TFIDF

July 13, 2018

Personalized cancer diagnosis

1. Business Problem

1.1. Description
Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/
Data: Memorial Sloan Kettering Cancer Center (MSKCC)
Download training_variants.zip and training_text.zip from Kaggle.
Context:
Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/discussion/35336#198462
Problem statement :
Classify the given genetic variations/mutations based on evidence from text-based clinical literature.
1.2. Source/Useful Links
Some articles and reference blogs about the problem statement

1. https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almost-everyone-who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25
2. https://www.youtube.com/watch?v=UwbuW7oK8rk
3. https://www.youtube.com/watch?v=qxXRKVompI8

1.3. Real-world/Business objectives and constraints.

- No low-latency requirement.
- Interpretability is important.
- Errors can be very costly.
- Probability of a data-point belonging to each class is needed.

```
<li> Apply All the models with tf-idf features (Replace CountVectorizer with tfidfVectorizer ar
<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
```

1.4. Assignment


```
<li> Apply All the models with tf-idf features (Replace CountVectorizer with tfidfVectorizer ar
<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
```

2. Machine Learning Problem Formulation

2.1. Data

2.1.1. Data Overview

- Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/data
- We have two data files: one conatins the information about the genetic mutations and the other contains the clinical evidence (text) that human experts/pathologists use to classify the genetic mutations.
- Both these data files are have a common column called ID
- Data file's information:

```
<li>
training_variants (ID , Gene, Variations, Class)
</li>
<li>
training_text (ID, Text)
</li>
```

2.1.2. Example Data Point

training_variants

ID,Gene,Variation,Class 0,FAM58A,Truncating Mutations,1 1,CBL,W802*,2 2,CBL,Q249E,2 ...

training_text

ID,Text 0||Cyclin-dependent kinases (CDKs) regulate a variety of fundamental cellular processes. CDK10 stands out as one of the last orphan CDKs for which no activating cyclin has been identified and no kinase activity revealed. Previous work has shown that CDK10 silencing increases ETS2 (v-ets erythroblastosis virus E26 oncogene homolog 2)-driven activation of the MAPK pathway, which confers tamoxifen resistance to breast cancer cells. The precise mechanisms by which CDK10 modulates ETS2 activity, and more generally the functions of CDK10, remain elusive. Here we demonstrate that CDK10 is a cyclin-dependent kinase by identifying cyclin M as an activating cyclin. Cyclin M, an orphan cyclin, is the product of FAM58A, whose mutations cause STAR syndrome, a human developmental anomaly whose features include toe syndactyly, telecanthus, and anogenital and renal malformations. We show that STAR syndrome-associated cyclin M mutants are unable to interact with CDK10. Cyclin M silencing phenocopies CDK10 silencing in increasing c-Raf and in conferring tamoxifen resistance to breast cancer cells. CDK10/cyclin M phosphorylates ETS2 in vitro, and in cells it positively controls ETS2 degradation by the proteasome. ETS2 protein levels are increased in cells derived from a STAR patient, and this increase is attributable to decreased cyclin M levels. Altogether, our results reveal an additional regulatory mechanism for ETS2, which plays key roles in cancer and development. They also shed light on the molecular mechanisms underlying STAR syndrome.Cyclin-dependent kinases (CDKs) play a pivotal role in the control of a number of fundamental cellular processes (1). The human genome contains 21 genes encoding proteins that can be considered as members of the CDK family owing to their sequence similarity with bona fide CDKs, those known to be activated by cyclins (2). Although discovered almost 20 y ago (3, 4), CDK10 remains one of the two CDKs without an identified cyclin partner. This knowledge gap has largely impeded the exploration of its biological functions. CDK10 can act as a positive cell cycle regulator in some cells (5, 6) or as a tumor suppressor in others (7, 8). CDK10 interacts with the ETS2 (v-ets erythroblastosis virus E26 oncogene homolog 2) transcription factor and inhibits its transcriptional activity through an unknown mechanism (9). CDK10 knockdown derepresses ETS2, which increases the expression of the c-Raf protein kinase, activates the MAPK pathway, and induces resistance of MCF7 cells to tamoxifen (6). ...

2.2. Mapping the real-world problem to an ML problem

2.2.1. Type of Machine Learning Problem

```
There are nine different classes a genetic mutation can be classified into => Multi cla
```

2.2.2. Performance Metric

Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation

Metric(s): * Multi class log-loss * Confusion matrix

2.2.3. Machine Learing Objectives and Constraints

Objective: Predict the probability of each data-point belonging to each of the nine classes.

