PersonalizedCancerDiagnosis-Hyperparameter

March 21, 2019

```
In [3]: import pandas as pd
        import matplotlib.pyplot as plt
        import re
        import time
        import warnings
        import numpy as np
        from nltk.corpus import stopwords
        from sklearn.decomposition import TruncatedSVD
        from sklearn.preprocessing import normalize
        from sklearn.feature_extraction.text import CountVectorizer
        from sklearn.manifold import TSNE
        import seaborn as sns
        from sklearn.neighbors import KNeighborsClassifier
        from sklearn.metrics import confusion_matrix
        from sklearn.metrics.classification import accuracy_score, log_loss
        from sklearn.feature_extraction.text import TfidfVectorizer
        from sklearn.linear_model import SGDClassifier
        from imblearn.over_sampling import SMOTE
        from collections import Counter
        from scipy.sparse import hstack
        from sklearn.multiclass import OneVsRestClassifier
        from sklearn.svm import SVC
        from sklearn.model_selection import StratifiedKFold
        from collections import Counter, defaultdict
        from sklearn.calibration import CalibratedClassifierCV
        from sklearn.naive_bayes import MultinomialNB
        from sklearn.naive_bayes import GaussianNB
        from sklearn.model_selection import train_test_split
        from sklearn.model_selection import GridSearchCV
        import math
        from sklearn.metrics import normalized_mutual_info_score
        from sklearn.ensemble import RandomForestClassifier
        warnings.filterwarnings("ignore")

        from mlxtend.classifier import StackingClassifier

        from sklearn import model_selection
        from sklearn.linear_model import LogisticRegression
```

```
In [4]: train_df = pd.read_pickle('train_df')
        test_df = pd.read_pickle('test_df')
        cv_df = pd.read_pickle('cv_df')
        from scipy import sparse

        train_gene_feature_onehotCoding = sparse.load_npz("train_gene_feature_onehotCoding.npz"
        train_variation_feature_onehotCoding = sparse.load_npz("train_variation_feature_onehot
        test_gene_feature_onehotCoding = sparse.load_npz("test_gene_feature_onehotCoding.npz")
        test_variation_feature_onehotCoding = sparse.load_npz("test_variation_feature_onehotCo
        cv_gene_feature_onehotCoding = sparse.load_npz("cv_gene_feature_onehotCoding.npz")
        cv_variation_feature_onehotCoding = sparse.load_npz("cv_variation_feature_onehotCoding
```

```
In [5]: train_y = np.array(list(train_df['Class']))
        test_y = np.array(list(test_df['Class']))
        cv_y = np.array(list(cv_df['Class']))
        y_train=np.load('y_train.npy')
        y_test=np.load('y_test.npy')
        y_cv=np.load('y_cv.npy')
```

```
In [47]: y_train
```

```
Out[47]: array([4, 1, 6, ..., 3, 5, 6], dtype=int64)
```

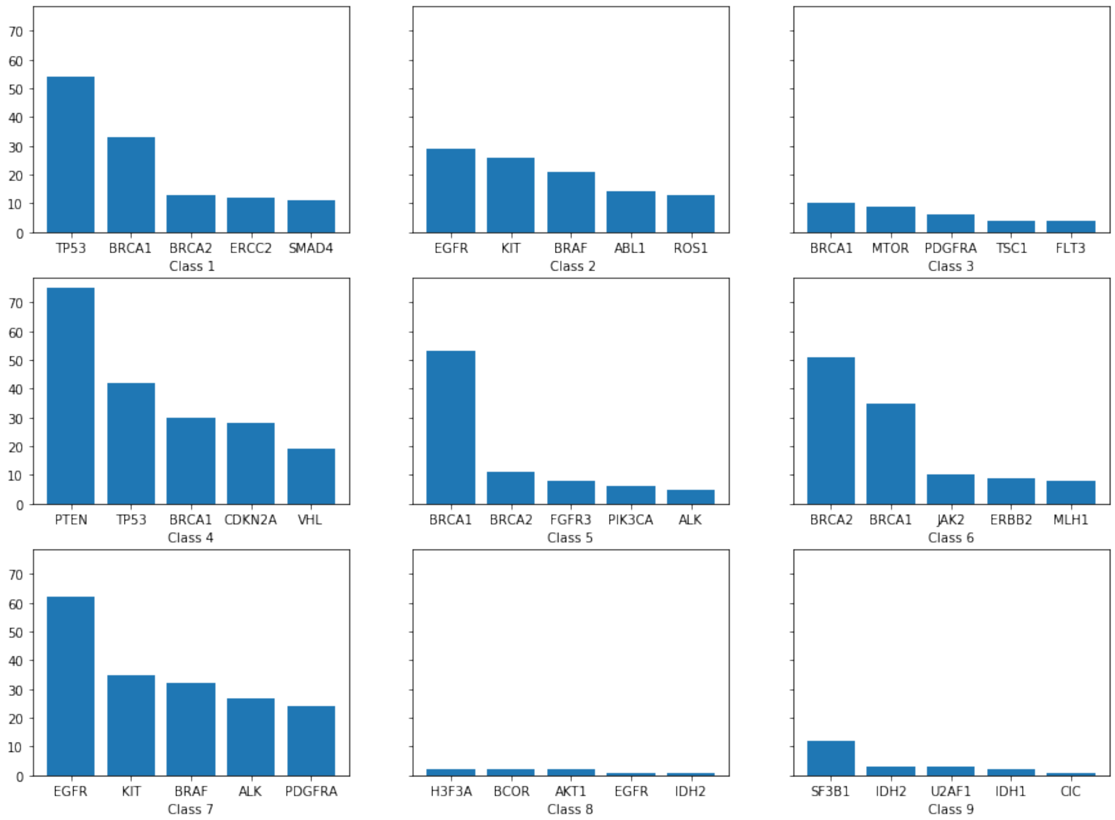
```
In [15]: print('Number of data points in train data:', train_df.shape[0])
         print('Number of data points in test data:', test_df.shape[0])
         print('Number of data points in cross validation data:', cv_df.shape[0])
```

```
Number of data points in train data: 2124
Number of data points in test data: 665
Number of data points in cross validation data: 532
```

0.1 Analysis on Gene Feature

0.2 Gene Frequency corresponding to each class

```
In [139]: fig, axes = plt.subplots(nrows=3, ncols=3, sharey=True, figsize=(15,11))
          i=1
          p=[' Class 1',' Class 2','Class 3','Class 4','Class 5','Class 6','Class 7','Class 8'
          for row in axes:
              for col in row:
                  c={}
                  c=train_df[train_df['Class']==i]['Gene'].value_counts()[0:5]

                  a=c.to_dict()
                  col.bar(list(a.keys()),list(a.values()))
                  col.set_xlabel(p[i-1])
                  i+=1
```



We can see that BRCA1 and BRCA2 has occurred many times in class 1,3,4,5,6.

0.2.1 Frequency of most occuring Genes corresponding to each class

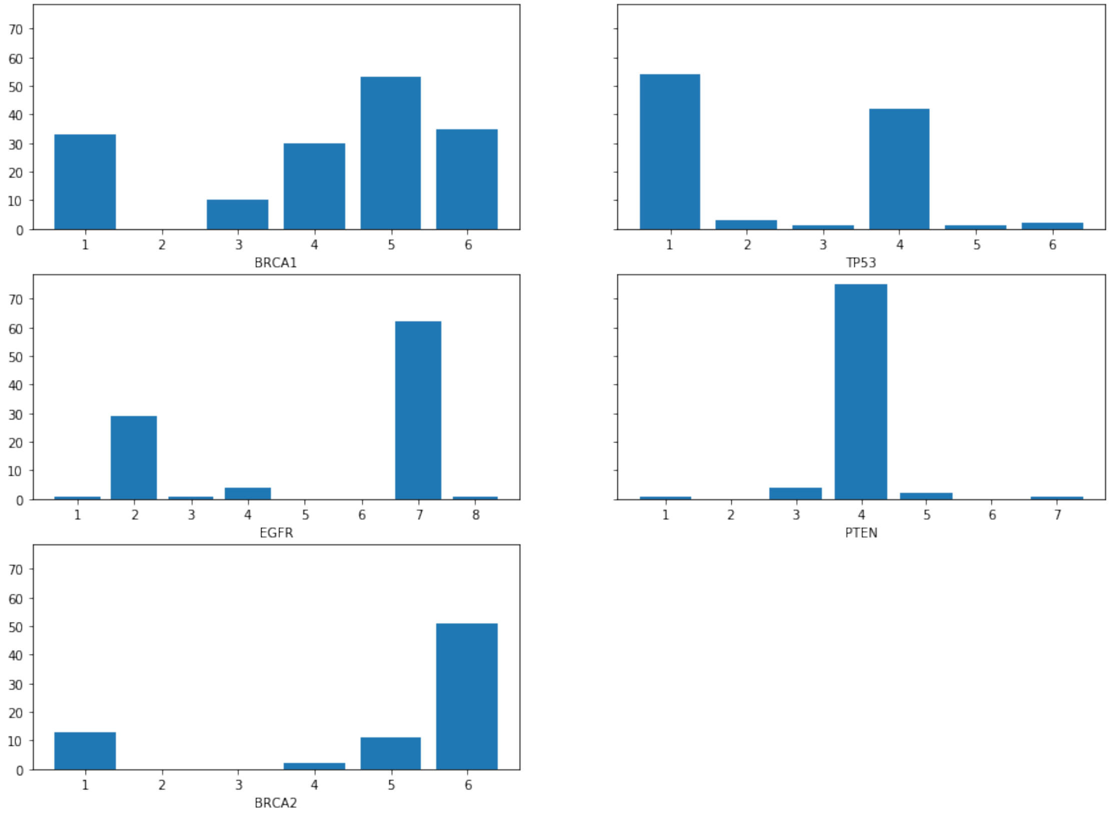
```
In [5]: train_df['Gene'].value_counts()[0:5]
```

```
Out[5]: BRCA1     161
        TP53      103
        EGFR       98
        PTEN       83
        BRCA2      77
        Name: Gene, dtype: int64
```

These are the most occuring genes

```
In [56]: fig, axes = plt.subplots(nrows=3, ncols=2, sharey=True, figsize=(15,11))
         i=0
         p=[' Class 1',' Class 2','Class 3','Class 4','Class 5','Class 6','Class 7','Class 8',
         gene=['BRCA1','TP53','EGFR','PTEN','BRCA2']
         for row in axes:
             for col in row:
                 c={}
                 if i<5:
```

```
            c=train_df[train_df['Gene']==gene[i]]['Class'].value_counts()
            a=c.to_dict()
            col.bar(list(a.keys()),list(a.values()))
            col.set_xlabel(gene[i])
            i+=1
axes[-1, -1].axis('off')
plt.show()
```



1. We can see that BRCA1 which is most occuring gene does not occur even once in class 2/7/8/9.
2. Class 7 contains more number of EGFR gene.
3. Class 9 does not contain any of the most occuring genes.

0.2.2 Analysis on Variation Feature

```
In [8]: counts=train_df['Variation'].value_counts().reset_index()
        counts.columns=['Occurence', 'Count']
        count_dict={}
        count_dict=counts.Count.value_counts()
        total=sum(count_dict.values)
        for a, b in count_dict.iteritems():
            print('{}% of variations has {} occurence'.format(np.round((b/total)*100,2 ),a))
```

```
98.65% of variations has 1 occurence
0.98% of variations has 2 occurence
0.1% of variations has 3 occurence
0.05% of variations has 60 occurence
0.05% of variations has 47 occurence
0.05% of variations has 45 occurence
0.05% of variations has 19 occurence
0.05% of variations has 4 occurence
```

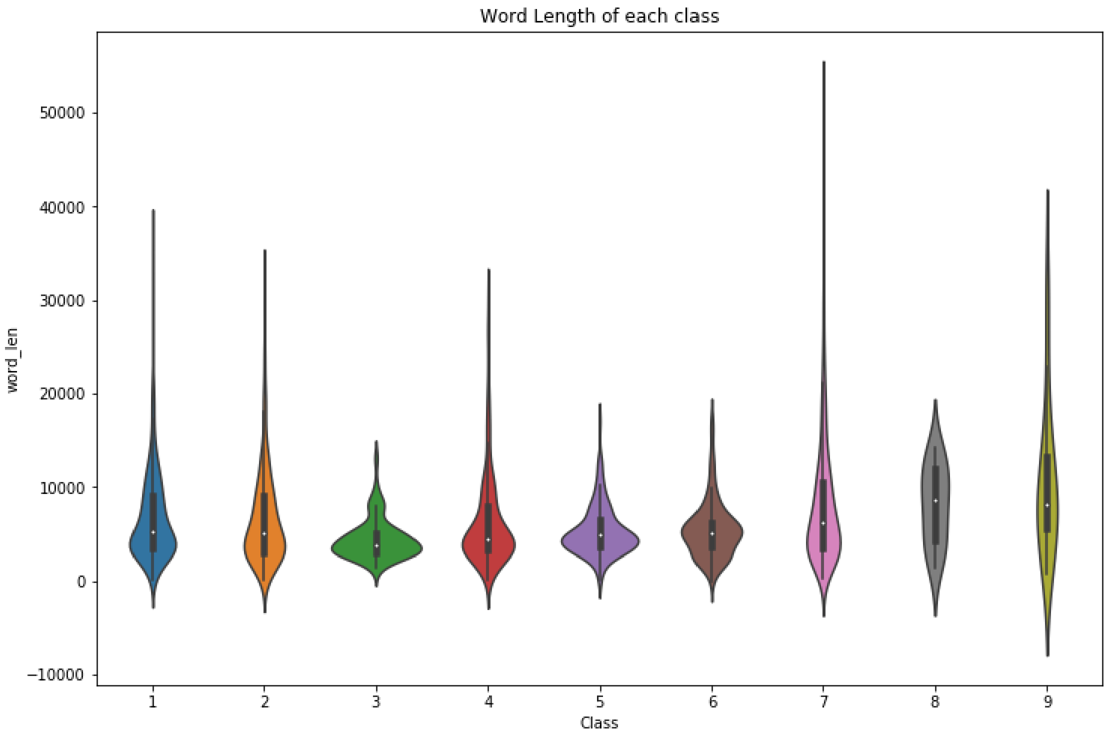
We can infer that 98.6% of variations are unique.

0.2.3 Analysis on Text Feature

```
In [113]: train_df.head(5)
```

```
Out[113]:         ID    Gene             Variation  Class  \
          2426  2426   BRCA1                  C64G      4
          636    636  CDKN1A  Truncating Mutations      1
          703    703   ERBB2                 E812K      6
          1455  1455   FGFR2                 K659N      7
          103    103    MSH6                 R976H      1

                                                     TEXT  word_len  char_len
          2426  published analyses effects missense mutations ...     17926    130265
          636   introduction loss control mammalian cell cycle...      7234     53047
          703   purpose mutations associated resistance kinase...      4961     37512
          1455  activating mutations tyrosine kinase domain re...      8077     59908
          103   msh6 gene one mismatch repair genes involved h...     13352    100388
```

```
In [11]: plt.figure(figsize=(12,8))
         sns.violinplot(x="Class", y="word_len", data=train_df)
         plt.title('Word Length of each class')
         plt.show()
```

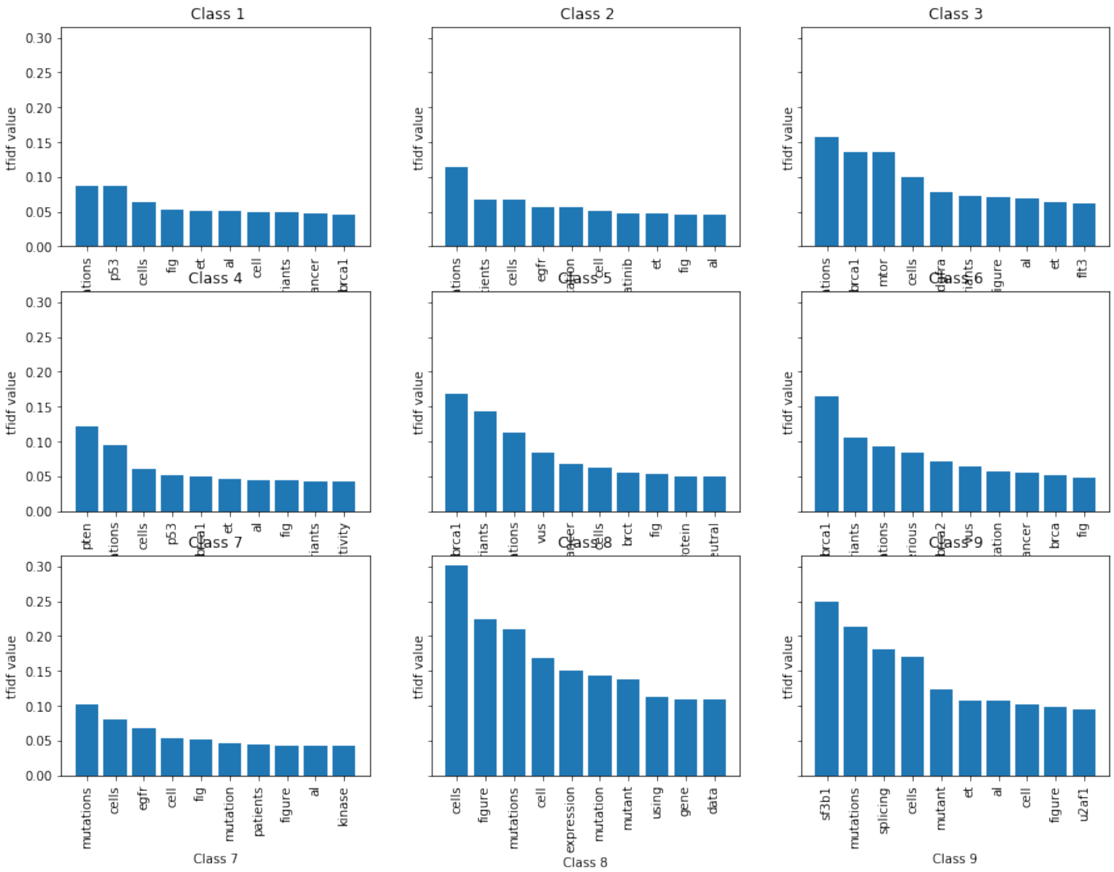


we can see that most classes have word length between 0 to 10000.

0.2.4 Words with top TFIDF Values

```
In [162]: fig, axes = plt.subplots(nrows=3, ncols=3, sharey=True, figsize=(15,11))
          count=1
          classes=[' Class 1',' Class 2','Class 3','Class 4','Class 5','Class 6','Class 7','Cla

          for row in axes:
              for col in row:
                  tf_idf_vect = TfidfVectorizer(min_df=10)
                  vec1=tf_idf_vect.fit_transform(train_df[train_df['Class']==count]['TEXT'])

                  features=pd.DataFrame(tf_idf_vect.get_feature_names())
                  mean_tf=np.mean(vec1,axis=0)
                  x=np.array(mean_tf)[0].tolist()
                  idf_values=sorted(x, reverse=True)
                  # taking top 20 features
                  important_feat=[]
                  important_feat=np.argsort((x))[::-1]
                  important_feat=important_feat[:10]
                  important_feat
                  imp_feat=[]
                  for index in important_feat:
```

```
    imp_feat.append(features.iloc[index])
x=np.array(imp_feat)
feature=[]
for i in x:
    for j in i:
        feature.append(j)
clas={}
c=0
common={}
for i in feature:
    common[i]=idf_values[c]
    c+=1
col.bar(list(common.keys()),list(common.values()))
col.set_xticklabels(list(common.keys()),rotation=90)
col.set_xlabel(classes[count-1])
col.set_title(classes[count-1])
col.set_ylabel('tfidf value')
count+=1
```



