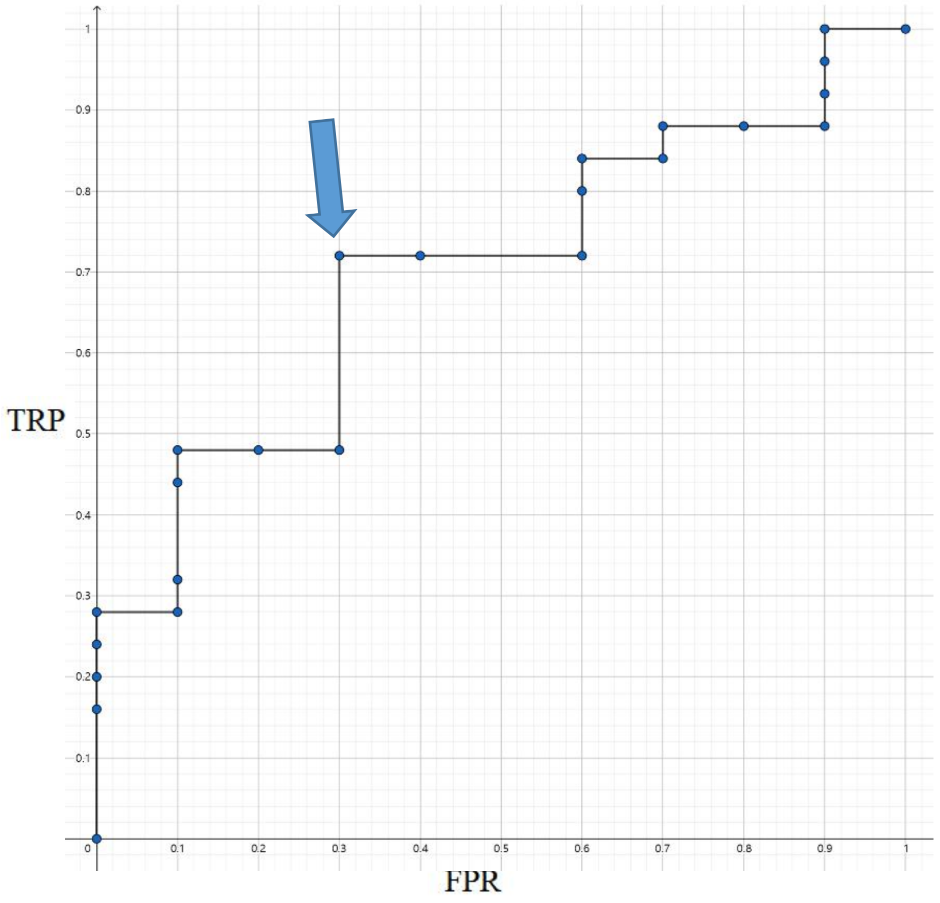


Figure 7: HMM ROC

From this ROC curve, we can see at the point where the arrow is pointing to, the TPR is around 0.7, and the FPR is around 0.3. And the FPR is decreasing from the previous point while the TPR remain the same. However, after this point, the TPR is crashing to lower than 0.5. Then, we find that this point happens at around score -2.7. The accuracy for this threshold is 0.71.

From the PR curve, we also see that while the threshold of score is around -2.7, it yields a Recall = 0.72 and Precision = 0.86. Therefore, we determined to draw the threshold around score = -2.7. That means, if the score is lower than -2.7, the file is more likely to be a benign, and if the score is higher than -2.7, it is more likely to be a Malware.

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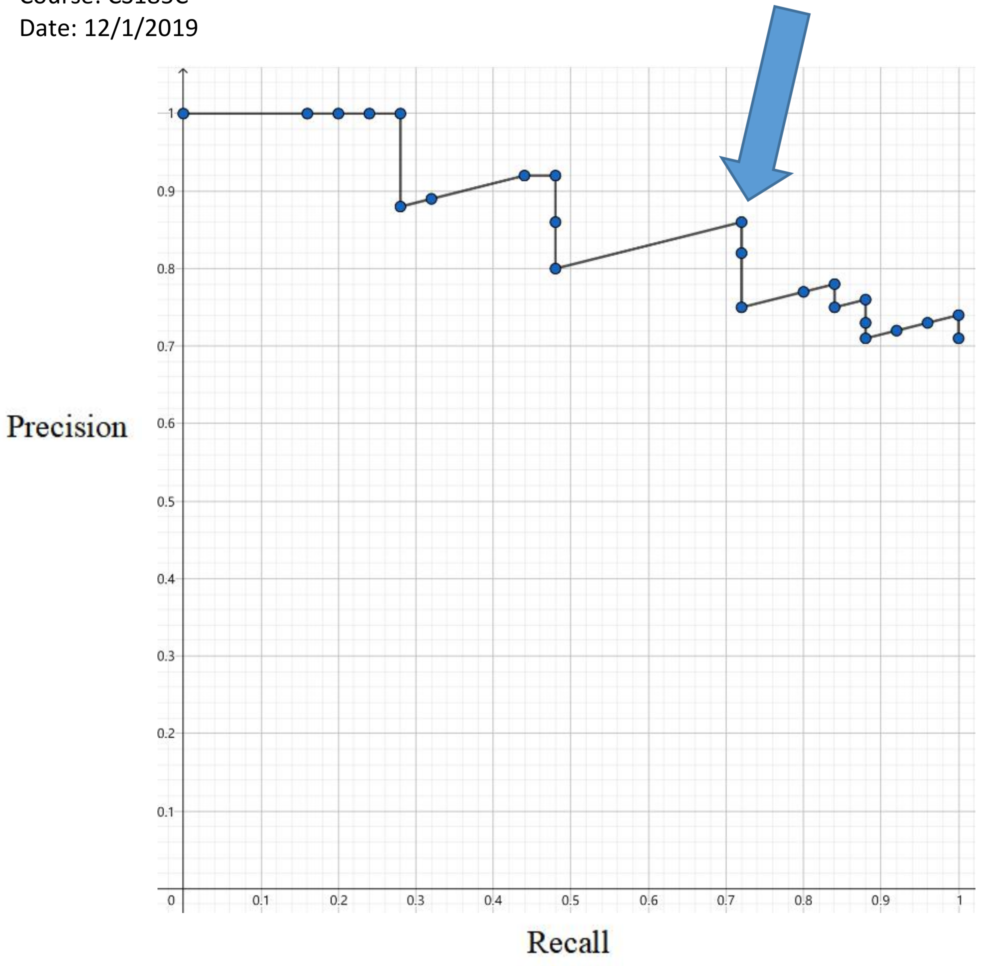

