

# CS 37300 Group Project Final Report

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Group Member:

Shupei Wang([wang3107@purdue.edu](mailto:wang3107@purdue.edu))

Yuxuan Yang([yang1329@purdue.edu](mailto:yang1329@purdue.edu))

Yuxing Chen([chen2689@purdue.edu](mailto:chen2689@purdue.edu))

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## Dataset Description and Pre-processing

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We use Higgs Boson dataset from [Kaggle](https://www.kaggle.com/datasets/cern/higgs-boson). The original dataset contains 250000 samples, each with 30 features and 1 label, 1 event id and 1 weight column. Although there is also another test dataset on the website, it doesn't contain label column so it cannot be used. So we sperate the training set to two parts, one for training and another one for testing. In data pre-processing, we ignored two columns: `eventid` and `weight`. Since the original data set is too large, we select 5000 samples. In the code it's index 120000 to 125000, given the original data should be independent of index. And another 5000 samples from index 125000 to 130000 for testing.

Also, the website states that "it can happen that for some entries some variables are meaningless or cannot be computed; in this case, their value is -999.0, which is outside the normal range of all variables". Regarding the -999 data, we are currently treating it like normal value, we considered getting rid of all these values by deleting all samples that contains a feature that has the value of -999, yet it could though not necessarily lead to bias, since test dataset also contain -999 features.

```

1 # Converting original labels to -1 and 1
2 s = list(np.where(data=='s'))
3 data[tuple(s)] = 1
4 b = list(np.where(data=='b'))
5 data[tuple(b)] = -1
6 data1 = data.astype(float)
7 # Select testing and training samples
8 data2 = data1[range(120000, 125000)] # testing samples
9 data1 = data1[range(125000,130000)] # training samples

```

In cleaned dataset, column 0 is `eventid`; 1-30 are features; 31 is `weight` which we will ignore; and 32 is label. After we done pre-processing, `x` contains training samples with features; `y` contains labels of training samples; `test_x` contains testing samples with features; and `test_y` contains labels of testing samples. Also, Based on the label, we separate the dataset to positive and negative samples:

```

1 X = data1[:,1:31]
2 y = data1[:,32]
3 test_x = data2[:, 1:31]
4 test_y = data2[:,32]
5
6 y.astype(int)
7 y=y.reshape(-1,1)
8 test_y.astype(int)
9 test_y.reshape(-1,1)
10 n,d = X.shape
11 pos = np.sum(y==1)
12 neg = np.sum(y==-1)
13 positive_samples = list(np.where(y==1)[0])
14 negative_samples = list(np.where(y==-1)[0])

```

## Validation and Hyperparameter Tuning

### Pre-tuning

At the start of hyperparameter tuning we first use first half of original training samples as training set and the second half as validation set:

```

1 train_samples = positive_samples[0:pos/2] + negative_samples[0:neg/2]
2 validation_samples = positive_samples[pos/2:] + negative_samples[neg/2:]

```

# Hyperparameter Tuning

The hyperparameters are `k` (number of nearest neighbors from k-nearest-neighbor) and `F` (number features after reduction in principal component analysis(PCA)). We use the two sets we got above as two folders in two-fold cross validation and we also use nested bootstrapping to tune hyperparameters 'k' and 'F' independently.

```
1  for F in range(8,15):
2      k_list = list(range(10,30))
3      for k in k_list:
4          # y_pred = np.zeros(len(X),int)
5          mu_fold1, z_fold1 = pclearn.run(F, X_fold1)
6          X_fold1_small = pcaproj.run(X_fold1, mu_fold1, z_fold1)
7          mu_fold2, z_fold2 = pclearn.run(F, X_fold2)
8          X_fold2_small = pcaproj.run(X_fold2, mu_fold2, z_fold2)
9          B = 1
10         y_pred = np.zeros(len(train_samples) + len(validation_samples), int)
11         err = bootstrapping.run(B, X_fold1_small, y[train_samples], k)
12         if err < best_err_1:
13             best_err_1 = err
14             best_k_1 = k
15             best_F_1 = F
16         temp = err
17
18         err = bootstrapping.run(B, X_fold2_small, y[validation_samples], k)
19         if err < best_err_2:
20             best_err_2 = err
21             best_k_2 = k
22             best_F_2 = F
23         plot_m[F-8][k-10] = (temp+err)/2
24     print "Final result is : " + str(best_k_1) + " " + str(best_k_2) + " " +
        str(best_err_1) + " " + str(best_err_2) + " " + str(best_F_1) + " " +
        str(best_F_2)
```