0.3 ML Models

```
In [4]: # This function plots the confusion matrices given y_i, y_i_hat.
        def plot_confusion_matrix(test_y, predict_y):
            C = confusion_matrix(test_y, predict_y)
            #C = 9,9 matrix, each cell (i,j) represents number of points of class i are predic

            A =(((C.T)/(C.sum(axis=1))).T)
            #divid each element of the confusion matrix with the sum of elements in that colum

            # C = [[1, 2],
            #     [3, 4]]
            # C.T = [[1, 3],
            #        [2, 4]]
            # C.sum(axis = 1)  axis=0 corresonds to columns and axis=1 corresponds to rows in
            # C.sum(axix =1) = [[3, 7]]
            # ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
            #                            [2/3, 4/7]]

            # ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]
            #                            [3/7, 4/7]]
            # sum of row elements = 1

            B =(C/C.sum(axis=0))
            #divid each element of the confusion matrix with the sum of elements in that row
            # C = [[1, 2],
            #     [3, 4]]
            # C.sum(axis = 0)  axis=0 corresonds to columns and axis=1 corresponds to rows in
            # C.sum(axix =0) = [[4, 6]]
            # (C/C.sum(axis=0)) = [[1/4, 2/6],
            #                       [3/4, 4/6]]

            labels = [1,2,3,4,5,6,7,8,9]
            # representing A in heatmap format
            print("-"*20, "Confusion matrix", "-"*20)
            plt.figure(figsize=(20,7))
            sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabel
            plt.xlabel('Predicted Class')
            plt.ylabel('Original Class')
            plt.show()

            print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
            plt.figure(figsize=(20,7))
            sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabel
            plt.xlabel('Predicted Class')
            plt.ylabel('Original Class')
            plt.show()
            # representing B in heatmap format
            print("-"*20, "Recall matrix (Row sum=1)", "-"*20)
            plt.figure(figsize=(20,7))
            sns.heatmap(A, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabel
            plt.xlabel('Predicted Class')
            plt.ylabel('Original Class')
            plt.show()
```

```
In [5]: # cls_text is a data frame
        # for every row in data fram consider the 'TEXT'
        # split the words by space
        # make a dict with those words
        # increment its count whenever we see that word

        def extract_dictionary_paddle(cls_text):
            dictionary = defaultdict(int)
            for index, row in cls_text.iterrows():
                for word in row['TEXT'].split():
                    dictionary[word] +=1
            return dictionary
```

```
In [6]: dict_list = []
        # dict_list =[] contains 9 dictoinaries each corresponds to a class
        for i in range(1,10):
            cls_text = train_df[train_df['Class']==i]
            # build a word dict based on the words in that class
            dict_list.append(extract_dictionary_paddle(cls_text))
            # append it to dict_list

        # dict_list[i] is build on i'th  class text data
        # total_dict is buid on whole training text data
        total_dict = extract_dictionary_paddle(train_df)
```

```
In [7]: def predict_and_plot_confusion_matrix(train_x, train_y,test_x, test_y, clf):
            clf.fit(train_x, train_y)
            sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig_clf.fit(train_x, train_y)
            pred_y = sig_clf.predict(test_x)

            # for calculating log_loss we willl provide the array of probabilities belongs to
            print("Log loss :",log_loss(test_y, sig_clf.predict_proba(test_x)))
            # calculating the number of data points that are misclassified
            print("Number of mis-classified points :", np.count_nonzero((pred_y- test_y))/test_
            plot_confusion_matrix(test_y, pred_y)
```

```
In [8]: def report_log_loss(train_x, train_y, test_x, test_y,  clf):
            clf.fit(train_x, train_y)
            sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig_clf.fit(train_x, train_y)
            sig_clf_probs = sig_clf.predict_proba(test_x)
            return log_loss(test_y, sig_clf_probs, eps=1e-15)

In [9]: # this function will be used just for naive bayes
        # for the given indices, we will print the name of the features
        # and we will check whether the feature present in the test point text or not
        def get_impfeature_names(indices, text, gene, var, no_features):
            gene_count_vec = CountVectorizer()
            var_count_vec = CountVectorizer()
            text_count_vec = CountVectorizer(min_df=3)

            gene_vec = gene_count_vec.fit(train_df['Gene'])
            var_vec  = var_count_vec.fit(train_df['Variation'])
            text_vec = text_count_vec.fit(train_df['TEXT'])

            fea1_len = len(gene_vec.get_feature_names())
            fea2_len = len(var_count_vec.get_feature_names())

            word_present = 0
            for i,v in enumerate(indices):
                if (v < fea1_len):
                    word = gene_vec.get_feature_names()[v]
                    yes_no = True if word == gene else False
                    if yes_no:
                        word_present += 1
                        print(i, "Gene feature [{}] present in test data point [{}]".format(wo
                elif (v < fea1_len+fea2_len):
                    word = var_vec.get_feature_names()[v-(fea1_len)]
                    yes_no = True if word == var else False
                    if yes_no:
                        word_present += 1
                        print(i, "variation feature [{}] present in test data point [{}]".forma
                else:
                    word = text_vec.get_feature_names()[v-(fea1_len+fea2_len)]
                    yes_no = True if word in text.split() else False
                    if yes_no:
                        word_present += 1
                        print(i, "Text feature [{}] present in test data point [{}]".format(wo

            print("Out of the top ",no_features," features ", word_present, "are present in que

In [10]: def get_imp_feature_names(text, indices, removed_ind = []):
             word_present = 0
             tabulte_list = []
             incresingorder_ind = 0
             for i in indices:
                 if i < train_gene_feature_onehotCoding.shape[1]:
                     tabulte_list.append([incresingorder_ind, "Gene", "Yes"])
                 elif i< 18:
                     tabulte_list.append([incresingorder_ind,"Variation", "Yes"])
                 if ((i > 17) & (i not in removed_ind)) :
                     word = train_text_features[i]
                     yes_no = True if word in text.split() else False
                     if yes_no:
                         word_present += 1
                     tabulte_list.append([incresingorder_ind,train_text_features[i], yes_no])
                 incresingorder_ind += 1
             print(word_present, "most importent features are present in our query point")
             print("-"*50)
             print("The features that are most importent of the ",predicted_cls[0]," class:")
             print (tabulate(tabulte_list, headers=["Index",'Feature name', 'Present or Not'])
```

5. Assignments

```
<li> Apply All the models with tf-idf features (Replace CountVectorizer with tfidfVectorizer an
<li> Instead of using all the words in the dataset, use only the top 1000 words based of tf-idf
<li>Apply Logistic regression with CountVectorizer Features, including both unigrams and bigram
<li> Try any of the feature engineering techniques discussed in the course to reduce the CV and
```

In [23]:
```
train_df.head()
```

Out[23]:
```
        ID    Gene             Variation  Class  \
2426  2426   BRCA1                  C64G      4
636    636  CDKN1A  Truncating Mutations      1
703    703   ERBB2                 E812K      6
1455  1455   FGFR2                 K659N      7
103    103    MSH6                 R976H      1

                                                   TEXT
2426  published analyses effects missense mutations ...
636   introduction loss control mammalian cell cycle...
703   purpose mutations associated resistance kinase...
1455  activating mutations tyrosine kinase domain re...
103   msh6 gene one mismatch repair genes involved h...
```

In [24]:
```
train_variation_feature_onehotCoding
```

Out[24]:
```
<2124x1964 sparse matrix of type '<class 'numpy.int64'>'
        with 2431 stored elements in Compressed Sparse Row format>
```

In [224]:
```
# building a CountVectorizer with all the words that occured minimum 3 times in trai
from sklearn.feature_extraction.text import TfidfVectorizer
text_vectorizer = TfidfVectorizer()
train_text_feature = text_vectorizer.fit_transform(train_df['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()
test_text_feature = text_vectorizer.transform(test_df['TEXT'])
cv_text_feature = text_vectorizer.transform(cv_df['TEXT'])
```

```
In [13]: print(train_variation_feature_onehotCoding.shape)
         print(train_gene_feature_onehotCoding.shape)
         train_text_feature.shape
```

```
(2124, 1964)
(2124, 229)
```

```
Out[13]: (2124, 126099)
```

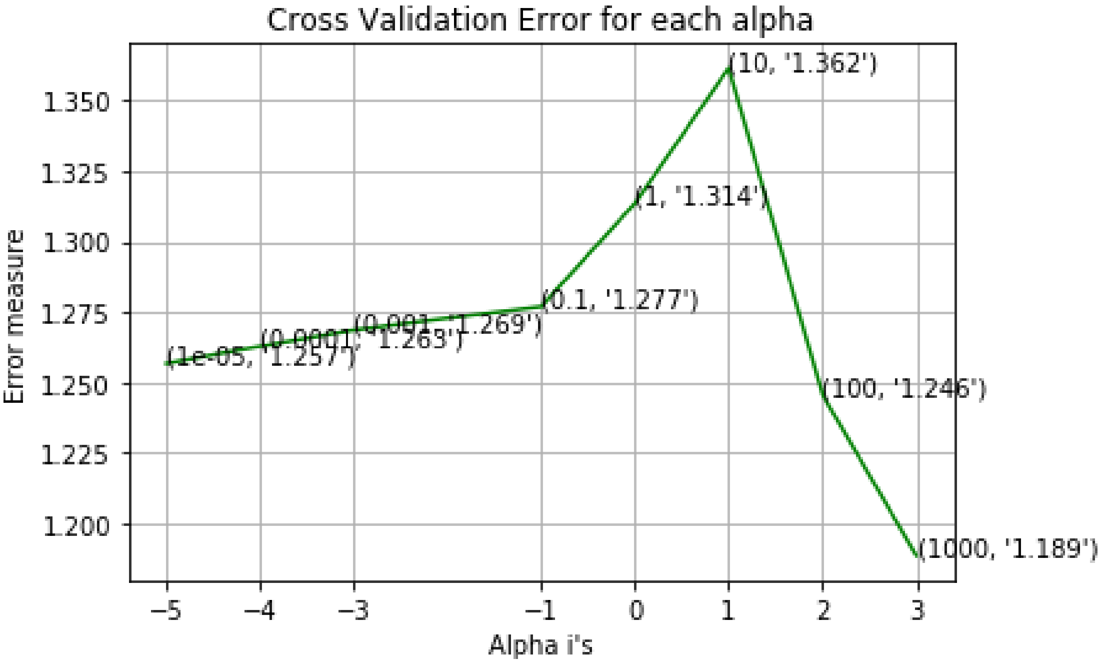
```
In [225]: train_text_feature = normalize(train_text_feature, axis=0)

          # we use the same vectorizer that was trained on train data

          # don't forget to normalize every feature
          test_text_feature = normalize(test_text_feature, axis=0)

          # we use the same vectorizer that was trained on train data

          # don't forget to normalize every feature
          cv_text_feature = normalize(cv_text_feature, axis=0)
```

```
In [29]: train_vec = hstack((train_gene_feature_onehotCoding,train_variation_feature_onehotCodi
         test_vec = hstack((test_gene_feature_onehotCoding,test_variation_feature_onehotCoding
         cv_vec = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehotCoding,cv_te
```

0.4 Naive Bayes

```
In [52]: alpha = [0.00001, 0.0001, 0.001, 0.1, 1, 10, 100,1000]
         cv_log_error_array = []
         for i in alpha:
             print("for alpha =", i)
             clf = MultinomialNB(alpha=i)
             clf.fit(train_vec, train_y)
             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_vec, train_y)
             sig_clf_probs = sig_clf.predict_proba(cv_vec)
             cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=
             # to avoid rounding error while multiplying probabilites we use log-probability e
             print("Log Loss :",log_loss(cv_y, sig_clf_probs))

         fig, ax = plt.subplots()
         ax.plot(np.log10(alpha), cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
             ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv_log_error_array[i]))
         plt.grid()
         plt.xticks(np.log10(alpha))
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
         plt.show()


         best_alpha = np.argmin(cv_log_error_array)
         clf = MultinomialNB(alpha=alpha[best_alpha])
         clf.fit(train_vec, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_vec, train_y)


         predict_y = sig_clf.predict_proba(train_vec)
         print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_l
         predict_y = sig_clf.predict_proba(cv_vec)
         print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
         predict_y = sig_clf.predict_proba(test_vec)
         print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_lo
```

```
for alpha = 1e-05
Log Loss : 1.2567927668300418
for alpha = 0.0001
Log Loss : 1.2629049300903104
for alpha = 0.001
Log Loss : 1.2686550032314035
for alpha = 0.1
Log Loss : 1.2770262355822313
for alpha = 1
Log Loss : 1.313619241850694
for alpha = 10
Log Loss : 1.3615423725765872
for alpha = 100
Log Loss : 1.2457778208833945
for alpha = 1000
Log Loss : 1.188761554861517
```

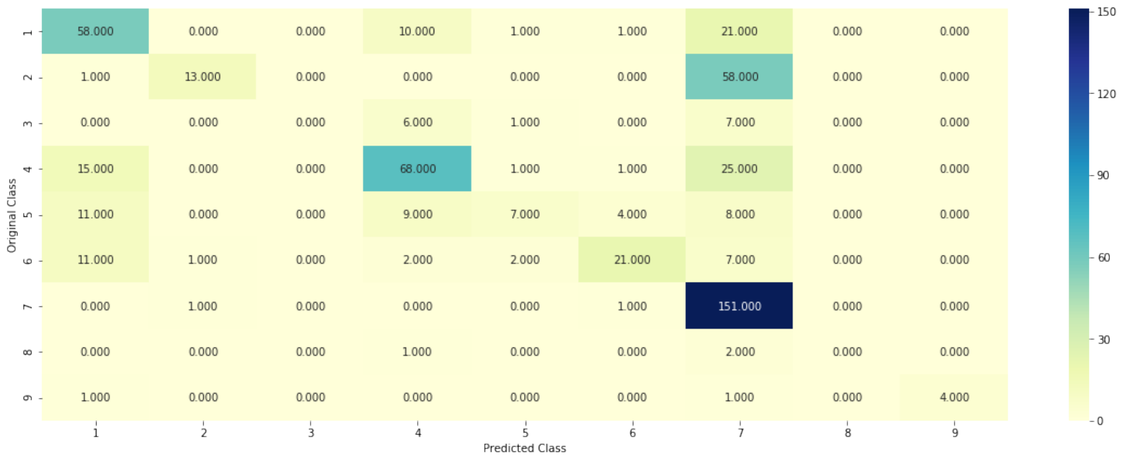


```
For values of best alpha =  1000 The train log loss is: 0.8376778669235427
For values of best alpha =  1000 The cross validation log loss is: 1.188761554861517
For values of best alpha =  1000 The test log loss is: 1.1764751736807895
```

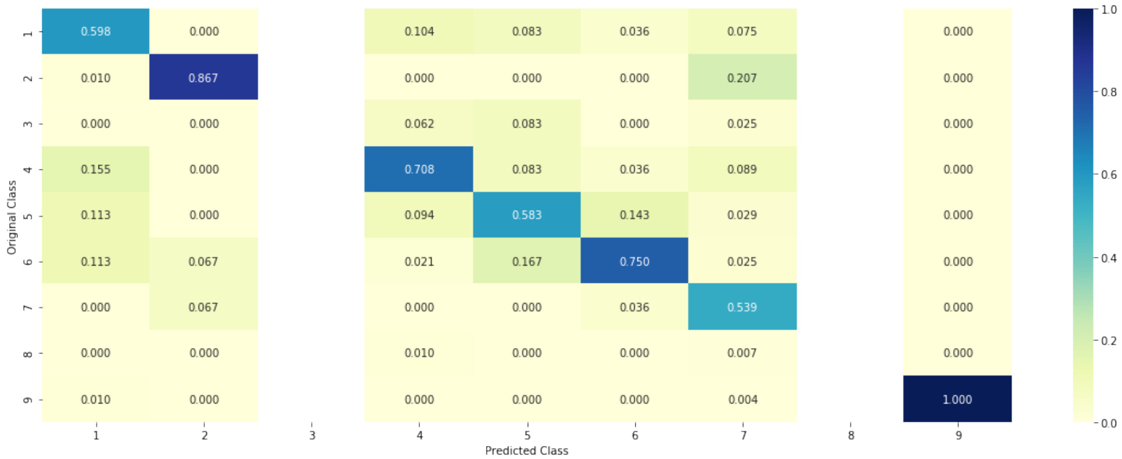
Testing the model with best hyper paramters

```
In [55]: clf = MultinomialNB(alpha=alpha[best_alpha])
         clf.fit(train_vec, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_vec, train_y)
         sig_clf_probs = sig_clf.predict_proba(cv_vec)
         # to avoid rounding error while multiplying probabilites we use log-probability estim
         print("Log Loss :",log_loss(cv_y, sig_clf_probs))
         print("Number of missclassified point :", np.count_nonzero((sig_clf.predict(cv_vec)-
         plot_confusion_matrix(cv_y, sig_clf.predict(cv_vec.toarray()))
```

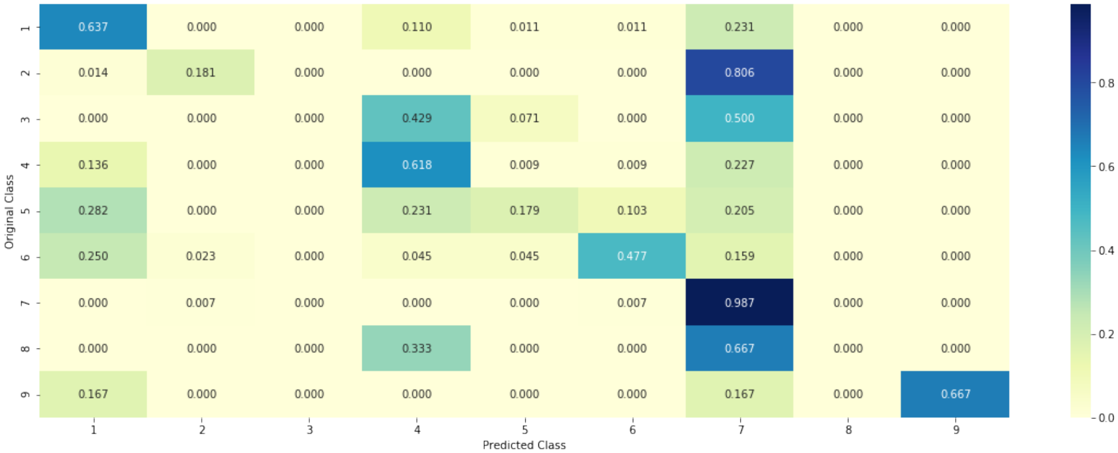
```
Log Loss : 1.188761554861517
Number of missclassified point : 0.39473684210526316
-------------------- Confusion matrix --------------------
```



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



```
-------------------- Recall matrix (Row sum=1) --------------------
```



0.4.1 Feature Importance, Correctly classified point

```
In [11]: # this function will be used just for naive bayes
         # for the given indices, we will print the name of the features
         # and we will check whether the feature present in the test point text or not
         # feature importance for tfidf features
         def get_impfeature_names_tf(indices, text, gene, var, no_features):
             gene_count_vec = CountVectorizer()
             var_count_vec = CountVectorizer()
             text_count_vec = TfidfVectorizer()

             gene_vec = gene_count_vec.fit(train_df['Gene'])
             var_vec  = var_count_vec.fit(train_df['Variation'])
             text_vec = text_count_vec.fit(train_df['TEXT'])

             fea1_len = len(gene_vec.get_feature_names())
             fea2_len = len(var_count_vec.get_feature_names())

             word_present = 0
             for i,v in enumerate(indices):
                 if (v < fea1_len):
                     word = gene_vec.get_feature_names()[v]
                     yes_no = True if word == gene else False
                     if yes_no:
                         word_present += 1
                         print(i, "Gene feature [{}] present in test data point [{}]".format(w
                 elif (v < fea1_len+fea2_len):
                     word = var_vec.get_feature_names()[v-(fea1_len)]
                     yes_no = True if word == var else False
                     if yes_no:
                         word_present += 1
```

```
                print(i, "variation feature [{}] present in test data point [{}]".form
        else:
            word = text_vec.get_feature_names()[v-(fea1_len+fea2_len)]
            yes_no = True if word in text.split() else False
            if yes_no:
                word_present += 1
                print(i, "Text feature [{}] present in test data point [{}]".format(wo

    print("Out of the top ",no_features," features ", word_present, "are present in qu
```

```
In [35]: test_vec=test_vec.tocsr()
```

```
In [57]: test_point_index = 1
         no_feature = 100
         predicted_cls = sig_clf.predict(test_vec[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         test_vec=test_vec.tocsr()
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_p
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names_tf(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Ge
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0161 0.0605 0.0191 0.0315 0.033  0.0213 0.8125 0.0038 0.002
Actual Class : 7
--------------------------------------------------
15 Text feature [cells] present in test data point [True]
16 Text feature [kinase] present in test data point [True]
20 Text feature [cell] present in test data point [True]
21 Text feature [presence] present in test data point [True]
22 Text feature [activated] present in test data point [True]
23 Text feature [contrast] present in test data point [True]
24 Text feature [activation] present in test data point [True]
25 Text feature [phosphorylation] present in test data point [True]
26 Text feature [inhibitor] present in test data point [True]
28 Text feature [also] present in test data point [True]
29 Text feature [shown] present in test data point [True]
30 Text feature [expressing] present in test data point [True]
31 Text feature [10] present in test data point [True]
32 Text feature [signaling] present in test data point [True]
33 Text feature [however] present in test data point [True]
34 Text feature [treated] present in test data point [True]
35 Text feature [independent] present in test data point [True]
37 Text feature [growth] present in test data point [True]
38 Text feature [suggest] present in test data point [True]
39 Text feature [found] present in test data point [True]
40 Text feature [compared] present in test data point [True]
```

```
41 Text feature [increased] present in test data point [True]
42 Text feature [similar] present in test data point [True]
43 Text feature [previously] present in test data point [True]
45 Text feature [tyrosine] present in test data point [True]
46 Text feature [inhibition] present in test data point [True]
47 Text feature [treatment] present in test data point [True]
48 Text feature [constitutively] present in test data point [True]
50 Text feature [addition] present in test data point [True]
52 Text feature [potential] present in test data point [True]
53 Text feature [well] present in test data point [True]
54 Text feature [figure] present in test data point [True]
56 Text feature [various] present in test data point [True]
57 Text feature [mutations] present in test data point [True]
58 Text feature [sensitive] present in test data point [True]
59 Text feature [obtained] present in test data point [True]
60 Text feature [may] present in test data point [True]
63 Text feature [showed] present in test data point [True]
64 Text feature [described] present in test data point [True]
65 Text feature [3b] present in test data point [True]
67 Text feature [constitutive] present in test data point [True]
68 Text feature [inhibitors] present in test data point [True]
70 Text feature [consistent] present in test data point [True]
71 Text feature [mutant] present in test data point [True]
72 Text feature [reported] present in test data point [True]
73 Text feature [total] present in test data point [True]
74 Text feature [including] present in test data point [True]
75 Text feature [using] present in test data point [True]
76 Text feature [respectively] present in test data point [True]
77 Text feature [mutation] present in test data point [True]
81 Text feature [confirmed] present in test data point [True]
83 Text feature [fig] present in test data point [True]
84 Text feature [proliferation] present in test data point [True]
87 Text feature [followed] present in test data point [True]
88 Text feature [inhibited] present in test data point [True]
89 Text feature [activating] present in test data point [True]
90 Text feature [concentrations] present in test data point [True]
91 Text feature [identified] present in test data point [True]
92 Text feature [approximately] present in test data point [True]
95 Text feature [two] present in test data point [True]
96 Text feature [approved] present in test data point [True]
97 Text feature [molecular] present in test data point [True]
98 Text feature [due] present in test data point [True]
99 Text feature [3a] present in test data point [True]
Out of the top  100  features  64 are present in query point
```

0.4.2 Feature Importance, Incorrectly classified point

```
In [68]: test_point_index = 350
         no_feature = 100
         predicted_cls = sig_clf.predict(test_vec[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names_tf(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Ge
```

```
Predicted Class : 1
Predicted Class Probabilities: [[0.5857 0.0275 0.0171 0.2585 0.0318 0.024  0.0492 0.0036 0.0026
Actual Class : 4
--------------------------------------------------
13 Text feature [protein] present in test data point [True]
14 Text feature [type] present in test data point [True]
15 Text feature [wild] present in test data point [True]
16 Text feature [one] present in test data point [True]
19 Text feature [dna] present in test data point [True]
20 Text feature [containing] present in test data point [True]
21 Text feature [two] present in test data point [True]
23 Text feature [region] present in test data point [True]
24 Text feature [either] present in test data point [True]
25 Text feature [binding] present in test data point [True]
26 Text feature [function] present in test data point [True]
27 Text feature [results] present in test data point [True]
28 Text feature [expression] present in test data point [True]
29 Text feature [therefore] present in test data point [True]
30 Text feature [reduced] present in test data point [True]
31 Text feature [also] present in test data point [True]
33 Text feature [using] present in test data point [True]
34 Text feature [role] present in test data point [True]
35 Text feature [loss] present in test data point [True]
36 Text feature [shown] present in test data point [True]
37 Text feature [control] present in test data point [True]
38 Text feature [specific] present in test data point [True]
39 Text feature [table] present in test data point [True]
40 Text feature [affect] present in test data point [True]
41 Text feature [human] present in test data point [True]
42 Text feature [effect] present in test data point [True]
43 Text feature [gene] present in test data point [True]
44 Text feature [however] present in test data point [True]
45 Text feature [indicate] present in test data point [True]
46 Text feature [possible] present in test data point [True]
47 Text feature [following] present in test data point [True]
49 Text feature [four] present in test data point [True]
50 Text feature [determined] present in test data point [True]
```