Figure 8: HMM PR

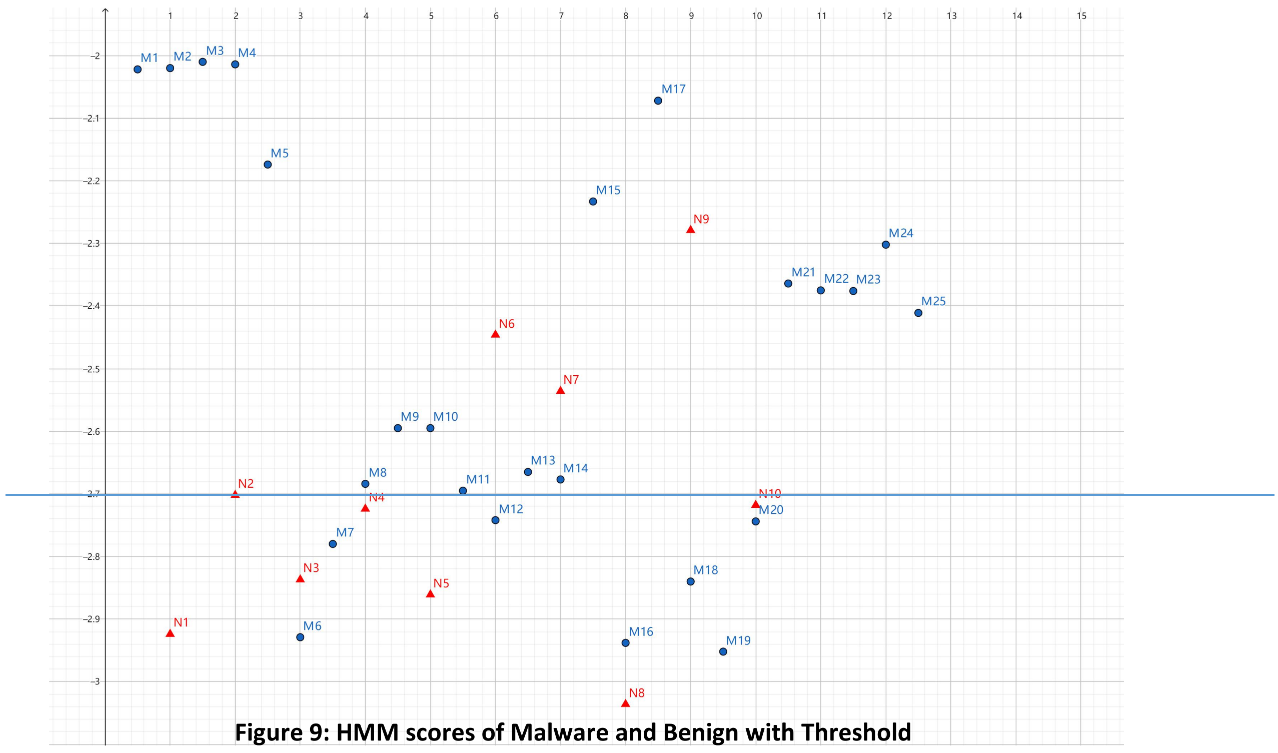

Figure 9: HMM scores of Malware and Benign with Threshold

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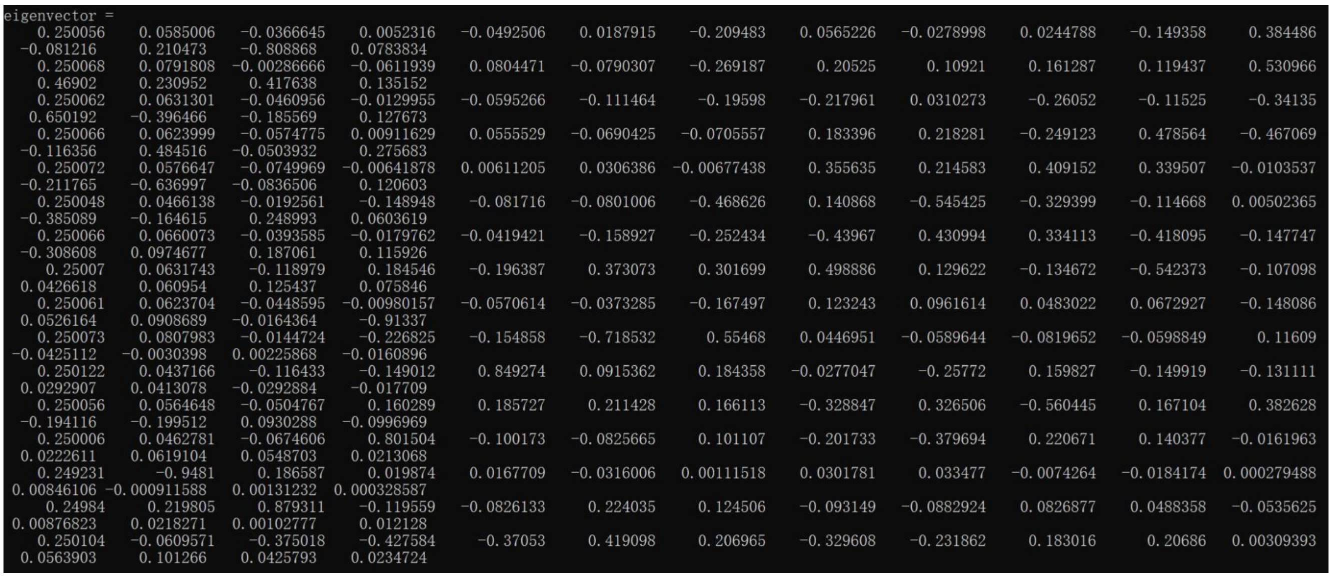
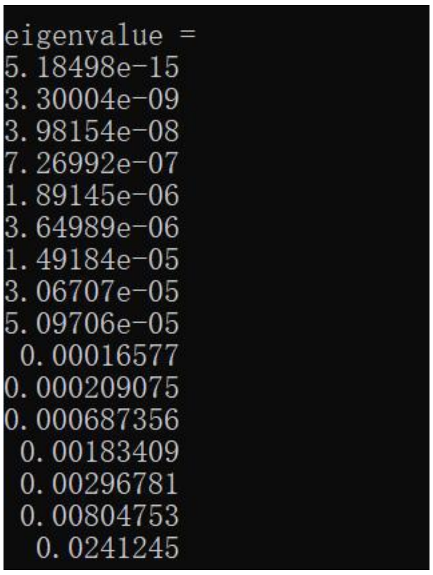
3.2 PCA result and Analysis

In the PCA process, we got the eigenvector and eigenvalue. And basing on the eigenvalue, we chose which eigenvector should be saved. We attached the result eigenvector, eigenvalue and significant eignvector of the 1st fold.