Constraints:

- Interpretability
- Class probabilities are needed.
- Penalize the errors in class probabilites => Metric is Log-loss.
- No Latency constraints.

2.3. Train, CV and Test Datasets

Split the dataset randomly into three parts train, cross validation and test with 64%,16%, 20% of data respectively

3. Exploratory Data Analysis

In [1]:
```
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.cross_validation 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
import nltk
from sklearn import model_selection
from sklearn.linear_model import LogisticRegression
```

```
C:\Users\suman\Anaconda3\lib\site-packages\sklearn\cross_validation.py:41: DeprecationWarning:
  "This module will be removed in 0.20.", DeprecationWarning)
```

3.1. Reading Data
3.1.1. Reading Gene and Variation Data

```
In [2]: data = pd.read_csv('training_variants')
        print('Number of data points : ', data.shape[0])
        print('Number of features : ', data.shape[1])
        print('Features : ', data.columns.values)
        data.head()
```

```
Number of data points :  3321
Number of features :  4
Features :  ['ID' 'Gene' 'Variation' 'Class']
```

Out[2]:

	ID	Gene	Variation	Class
0	0	FAM58A	Truncating Mutations	1
1	1	CBL	W802*	2
2	2	CBL	Q249E	2
3	3	CBL	N454D	3
4	4	CBL	L399V	4

```
training_variants is a comma separated file containing the description of the genetic mutation
Fields are
<ul>
    <li><b>ID : </b>the id of the row used to link the mutation to the clinical evidence</li>
    <li><b>Gene : </b>the gene where this genetic mutation is located </li>
    <li><b>Variation : </b>the aminoacid change for this mutations </li>
```

```
    <li><b>Class :</b> 1-9 the class this genetic mutation has been classified on</li>
</ul>
```

3.1.2. Reading Text Data

```
In [3]: # note the seprator in this file
        data_text =pd.read_csv("training_text",sep="\|\|",engine="python",names=["ID","TEXT"],
        print('Number of data points : ', data_text.shape[0])
        print('Number of features : ', data_text.shape[1])
        print('Features : ', data_text.columns.values)
        data_text.head()
```

```
Number of data points :  3321
Number of features :  2
Features :  ['ID' 'TEXT']
```

Out[3]:

	ID	TEXT
0	0	Cyclin-dependent kinases (CDKs) regulate a var...
1	1	Abstract Background Non-small cell lung canc...
2	2	Abstract Background Non-small cell lung canc...
3	3	Recent evidence has demonstrated that acquired...
4	4	Oncogenic mutations in the monomeric Casitas B...

3.1.3. Preprocessing of text

```
In [4]: # loading stop words from nltk library
        stop_words = set(stopwords.words('english'))
        #sno = nltk.stem.SnowballStemmer('english') #initialising the snowball stemmer

        def nlp_preprocessing(total_text, index, column):
            if type(total_text) is not int:
                string = ""
                # replace every special char with space
                total_text = re.sub('[^a-zA-Z0-9\n]', ' ', str(total_text))
                # replace multiple spaces with single space
                total_text = re.sub('\s+',' ', total_text)
                # converting all the chars into lower-case.
                total_text = total_text.lower()
                for word in total_text.split():
                # if the word is a not a stop word then retain that word from the data
                    #word=(sno.stem(word.lower())).encode('utf8')
                    #    print(word)
                    if not word in stop_words:
                        string += word + " "

                data_text[column][index] = string
```

```
In [5]: #text processing stage.
        start_time = time.clock()
```

```python
for index, row in data_text.iterrows():
    nlp_preprocessing(row['TEXT'], index, 'TEXT')
print('Time took for preprocessing the text :',time.clock() - start_time, "seconds")
```

```
Time took for preprocessing the text : 250.23175305309593 seconds
```

In [6]:
```python
#merging both gene_variations and text data based on ID
result = pd.merge(data, data_text,on='ID', how='left')
result.head()
```

Out[6]:
```
   ID    Gene             Variation  Class  \
0   0  FAM58A  Truncating Mutations      1
1   1     CBL                 W802*      2
2   2     CBL                 Q249E      2
3   3     CBL                 N454D      3
4   4     CBL                 L399V      4

                                                TEXT
0  cyclin dependent kinases cdks regulate variety...
1  abstract background non small cell lung cancer...
2  abstract background non small cell lung cancer...
3  recent evidence demonstrated acquired uniparen...
4  oncogenic mutations monomeric casitas b lineag...
```