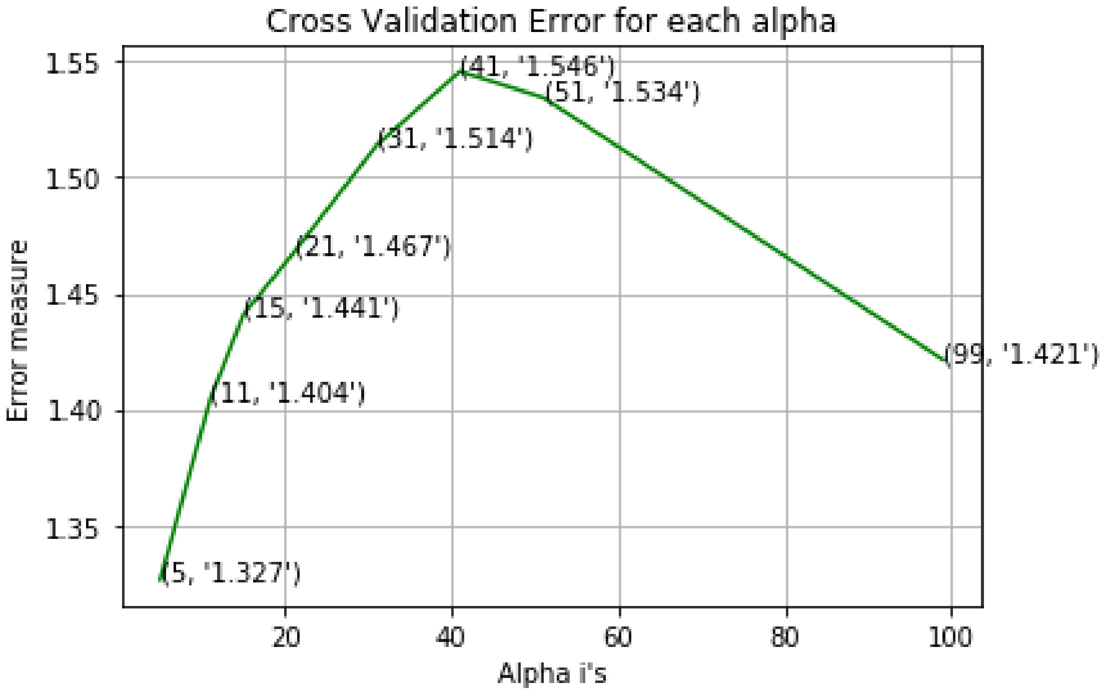
```
51 Text feature [three] present in test data point [True]
53 Text feature [similar] present in test data point [True]
54 Text feature [important] present in test data point [True]
55 Text feature [critical] present in test data point [True]
56 Text feature [respectively] present in test data point [True]
60 Text feature [amino] present in test data point [True]
61 Text feature [well] present in test data point [True]
62 Text feature [previous] present in test data point [True]
65 Text feature [form] present in test data point [True]
66 Text feature [analysis] present in test data point [True]
67 Text feature [indicating] present in test data point [True]
68 Text feature [complex] present in test data point [True]
69 Text feature [indicated] present in test data point [True]
70 Text feature [proteins] present in test data point [True]
71 Text feature [previously] present in test data point [True]
73 Text feature [addition] present in test data point [True]
75 Text feature [corresponding] present in test data point [True]
77 Text feature [even] present in test data point [True]
78 Text feature [compared] present in test data point [True]
81 Text feature [result] present in test data point [True]
82 Text feature [least] present in test data point [True]
83 Text feature [25] present in test data point [True]
84 Text feature [used] present in test data point [True]
85 Text feature [including] present in test data point [True]
87 Text feature [acids] present in test data point [True]
88 Text feature [significant] present in test data point [True]
91 Text feature [may] present in test data point [True]
92 Text feature [within] present in test data point [True]
93 Text feature [essential] present in test data point [True]
94 Text feature [observed] present in test data point [True]
95 Text feature [furthermore] present in test data point [True]
97 Text feature [terminal] present in test data point [True]
Out of the top  100  features  65 are present in query point
```

0.4.3 K Nearest Neighbour Classification

```
In [69]: alpha = [5, 11, 15, 21, 31, 41, 51, 99]
         cv_log_error_array = []
         for i in alpha:
             print("for alpha =", i)
             clf = KNeighborsClassifier(n_neighbors=i)
             clf.fit(train_vec, train_y)
             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_vec, train_y)
             sig_clf_probs = sig_clf.predict_proba(cv_vec)
             cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=
             # to avoid rounding error while multiplying probabilites we use log-probability e
```

```
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()


best_alpha = np.argmin(cv_log_error_array)
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train_vec, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_vec, train_y)

predict_y = sig_clf.predict_proba(train_vec)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_l
predict_y = sig_clf.predict_proba(test_vec)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
predict_y = sig_clf.predict_proba(cv_vec)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l
```

```
for alpha = 5
Log Loss : 1.3265398215899902
for alpha = 11
Log Loss : 1.4042284081495355
for alpha = 15
Log Loss : 1.4409212647173233
for alpha = 21
Log Loss : 1.467403544557008
for alpha = 31
Log Loss : 1.5138769837737722
for alpha = 41
Log Loss : 1.5456574333802615
for alpha = 51
Log Loss : 1.5343982678526018
for alpha = 99
Log Loss : 1.4213936169591672
```

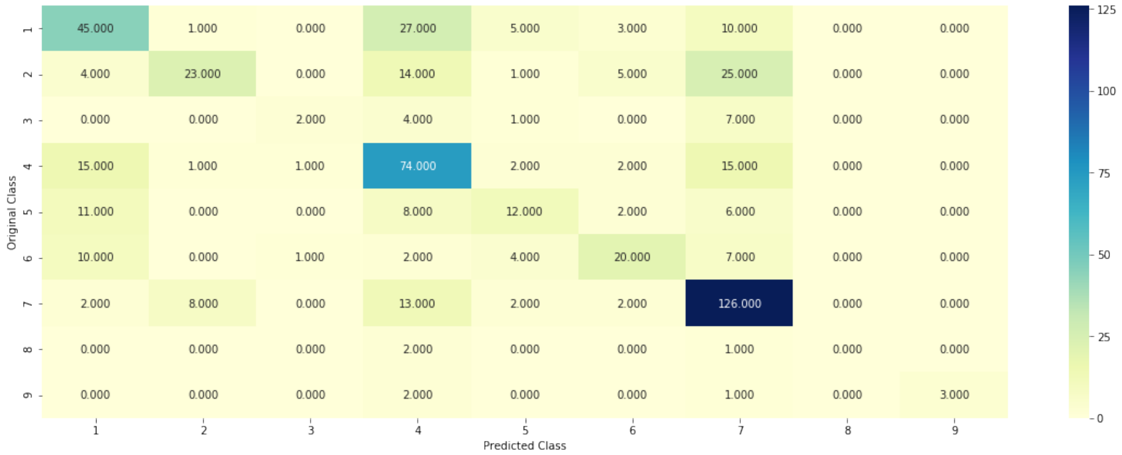


```
For values of best alpha =  5 The train log loss is: 1.020680894820197
For values of best alpha =  5 The cross validation log loss is: 1.3290953937242058
For values of best alpha =  5 The test log loss is: 1.3265398215899902
```

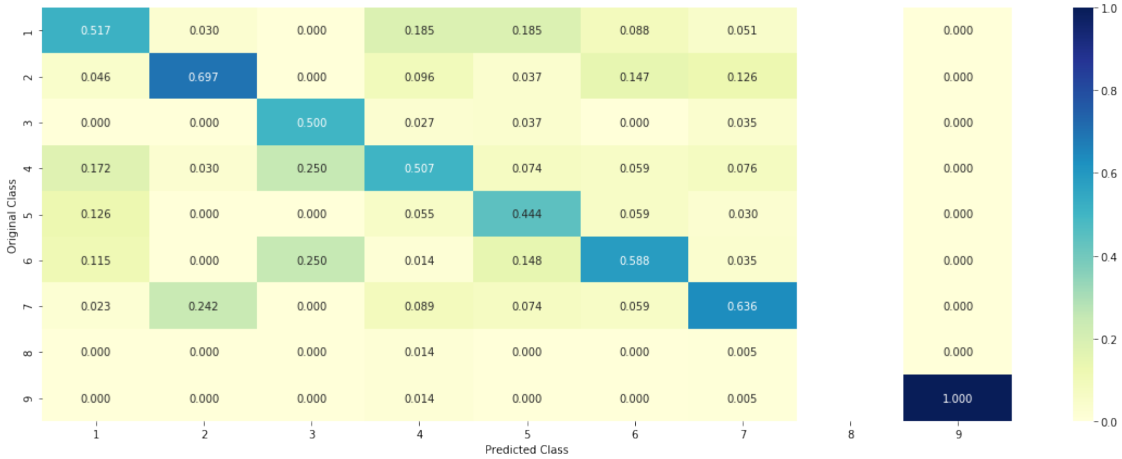
Testing the model with best hyper paramters

```
In [70]: clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
         predict_and_plot_confusion_matrix(train_vec, train_y, cv_vec, cv_y, clf)
```

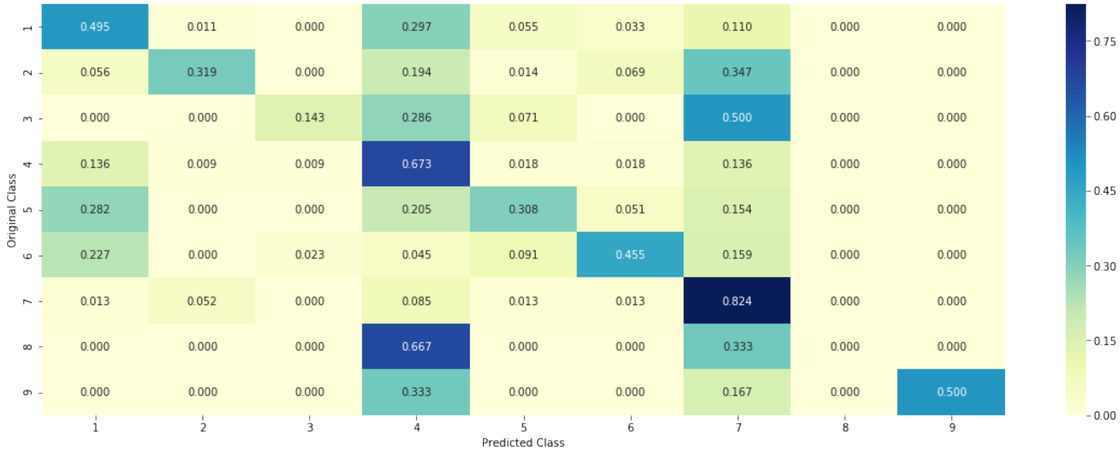
```
Log loss : 1.3265398215899902
Number of mis-classified points : 0.4266917293233083
-------------------- Confusion matrix --------------------
```



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



```
-------------------- Recall matrix (Row sum=1) --------------------
```



Feature Importance, Inorrectly classified point

```
In [77]: clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
         clf.fit(train_vec, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_vec, train_y)

         test_point_index = 1

         predicted_cls = sig_clf.predict(test_vec[0].reshape(1,-1))
         print("Predicted Class :", predicted_cls[0])
         print("Actual Class :", test_y[test_point_index])
         neighbors = clf.kneighbors(test_vec[test_point_index].reshape(1, -1), alpha[best_alpha
         print("The ",alpha[best_alpha]," nearest neighbours of the test points belongs to clas
         print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

```
Predicted Class : 4
Actual Class : 7
The  5  nearest neighbours of the test points belongs to classes [7 7 7 7 7]
Fequency of nearest points : Counter({7: 5})
```

Feature Importance, Correctly classified point

```
In [74]: clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
         clf.fit(train_vec, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_vec, train_y)

         test_point_index = 1
```

```
predicted_cls = sig_clf.predict(test_vec[test_point_index].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Actual Class :", test_y[test_point_index])
neighbors = clf.kneighbors(test_vec[test_point_index].reshape(1, -1), alpha[best_alpha
print("the k value for knn is",alpha[best_alpha],"and the nearest neighbours of the t
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

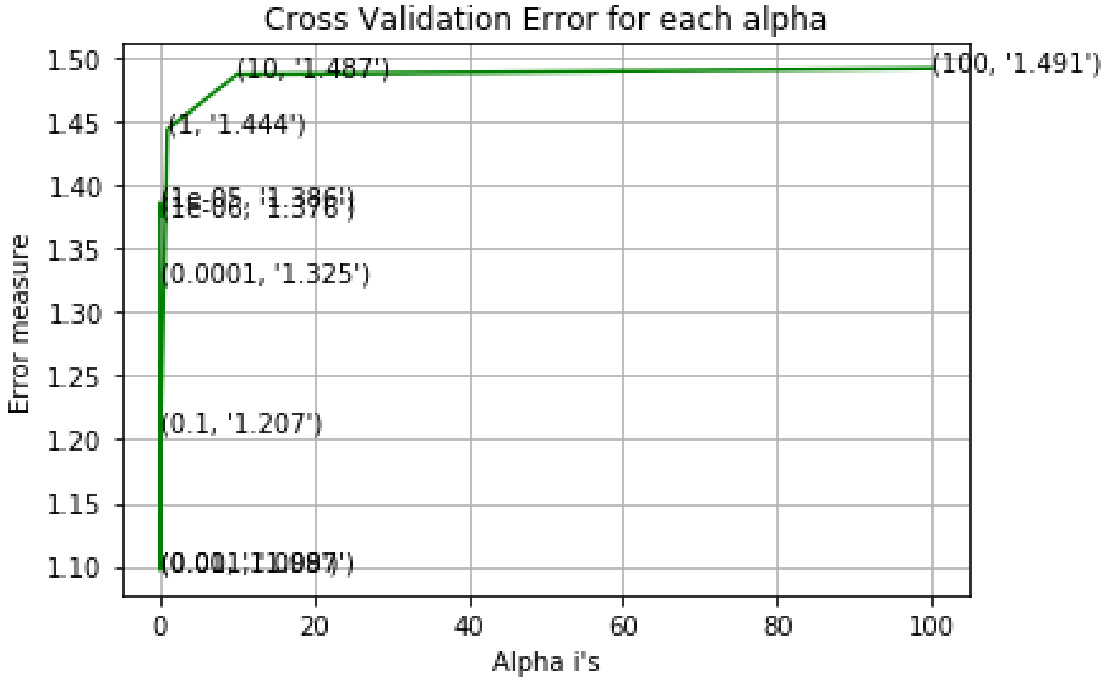
```
Predicted Class : 7
Actual Class : 7
the k value for knn is 5 and the nearest neighbours of the test points belongs to classes [7 7
Fequency of nearest points : Counter({7: 5})
```

0.4.4 Logistic Regression with class balancing

```
In [78]: alpha = [10 ** x for x in range(-6, 3)]
         cv_log_error_array = []
         for i in alpha:
             print("for alpha =", i)
             clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='log', r
             clf.fit(train_vec, train_y)
             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_vec, train_y)
             sig_clf_probs = sig_clf.predict_proba(cv_vec)
             cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=
             # to avoid rounding error while multiplying probabilites we use log-probability e
             print("Log Loss :",log_loss(cv_y, sig_clf_probs))

         fig, ax = plt.subplots()
         ax.plot(alpha, cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
             ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
         plt.show()


         best_alpha = np.argmin(cv_log_error_array)
         clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', l
         clf.fit(train_vec, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_vec, train_y)

         predict_y = sig_clf.predict_proba(train_vec)
         print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_
         predict_y = sig_clf.predict_proba(cv_vec)
```

```
        print('For values of best alpha = ', alpha[best_alpha], "The cross validation log los
        predict_y = sig_clf.predict_proba(test_vec)
        print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l
```

```
for alpha = 1e-06
Log Loss : 1.3762267471928669
for alpha = 1e-05
Log Loss : 1.3858761287675025
for alpha = 0.0001
Log Loss : 1.3251788401733469
for alpha = 0.001
Log Loss : 1.0974391839339572
for alpha = 0.01
Log Loss : 1.098482224226122
for alpha = 0.1
Log Loss : 1.206796920687988
for alpha = 1
Log Loss : 1.4435460203183215
for alpha = 10
Log Loss : 1.486851536803223
for alpha = 100
Log Loss : 1.4914874092809136
```

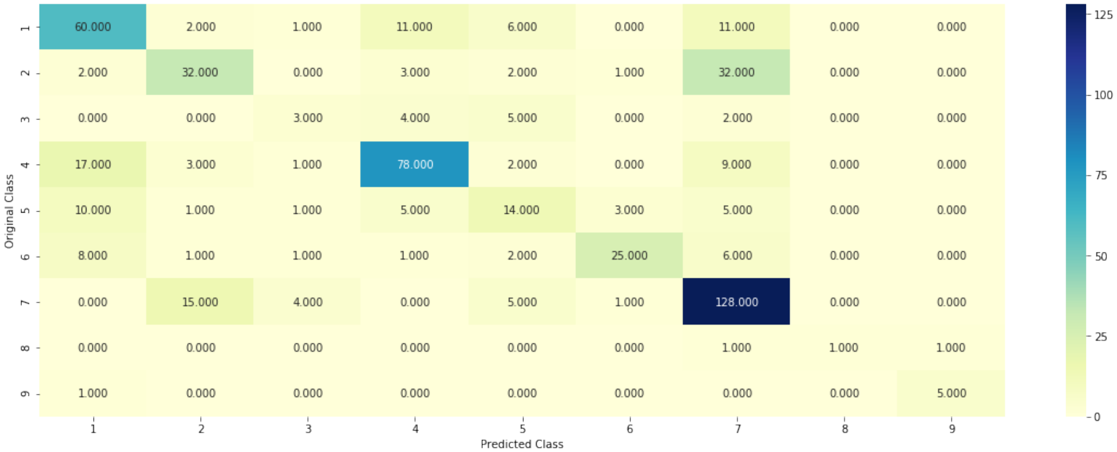


```
For values of best alpha =  0.001 The train log loss is: 0.5611355366800372
For values of best alpha =  0.001 The cross validation log loss is: 1.0974391839339572
For values of best alpha =  0.001 The test log loss is: 1.0649284801253855
```

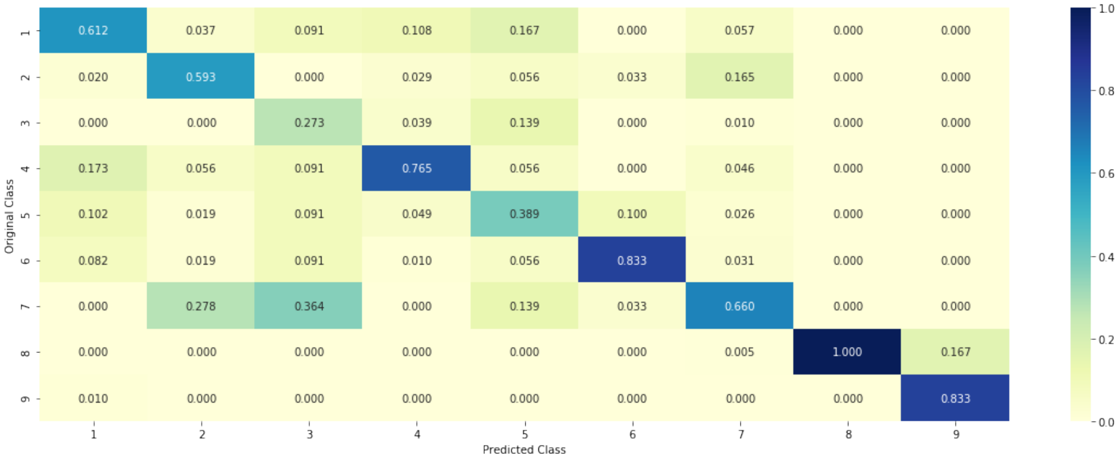
Testing the model with best hyper paramters

```
In [80]: ### clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2
         predict_and_plot_confusion_matrix(train_vec, train_y, cv_vec, cv_y, clf)
```

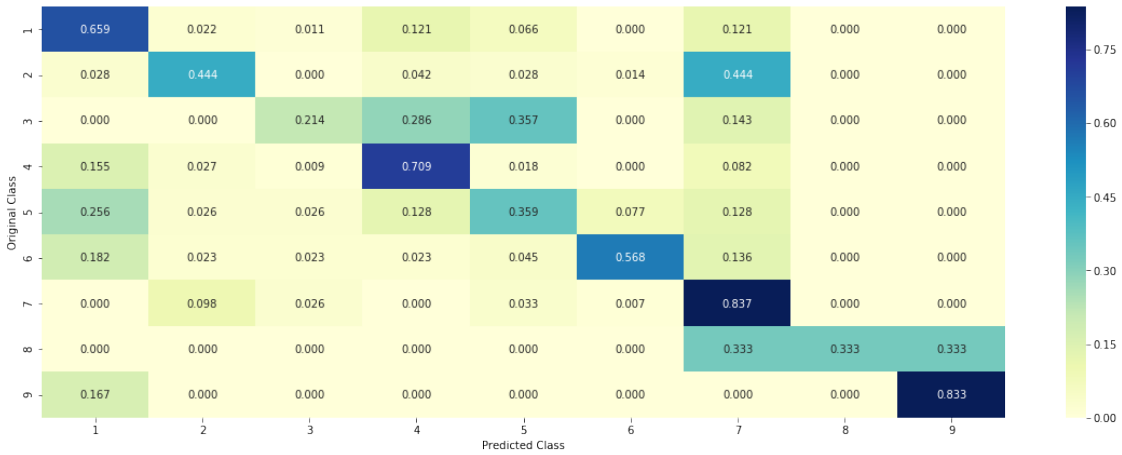
```
Log loss : 1.0974391839339572
Number of mis-classified points : 0.34962406015037595
-------------------- Confusion matrix --------------------
```