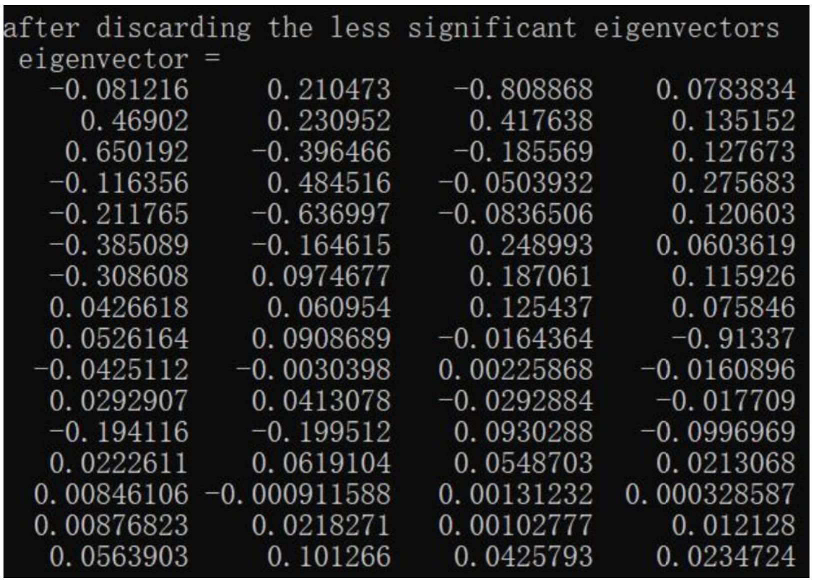


```
eigenvector =
    0.250056   0.0585006  -0.0366645   0.0052316  -0.0492506   0.0187915   -0.209483   0.0565226  -0.0278998   0.0244788   -0.149358    0.384486
  -0.081216    0.210473   -0.808868   0.0783834
    0.250068   0.0791808 -0.00286666  -0.0611939   0.0804471  -0.0790307   -0.269187     0.20525     0.10921    0.161287    0.119437    0.530966
    0.46902    0.230952    0.417638    0.135152
    0.250062   0.0631301  -0.0460956  -0.0129955  -0.0595266   -0.111464    -0.19598   -0.217961   0.0310273    -0.26052    -0.11525    -0.34135
   0.650192   -0.396466   -0.185569    0.127673
    0.250066   0.0623999  -0.0574775  0.00911629   0.0555529  -0.0690425  -0.0705557    0.183396    0.218281   -0.249123    0.478564   -0.467069
  -0.116356    0.484516  -0.0503932    0.275683
    0.250072   0.0576647  -0.0749969 -0.00641878  0.00611205   0.0306386 -0.00677438    0.355635    0.214583    0.409152    0.339507  -0.0103537
  -0.211765   -0.636997  -0.0836506    0.120603
    0.250048   0.0466138  -0.0192561   -0.148948   -0.081716  -0.0801006   -0.468626    0.140868   -0.545425   -0.329399   -0.114668  0.00502365
  -0.385089   -0.164615    0.248993   0.0603619
    0.250066   0.0660073  -0.0393585  -0.0179762  -0.0419421   -0.158927   -0.252434    -0.43967    0.430994    0.334113   -0.418095   -0.147747
  -0.308608   0.0974677    0.187061    0.115926
     0.25007   0.0631743   -0.118979    0.184546   -0.196387    0.373073    0.301699    0.498886    0.129622   -0.134672   -0.542373   -0.107098
  0.0426618    0.060954    0.125437    0.075846
    0.250061   0.0623704  -0.0448595 -0.00980157  -0.0570614  -0.0373285   -0.167497    0.123243   0.0961614   0.0483022   0.0672927   -0.148086
  0.0526164   0.0908689  -0.0164364    -0.91337
    0.250073   0.0807983  -0.0144724   -0.226825   -0.154858   -0.718532     0.55468   0.0446951  -0.0589644  -0.0819652  -0.0598849     0.11609
 -0.0425112  -0.0030398  0.00225868  -0.0160896
    0.250122   0.0437166   -0.116433   -0.149012    0.849274   0.0915362    0.184358  -0.0277047    -0.25772    0.159827   -0.149919   -0.131111
  0.0292907   0.0413078  -0.0292884   -0.017709
    0.250056   0.0564648  -0.0504767    0.160289    0.185727    0.211428    0.166113   -0.328847    0.326506   -0.560445    0.167104    0.382628
  -0.194116   -0.199512   0.0930288  -0.0996969
    0.250006   0.0462781  -0.0674606    0.801504   -0.100173  -0.0825665    0.101107   -0.201733   -0.379694    0.220671    0.140377  -0.0161963
  0.0222611   0.0619104   0.0548703   0.0213068
    0.249231     -0.9481    0.186587    0.019874   0.0167709  -0.0316006  0.00111518   0.0301781    0.033477  -0.0074264  -0.0184174 0.000279488
 0.00846106 -0.000911588 0.00131232 0.000328587
     0.24984    0.219805    0.879311   -0.119559  -0.0826133    0.224035    0.124506   -0.093149  -0.0882924   0.0826877   0.0488358  -0.0535625
 0.00876823   0.0218271  0.00102777    0.012128
    0.250104  -0.0609571   -0.375018   -0.427584    -0.37053    0.419098    0.206965   -0.329608   -0.231862    0.183016     0.20686  0.00309393
  0.0563903    0.101266   0.0425793   0.0234724
```

Figure 10: 16*16 Eigenvector Space



```
eigenvalue =
5.18498e-15
3.30004e-09
3.98154e-08
7.26992e-07
1.89145e-06
3.64989e-06
1.49184e-05
3.06707e-05
5.09706e-05
 0.00016577
0.000209075
0.000687356
 0.00183409
 0.00296781
 0.00804753
  0.0241245
```



```
after discarding the less significant eigenvectors
 eigenvector =
   -0.081216     0.210473    -0.808868    0.0783834
     0.46902     0.230952     0.417638     0.135152
    0.650192    -0.396466    -0.185569     0.127673
   -0.116356     0.484516   -0.0503932     0.275683
   -0.211765    -0.636997   -0.0836506     0.120603
   -0.385089    -0.164615     0.248993    0.0603619
   -0.308608    0.0974677     0.187061     0.115926
   0.0426618     0.060954     0.125437     0.075846
   0.0526164    0.0908689   -0.0164364     -0.91337
  -0.0425112   -0.0030398   0.00225868   -0.0160896
   0.0292907    0.0413078   -0.0292884    -0.017709
   -0.194116    -0.199512    0.0930288   -0.0996969
   0.0222611    0.0619104    0.0548703    0.0213068
  0.00846106 -0.000911588   0.00131232  0.000328587
  0.00876823    0.0218271   0.00102777     0.012128
   0.0563903     0.101266    0.0425793    0.0234724
```

Figure 11: Eigenvalue

Figure 12: Significant Eigenvector

Then we projected the matrix A onto those significant eigenvector and gained the score matrix.

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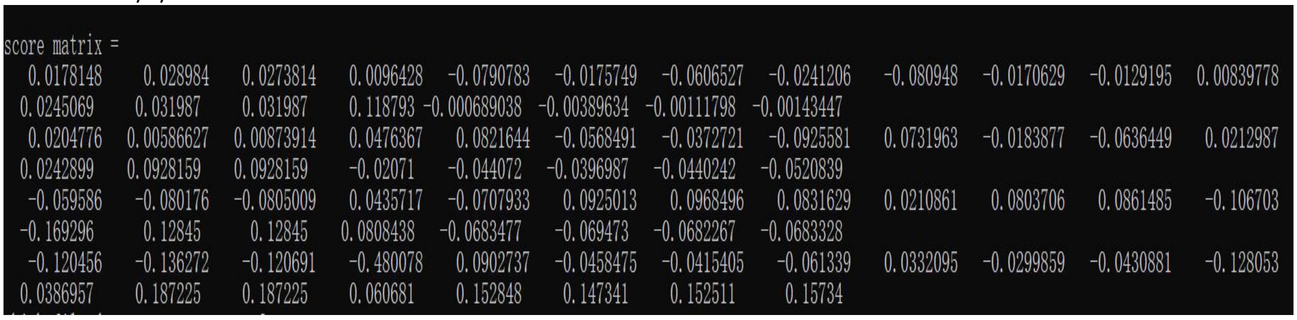


```
score matrix =
   0.0178148     0.028984    0.0273814    0.0096428   -0.0790783   -0.0175749   -0.0606527   -0.0241206    -0.080948   -0.0170629   -0.0129195   0.00839778
  0.0245069     0.031987     0.031987     0.118793 -0.000689038  -0.00389634  -0.00111798  -0.00143447
   0.0204776   0.00586627   0.00873914    0.0476367    0.0821644   -0.0568491   -0.0372721   -0.0925581    0.0731963   -0.0183877   -0.0636449    0.0212987
  0.0242899    0.0928159    0.0928159     -0.02071    -0.044072   -0.0396987   -0.0440242   -0.0520839
   -0.059586    -0.080176   -0.0805009    0.0435717   -0.0707933    0.0925013    0.0968496    0.0831629    0.0210861    0.0803706    0.0861485    -0.106703
  -0.169296      0.12845      0.12845    0.0808438   -0.0683477    -0.069473   -0.0682267   -0.0683328
   -0.120456    -0.136272    -0.120691    -0.480078    0.0902737   -0.0458475   -0.0415405    -0.061339    0.0332095   -0.0299859   -0.0430881    -0.128053
  0.0386957     0.187225     0.187225     0.060681     0.152848     0.147341     0.152511      0.15734
```

Figure 13: 4*20 Score Matrix

After we did 5 Cross Validations, we got the PCA scores for the Malware and benign as figure 14.