3.1.4. Test, Train and Cross Validation Split

3.1.4.1. Splitting data into train, test and cross validation (64:20:16)

In [7]:
```python
y_true = result['Class'].values
result.Gene      = result.Gene.str.replace('\s+', '_')
result.Variation = result.Variation.str.replace('\s+', '_')

# split the data into test and train by maintaining same distribution of output varaib
X_train, test_df, y_train, y_test = train_test_split(result, y_true, stratify=y_true, 
# split the train data into train and cross validation by maintaining same distributio
train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train, stratify=y_train, 
```

We split the data into train, test and cross validation data sets, preserving the ratio of class distribution in the original data set

In [8]:
```python
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])
train_df['TEXT'].shape
```

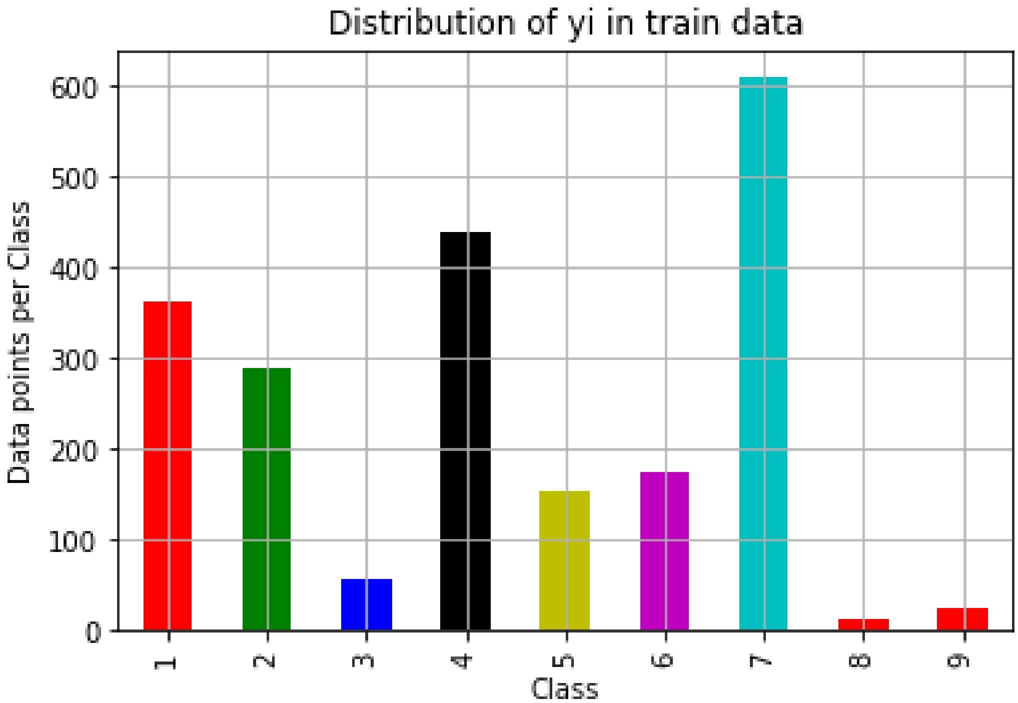
```
Number of data points in train data: 2124
Number of data points in test data: 665
Number of data points in cross validation data: 532
```

Out[8]: (2124,)