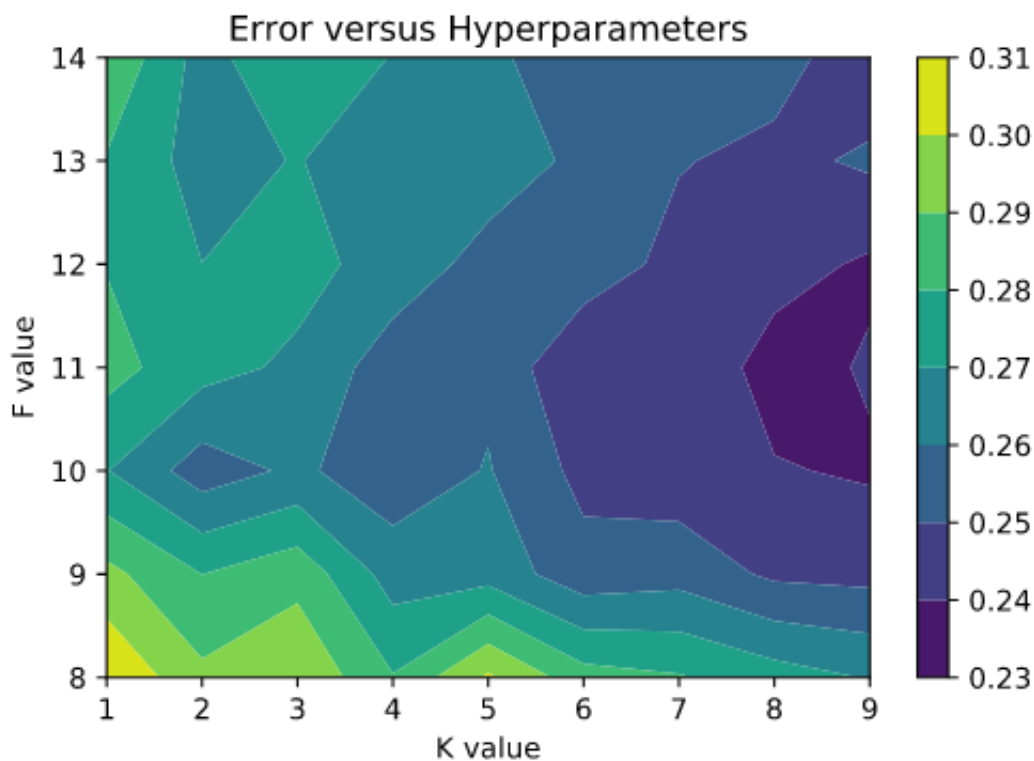
During hyperparameter tuning, we store the average error we get from two-fold cross validation. To visualize how error change with hyperparameters, we use contour map.

```

1 import matplotlib.pyplot as pp
2 x = range(10,30)
3 Y = range(8,15)
4 Z = plot_m
5 fig,ax = pp.subplots(1,1)
6 cp = ax.contourf(x, Y, Z)
7 fig.colorbar(cp)
8 ax.set_title("Error versus Hyperparameters")
9 ax.set_xlabel("K value")
10 ax.set_ylabel("F value")
11 pp.show()

```

We first use `k` in range of (1,10). However the plot we get look like this:



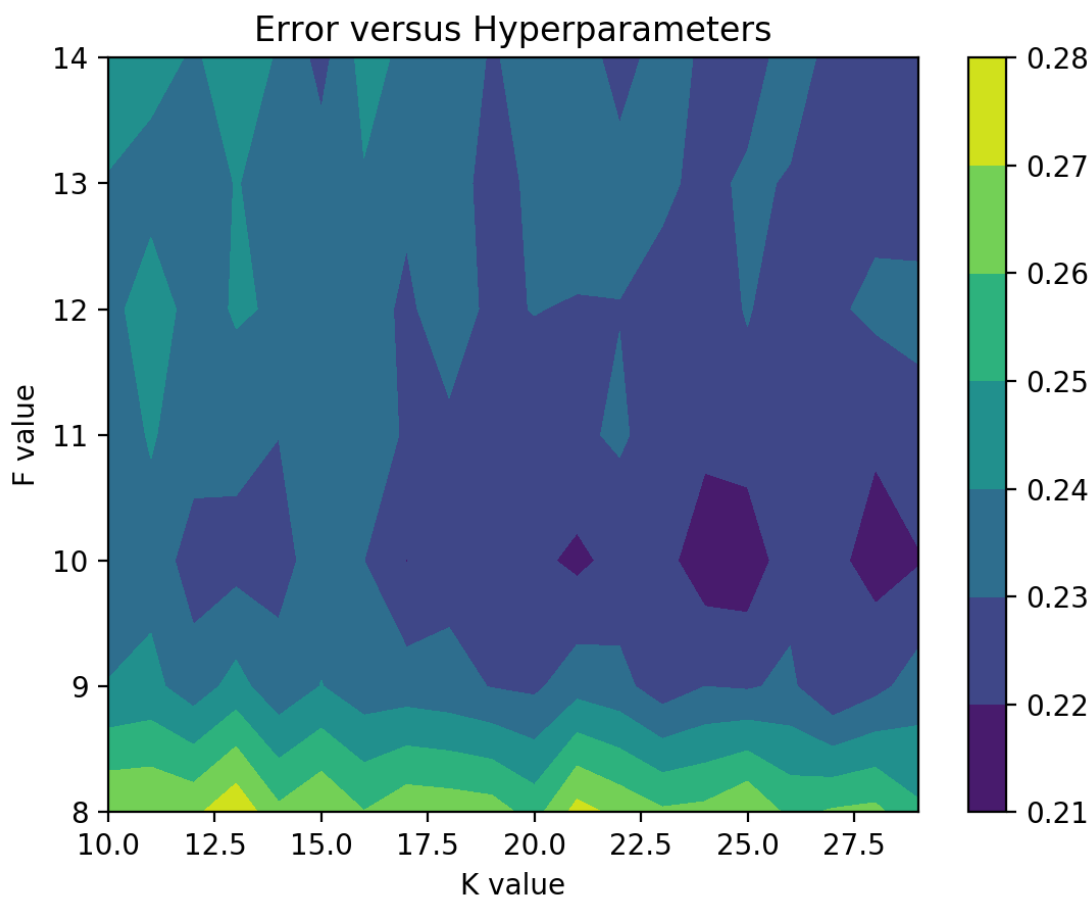
We observe that the error is still decreasing while `k` increasing. So, we decide to increasing `k` value to range(10,30). We will discuss more about the plot in result section.

## Results

Since we generate random numbers in bootstrapping, the graph and result of each run may have slight difference. However, both hyperparameter values will always in the fixed range. And classification error won't change a lot (around 0.22).

## Error versus Hyperparameters Plot

After we changed `k` to `range(10,30)` like we mentioned above, we can get a plot similar to this one. We observe this is more reasonable. We can clearly see the best number of features, `F` is around 10 and best number of nearest neighbors, `k`, is around 25.



## Classification Error

We also use the best `k` and best `F` we get from hyperparameter tuning for both sets to predict test samples and get classification error:

```
1 #Find best k and F based on the min error
2 best_err = np.amin(plot_m)
3 best_k = np.where(plot_m==best_err)[1][0] + 10
4 best_F = np.where(plot_m==best_err)[0][0] + 8
5
6 mu_fold1, z_fold1 = pclearn.run(best_F, X_fold1)
```

```

7 X_fold1_small = pcaproj.run(X_fold1, mu_fold1, Z_fold1)
8 mu_fold2, Z_fold2 = pcalearn.run(best_F, X_fold2)
9 X_fold2_small = pcaproj.run(X_fold2, mu_fold1, Z_fold1)
10
11 alg = KNeighborsClassifier(n_neighbors = best_k,algorithm='auto')
12 alg.fit(X_fold1_small,np.ravel(y[train_samples]))
13 y_pred[validation_samples] = alg.predict(X_fold2_small)
14
15
16 X_fold1_small = pcaproj.run(X_fold1, mu_fold2, Z_fold2)
17 X_fold2_small = pcaproj.run(X_fold2, mu_fold2, Z_fold2)
18
19 alg = KNeighborsClassifier(n_neighbors = best_k,algorithm='auto')
20 alg.fit(X_fold2_small,np.ravel(y[validation_samples]))
21 y_pred[train_samples] = alg.predict(X_fold1_small)
22
23 err = np.mean(y != np.array([y_pred]).T)
24
25 print "Classification Error:" + str(err)

```

As mentioned above, we have random values in bootstrapping. But the error we get is always around 0.22. Also, one interesting finding is that if we continue increasing `k` range, the best `k` value will continue increasing. But the classification error will still be around 0.22. That's why we think `range(10,30)` is enough for this dataset.