	PCA on Reg Frequence
Cleaman1	0.06181
Cleaman2	0.02227
Cleaman3	0.01600
Cleaman4	0.01603
Cleaman5	0.2989
Securityshield1	0.06035
Securityshield2	0.1114
Securityshield3	0.01329
Securityshield4	0.05168
Securityshield5	0.01770
Winwebsec1	0.01455
Winwebsec2	0.08123
Winwebsec3	0.05356
Winwebsec4	0.01491
Winwebsec5	0.05698
Zbot1	0.04066
Zbot2	0.1539
Zbot3	0.2046
Zbot4	0.04062
Zbot5	0.1411
Zeroaccess1	0.0005145
Zeroaccess2	0.0003901
Zeroaccess3	0.007353
Zeroaccess4	0.0006864
Zeroaccess5	0.008226

	PCA on Reg Frequence
ChromeSetup	0.1111
Devenv	0.1022
GrammarlySetup	0.1066
IdeaIU	0.0826
LockDownBrowser	0.1032
ScoringHMM	0.08353
Setup (nxt-g installer v2.0f6 (windows))	0.1347
VirtualBox-6.0.14-133895-Win	0.1077
Webexapp	0.1214
WPSOffice	0.1034

Figure 14: PCA Scores

From figure 14, we can easily see that PCA with the register frequency has a significant result on the Malware detection since most of the Malware scores are much smaller than the benign scores.

We also drew a graph for these scores:

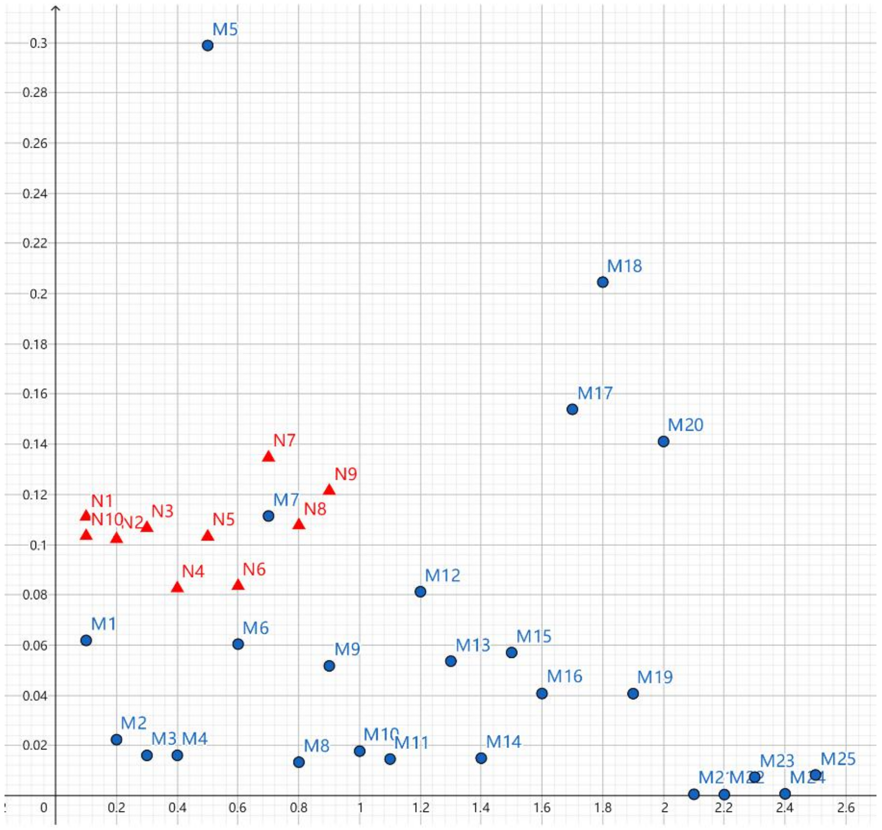


Figure 15: PCA Scores

The blue circles show us the Malware and the red triangles show us the benign. The lower score means the smaller distance between the training sample and scoring sample. That is, if the score is near 0, it means the score sample is much closer to the training sample. From figure 15, we see that most of the scoring Malware samples are close to the training Malware samples. And the benign samples are grouping together and far away from the training samples.

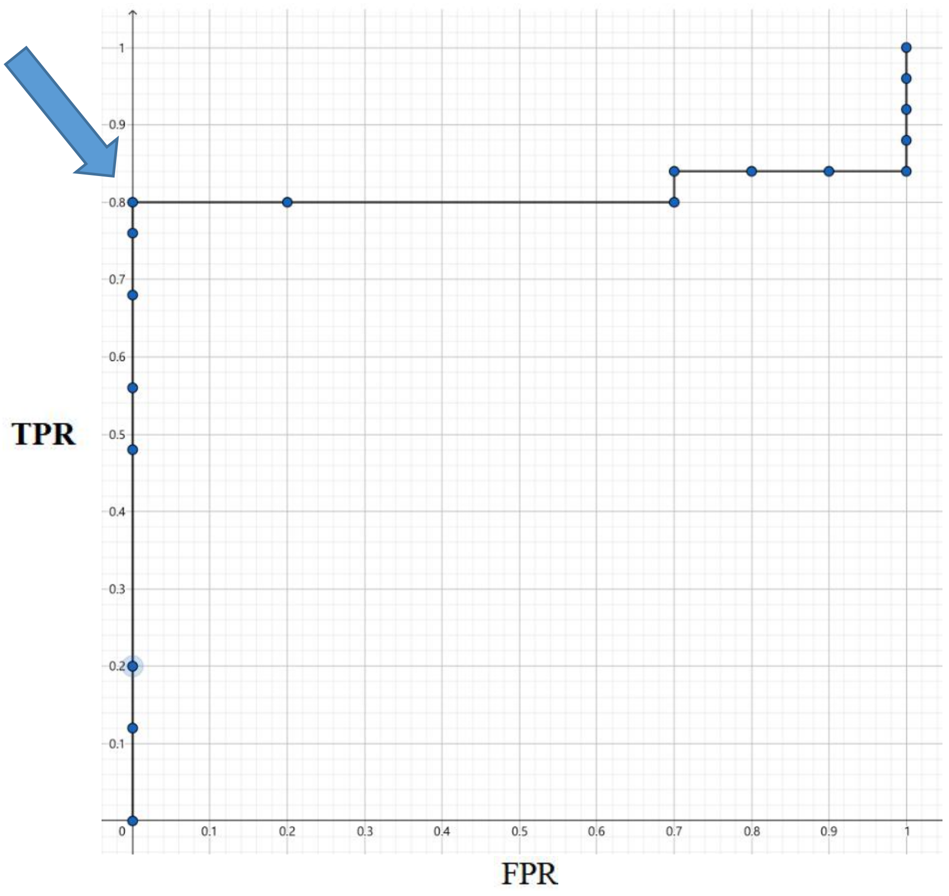


Figure 16: PCA Scores

As our arrow shown, the FPR =0 and TPR = 0.8. And after this point, the TPR is decreasing quickly. When the threshold is around 0.08, we can obtain this FPR and TPR. That means, if we set score =0.08 as a threshold, we can have a 0 FPR, but 0.8 TPR, and

$$Accuracy = \frac{20+10}{25+10} = \frac{30}{35} = 0.86$$

As the arrow point on the figure 17, when score = 0.08, the precision reach 1 and recall keeps at 0.8. Therefore, we can determine that, if the score is lower than 0.08, the scoring sample is most likely to be a Malware while the scoring sample is classified as a benign if the score is higher than 0.08.