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



```
-------------------- Recall matrix (Row sum=1) --------------------
```



	1	2	3	4	5	6	7	8	9
1	0.659	0.022	0.011	0.121	0.066	0.000	0.121	0.000	0.000
2	0.028	0.444	0.000	0.042	0.028	0.014	0.444	0.000	0.000
3	0.000	0.000	0.214	0.286	0.357	0.000	0.143	0.000	0.000
4	0.155	0.027	0.009	0.709	0.018	0.000	0.082	0.000	0.000
5	0.256	0.026	0.026	0.128	0.359	0.077	0.128	0.000	0.000
6	0.182	0.023	0.023	0.023	0.045	0.568	0.136	0.000	0.000
7	0.000	0.098	0.026	0.000	0.033	0.007	0.837	0.000	0.000
8	0.000	0.000	0.000	0.000	0.000	0.000	0.333	0.333	0.333
9	0.167	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.833

Feature Importance, Correctly classified point

```
In [81]: # from tabulate import tabulate
         clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', lo
         clf.fit(train_vec,train_y)
         test_point_index = 1
         no_feature = 500
         predicted_cls = sig_clf.predict(test_vec[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names_tf(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['G
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0241 0.0467 0.0147 0.0246 0.0221 0.0141 0.8443 0.0048 0.004
Actual Class : 7
--------------------------------------------------
36 Text feature [constitutive] present in test data point [True]
65 Text feature [constitutively] present in test data point [True]
114 Text feature [activated] present in test data point [True]
158 Text feature [phosphotyrosine] present in test data point [True]
235 Text feature [activation] present in test data point [True]
371 Text feature [technology] present in test data point [True]
455 Text feature [interleukin] present in test data point [True]
488 Text feature [kinase] present in test data point [True]
Out of the top  500  features  8 are present in query point
```

Feature Importance, Incorrectly classified point

```
In [82]: test_point_index = 100
         no_feature = 500
         predicted_cls = sig_clf.predict(test_vec[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names_tf(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['G
```

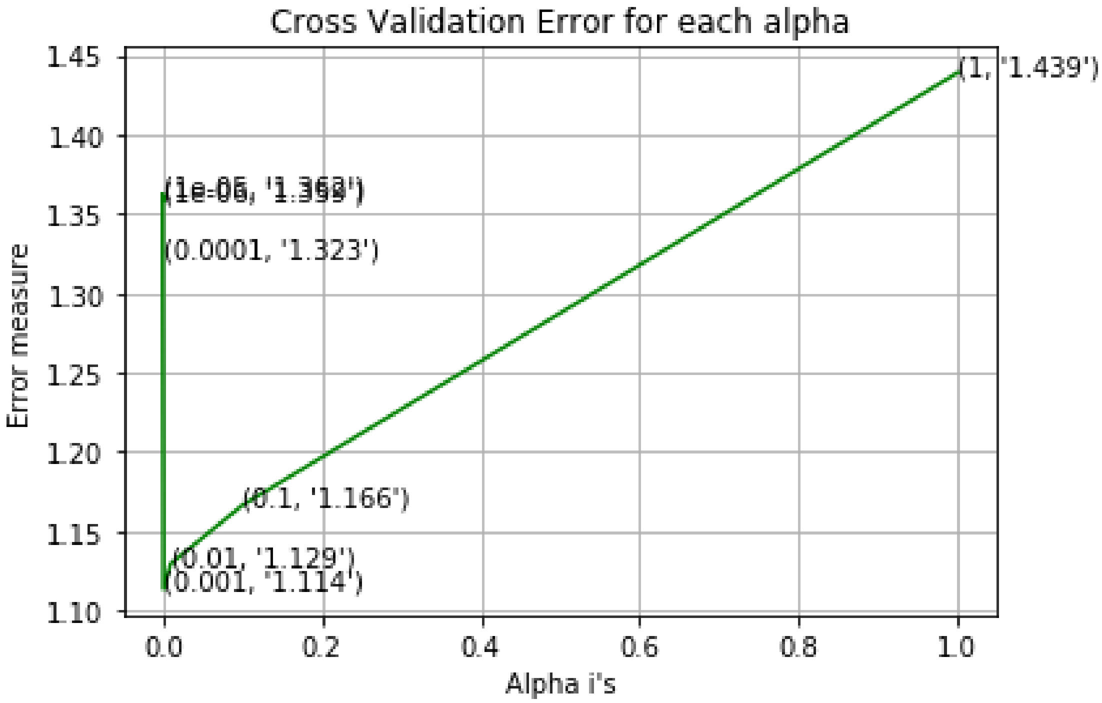
```
Predicted Class : 2
Predicted Class Probabilities: [[0.1653 0.2326 0.0324 0.1208 0.1394 0.0842 0.2039 0.0101 0.011
Actual Class : 6
--------------------------------------------------
116 Text feature [subgroup] present in test data point [True]
261 Text feature [median] present in test data point [True]
404 Text feature [formalin] present in test data point [True]
412 Text feature [therapy] present in test data point [True]
494 Text feature [ffpe] present in test data point [True]
Out of the top  500  features  5 are present in query point
```

0.4.5 Logistic Regression without class balancing

```
In [83]: alpha = [10 ** x for x in range(-6, 1)]
         cv_log_error_array = []
         for i in alpha:
             print("for alpha =", i)
             clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
             clf.fit(train_vec, train_y)
             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_vec, train_y)
             sig_clf_probs = sig_clf.predict_proba(cv_vec)
             cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=
             print("Log Loss :",log_loss(cv_y, sig_clf_probs))

         fig, ax = plt.subplots()
         ax.plot(alpha, cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
             ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
         plt.show()
```

```
    best_alpha = np.argmin(cv_log_error_array)
    clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=4
    clf.fit(train_vec, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_vec, train_y)

    predict_y = sig_clf.predict_proba(train_vec)
    print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_
    predict_y = sig_clf.predict_proba(cv_vec)
    print('For values of best alpha = ', alpha[best_alpha], "The cross validation log los
    predict_y = sig_clf.predict_proba(test_vec)
    print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l
```

```
for alpha = 1e-06
Log Loss : 1.3587304074753803
for alpha = 1e-05
Log Loss : 1.3624834639880334
for alpha = 0.0001
Log Loss : 1.3225394674388362
for alpha = 0.001
Log Loss : 1.1135641054292025
for alpha = 0.01
Log Loss : 1.1294188383338022
for alpha = 0.1
Log Loss : 1.1662444045999807
for alpha = 1
Log Loss : 1.438973960607487
```

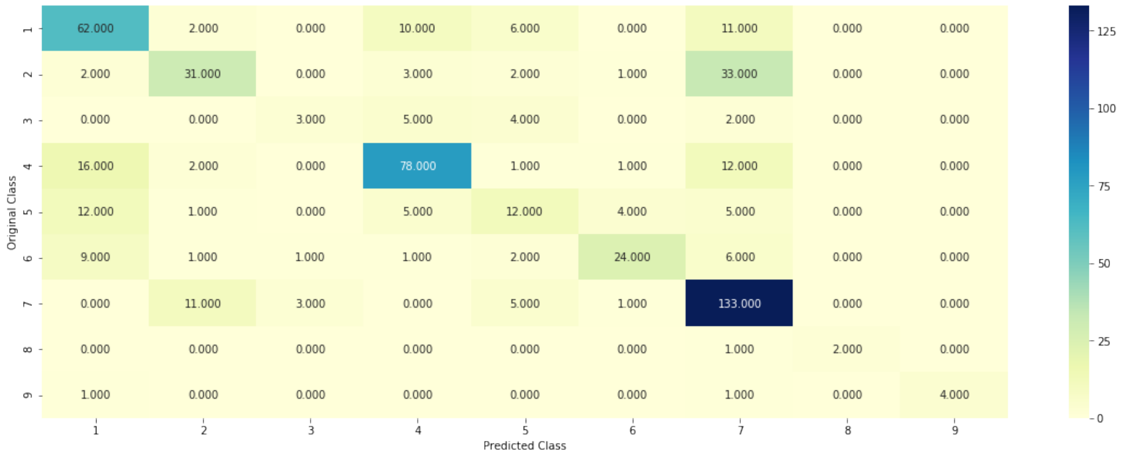


```
For values of best alpha =  0.001 The train log loss is: 0.5565790044926407
For values of best alpha =  0.001 The cross validation log loss is: 1.1135641054292025
For values of best alpha =  0.001 The test log loss is: 1.0729974789587016
```

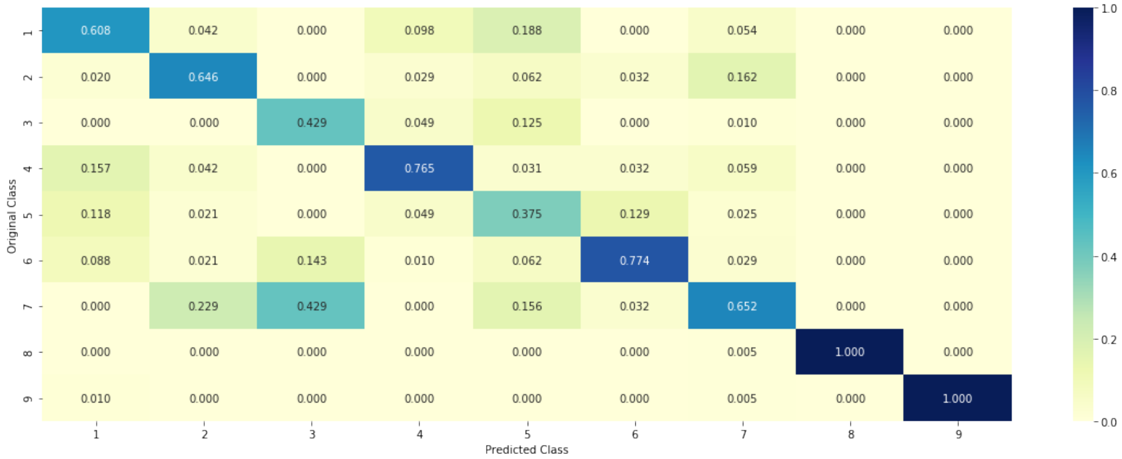
Testing the model with best hyper paramters

```
In [87]: clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=4
         predict_and_plot_confusion_matrix(train_vec, train_y, cv_vec, cv_y, clf)
```

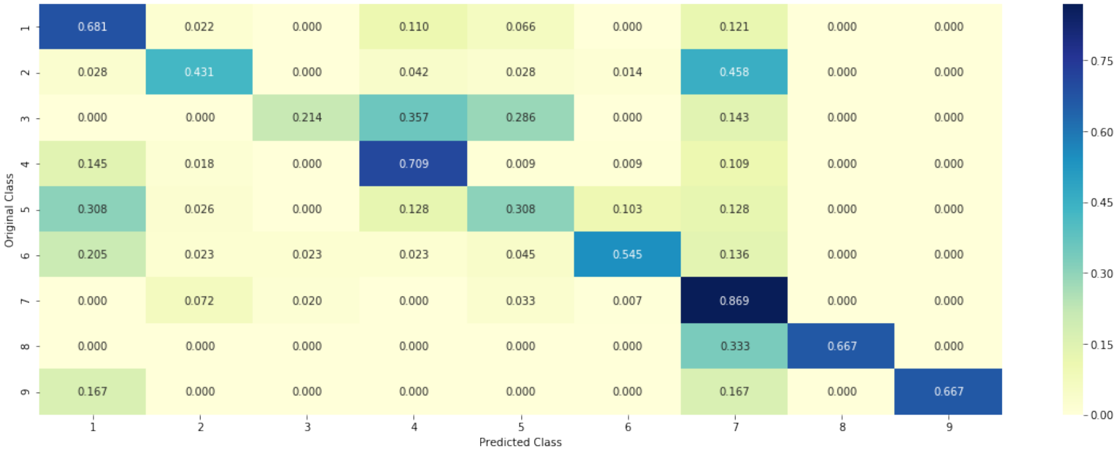
```
Log loss : 1.1135641054292025
Number of mis-classified points : 0.34398496240601506
-------------------- Confusion matrix --------------------
```



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



```
-------------------- Recall matrix (Row sum=1) --------------------
```



Feature Importance, Correctly classified point

```
In [85]: clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=4
         clf.fit(train_vec,train_y)
         test_point_index = 1
         no_feature = 500
         predicted_cls = sig_clf.predict(test_vec[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names_tf(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['G
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0292 0.0523 0.01   0.0309 0.0189 0.0136 0.8383 0.0046 0.002
Actual Class : 7
--------------------------------------------------
70 Text feature [constitutively] present in test data point [True]
101 Text feature [constitutive] present in test data point [True]
130 Text feature [activated] present in test data point [True]
200 Text feature [activation] present in test data point [True]
278 Text feature [phosphotyrosine] present in test data point [True]
299 Text feature [inhibited] present in test data point [True]
320 Text feature [technology] present in test data point [True]
376 Text feature [tyrosyl] present in test data point [True]
393 Text feature [kinase] present in test data point [True]
395 Text feature [phosphorylation] present in test data point [True]
413 Text feature [independence] present in test data point [True]
414 Text feature [ligand] present in test data point [True]
421 Text feature [py] present in test data point [True]
```

```
426 Text feature [interleukin] present in test data point [True]
439 Text feature [oncogene] present in test data point [True]
482 Text feature [expressing] present in test data point [True]
Out of the top  500  features  16 are present in query point
```

Feature Importance, Incorrectly classified point

```
In [86]: test_point_index = 100
         no_feature = 500
         predicted_cls = sig_clf.predict(test_vec[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names_tf(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Ge
```

```
Predicted Class : 2
Predicted Class Probabilities: [[0.1703 0.2399 0.0204 0.1178 0.1314 0.0821 0.223  0.0096 0.0055
Actual Class : 6
--------------------------------------------------
106 Text feature [subgroup] present in test data point [True]
268 Text feature [median] present in test data point [True]
326 Text feature [ffpe] present in test data point [True]
388 Text feature [therapy] present in test data point [True]
391 Text feature [formalin] present in test data point [True]
Out of the top  500  features  5 are present in query point
```

0.4.6 Random Forest Classifier

```
In [88]: alpha = [100,200,500,1000,2000]
         max_depth = [5, 10]
         cv_log_error_array = []
         for i in alpha:
             for j in max_depth:
                 print("for n_estimators =", i,"and max depth = ", j)
                 clf = RandomForestClassifier(n_estimators=i, criterion='gini', max_depth=j, ra
                 clf.fit(train_vec, train_y)
                 sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
                 sig_clf.fit(train_vec, train_y)
                 sig_clf_probs = sig_clf.predict_proba(cv_vec)
                 cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, e
                 print("Log Loss :",log_loss(cv_y, sig_clf_probs))

         '''fig, ax = plt.subplots()
         features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
```

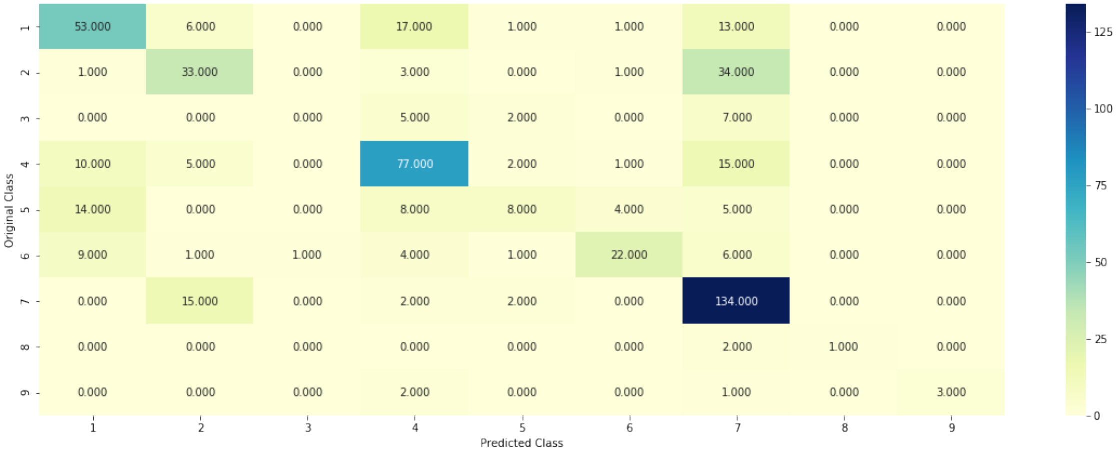
```
        ax.plot(features, cv_log_error_array,c='g')
        for i, txt in enumerate(np.round(cv_log_error_array,3)):
            ax.annotate((alpha[int(i/2)],max_depth[int(i%2)],str(txt)), (features[i],cv_log_e
        plt.grid()
        plt.title("Cross Validation Error for each alpha")
        plt.xlabel("Alpha i's")
        plt.ylabel("Error measure")
        plt.show()
        '''

        best_alpha = np.argmin(cv_log_error_array)
        clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini',
        clf.fit(train_vec, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_vec, train_y)

        predict_y = sig_clf.predict_proba(train_vec)
        print('For values of best estimator = ', alpha[int(best_alpha/2)], "The train log loss
        predict_y = sig_clf.predict_proba(cv_vec)
        print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross validati
        predict_y = sig_clf.predict_proba(test_vec)
        print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss
```

```
for n_estimators = 100 and max depth =  5
Log Loss : 1.2417309452150282
for n_estimators = 100 and max depth =  10
Log Loss : 1.1912829351753556
for n_estimators = 200 and max depth =  5
Log Loss : 1.228500684679421
for n_estimators = 200 and max depth =  10
Log Loss : 1.1812957438294787
for n_estimators = 500 and max depth =  5
Log Loss : 1.2236113739683498
for n_estimators = 500 and max depth =  10
Log Loss : 1.1763219005393661
for n_estimators = 1000 and max depth =  5
Log Loss : 1.2277077844020792
for n_estimators = 1000 and max depth =  10
Log Loss : 1.1740521033604074
for n_estimators = 2000 and max depth =  5
Log Loss : 1.2279677047180988
for n_estimators = 2000 and max depth =  10
Log Loss : 1.1721777847644939
For values of best estimator =  2000 The train log loss is: 0.6786572369508065
For values of best estimator =  2000 The cross validation log loss is: 1.1721777847644936
For values of best estimator =  2000 The test log loss is: 1.1609443840222373
```

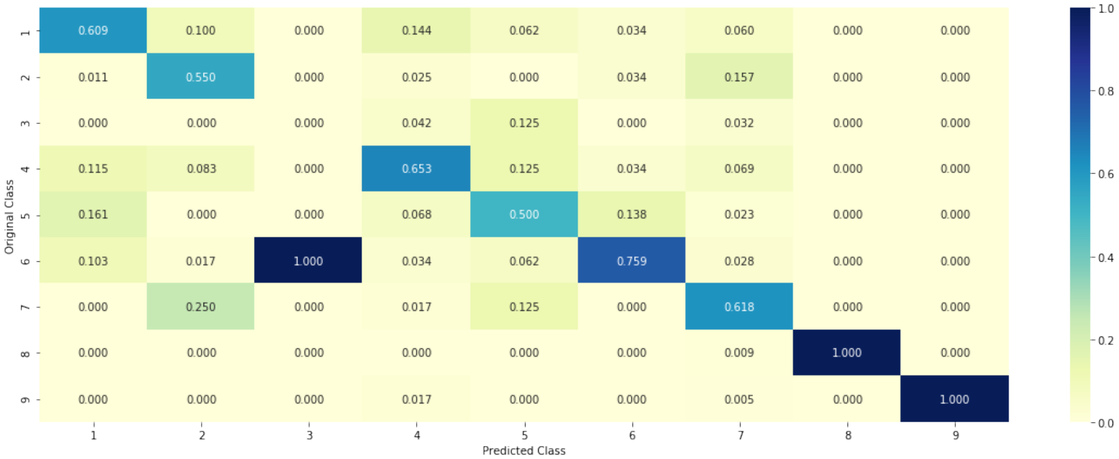
Testing the model with best hyper paramters

```
In [89]: clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini',
         predict_and_plot_confusion_matrix(train_vec, train_y,cv_vec,cv_y, clf)
```

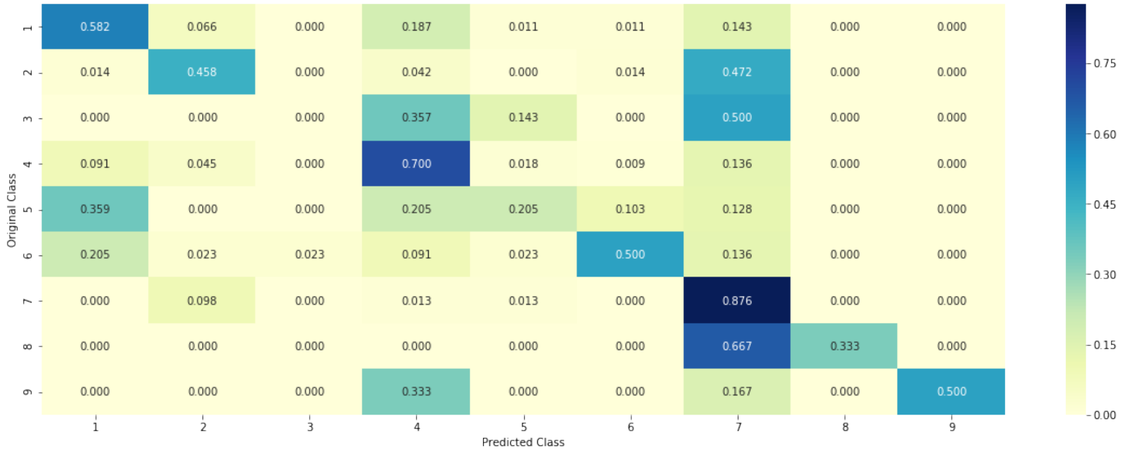
```
Log loss : 1.1721777847644936
Number of mis-classified points : 0.37781954887218044
-------------------- Confusion matrix --------------------
```



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



```
-------------------- Recall matrix (Row sum=1) --------------------
```