## ROC Curve

We also implement calculation of TPR and FPR and plot ROC curve:

```

1 def plot_roc_curve(fpr, tpr):
2     plt.plot(fpr, tpr, color='orange', label='ROC')
3     plt.plot([0, 1], [0, 1], color='darkblue', linestyle='--')
4     plt.xlabel('False Positive Rate')
5     plt.ylabel('True Positive Rate')
6     plt.title('Receiver Operating Characteristic (ROC) Curve')
7     plt.legend()
8     plt.show()
9
10 alg = KNeighborsClassifier(n_neighbors = best_k,algorithm='auto')
11 alg.fit(X,np.ravel(y))
12 probs = alg.predict_proba(test_X)
13 probs = probs[:,1]
14 #print np.array([probs]).T.shape, test_y.shape
15 fpr = np.zeros(22)

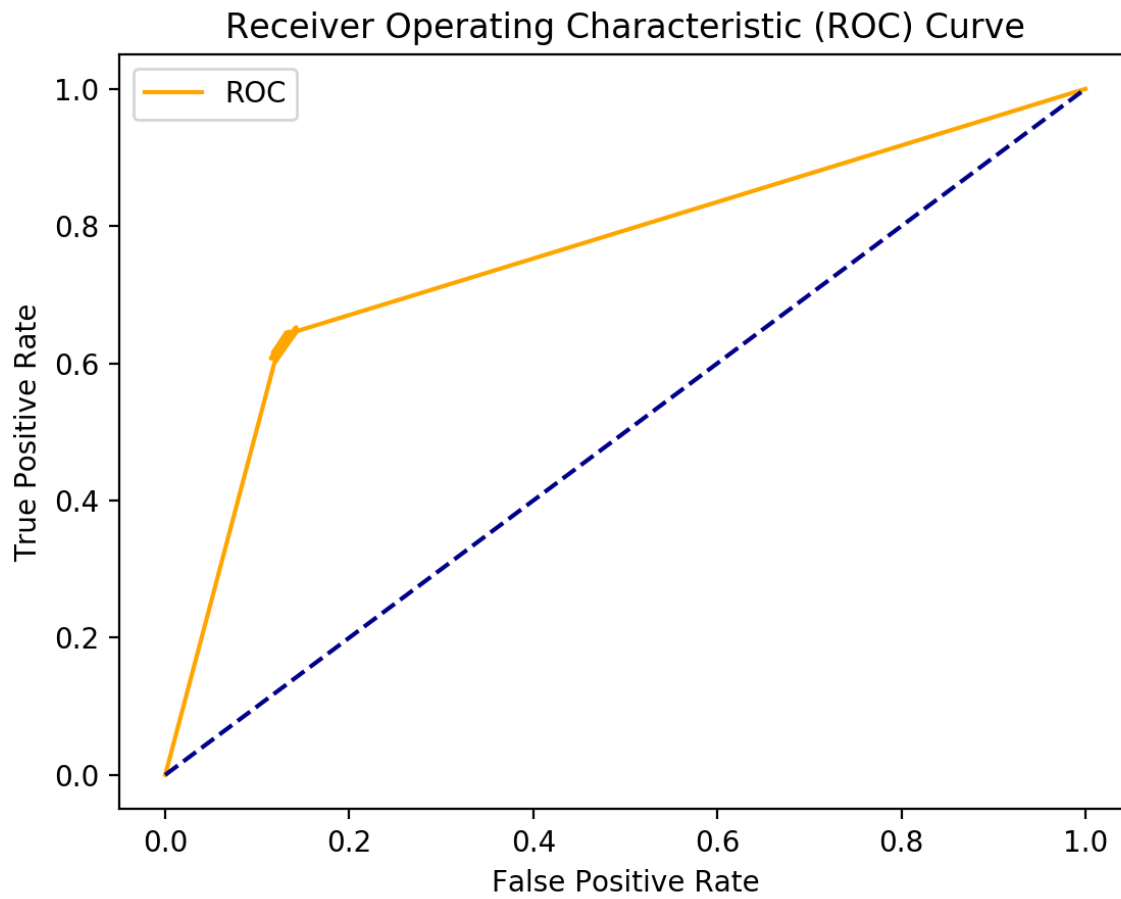
```

```

16 tpr = np.zeros(22)
17 P_label = list(np.where(test_y == 1))
18 P_label = np.asarray(P_label)
19 P_label = P_label.size
20 N_label = list(np.where(test_y == -1))
21 N_label = np.asarray(N_label)
22 N_label = N_label.size
23 for i in range(2,30):
24     #print i
25     alg = KNeighborsClassifier(n_neighbors = i, algorithm='auto')
26     alg.fit(X, np.ravel(y))
27     probs = alg.predict(test_X)
28     TP = 0
29     FP = 0
30     for j in range(0,len(test_y)):
31         if test_y[j] == 1 and probs[j] == 1:
32             TP = TP + 1
33         if test_y[j] == -1 and probs[j] == 1:
34             FP = FP + 1
35     fpr[i-9] = FP*1.0/N_label
36     tpr[i-9] = TP*1.0/P_label
37     #print TP,FP
38 fpr[0] = 0
39 fpr[21] = 1
40 tpr[0] = 0
41 tpr[21] = 1
42 print fpr,tpr
43 plot_roc_curve(fpr,tpr)

```

The curve we get looks like this:



The reason we get a curve like this but not a "smoother" curve may be FPR and TPR won't change a lot with hyperparameter.