Student Name: Zizhao Guan, Ibrahim Ansari
Instructor: Mark Stamp
Course: CS185C
Date: 12/1/2019

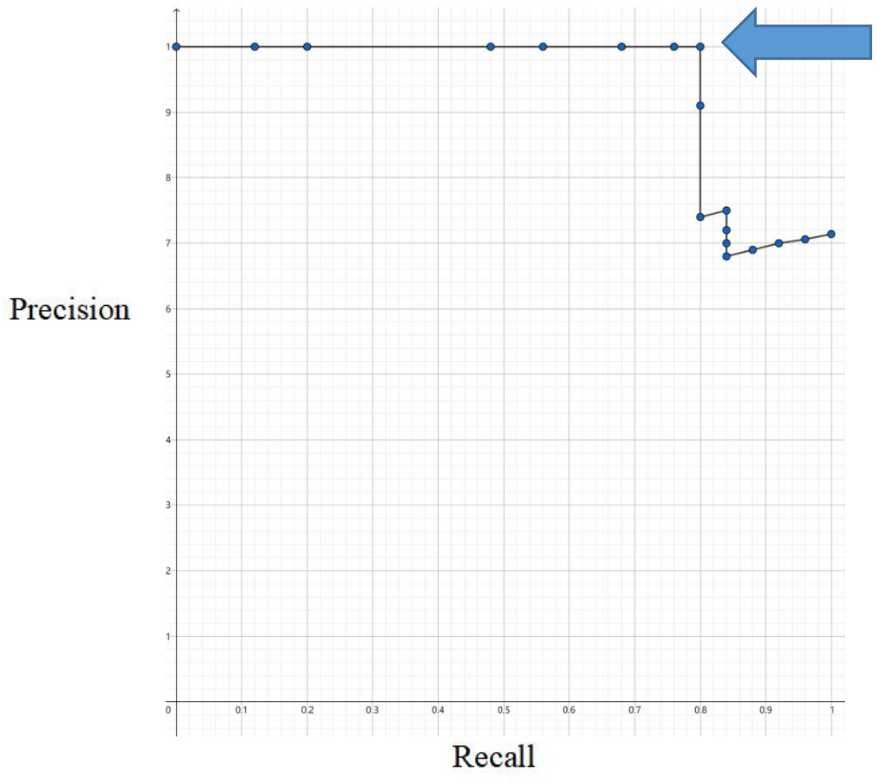


Figure 17: PCA Scores

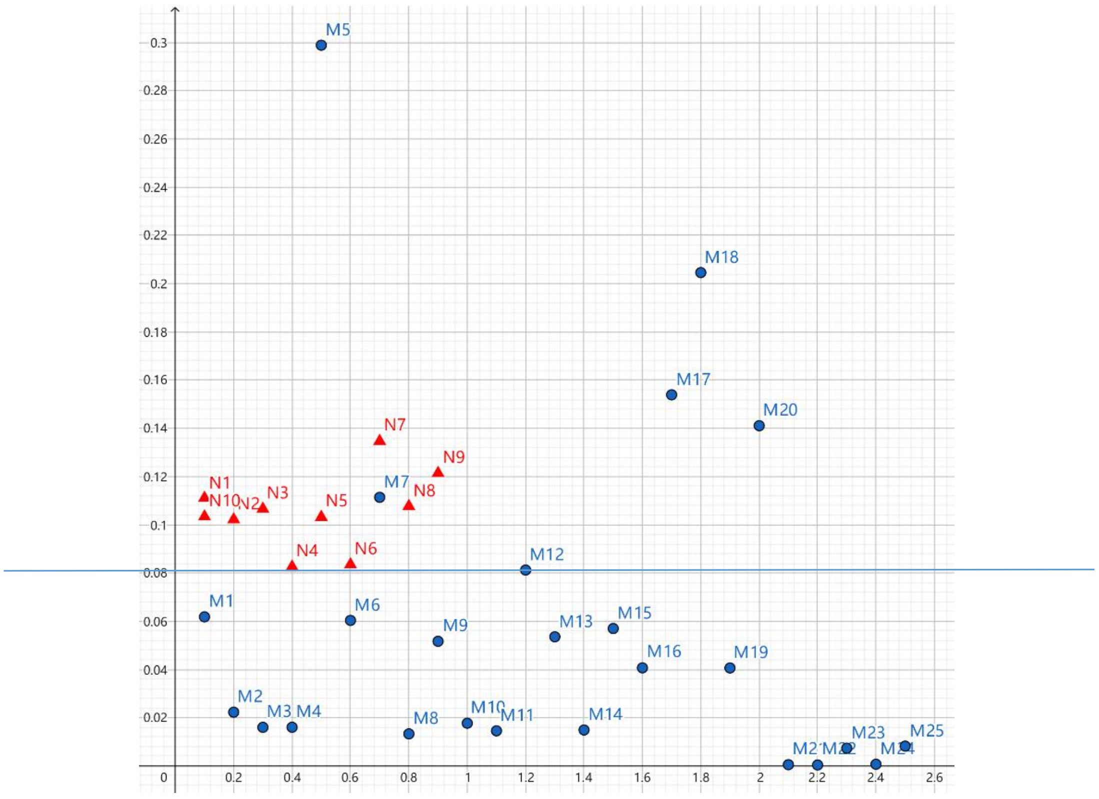


Figure 18: PCA Scores with Threshold

Student Name: Zizhao Guan, Ibrahim Ansari
Instructor: Mark Stamp
Course: CS185C
Date: 12/1/2019

3.3 MLP on both HMM and PCA Scores

	HMM on Opcode	PCA on Reg Frequence
Cleaman1	-2.022	0.06181
Cleaman2	-2.020	0.02227
Cleaman3	-2.010	0.01600
Cleaman4	-2.014	0.01603
Cleaman5	-2.174	0.2989
Securityshield1	-2.929	0.06035
Securityshield2	-2.780	0.1114
Securityshield3	-2.684	0.01329
Securityshield4	-2.740	0.05168
Securityshield5	-2.595	0.01770
Winwebsec1	-2.695	0.01455
Winwebsec2	-2.742	0.08123
Winwebsec3	-2.665	0.05356
Winwebsec4	-2.677	0.01491
Winwebsec5	-2.233	0.05698
Zbot1	-2.938	0.04066
Zbot2	-2.072	0.1539
Zbot3	-2.840	0.2046
Zbot4	-2.952	0.04062
Zbot5	-2.744	0.1411
Zeroaccess1	-2.364	0.0005145
Zeroaccess2	-2.375	0.0003901
Zeroaccess3	-2.376	0.007353
Zeroaccess4	-2.302	0.0006864
Zeroaccess5	-2.411	0.008226

	HMM on Opcode	PCA on Reg Frequence
ChromeSetup	-2.924	0.1111
Devenv	-2.702	0.1022
GrammarlySetup	-2.837	0.1066
IdeaIU	-2.724	0.0826
LockDownBrowser	-2.861	0.1032
ScoringHMM	-2.446	0.08353
Setup (nxt-g installer v2.0f6 (windows))	-2.536	0.1347
VirtualBox-6.0.14-133895-Win	-3.036	0.1077
Webexapp	-2.279	0.1214
WPSOffice	-2.718	0.1034