Feature Importance, Correctly classified point

```
In [90]: # test_point_index = 10
         clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini',
         clf.fit(train_vec, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_vec, train_y)

         test_point_index = 1
         no_feature = 100
         predicted_cls = sig_clf.predict(test_vec[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.feature_importances_)
         print("-"*50)
         get_impfeature_names_tf(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0294 0.1412 0.0157 0.0274 0.0374 0.0274 0.7136 0.0045 0.003
Actual Class : 7
--------------------------------------------------
0 Text feature [activating] present in test data point [True]
1 Text feature [kinase] present in test data point [True]
2 Text feature [activation] present in test data point [True]
3 Text feature [tyrosine] present in test data point [True]
4 Text feature [phosphorylation] present in test data point [True]
5 Text feature [treatment] present in test data point [True]
6 Text feature [inhibitor] present in test data point [True]
7 Text feature [activated] present in test data point [True]
8 Text feature [oncogenic] present in test data point [True]
```

```
9 Text feature [inhibitors] present in test data point [True]
10 Text feature [function] present in test data point [True]
11 Text feature [therapy] present in test data point [True]
12 Text feature [constitutive] present in test data point [True]
13 Text feature [growth] present in test data point [True]
15 Text feature [signaling] present in test data point [True]
16 Text feature [drug] present in test data point [True]
18 Text feature [constitutively] present in test data point [True]
22 Text feature [trials] present in test data point [True]
23 Text feature [resistance] present in test data point [True]
24 Text feature [inhibition] present in test data point [True]
25 Text feature [receptor] present in test data point [True]
28 Text feature [treated] present in test data point [True]
31 Text feature [months] present in test data point [True]
32 Text feature [clinical] present in test data point [True]
33 Text feature [protein] present in test data point [True]
37 Text feature [kinases] present in test data point [True]
40 Text feature [dose] present in test data point [True]
41 Text feature [proliferation] present in test data point [True]
45 Text feature [ic50] present in test data point [True]
47 Text feature [amplification] present in test data point [True]
48 Text feature [patients] present in test data point [True]
54 Text feature [expressing] present in test data point [True]
60 Text feature [phospho] present in test data point [True]
61 Text feature [advanced] present in test data point [True]
62 Text feature [potential] present in test data point [True]
63 Text feature [oncogene] present in test data point [True]
65 Text feature [cells] present in test data point [True]
66 Text feature [resistant] present in test data point [True]
68 Text feature [autophosphorylation] present in test data point [True]
70 Text feature [nsclc] present in test data point [True]
72 Text feature [independent] present in test data point [True]
75 Text feature [ligand] present in test data point [True]
77 Text feature [phosphorylated] present in test data point [True]
81 Text feature [patient] present in test data point [True]
82 Text feature [effective] present in test data point [True]
84 Text feature [predicted] present in test data point [True]
85 Text feature [sensitive] present in test data point [True]
88 Text feature [inhibited] present in test data point [True]
89 Text feature [active] present in test data point [True]
94 Text feature [sensitivity] present in test data point [True]
95 Text feature [response] present in test data point [True]
96 Text feature [cell] present in test data point [True]
97 Text feature [survival] present in test data point [True]
99 Text feature [tki] present in test data point [True]
Out of the top  100  features  54 are present in query point
```

Feature Importance, Incorrectly classified point

```
In [91]: test_point_index = 100
         no_feature = 100
         predicted_cls = sig_clf.predict(test_vec[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
         print("Actuall Class :", test_y[test_point_index])
         indices = np.argsort(-clf.feature_importances_)
         print("-"*50)
         get_impfeature_names_tf(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],
```

```
Predicted Class : 2
Predicted Class Probabilities: [[0.2245 0.2781 0.0249 0.1615 0.0702 0.0635 0.1603 0.0086 0.0084
Actuall Class : 6
--------------------------------------------------
1 Text feature [kinase] present in test data point [True]
3 Text feature [tyrosine] present in test data point [True]
5 Text feature [treatment] present in test data point [True]
6 Text feature [inhibitor] present in test data point [True]
9 Text feature [inhibitors] present in test data point [True]
10 Text feature [function] present in test data point [True]
11 Text feature [therapy] present in test data point [True]
13 Text feature [growth] present in test data point [True]
14 Text feature [suppressor] present in test data point [True]
25 Text feature [receptor] present in test data point [True]
26 Text feature [therapeutic] present in test data point [True]
32 Text feature [clinical] present in test data point [True]
33 Text feature [protein] present in test data point [True]
47 Text feature [amplification] present in test data point [True]
48 Text feature [patients] present in test data point [True]
49 Text feature [variants] present in test data point [True]
52 Text feature [functional] present in test data point [True]
54 Text feature [expressing] present in test data point [True]
56 Text feature [factor] present in test data point [True]
57 Text feature [harboring] present in test data point [True]
59 Text feature [stability] present in test data point [True]
62 Text feature [potential] present in test data point [True]
63 Text feature [oncogene] present in test data point [True]
65 Text feature [cells] present in test data point [True]
69 Text feature [brca1] present in test data point [True]
71 Text feature [functions] present in test data point [True]
72 Text feature [independent] present in test data point [True]
80 Text feature [variant] present in test data point [True]
81 Text feature [patient] present in test data point [True]
85 Text feature [sensitive] present in test data point [True]
90 Text feature [repair] present in test data point [True]
91 Text feature [pathway] present in test data point [True]
94 Text feature [sensitivity] present in test data point [True]
```

```
95 Text feature [response] present in test data point [True]
96 Text feature [cell] present in test data point [True]
97 Text feature [survival] present in test data point [True]
Out of the top  100  features  36 are present in query point
```

0.4.7 Stack the models

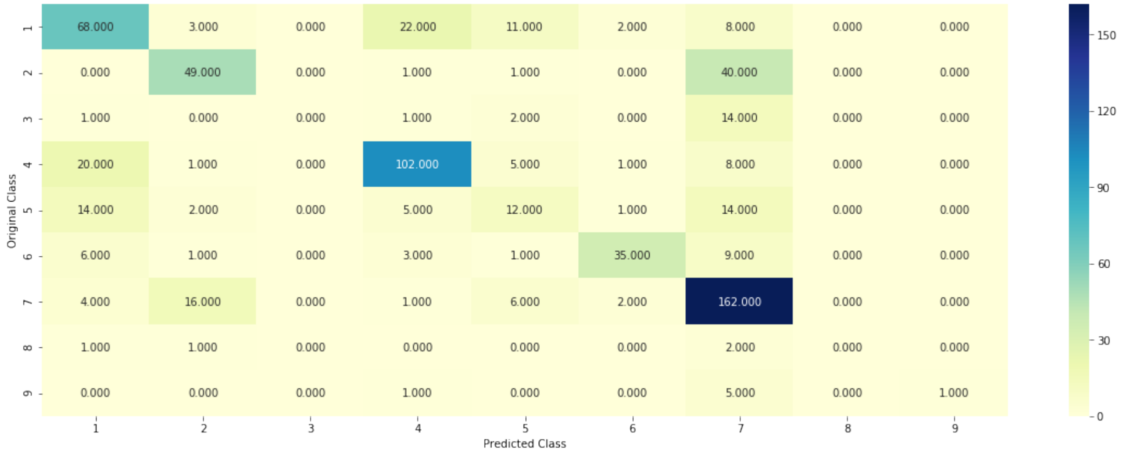
```
In [92]: clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class_weight='balanced', r
         clf1.fit(train_vec, train_y)
         sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")

         clf2 = SGDClassifier(alpha=1, penalty='l2', loss='hinge', class_weight='balanced', ran
         clf2.fit(train_vec, train_y)
         sig_clf2 = CalibratedClassifierCV(clf2, method="sigmoid")


         clf3 = MultinomialNB(alpha=0.001)
         clf3.fit(train_vec, train_y)
         sig_clf3 = CalibratedClassifierCV(clf3, method="sigmoid")

         sig_clf1.fit(train_vec, train_y)
         print("Logistic Regression :  Log Loss: %0.2f" % (log_loss(cv_y, sig_clf1.predict_prob
         sig_clf2.fit(train_vec, train_y)
         print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf2.predict_p
         sig_clf3.fit(train_vec, train_y)
         print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba(cv_vec
         print("-"*50)
         alpha = [0.0001,0.001,0.01,0.1,1,10]
         best_alpha = 999
         for i in alpha:
             lr = LogisticRegression(C=i)
             sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classi
             sclf.fit(train_vec, train_y)
             print("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" % (i, log_
             log_error =log_loss(cv_y, sclf.predict_proba(cv_vec))
             if best_alpha > log_error:
                 best_alpha = log_error
```

```
Logistic Regression :  Log Loss: 1.11
Support vector machines : Log Loss: 1.49
Naive Bayes : Log Loss: 1.27
--------------------------------------------------
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 2.178
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 2.038
Stacking Classifer : for the value of alpha: 0.010000 Log Loss: 1.516
Stacking Classifer : for the value of alpha: 0.100000 Log Loss: 1.130
Stacking Classifer : for the value of alpha: 1.000000 Log Loss: 1.218
Stacking Classifer : for the value of alpha: 10.000000 Log Loss: 1.464
```

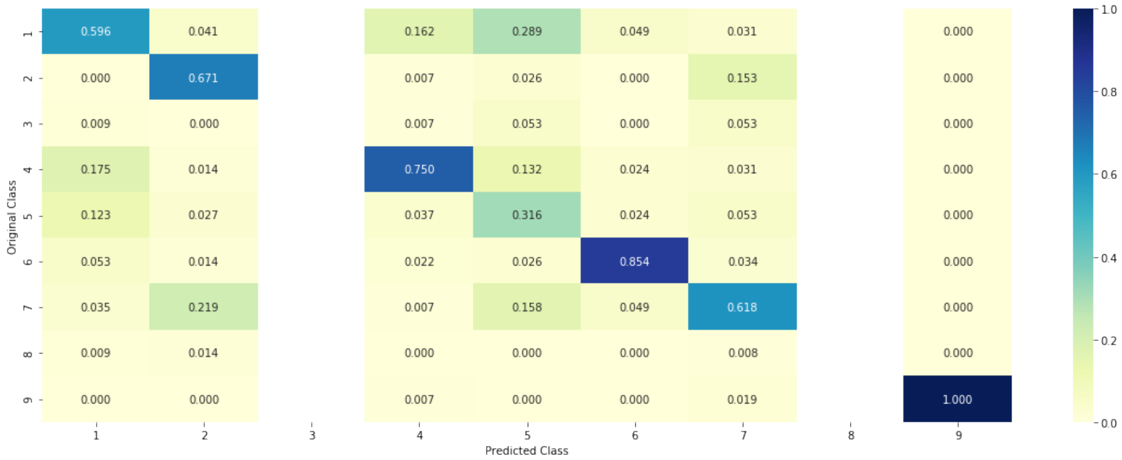
Testing the model with best hyper paramters

```
In [93]: lr = LogisticRegression(C=0.1)
         sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier
         sclf.fit(train_vec, train_y)

         log_error = log_loss(train_y, sclf.predict_proba(train_vec))
         print("Log loss (train) on the stacking classifier :",log_error)

         log_error = log_loss(cv_y, sclf.predict_proba(cv_vec))
         print("Log loss (CV) on the stacking classifier :",log_error)

         log_error = log_loss(test_y, sclf.predict_proba(test_vec))
         print("Log loss (test) on the stacking classifier :",log_error)

         print("Number of missclassified point :", np.count_nonzero((sclf.predict(test_vec)- te
         plot_confusion_matrix(test_y=test_y, predict_y=sclf.predict(test_vec))
```

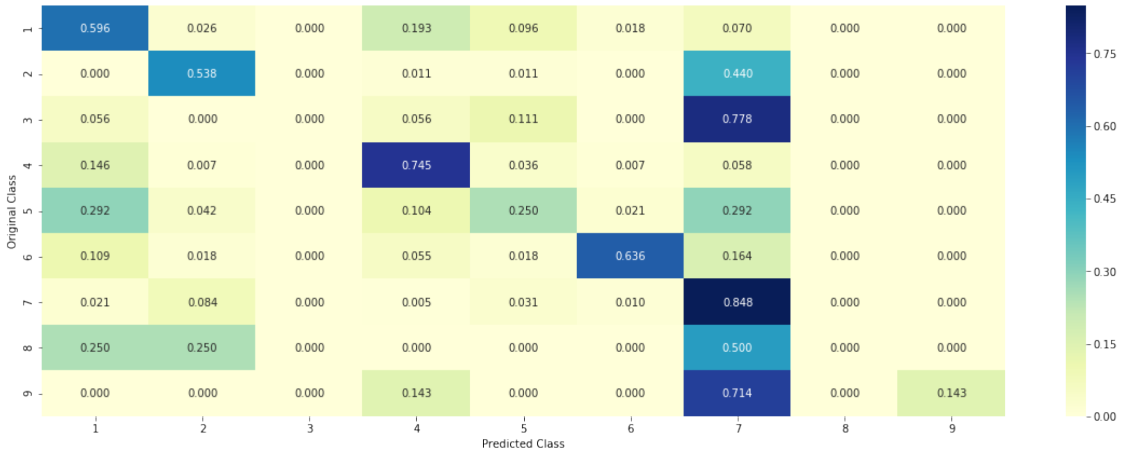
```
Log loss (train) on the stacking classifier : 0.6328410190333948
Log loss (CV) on the stacking classifier : 1.1296450689631101
Log loss (test) on the stacking classifier : 1.1091185225239562
Number of missclassified point : 0.3548872180451128
-------------------- Confusion matrix --------------------
```



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



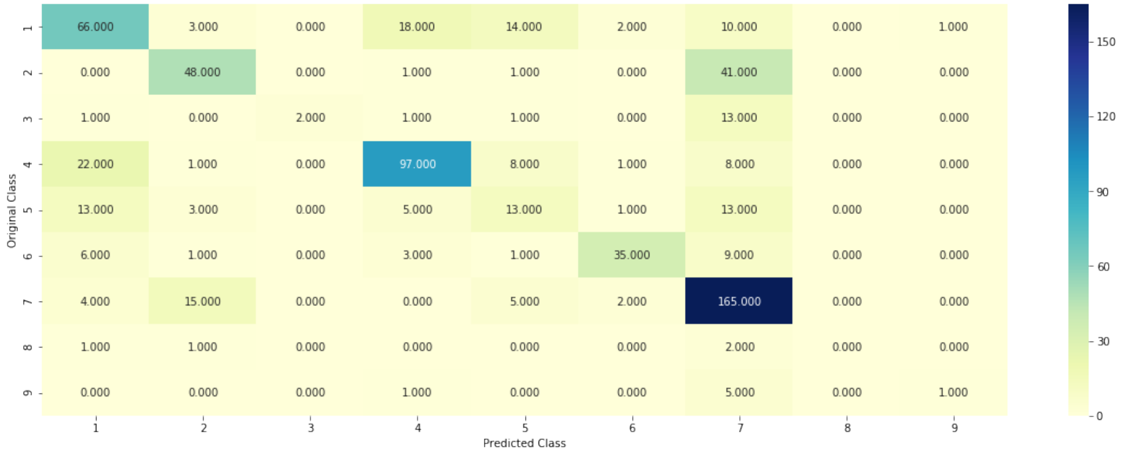
```
-------------------- Recall matrix (Row sum=1) --------------------
```



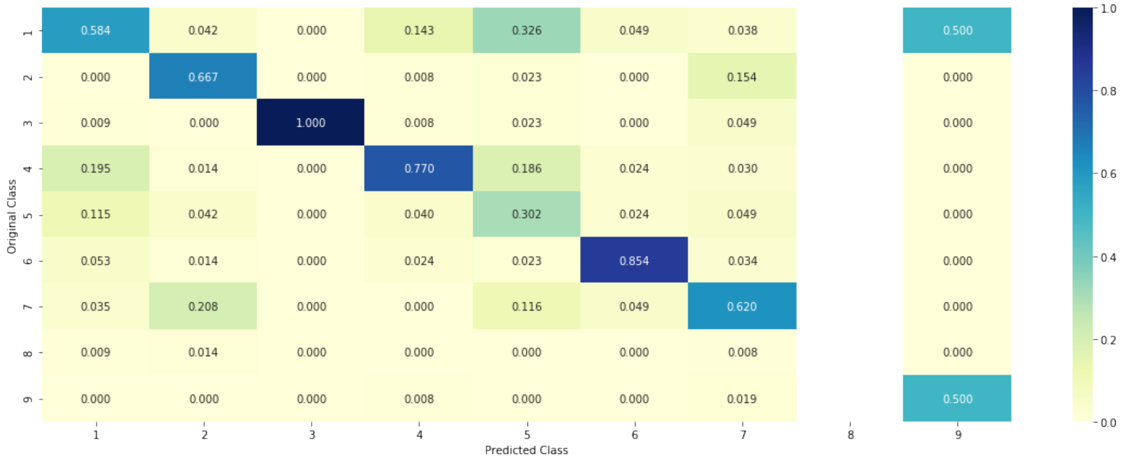
0.4.8 Maximum Voting classifier

```
In [94]: #Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassi
         from sklearn.ensemble import VotingClassifier
         vclf = VotingClassifier(estimators=[('lr', sig_clf1), ('svc', sig_clf2), ('rf', sig_cl
         vclf.fit(train_vec, train_y)
         print("Log loss (train) on the VotingClassifier :", log_loss(train_y, vclf.predict_pro
         print("Log loss (CV) on the VotingClassifier :", log_loss(cv_y, vclf.predict_proba(cv_
         print("Log loss (test) on the VotingClassifier :", log_loss(test_y, vclf.predict_proba
         print("Number of missclassified point :", np.count_nonzero((vclf.predict(test_vec)- te
         plot_confusion_matrix(test_y=test_y, predict_y=vclf.predict(test_vec))
```

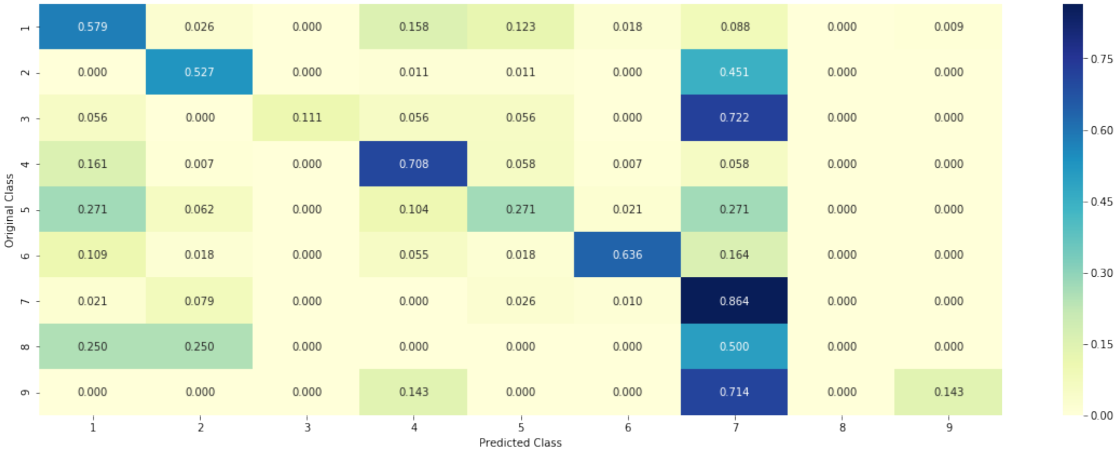
```
Log loss (train) on the VotingClassifier : 0.8565659723221687
Log loss (CV) on the VotingClassifier : 1.1576533848750443
Log loss (test) on the VotingClassifier : 1.1643755127972553
Number of missclassified point : 0.35789473684210527
-------------------- Confusion matrix --------------------
```



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



```
-------------------- Recall matrix (Row sum=1) --------------------
```



0.5 Instead of using all the words in the dataset, use only the top 1000 words based of tf-idf values

```
In [15]: text_vectorizer.idf_.shape

Out[15]: (126099,)

In [16]: train_text_feature.shape

Out[16]: (2124, 126099)

In [17]: df=pd.DataFrame(text_vectorizer.get_feature_names())

In [18]: mean_tf=np.mean(train_text_feature,axis=0)
         mean_tf

Out[18]: matrix([[0.00410664, 0.00943086, 0.00065508, ..., 0.00047081, 0.00047081,
                  0.00047081]])

In [19]: x=np.array(mean_tf)[0].tolist()

In [20]: important_feat=[]
         important_feat=np.argsort((x))[::-1]
         important_feat=important_feat[:1000]
         important_feat.shape

Out[20]: (1000,)

In [21]: np.argmax(mean_tf)

Out[21]: 19795

In [22]: np.max(mean_tf)
```

```
Out[22]: 0.019041245324341777
```

```
In [23]: imp_feat=[]
         for index in important_feat:
             imp_feat.append(df.iloc[index])
```

```
In [24]: x=np.array(imp_feat)
         feature=[]
         for i in x:
             for j in i:
                 feature.append(j)
```

```
In [25]: text_vectorizer=TfidfVectorizer()
         text_vectorizer.fit(feature)
         train=text_vectorizer.transform(train_df['TEXT'])
         test=text_vectorizer.transform(test_df['TEXT'])
         cv=text_vectorizer.transform(cv_df['TEXT'])
```