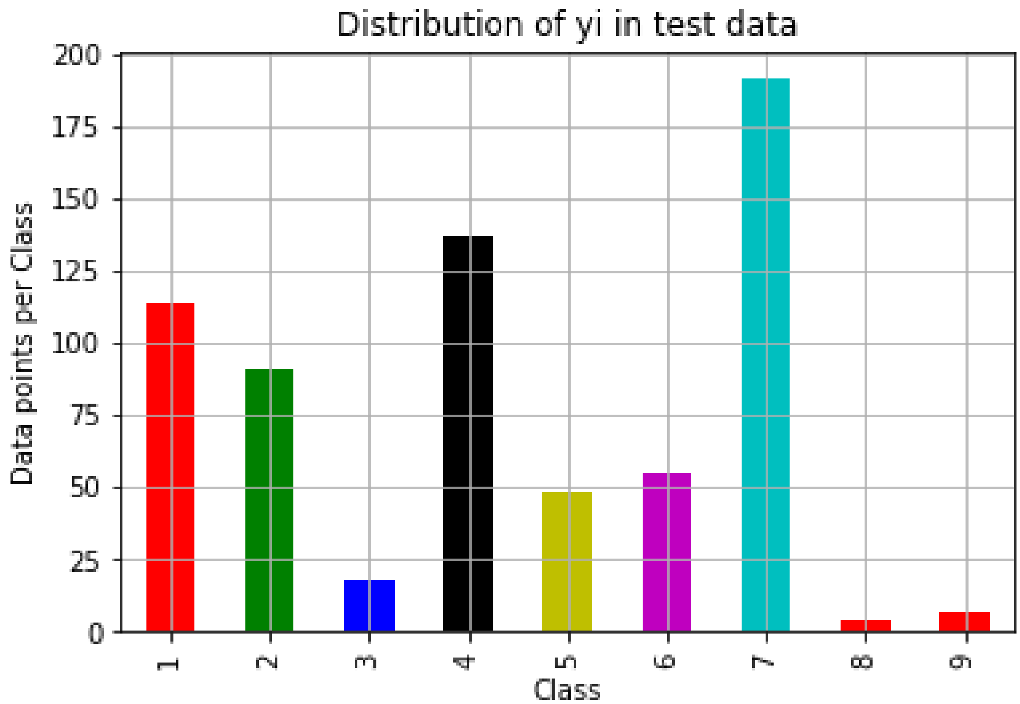
3.1.4.2. Distribution of y_i's in Train, Test and Cross Validation datasets

```
In [9]: # it returns a dict, keys as class labels and values as the number of data points in th
        train_class_distribution = train_df['Class'].value_counts().sortlevel()
        test_class_distribution = test_df['Class'].value_counts().sortlevel()
        cv_class_distribution = cv_df['Class'].value_counts().sortlevel()

        my_colors = ['r', 'g', 'b', 'k', 'y', 'm', 'c']
        train_class_distribution.plot(kind='bar', color=my_colors)
        plt.xlabel('Class')
        plt.ylabel('Data points per Class')
        plt.title('Distribution of yi in train data')
        plt.grid()
        plt.show()

        # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
        # -(train_class_distribution.values): the minus sign will give us in decreasing order
        sorted_yi = np.argsort(-train_class_distribution.values)
        for i in sorted_yi:
            print('Number of data points in class', i+1, ':',train_class_distribution.values[i]


        print('-'*80)
        my_colors = ['r', 'g', 'b', 'k', 'y', 'm', 'c']
        test_class_distribution.plot(kind='bar', color=my_colors)
        plt.xlabel('Class')
        plt.ylabel('Data points per Class')
        plt.title('Distribution of yi in test data')
        plt.grid()
        plt.show()

        # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
        # -(train_class_distribution.values): the minus sign will give us in decreasing order
        sorted_yi = np.argsort(-test_class_distribution.values)
        for i in sorted_yi:
            print('Number of data points in class', i+1, ':',test_class_distribution.values[i]

        print('-'*80)
        my_colors = ['r', 'g', 'b', 'k', 'y', 'm', 'c']
        cv_class_distribution.plot(kind='bar', color=my_colors)
        plt.xlabel('Class')
        plt.ylabel('Data points per Class')
        plt.title('Distribution of yi in cross validation data')
        plt.grid()
        plt.show()
```