Figure 19: HMM and PCA Scores

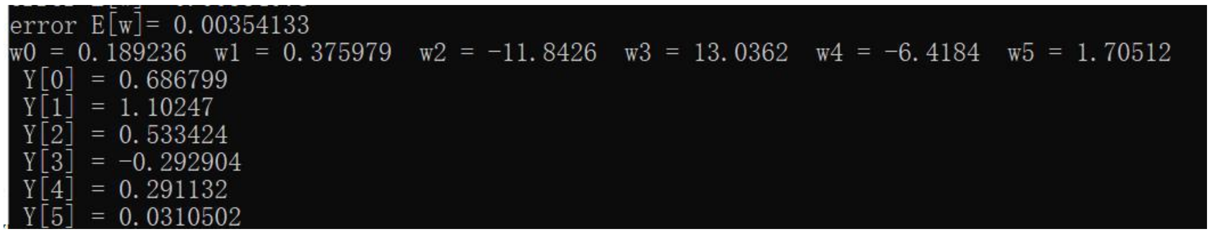
Before we chose the data set using the threshold we determine above, we chose the training data from the HMM and PCA scores of the Malware. For example, we chose only 3 Zbot scores:

Zbot2	-2.072	0.1539
Zbot3	-2.840	0.2046
Zbot5	-2.744	0.1411

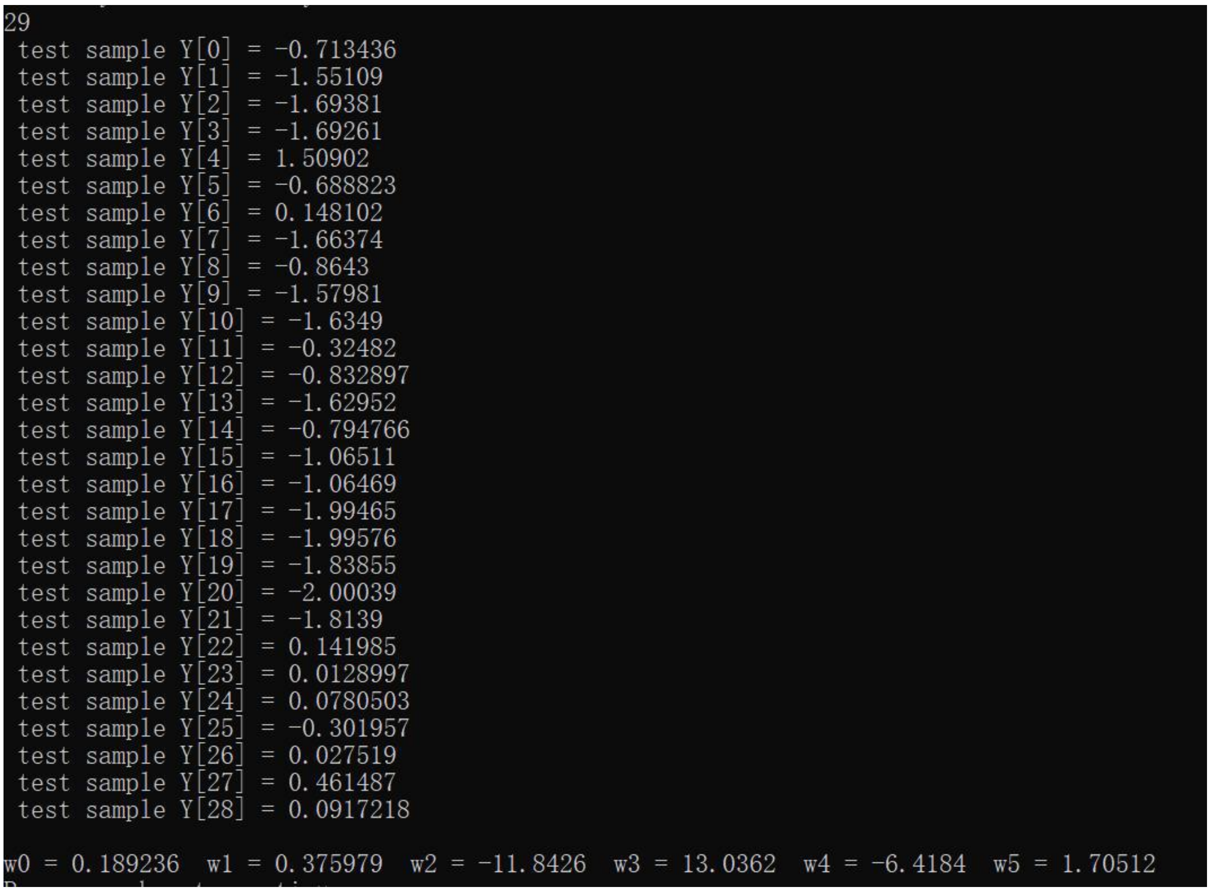
And we choose 3 benign scores:

ScoringHMM	-2.446	0.08353
Webexapp	-2.279	0.1214
WPSOffice	-2.718	0.1034

Then we got the training scores and testing scores:



```
error E[w]= 0.00354133
w0 = 0.189236  w1 = 0.375979  w2 = -11.8426  w3 = 13.0362  w4 = -6.4184  w5 = 1.70512
 Y[0] = 0.686799
 Y[1] = 1.10247
 Y[2] = 0.533424
 Y[3] = -0.292904
 Y[4] = 0.291132
 Y[5] = 0.0310502
```



```
29
 test sample Y[0] = -0.713436
 test sample Y[1] = -1.55109
 test sample Y[2] = -1.69381
 test sample Y[3] = -1.69261
 test sample Y[4] = 1.50902
 test sample Y[5] = -0.688823
 test sample Y[6] = 0.148102
 test sample Y[7] = -1.66374
 test sample Y[8] = -0.8643
 test sample Y[9] = -1.57981
 test sample Y[10] = -1.6349
 test sample Y[11] = -0.32482
 test sample Y[12] = -0.832897
 test sample Y[13] = -1.62952
 test sample Y[14] = -0.794766
 test sample Y[15] = -1.06511
 test sample Y[16] = -1.06469
 test sample Y[17] = -1.99465
 test sample Y[18] = -1.99576
 test sample Y[19] = -1.83855
 test sample Y[20] = -2.00039
 test sample Y[21] = -1.8139
 test sample Y[22] = 0.141985
 test sample Y[23] = 0.0128997
 test sample Y[24] = 0.0780503
 test sample Y[25] = -0.301957
 test sample Y[26] = 0.027519
 test sample Y[27] = 0.461487
 test sample Y[28] = 0.0917218

w0 = 0.189236  w1 = 0.375979  w2 = -11.8426  w3 = 13.0362  w4 = -6.4184  w5 = 1.70512
```

Figure 20: MLP Scores of Sandom Training Sample

If the score is higher than 0.5, we would round it to 1, and if lower than 0.5, we would round it to 0. And “1” means, it’s Malware when “0” means its benign. Then, we calculated the accuracy basing on the classification in the figure 20.