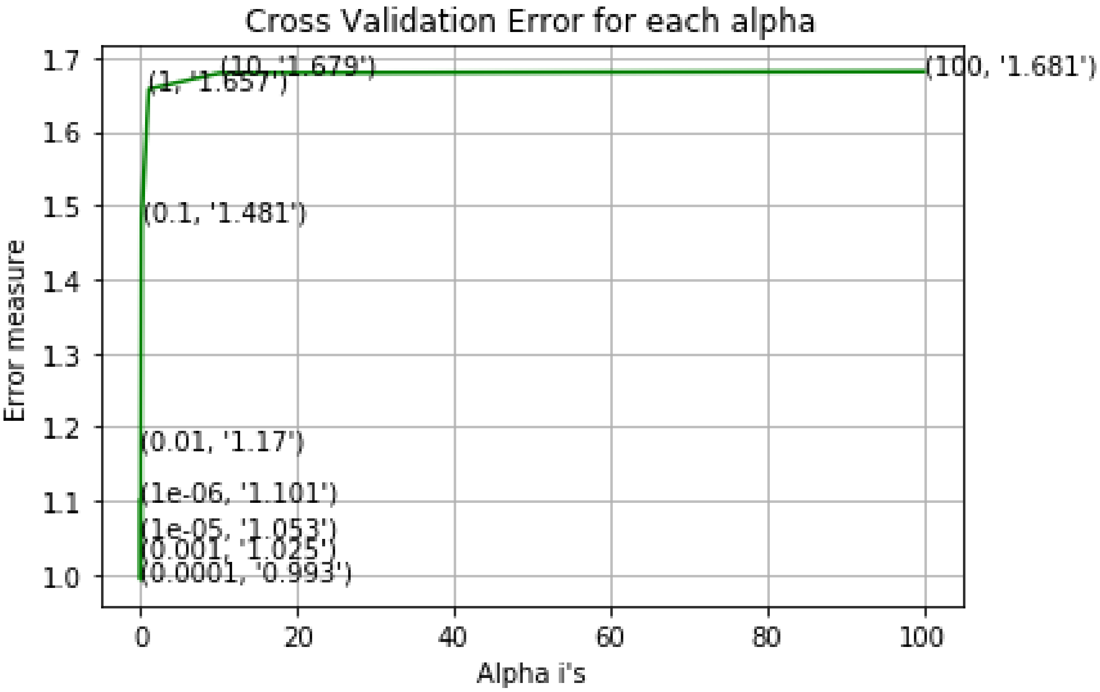
```
In [26]: train_vec = hstack((train_gene_feature_onehotCoding,train_variation_feature_onehotCodi
         test_vec = hstack((test_gene_feature_onehotCoding,test_variation_feature_onehotCoding
         cv_vec = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehotCoding,cv))
```

0.5.1 Logistic Regression with class Balance

```
In [132]: alpha = [10 ** x for x in range(-6, 3)]
          cv_log_error_array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='log', r
              clf.fit(train_vec, train_y)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(train_vec, train_y)
              sig_clf_probs = sig_clf.predict_proba(cv_vec)
              cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=
              # to avoid rounding error while multiplying probabilites we use log-probability
              print("Log Loss :",log_loss(cv_y, sig_clf_probs))

          fig, ax = plt.subplots()
          ax.plot(alpha, cv_log_error_array,c='g')
          for i, txt in enumerate(np.round(cv_log_error_array,3)):
              ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()


          best_alpha = np.argmin(cv_log_error_array)
```

```
        clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', l
        clf.fit(train_vec, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_vec, train_y)

        predict_y = sig_clf.predict_proba(train_vec)
        print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_
        predict_y = sig_clf.predict_proba(cv_vec)
        print('For values of best alpha = ', alpha[best_alpha], "The cross validation log los
        predict_y = sig_clf.predict_proba(test_vec)
        print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l
```

```
for alpha = 1e-06
Log Loss : 1.1011976653190054
for alpha = 1e-05
Log Loss : 1.0525242861483708
for alpha = 0.0001
Log Loss : 0.9932250639803677
for alpha = 0.001
Log Loss : 1.0253601459328905
for alpha = 0.01
Log Loss : 1.1704809031082442
for alpha = 0.1
Log Loss : 1.4806280813212045
for alpha = 1
Log Loss : 1.6569474163813263
for alpha = 10
Log Loss : 1.6786255997965651
for alpha = 100
Log Loss : 1.680908657292085
```

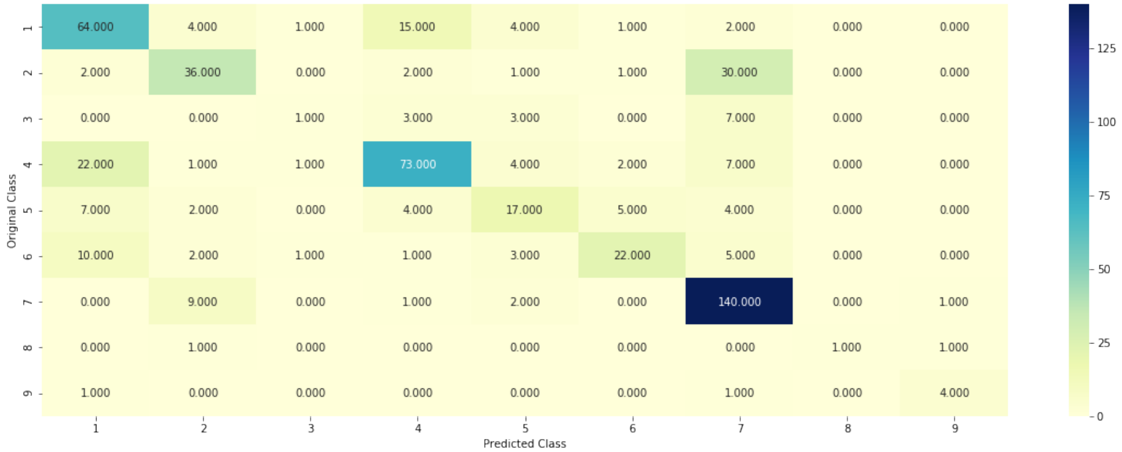


```
For values of best alpha =  0.0001 The train log loss is: 0.4627039169136912
For values of best alpha =  0.0001 The cross validation log loss is: 0.9932250639803677
For values of best alpha =  0.0001 The test log loss is: 1.0185008365416044
```

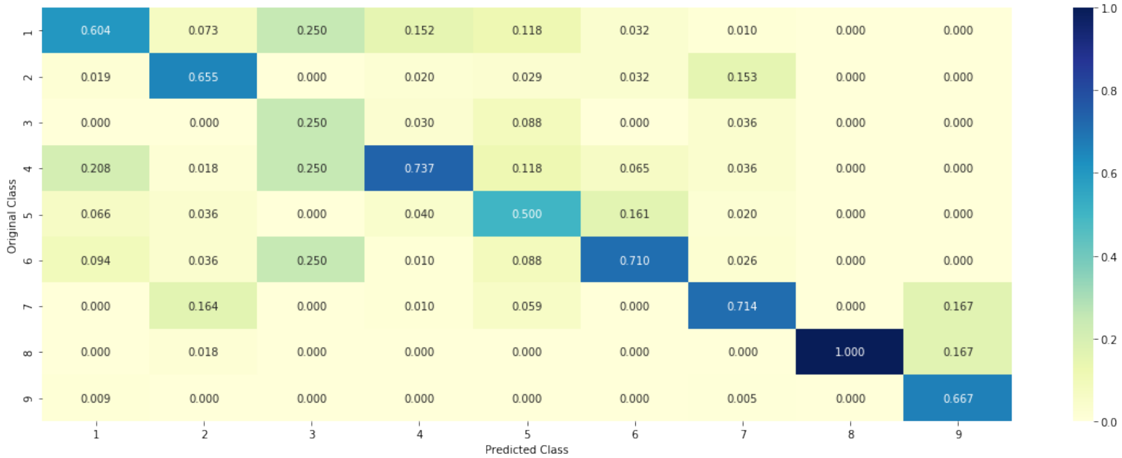
Testing the model with best hyper paramters

```
In [133]: clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', l
          predict_and_plot_confusion_matrix(train_vec, train_y, cv_vec, cv_y, clf)
```

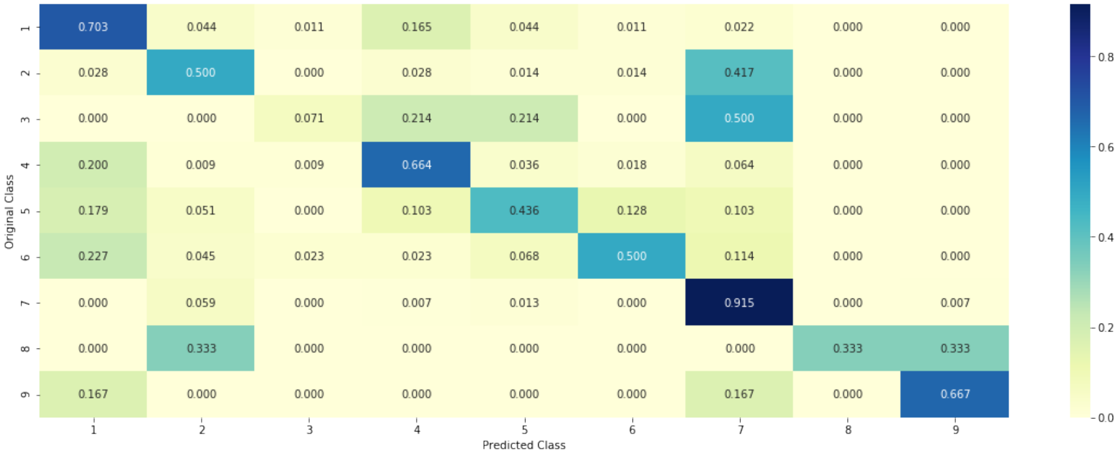
```
Log loss : 0.9932250639803677
Number of mis-classified points : 0.32706766917293234
-------------------- Confusion matrix --------------------
```



-------------------- Precision matrix (Columm Sum=1) --------------------



-------------------- Recall matrix (Row sum=1) --------------------



```
In [113]: text_vectorizer
```

```
Out[113]: (2124, 1000)
```

```
In [137]: test_vec=test_vec.tocsr()
```

```
In [27]: #Feature importance for tfidf with 1000 features
         def get_impfeature_names_tf_imp(indices, text, gene, var, no_features):
             gene_count_vec = CountVectorizer()
             var_count_vec = CountVectorizer()


             gene_vec = gene_count_vec.fit(train_df['Gene'])
             var_vec  = var_count_vec.fit(train_df['Variation'])


             fea1_len = len(gene_vec.get_feature_names())
             fea2_len = len(var_count_vec.get_feature_names())

             word_present = 0
             for i,v in enumerate(indices):
                 if (v < fea1_len):
                     word = gene_vec.get_feature_names()[v]
                     yes_no = True if word == gene else False
                     if yes_no:
                         word_present += 1
                         print(i, "Gene feature [{}] present in test data point [{}]".format(wo
                 elif (v < fea1_len+fea2_len):
                     word = var_vec.get_feature_names()[v-(fea1_len)]
                     yes_no = True if word == var else False
                     if yes_no:
                         word_present += 1
```

```
                print(i, "variation feature [{}] present in test data point [{}]".form
        else:
            word = text_vectorizer.get_feature_names()[v-(fea1_len+fea2_len)]
            yes_no = True if word in text.split() else False
            if yes_no:
                word_present += 1
                print(i, "Text feature [{}] present in test data point [{}]".format(wo

    print("Out of the top ",no_features," features ", word_present, "are present in qu
```

Feature Importance, Correctly classified point

```
In [139]: # from tabulate import tabulate
          clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', l
          clf.fit(train_vec,train_y)
          test_point_index = 1
          no_feature = 500
          predicted_cls = sig_clf.predict(test_vec[test_point_index])
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names_tf_imp(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0204 0.1397 0.0162 0.0211 0.0532 0.0178 0.7217 0.0065 0.0034
Actual Class : 7
--------------------------------------------------
0 Text feature [activation] present in test data point [True]
17 Text feature [mutant] present in test data point [True]
18 Text feature [oncogenic] present in test data point [True]
20 Text feature [high] present in test data point [True]
21 Text feature [cells] present in test data point [True]
22 Text feature [tyrosine] present in test data point [True]
26 Text feature [cancers] present in test data point [True]
28 Text feature [signaling] present in test data point [True]
58 Text feature [fig] present in test data point [True]
65 Text feature [12] present in test data point [True]
71 Text feature [increased] present in test data point [True]
78 Text feature [fold] present in test data point [True]
90 Text feature [proliferation] present in test data point [True]
93 Text feature [per] present in test data point [True]
98 Text feature [also] present in test data point [True]
113 Text feature [previously] present in test data point [True]
135 Text feature [activated] present in test data point [True]
149 Text feature [mutants] present in test data point [True]
158 Text feature [total] present in test data point [True]
```

```
163 Text feature [wt] present in test data point [True]
219 Text feature [inhibitor] present in test data point [True]
224 Text feature [genomic] present in test data point [True]
255 Text feature [expressing] present in test data point [True]
261 Text feature [common] present in test data point [True]
285 Text feature [positive] present in test data point [True]
288 Text feature [presence] present in test data point [True]
292 Text feature [obtained] present in test data point [True]
306 Text feature [reported] present in test data point [True]
317 Text feature [found] present in test data point [True]
325 Text feature [two] present in test data point [True]
345 Text feature [kinase] present in test data point [True]
378 Text feature [10] present in test data point [True]
388 Text feature [14] present in test data point [True]
390 Text feature [cdna] present in test data point [True]
394 Text feature [could] present in test data point [True]
397 Text feature [survival] present in test data point [True]
400 Text feature [tissue] present in test data point [True]
404 Text feature [inhibited] present in test data point [True]
406 Text feature [tumor] present in test data point [True]
429 Text feature [000] present in test data point [True]
434 Text feature [patients] present in test data point [True]
452 Text feature [constitutively] present in test data point [True]
465 Text feature [18] present in test data point [True]
483 Text feature [alterations] present in test data point [True]
491 Text feature [deletion] present in test data point [True]
496 Text feature [50] present in test data point [True]
498 Text feature [approximately] present in test data point [True]
Out of the top  500  features  47 are present in query point
```

Feature Importance, Incorrectly classified point

```
In [142]: test_point_index = 300
          no_feature = 500
          predicted_cls = sig_clf.predict(test_vec[test_point_index])
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names_tf_imp(indices[0], test_df['TEXT'].iloc[test_point_index],test_c
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0321 0.1555 0.0147 0.0322 0.0776 0.0115 0.6683 0.005  0.003
Actual Class : 2
--------------------------------------------------
0 Text feature [activation] present in test data point [True]
```

```
12 Text feature [somatic] present in test data point [True]
13 Text feature [downstream] present in test data point [True]
17 Text feature [mutant] present in test data point [True]
20 Text feature [high] present in test data point [True]
21 Text feature [cells] present in test data point [True]
22 Text feature [tyrosine] present in test data point [True]
28 Text feature [signaling] present in test data point [True]
58 Text feature [fig] present in test data point [True]
65 Text feature [12] present in test data point [True]
71 Text feature [increased] present in test data point [True]
78 Text feature [fold] present in test data point [True]
90 Text feature [proliferation] present in test data point [True]
98 Text feature [also] present in test data point [True]
99 Text feature [pathways] present in test data point [True]
113 Text feature [previously] present in test data point [True]
121 Text feature [factor] present in test data point [True]
135 Text feature [activated] present in test data point [True]
149 Text feature [mutants] present in test data point [True]
158 Text feature [total] present in test data point [True]
163 Text feature [wt] present in test data point [True]
182 Text feature [levels] present in test data point [True]
189 Text feature [position] present in test data point [True]
224 Text feature [genomic] present in test data point [True]
255 Text feature [expressing] present in test data point [True]
261 Text feature [common] present in test data point [True]
287 Text feature [2a] present in test data point [True]
288 Text feature [presence] present in test data point [True]
292 Text feature [obtained] present in test data point [True]
295 Text feature [transcription] present in test data point [True]
306 Text feature [reported] present in test data point [True]
312 Text feature [tissues] present in test data point [True]
317 Text feature [found] present in test data point [True]
325 Text feature [two] present in test data point [True]
345 Text feature [kinase] present in test data point [True]
378 Text feature [10] present in test data point [True]
388 Text feature [14] present in test data point [True]
390 Text feature [cdna] present in test data point [True]
394 Text feature [could] present in test data point [True]
397 Text feature [survival] present in test data point [True]
400 Text feature [tissue] present in test data point [True]
404 Text feature [inhibited] present in test data point [True]
406 Text feature [tumor] present in test data point [True]
425 Text feature [coding] present in test data point [True]
434 Text feature [patients] present in test data point [True]
445 Text feature [factors] present in test data point [True]
448 Text feature [activate] present in test data point [True]
452 Text feature [constitutively] present in test data point [True]
463 Text feature [without] present in test data point [True]
```

```
465 Text feature [18] present in test data point [True]
470 Text feature [higher] present in test data point [True]
479 Text feature [product] present in test data point [True]
483 Text feature [alterations] present in test data point [True]
493 Text feature [transformation] present in test data point [True]
496 Text feature [50] present in test data point [True]
498 Text feature [approximately] present in test data point [True]
Out of the top  500  features  56 are present in query point
```

```
In [28]: test_vec=test_vec.tocsr()
```

1 Apply Logistic regression with CountVectorizer Features, including both unigrams and bigrams

```
In [143]: text_vectorizer = CountVectorizer(min_df=3,ngram_range=(1,2))
          train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
          # getting all the feature names (words)
          train_text_features= text_vectorizer.get_feature_names()


          print("Total number of unique words in train data :", len(train_text_features))
```

```
Total number of unique words in train data : 796397
```

```
In [144]: # don't forget to normalize every feature
          train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding, axis=0)

          # we use the same vectorizer that was trained on train data
          test_text_feature_onehotCoding = text_vectorizer.transform(test_df['TEXT'])
          # don't forget to normalize every feature
          test_text_feature_onehotCoding = normalize(test_text_feature_onehotCoding, axis=0)

          # we use the same vectorizer that was trained on train data
          cv_text_feature_onehotCoding = text_vectorizer.transform(cv_df['TEXT'])
          # don't forget to normalize every feature
          cv_text_feature_onehotCoding = normalize(cv_text_feature_onehotCoding, axis=0)
```

```
In [145]: train_vec = hstack((train_gene_feature_onehotCoding,train_variation_feature_onehotCo
          test_vec = hstack((test_gene_feature_onehotCoding,test_variation_feature_onehotCodin
          cv_vec = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehotCoding,cv_t
```

1.0.1 Logistic regression

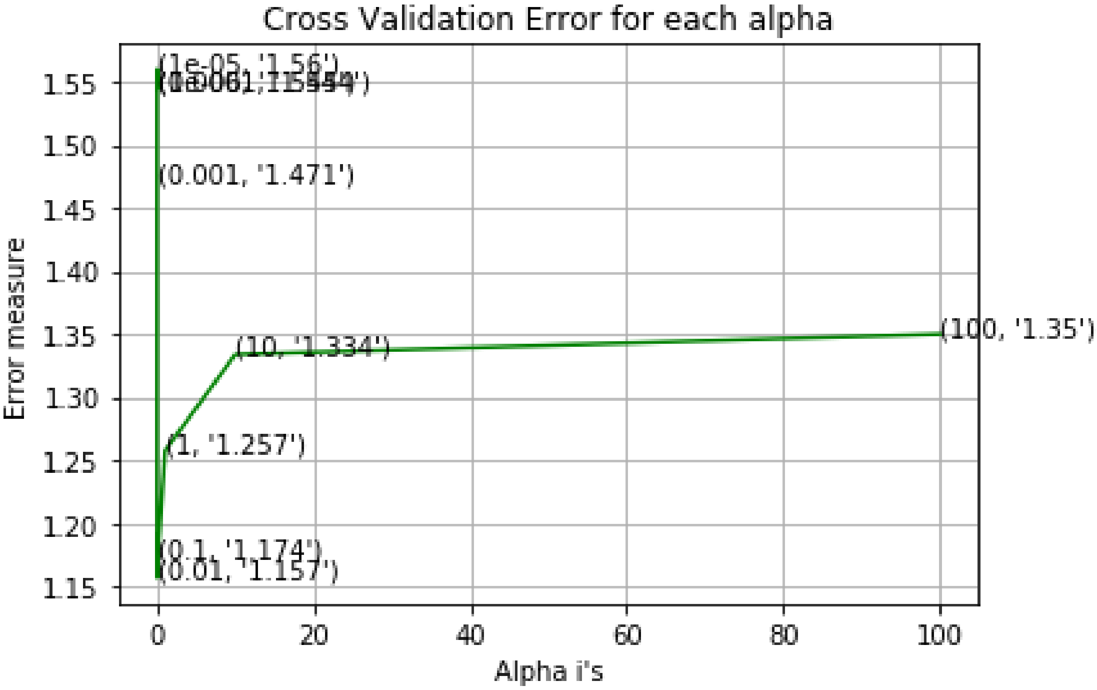
```
In [12]: #feature importance for 2gram BoW
         def get_impfeature_names_bow_2gram(indices, text, gene, var, no_features):
             gene_count_vec = CountVectorizer()
```

```
    var_count_vec = CountVectorizer()
    text_count_vec = CountVectorizer(min_df=3,ngram_range=(1,2))

    gene_vec = gene_count_vec.fit(train_df['Gene'])
    var_vec  = var_count_vec.fit(train_df['Variation'])
    text_vec = text_count_vec.fit(train_df['TEXT'])

    fea1_len = len(gene_vec.get_feature_names())
    fea2_len = len(var_count_vec.get_feature_names())

    word_present = 0
    for i,v in enumerate(indices):
        if (v < fea1_len):
            word = gene_vec.get_feature_names()[v]
            yes_no = True if word == gene else False
            if yes_no:
                word_present += 1
                print(i, "Gene feature [{}] present in test data point [{}]".format(wo
        elif (v < fea1_len+fea2_len):
            word = var_vec.get_feature_names()[v-(fea1_len)]
            yes_no = True if word == var else False
            if yes_no:
                word_present += 1
                print(i, "variation feature [{}] present in test data point [{}]".form
        else:
            word = text_vec.get_feature_names()[v-(fea1_len+fea2_len)]
            yes_no = True if word in text.split() else False
            if yes_no:
                word_present += 1
                print(i, "Text feature [{}] present in test data point [{}]".format(wo

    print("Out of the top ",no_features," features ", word_present, "are present in qu
```

```
In [146]: alpha = [10 ** x for x in range(-6, 3)]
          cv_log_error_array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='log', r
              clf.fit(train_vec, train_y)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(train_vec, train_y)
              sig_clf_probs = sig_clf.predict_proba(cv_vec)
              cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=
              # to avoid rounding error while multiplying probabilites we use log-probability
              print("Log Loss :",log_loss(cv_y, sig_clf_probs))

          fig, ax = plt.subplots()
          ax.plot(alpha, cv_log_error_array,c='g')
```

```
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', l
clf.fit(train_vec, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_vec, train_y)

predict_y = sig_clf.predict_proba(train_vec)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_
predict_y = sig_clf.predict_proba(cv_vec)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log los
predict_y = sig_clf.predict_proba(test_vec)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l
```

```
for alpha = 1e-06
Log Loss : 1.5452224097324696
for alpha = 1e-05
Log Loss : 1.559690091434177
for alpha = 0.0001
Log Loss : 1.5438538989527038
for alpha = 0.001
Log Loss : 1.4707385242692435
for alpha = 0.01
Log Loss : 1.1566704885794588
for alpha = 0.1
Log Loss : 1.1744047319616486
for alpha = 1
Log Loss : 1.2573623352622487
for alpha = 10
Log Loss : 1.3337836693304905
for alpha = 100
Log Loss : 1.3498408414671528
```