$$Accuracy = \frac{11}{35} = 0.31$$

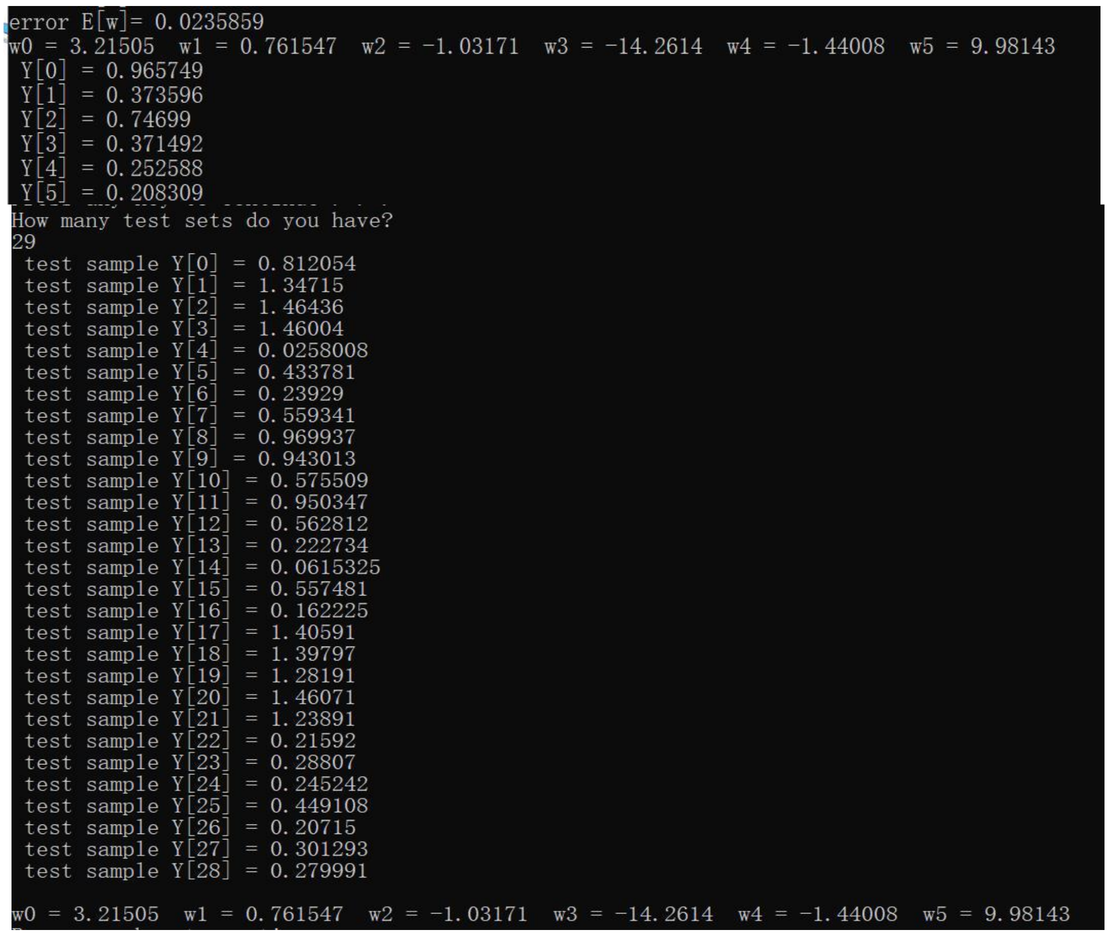
The accuracy is very low.

But when we chose the training data basing on the threshold we determined before. For example, we choose

Securityshield3	-2.684	0.01329
Winwebsec2	-2.742	0.08123
Winwebsec5	-2.233	0.05698

IdeaIU	-2.724	0.0826
LockDownBrowser	-2.861	0.1032
VirtualBox-6.0.14-133895 -Win	-3.036	0.1077

We had the training scores and testing scores as below:



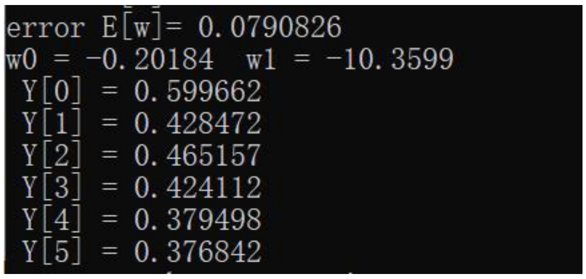
```
error E[w]= 0.0235859
w0 = 3.21505  w1 = 0.761547  w2 = -1.03171  w3 = -14.2614  w4 = -1.44008  w5 = 9.98143
 Y[0] = 0.965749
 Y[1] = 0.373596
 Y[2] = 0.74699
 Y[3] = 0.371492
 Y[4] = 0.252588
 Y[5] = 0.208309
How many test sets do you have?
29
 test sample Y[0] = 0.812054
 test sample Y[1] = 1.34715
 test sample Y[2] = 1.46436
 test sample Y[3] = 1.46004
 test sample Y[4] = 0.0258008
 test sample Y[5] = 0.433781
 test sample Y[6] = 0.23929
 test sample Y[7] = 0.559341
 test sample Y[8] = 0.969937
 test sample Y[9] = 0.943013
 test sample Y[10] = 0.575509
 test sample Y[11] = 0.950347
 test sample Y[12] = 0.562812
 test sample Y[13] = 0.222734
 test sample Y[14] = 0.0615325
 test sample Y[15] = 0.557481
 test sample Y[16] = 0.162225
 test sample Y[17] = 1.40591
 test sample Y[18] = 1.39797
 test sample Y[19] = 1.28191
 test sample Y[20] = 1.46071
 test sample Y[21] = 1.23891
 test sample Y[22] = 0.21592
 test sample Y[23] = 0.28807
 test sample Y[24] = 0.245242
 test sample Y[25] = 0.449108
 test sample Y[26] = 0.20715
 test sample Y[27] = 0.301293
 test sample Y[28] = 0.279991

w0 = 3.21505  w1 = 0.761547  w2 = -1.03171  w3 = -14.2614  w4 = -1.44008  w5 = 9.98143
```

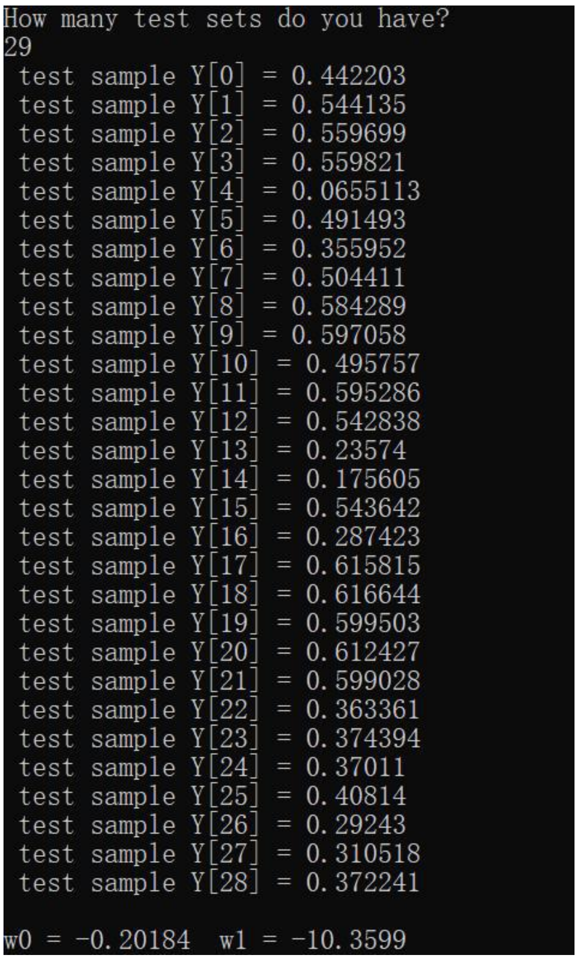
Figure 21: MLP Scores of Training Sample Basing on Threshold

The $Accuracy = \frac{28}{35} = 0.8$

And we also used singler layer perceptron to train and classify on these samples, and we gained:



```
error E[w]= 0.0790826
w0 = -0.20184  w1 = -10.3599
 Y[0] = 0.599662
 Y[1] = 0.428472
 Y[2] = 0.465157
 Y[3] = 0.424112
 Y[4] = 0.379498
 Y[5] = 0.376842
```



```
How many test sets do you have?
29
 test sample Y[0] = 0.442203
 test sample Y[1] = 0.544135
 test sample Y[2] = 0.559699
 test sample Y[3] = 0.559821
 test sample Y[4] = 0.0655113
 test sample Y[5] = 0.491493
 test sample Y[6] = 0.355952
 test sample Y[7] = 0.504411
 test sample Y[8] = 0.584289
 test sample Y[9] = 0.597058
 test sample Y[10] = 0.495757
 test sample Y[11] = 0.595286
 test sample Y[12] = 0.542838
 test sample Y[13] = 0.23574
 test sample Y[14] = 0.175605
 test sample Y[15] = 0.543642
 test sample Y[16] = 0.287423
 test sample Y[17] = 0.615815
 test sample Y[18] = 0.616644
 test sample Y[19] = 0.599503
 test sample Y[20] = 0.612427
 test sample Y[21] = 0.599028
 test sample Y[22] = 0.363361
 test sample Y[23] = 0.374394
 test sample Y[24] = 0.37011
 test sample Y[25] = 0.40814
 test sample Y[26] = 0.29243
 test sample Y[27] = 0.310518
 test sample Y[28] = 0.372241

w0 = -0.20184  w1 = -10.3599
```

Figure 22: Single Layer Perceptron Scores of Training Sample Basing on Threshold

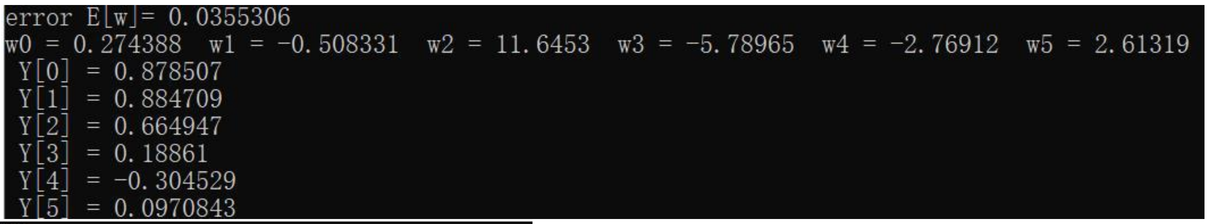
$Accuracy = \frac{25}{35} = 0.71$

From these experiments, we knew that when we set up the MLP or single layer perceptron, it's very important to choose the training data that corresponding to the threshold.

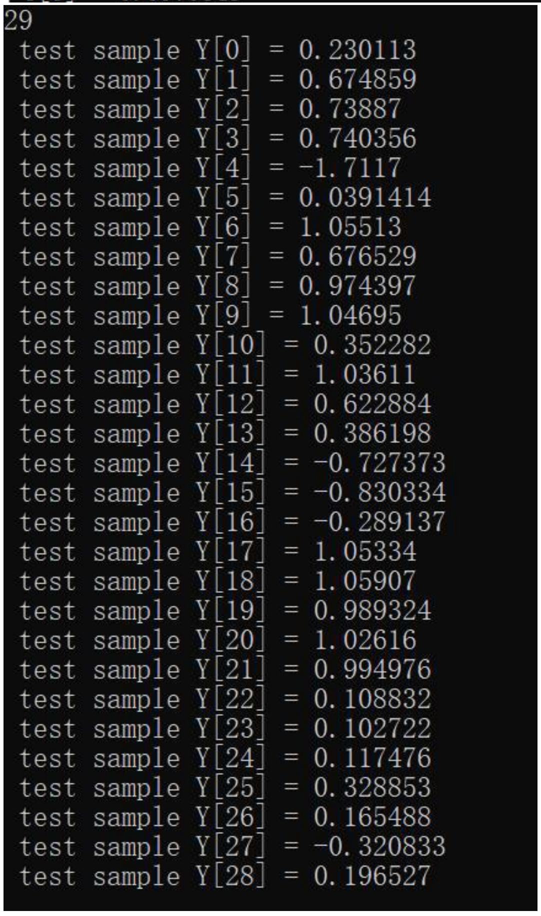
And we also want to know which score from HMM or PCA has more impact on the MLP training. Therefore, we decide to make some change to the training samples. We again chose the Malware scores from Zbot family but with low HMM score (we said lower HMM score is more likely to be classified as benign) and also low PCA score (lower PCA score is more likely to be classified as Malare). And we also chose the benign that has higher HMM scores and higher PCA score.

Zbot1	-2.938	0.04066
Zbot4	-2.952	0.04062
Securityshield1	-2.929	0.06035
ScoringHMM	-2.446	0.08353
Webexapp	-2.279	0.1214
WPSOffice	-2.718	0.1034

Then we obtained the result as below:



```
error E[w]= 0.0355306
w0 = 0.274388  w1 = -0.508331  w2 = 11.6453  w3 = -5.78965  w4 = -2.76912  w5 = 2.61319
 Y[0] = 0.878507
 Y[1] = 0.884709
 Y[2] = 0.664947
 Y[3] = 0.18861
 Y[4] = -0.304529
 Y[5] = 0.0970843
```



```
29
 test sample Y[0] = 0.230113
 test sample Y[1] = 0.674859
 test sample Y[2] = 0.73887
 test sample Y[3] = 0.740356
 test sample Y[4] = -1.7117
 test sample Y[5] = 0.0391414
 test sample Y[6] = 1.05513
 test sample Y[7] = 0.676529
 test sample Y[8] = 0.974397
 test sample Y[9] = 1.04695
 test sample Y[10] = 0.352282
 test sample Y[11] = 1.03611
 test sample Y[12] = 0.622884
 test sample Y[13] = 0.386198
 test sample Y[14] = -0.727373
 test sample Y[15] = -0.830334
 test sample Y[16] = -0.289137
 test sample Y[17] = 1.05334
 test sample Y[18] = 1.05907
 test sample Y[19] = 0.989324
 test sample Y[20] = 1.02616
 test sample Y[21] = 0.994976
 test sample Y[22] = 0.108832
 test sample Y[23] = 0.102722
 test sample Y[24] = 0.117476
 test sample Y[25] = 0.328853
 test sample Y[26] = 0.165488
 test sample Y[27] = -0.320833
 test sample Y[28] = 0.196527
```

Figure 22:MLP Score

$$Accuracy = \frac{27}{35} = 0.77$$

Therefore, now we know that if we choose the Malware samples (that have lower PCA score) and the benign samples (that have higher PCA score) to be the MLP training sample, we will probably get the model with higher accuracy. That is, PCA plays an important role when we train a MLP.

4. Conclusion

From this project, we found that PCA with register frequency played very good in Malware detection, it yielded an accuracy with 0.86. HMM with Opcode sequence also had an accuracy with 0.71, but the malware and benign samples were hardly separated. However, the choices of benign samples in this project maybe not so good. In this situation, PCA can solve this problem effectively. Furthermore, with the correct choice of training samples (especially choosing the samples with significant PCA scores), MLP can perform better than HMM. It yielded an 0.8 accuracy in this project.