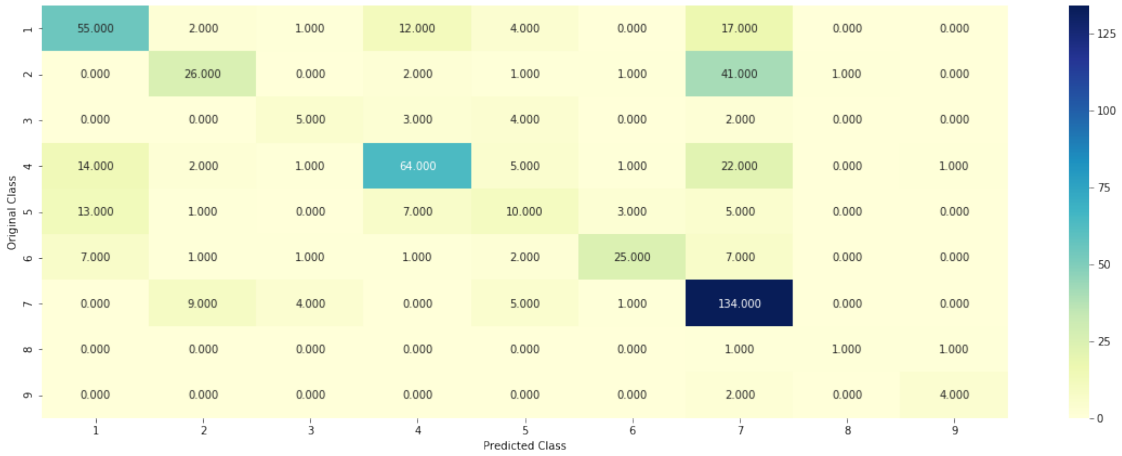


```
For values of best alpha =  0.01 The train log loss is: 0.8472646352615477
For values of best alpha =  0.01 The cross validation log loss is: 1.1566704885794588
For values of best alpha =  0.01 The test log loss is: 1.176842431113536
```

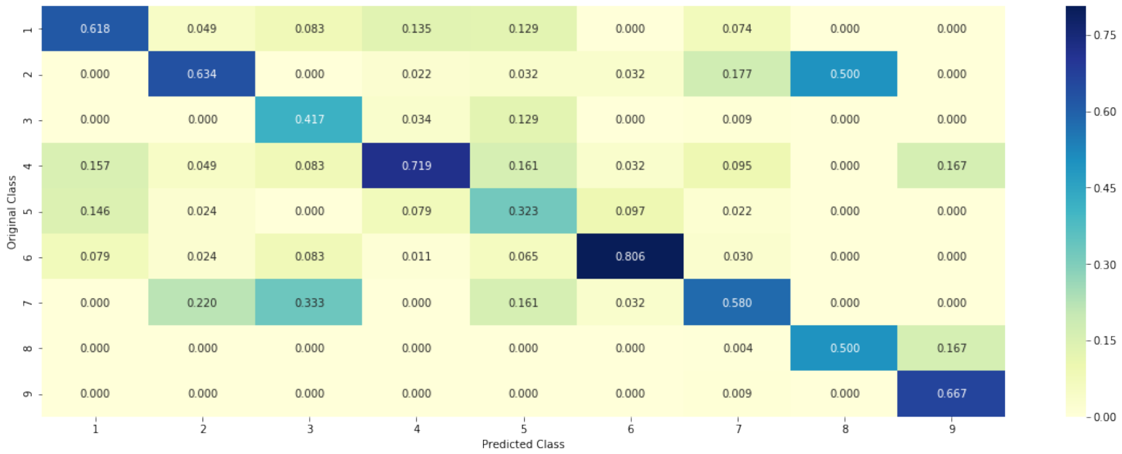
Testing the model with best hyper paramters

```
In [147]: clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', l
          predict_and_plot_confusion_matrix(train_vec, train_y, cv_vec, cv_y, clf)
```

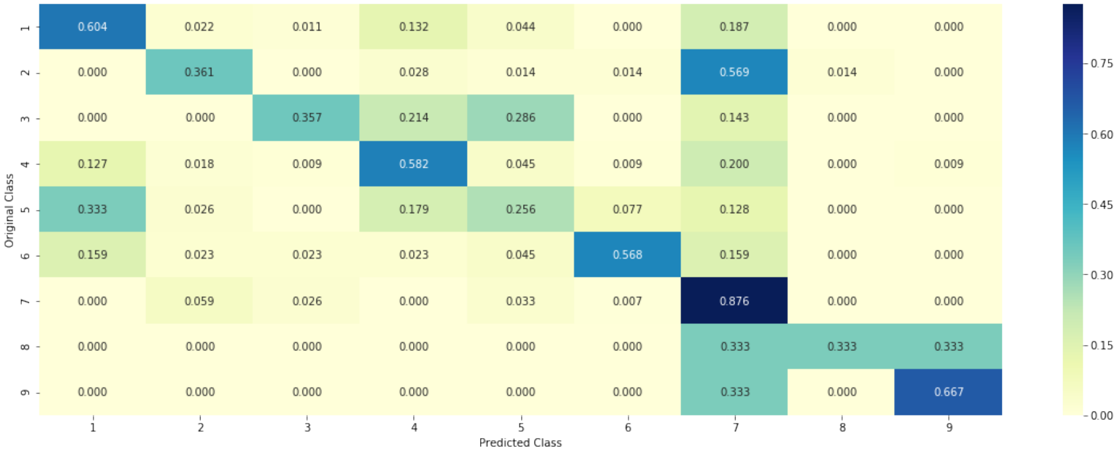
```
Log loss : 1.1566704885794588
Number of mis-classified points : 0.39097744360902253
-------------------- Confusion matrix --------------------
```



-------------------- Precision matrix (Columm Sum=1) --------------------



-------------------- Recall matrix (Row sum=1) --------------------



```
In [227]: text_count_vec = CountVectorizer(min_df=3,ngram_range=(1,2))
          text_vec = text_count_vec.fit(train_df['TEXT'])
```

feature Importance, Correctly classified point

```
In [150]: test_vec=test_vec.tocsr()
```

```
In [156]: # from tabulate import tabulate
          clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', l
          clf.fit(train_vec,train_y)
          test_point_index = 1
          no_feature = 1000
          predicted_cls = sig_clf.predict(test_vec[test_point_index])
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names_bow_2gram(indices[0], test_df['TEXT'].iloc[test_point_index],tes
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0698 0.0799 0.015  0.0559 0.0225 0.0274 0.7194 0.0048 0.0053
Actual Class : 7
--------------------------------------------------
882 Text feature [constitutively] present in test data point [True]
Out of the top  1000  features  1 are present in query point
```

Feature Importance, Incorrectly classified point

```
In [157]: test_point_index = 100
          no_feature = 1000
          predicted_cls = sig_clf.predict(test_vec[test_point_index])
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_vec[test_
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names_bow_2gram(indices[0], test_df['TEXT'].iloc[test_point_index],tes
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.1959 0.1817 0.0238 0.1397 0.0762 0.0701 0.2992 0.006  0.0074
Actual Class : 6
--------------------------------------------------
Out of the top  1000  features  0 are present in query point
```

1.1 Feature Engineering

```
In [158]: train_df.head()
```

```
Out[158]:         ID    Gene             Variation  Class  \
          2426  2426   BRCA1                  C64G      4
          636    636  CDKN1A  Truncating Mutations      1
          703    703   ERBB2                 E812K      6
          1455  1455   FGFR2                 K659N      7
          103    103    MSH6                 R976H      1

                                                             TEXT
          2426  published analyses effects missense mutations ...
          636   introduction loss control mammalian cell cycle...
          703   purpose mutations associated resistance kinase...
          1455  activating mutations tyrosine kinase domain re...
          103   msh6 gene one mismatch repair genes involved h...
```

1.1.1 Text word length, character length and variation length as features

```
In [10]: train_df['word_len']=train_df['TEXT'].apply(lambda x : len(x.split()))
         train_df['char_len']=train_df['TEXT'].apply(lambda x : len(x))
         test_df['word_len']=test_df['TEXT'].apply(lambda x : len(x.split()))
         test_df['char_len']=test_df['TEXT'].apply(lambda x : len(x))
         cv_df['word_len']=cv_df['TEXT'].apply(lambda x : len(x.split()))
         cv_df['char_len']=cv_df['TEXT'].apply(lambda x : len(x))
         train_df.head()
```

```
Out[10]:         ID    Gene             Variation  Class  \
         2426  2426   BRCA1                  C64G      4
         636    636  CDKN1A  Truncating Mutations      1
         703    703   ERBB2                 E812K      6
         1455  1455   FGFR2                 K659N      7
         103    103    MSH6                 R976H      1
```

```
                                                   TEXT  word_len  char_len
2426  published analyses effects missense mutations ...     17926    130265
636   introduction loss control mammalian cell cycle...      7234     53047
703   purpose mutations associated resistance kinase...      4961     37512
1455  activating mutations tyrosine kinase domain re...      8077     59908
103   msh6 gene one mismatch repair genes involved h...     13352    100388
```

```
In [14]: word_len_train=np.reshape(np.array(train_df['word_len']),(train_df['word_len'].shape[0
         char_len_train=np.reshape(np.array(train_df['char_len']),(train_df['char_len'].shape[0
         word_len_test=np.reshape(np.array(test_df['word_len']),(test_df['word_len'].shape[0],
         char_len_test=np.reshape(np.array(test_df['char_len']),(test_df['char_len'].shape[0],
         word_len_cv=np.reshape(np.array(cv_df['word_len']),(cv_df['word_len'].shape[0],1))
         char_len_cv=np.reshape(np.array(cv_df['char_len']),(cv_df['char_len'].shape[0],1))
```

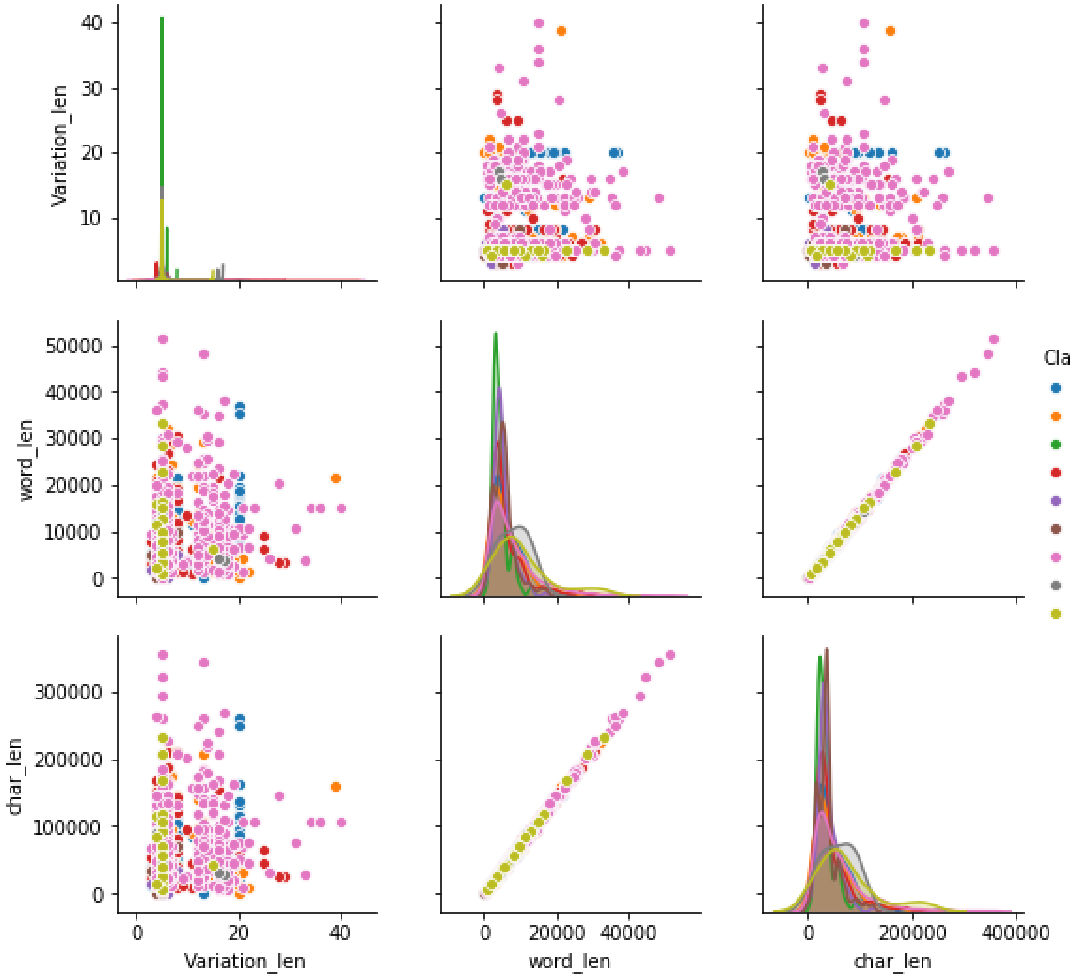
```
In [170]: train_df['Variation_len']=train_df['Variation'].apply(lambda x: len(x))
          test_df['Variation_len']=test_df['Variation'].apply(lambda x: len(x))
          cv_df['Variation_len']=cv_df['Variation'].apply(lambda x: len(x))
```

```
In [171]: train_df.head()
```

```
Out[171]:         ID    Gene             Variation  Class  \
          2426  2426   BRCA1                  C64G      4
          636    636  CDKN1A  Truncating Mutations      1
          703    703   ERBB2                 E812K      6
          1455  1455   FGFR2                 K659N      7
          103    103    MSH6                 R976H      1

                                                         TEXT  word_len  char_len  \
          2426  published analyses effects missense mutations ...     17926    130265
          636   introduction loss control mammalian cell cycle...      7234     53047
          703   purpose mutations associated resistance kinase...      4961     37512
          1455  activating mutations tyrosine kinase domain re...      8077     59908
          103   msh6 gene one mismatch repair genes involved h...     13352    100388

                Variation_len
          2426              4
          636              20
          703               5
          1455              5
          103               5
```

```
In [244]: fig = plt.figure(figsize=(20,15))
          sns.pairplot(train_df,hue='Class',vars=["Variation_len",'word_len','char_len'])
          plt.show()
```

```
<Figure size 1440x1080 with 0 Axes>
```



we can see that the features are not helping in classification and also adding these features did not improve the models.

1.1.2 Truncated svd to reduce the dimensions

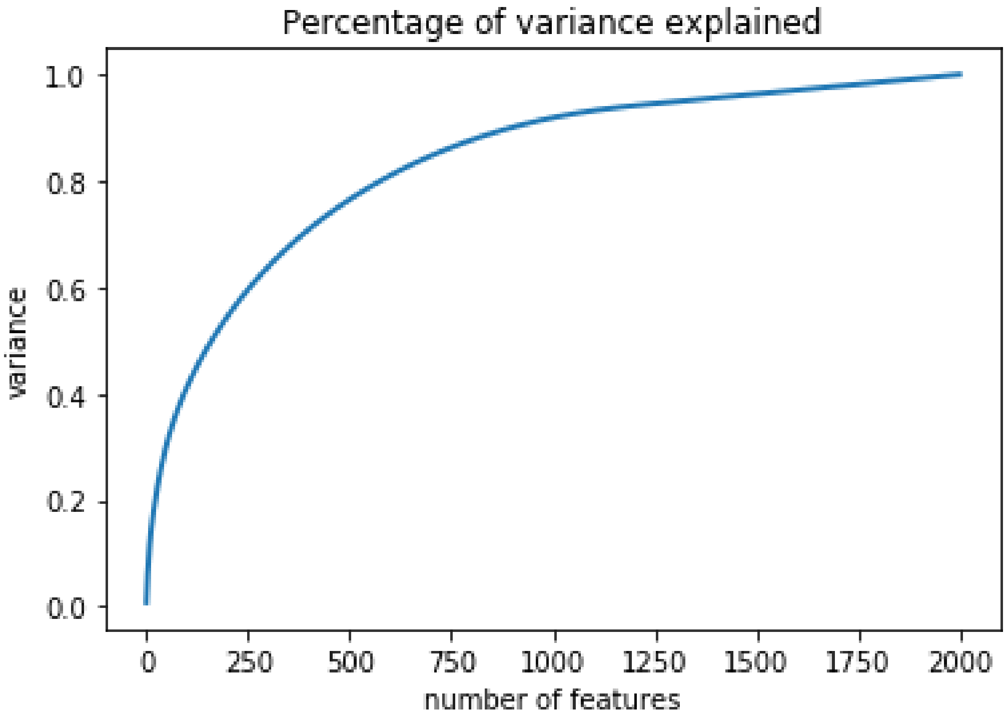
```
In [207]: from sklearn.feature_extraction.text import TfidfVectorizer
          text_vectorizer = TfidfVectorizer(max_features=10000)
          train_text_feature = text_vectorizer.fit_transform(train_df['TEXT'])
          # getting all the feature names (words)
          train_text_features= text_vectorizer.get_feature_names()
          test_text_feature = text_vectorizer.transform(test_df['TEXT'])
          cv_text_feature = text_vectorizer.transform(cv_df['TEXT'])
```

```
In [208]: train_text_feature = normalize(train_text_feature, axis=0)

          # don't forget to normalize every feature
          test_text_feature = normalize(test_text_feature, axis=0)
```

```
        cv_text_feature = normalize(cv_text_feature, axis=0)
```

```
In [211]: #stacking the features
          train_vec = hstack((train_gene_feature_onehotCoding,train_variation_feature_onehotCoc
          test_vec = hstack((test_gene_feature_onehotCoding,test_variation_feature_onehotCodin
          cv_vec = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehotCoding,cv_te
```

```
In [213]: #using tsvd to reduce the dimensions
          from sklearn.decomposition import TruncatedSVD
          from tqdm import tqdm
          #applying truncated svd with n_components =1000
          tsvd =TruncatedSVD(algorithm="randomized",n_components=2000, n_iter=7,\
                             random_state=42,tol=0.0)
          X_reduced = tsvd.fit_transform(train_vec)

          #plotting the percentage of the variance explained by the features
          percentage_variance_explained=tsvd.explained_variance_/sum(tsvd.explained_variance_)
          cum_variance_explained=np.cumsum(percentage_variance_explained)
          plt.plot(cum_variance_explained,linewidth='2')
          plt.xlabel("number of features")
          plt.ylabel("variance")
          plt.title("Percentage of variance explained")
          plt.show()
```

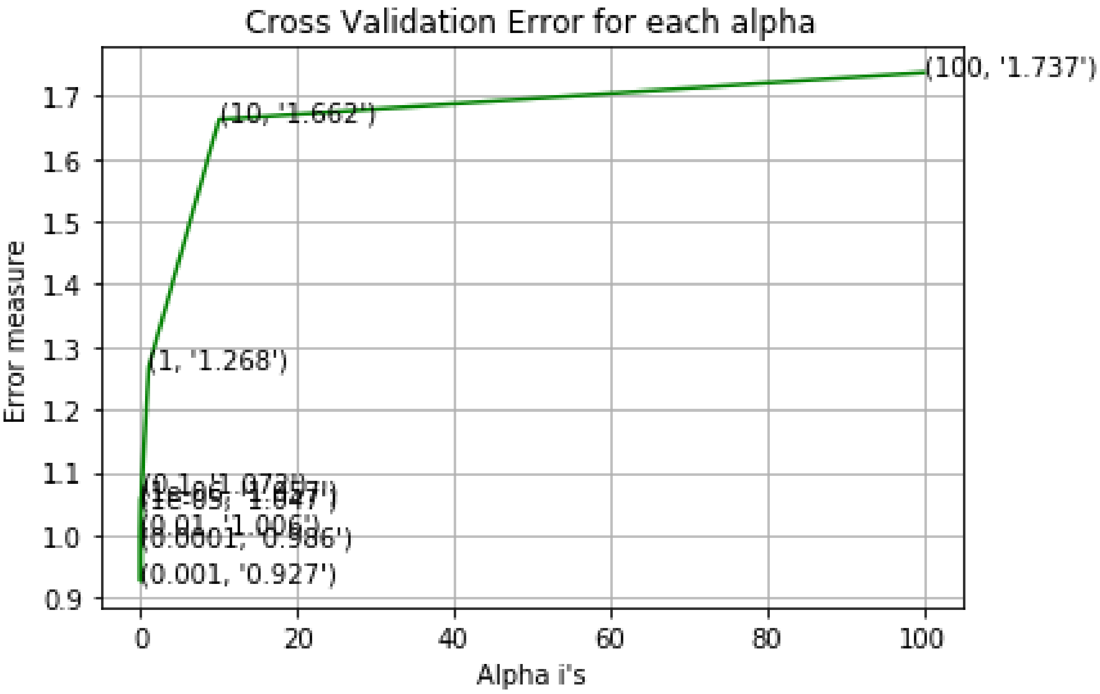


```
In [220]: tsvd =TruncatedSVD(algorithm="randomized",n_components=1500, n_iter=7,\
                             random_state=42,tol=0.0)
          tra = tsvd.fit_transform(train_vec)
          tes=tsvd.transform(test_vec)
          c=tsvd.transform(cv_vec)
```

1.2 Logistic Regression with Balancing

```
In [221]: alpha = [10 ** x for x in range(-6, 3)]
          cv_log_error_array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='log', 
              clf.fit(tra, train_y)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(tra, train_y)
              sig_clf_probs = sig_clf.predict_proba(c)
              cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps
              # to avoid rounding error while multiplying probabilites we use log-probability 
              print("Log Loss :",log_loss(cv_y, sig_clf_probs))

          fig, ax = plt.subplots()
          ax.plot(alpha, cv_log_error_array,c='g')
          for i, txt in enumerate(np.round(cv_log_error_array,3)):
              ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()


          best_alpha = np.argmin(cv_log_error_array)
          clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', 
          clf.fit(tra, train_y)
          sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(tra, train_y)

          predict_y = sig_clf.predict_proba(tra)
          print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log
          predict_y = sig_clf.predict_proba(c)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log lo
          predict_y = sig_clf.predict_proba(tes)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_

for alpha = 1e-06
Log Loss : 1.0570658874759329
for alpha = 1e-05
```

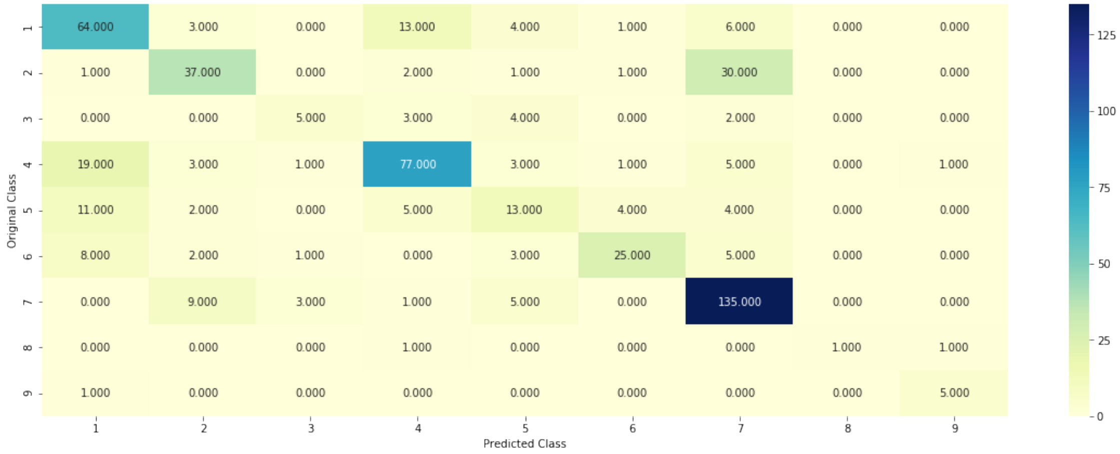
```
Log Loss : 1.0465970705661962
for alpha = 0.0001
Log Loss : 0.9864306000414919
for alpha = 0.001
Log Loss : 0.9266671112993817
for alpha = 0.01
Log Loss : 1.0057874102939246
for alpha = 0.1
Log Loss : 1.0717122327927189
for alpha = 1
Log Loss : 1.267646051437711
for alpha = 10
Log Loss : 1.6622461851007915
for alpha = 100
Log Loss : 1.7372144829297962
```



```
For values of best alpha =  0.001 The train log loss is: 0.5726296501912288
For values of best alpha =  0.001 The cross validation log loss is: 0.9266671112993817
For values of best alpha =  0.001 The test log loss is: 0.9706599524824131
```

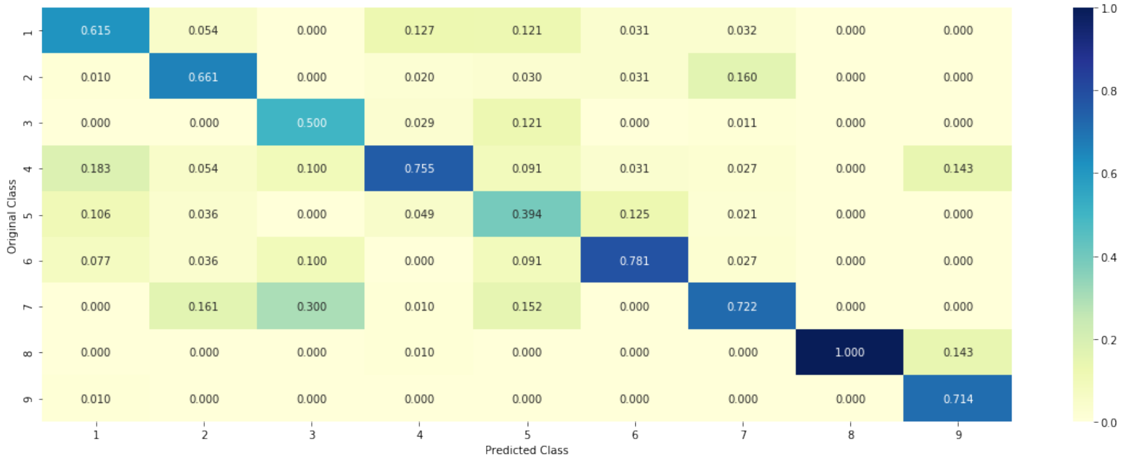
```
In [222]: clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', 
          predict_and_plot_confusion_matrix(tra, train_y, c, cv_y, clf)
```

```
Log loss : 0.9266671112993817
Number of mis-classified points : 0.31954887218045114
-------------------- Confusion matrix --------------------
```



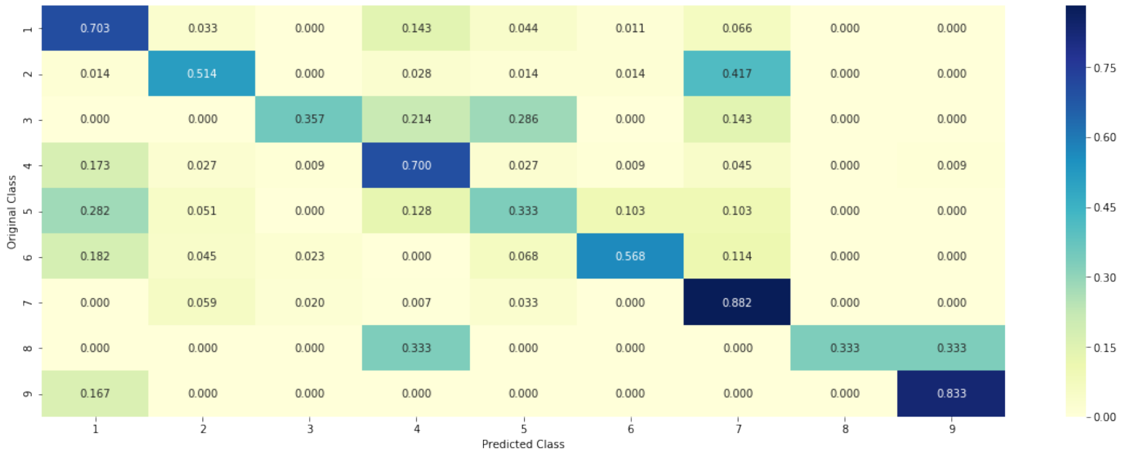
	1	2	3	4	5	6	7	8	9
1	64.000	3.000	0.000	13.000	4.000	1.000	6.000	0.000	0.000
2	1.000	37.000	0.000	2.000	1.000	1.000	30.000	0.000	0.000
3	0.000	0.000	5.000	3.000	4.000	0.000	2.000	0.000	0.000
4	19.000	3.000	1.000	77.000	3.000	1.000	5.000	0.000	1.000
5	11.000	2.000	0.000	5.000	13.000	4.000	4.000	0.000	0.000
6	8.000	2.000	1.000	0.000	3.000	25.000	5.000	0.000	0.000
7	0.000	9.000	3.000	1.000	5.000	0.000	135.000	0.000	0.000
8	0.000	0.000	0.000	1.000	0.000	0.000	0.000	1.000	1.000
9	1.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	5.000

```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



	1	2	3	4	5	6	7	8	9
1	0.615	0.054	0.000	0.127	0.121	0.031	0.032	0.000	0.000
2	0.010	0.661	0.000	0.020	0.030	0.031	0.160	0.000	0.000
3	0.000	0.000	0.500	0.029	0.121	0.000	0.011	0.000	0.000
4	0.183	0.054	0.100	0.755	0.091	0.031	0.027	0.000	0.143
5	0.106	0.036	0.000	0.049	0.394	0.125	0.021	0.000	0.000
6	0.077	0.036	0.100	0.000	0.091	0.781	0.027	0.000	0.000
7	0.000	0.161	0.300	0.010	0.152	0.000	0.722	0.000	0.000
8	0.000	0.000	0.000	0.010	0.000	0.000	0.000	1.000	0.143
9	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.714

```
-------------------- Recall matrix (Row sum=1) --------------------
```

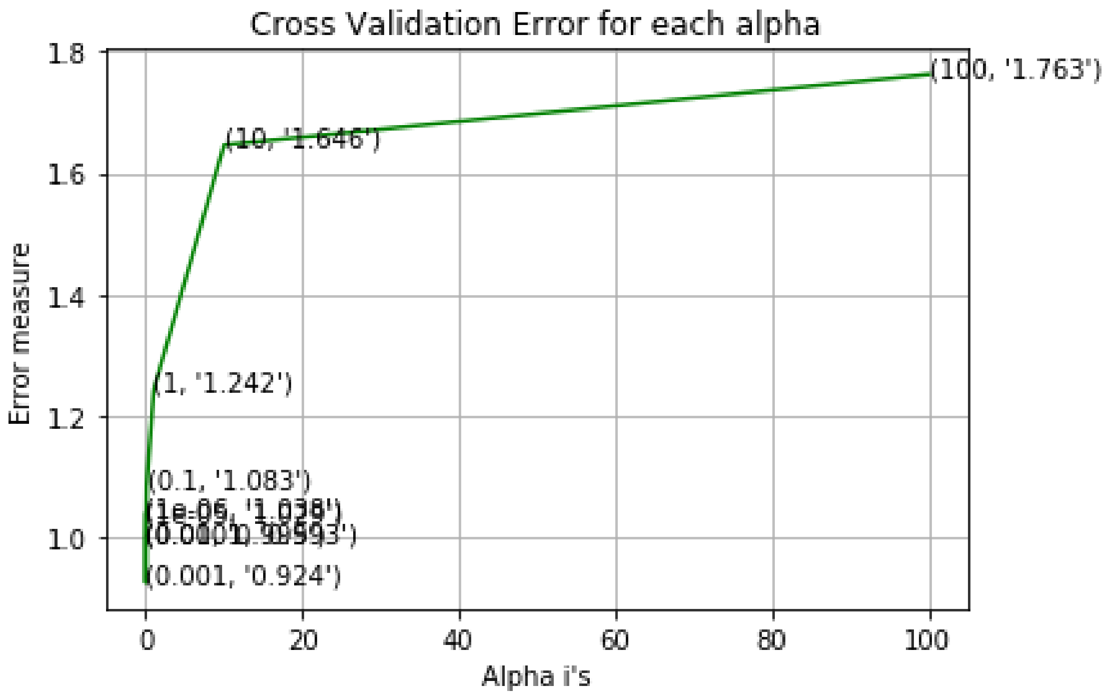


1.2.1 Logistic Regression without Class Balance

```
In [239]: alpha = [10 ** x for x in range(-6, 3)]
          cv_log_error_array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier( alpha=i, penalty='l2', loss='log', random_state=42)
              clf.fit(tra, train_y)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(tra, train_y)
              sig_clf_probs = sig_clf.predict_proba(c)
              cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps
              # to avoid rounding error while multiplying probabilites we use log-probability
              print("Log Loss :",log_loss(cv_y, sig_clf_probs))

          fig, ax = plt.subplots()
          ax.plot(alpha, cv_log_error_array,c='g')
          for i, txt in enumerate(np.round(cv_log_error_array,3)):
              ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()


          best_alpha = np.argmin(cv_log_error_array)
          clf = SGDClassifier( alpha=alpha[best_alpha], penalty='l2', loss='log', random_state
          clf.fit(tra, train_y)
          sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(tra, train_y)
```

```
        predict_y = sig_clf.predict_proba(tra)
        print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_
        predict_y = sig_clf.predict_proba(c)
        print('For values of best alpha = ', alpha[best_alpha], "The cross validation log los
        predict_y = sig_clf.predict_proba(tes)
        print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l
```

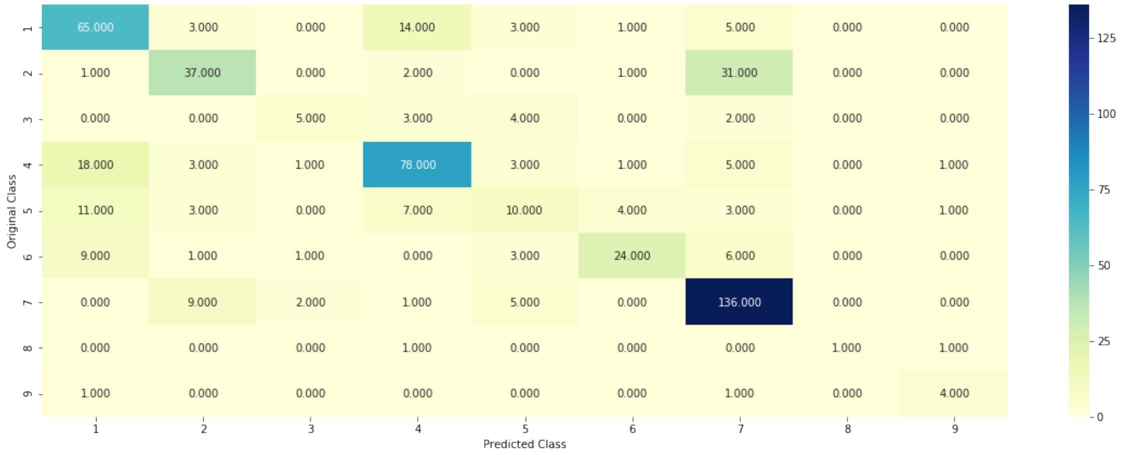
```
for alpha = 1e-06
Log Loss : 1.0376463311304114
for alpha = 1e-05
Log Loss : 1.0288008319989888
for alpha = 0.0001
Log Loss : 0.9930706350433093
for alpha = 0.001
Log Loss : 0.9241393237294904
for alpha = 0.01
Log Loss : 0.9950353774753347
for alpha = 0.1
Log Loss : 1.0832774813439614
for alpha = 1
Log Loss : 1.241828571935979
for alpha = 10
Log Loss : 1.6463772476034435
for alpha = 100
Log Loss : 1.7628574422286374
```



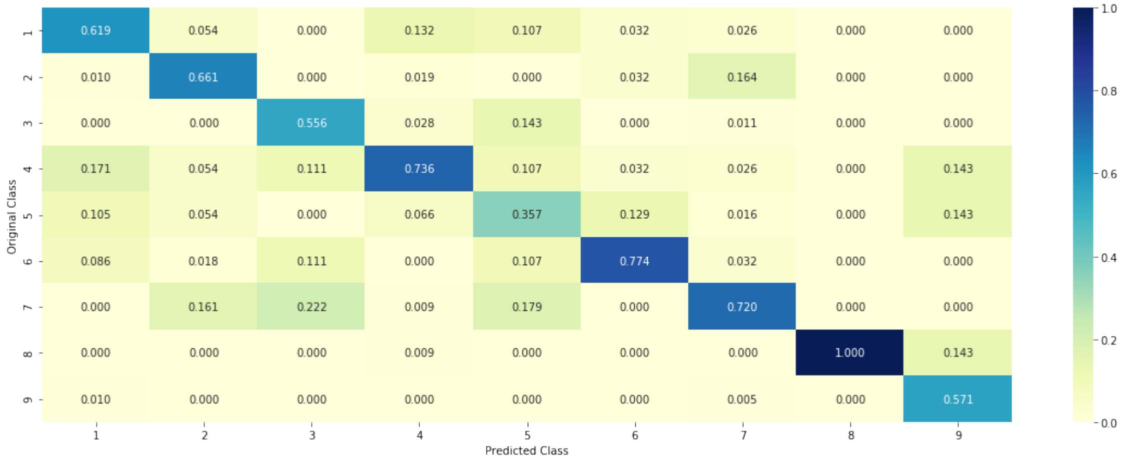
```
For values of best alpha =  0.001 The train log loss is: 0.5605561048509772
For values of best alpha =  0.001 The cross validation log loss is: 0.9241393237294904
For values of best alpha =  0.001 The test log loss is: 0.9642156482902127
```

```
In [240]: clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=
          predict_and_plot_confusion_matrix(tra, train_y, c, cv_y, clf)
```

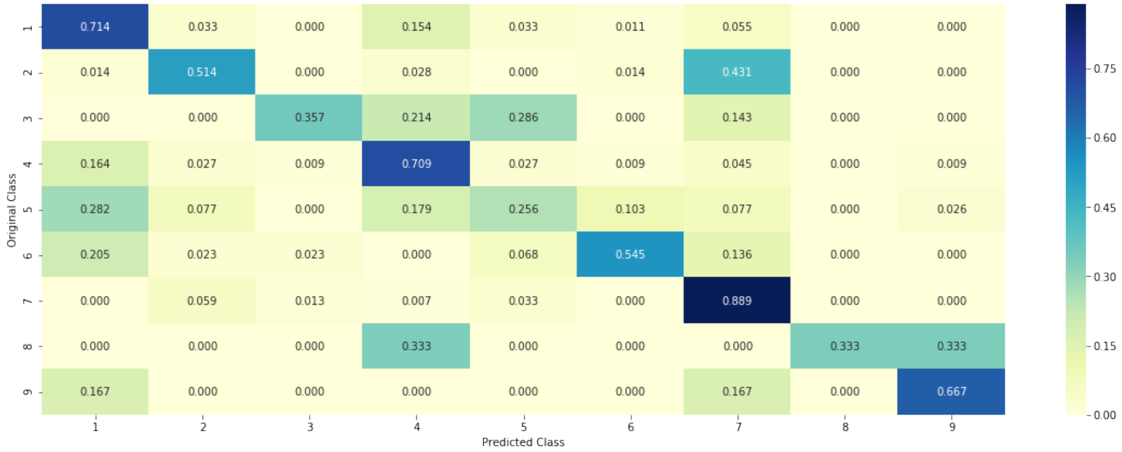
```
Log loss : 0.9241393237294904
Number of mis-classified points : 0.3233082706766917
-------------------- Confusion matrix --------------------
```



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



```
-------------------- Recall matrix (Row sum=1) --------------------
```



	1	2	3	4	5	6	7	8	9
1	0.714	0.033	0.000	0.154	0.033	0.011	0.055	0.000	0.000
2	0.014	0.514	0.000	0.028	0.000	0.014	0.431	0.000	0.000
3	0.000	0.000	0.357	0.214	0.286	0.000	0.143	0.000	0.000
4	0.164	0.027	0.009	0.709	0.027	0.009	0.045	0.000	0.009
5	0.282	0.077	0.000	0.179	0.256	0.103	0.077	0.000	0.026
6	0.205	0.023	0.023	0.000	0.068	0.545	0.136	0.000	0.000
7	0.000	0.059	0.013	0.007	0.033	0.000	0.889	0.000	0.000
8	0.000	0.000	0.000	0.333	0.000	0.000	0.000	0.333	0.333
9	0.167	0.000	0.000	0.000	0.000	0.000	0.167	0.000	0.667

1.3 Conclusion

Objective:Classify the given genetic variations/mutations based on evidence from text-based clinical literature.

1. We are given a dataset with 3321 rows and 5 columns: ID , Gene, Variations, Text, Class of which Class is a multiclass column containing the 9 classes.
2. We preprocess the data and split into train, test and cv set.
3. We perform EDA on the dataset to know about the distribution of the data and get more insights about the data and featurize the data using responsecoding and onehotencoding method.
4. We then check if distribution is stable across train test and cv set and then check how important gene and variation feature is in classifying the model.
5. We then apply various model like logistic Regression, Naive Bayes, Random Forest, Voting classifier etc and compare them.
6. We use multiclass log loss as error metric, confusion matrix as performance metric and also check the number of misclassified points.
7. Since interpretibility is important we used only models which are interpretable and got the feature importance.
8. We then try to reduce the log loss using other techniques like tfidf vectorization, BoW Vectorization with 2 gram and tsvd.

```
In [241]: from prettytable import PrettyTable

          x=PrettyTable()
```

```
x.field_names=['Algorithm','Vectorizer','penalty','alpha','CV Log loss','Test Log Los
x.add_row(["Naive Bayes","TFIDF",'-',1,1.188, 1.176,39.47])
x.add_row(["KNN","TFIDF",'-',5,1.329 ,1.326,  42.66 ])
x.add_row(["Logistic Regression (Balanced) ","TFIDF",'l2',0.001,1.097, 1.064, 34.96
x.add_row(["Logistic Regression","TFIDF",'l2',0.001,1.113, 1.072 ,34.39 ])
x.add_row(["Random Forest","TFIDF",'-',2000,1.172, 1.16, 37.78 ])
x.add_row(["Stacking","TFIDF",'-','-',1.129 ,1.109, 35.48 ])
x.add_row(["Logistic Regression (Balanced)","TFIDF-1000",'l2',0.0001,0.9932, 1.018 ,
x.add_row(["Logistic Regression (Balanced)","BoW 2 gram",'l2',0.01,1.156 ,1.176, 39.
x.add_row(["Logistic Regression (Balanced)","TFIDF-TSVD",'l2',0.001,0.9266, 0.9706,
x.add_row(["Logistic Regression","TFIDF-TSVD",'l2',0.001,0.924, 0.964, 32.33])


print(x)
```

```
+---------------------------------+------------+---------+--------+-------------+--------------
|            Algorithm            | Vectorizer | penalty | alpha  | CV Log loss | Test Log Loss
+---------------------------------+------------+---------+--------+-------------+--------------
|           Naive Bayes           |   TFIDF    |    -    |   1    |    1.188    |     1.176
|               KNN               |   TFIDF    |    -    |   5    |    1.329    |     1.326
| Logistic Regression (Balanced)  |   TFIDF    |    l2   | 0.001  |    1.097    |     1.064
|       Logistic Regression       |   TFIDF    |    l2   | 0.001  |    1.113    |     1.072
|          Random Forest          |   TFIDF    |    -    |  2000  |    1.172    |      1.16
|             Stacking            |   TFIDF    |    -    |   -    |    1.129    |     1.109
|  Logistic Regression (Balanced) | TFIDF-1000 |    l2   | 0.0001 |    0.9932   |     1.018
|  Logistic Regression (Balanced) | BoW 2 gram |    l2   |  0.01  |    1.156    |     1.176
|  Logistic Regression (Balanced) | TFIDF-TSVD |    l2   | 0.001  |    0.9266   |     0.9706
|       Logistic Regression       | TFIDF-TSVD |    l2   | 0.001  |    0.924    |     0.964
+---------------------------------+------------+---------+--------+-------------+--------------
```

Logistic Regression with TFIDf using tsvd reduced features has the log loss of 0.97 and lowest percent of misclassified points .

```
In [ ]:
```