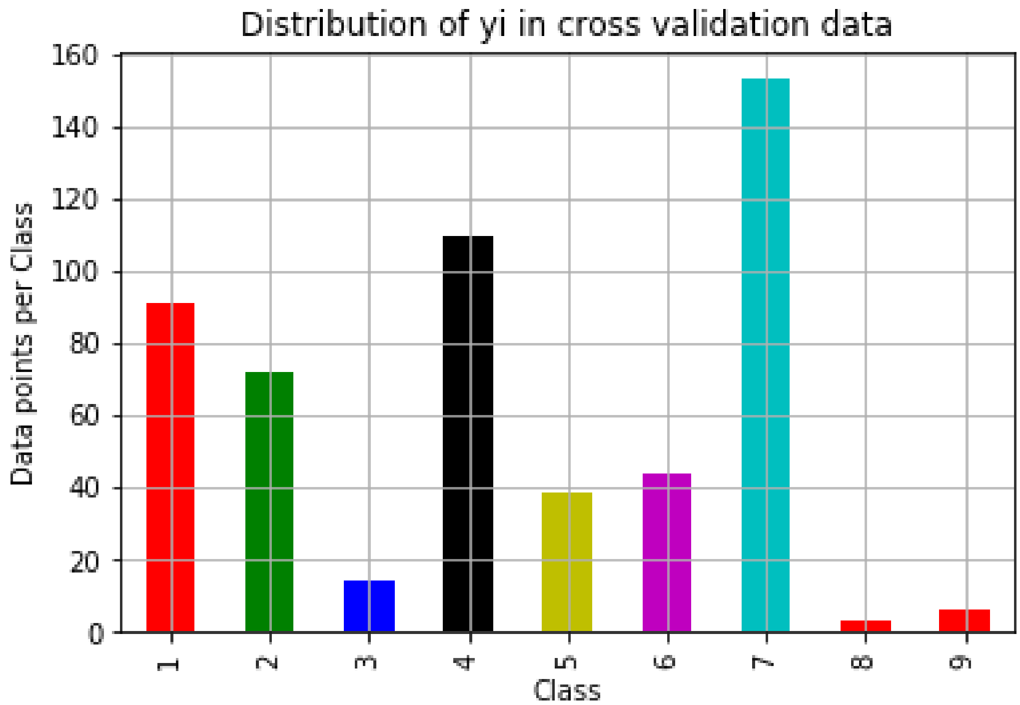
```
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',cv_class_distribution.values[i],
```




```
Number of data points in class 7 : 609 ( 28.672 %)
Number of data points in class 4 : 439 ( 20.669 %)
Number of data points in class 1 : 363 ( 17.09 %)
Number of data points in class 2 : 289 ( 13.606 %)
Number of data points in class 6 : 176 ( 8.286 %)
Number of data points in class 5 : 155 ( 7.298 %)
Number of data points in class 3 : 57 ( 2.684 %)
Number of data points in class 9 : 24 ( 1.13 %)
Number of data points in class 8 : 12 ( 0.565 %)
--------------------------------------------------------------------------------
```




```
Number of data points in class 7 : 191 ( 28.722 %)
Number of data points in class 4 : 137 ( 20.602 %)
Number of data points in class 1 : 114 ( 17.143 %)
Number of data points in class 2 : 91 ( 13.684 %)
Number of data points in class 6 : 55 ( 8.271 %)
Number of data points in class 5 : 48 ( 7.218 %)
Number of data points in class 3 : 18 ( 2.707 %)
Number of data points in class 9 : 7 ( 1.053 %)
Number of data points in class 8 : 4 ( 0.602 %)
--------------------------------------------------------------------------------
```




```
Number of data points in class 7 : 153 ( 28.759 %)
Number of data points in class 4 : 110 ( 20.677 %)
Number of data points in class 1 : 91 ( 17.105 %)
Number of data points in class 2 : 72 ( 13.534 %)
Number of data points in class 6 : 44 ( 8.271 %)
Number of data points in class 5 : 39 ( 7.331 %)
Number of data points in class 3 : 14 ( 2.632 %)
Number of data points in class 9 : 6 ( 1.128 %)
Number of data points in class 8 : 3 ( 0.564 %)
```

3.2 Prediction using a 'Random' Model

In a 'Random' Model, we generate the NINE class probabilites randomly such that they sum to 1.

```
In [10]: # 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 pred

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

             # C = [[1, 2],
```

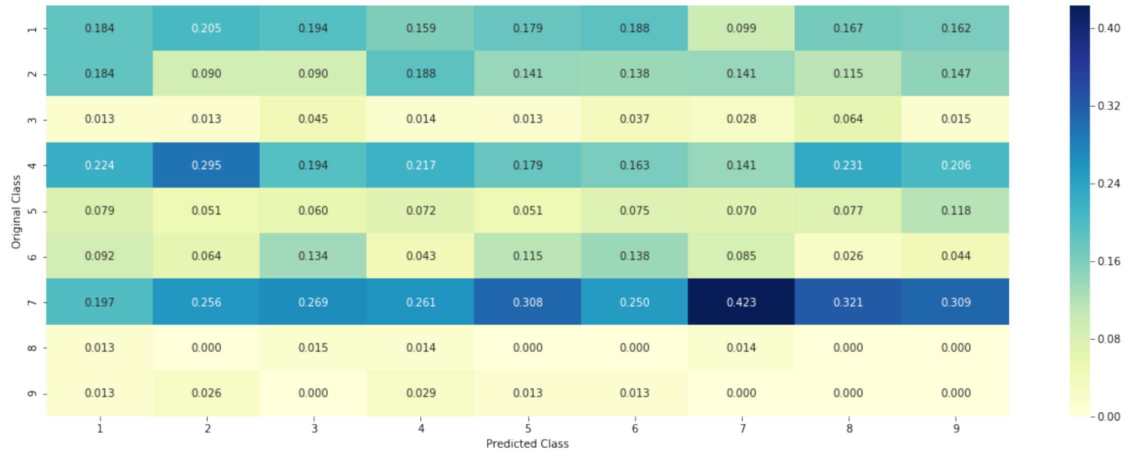
```
#     [3, 4]]
# C.T = [[1, 3],
#        [2, 4]]
# C.sum(axis = 1)  axis=0 corresonds to columns and axis=1 corresponds to rows in
# C.sum(axix =1) = [[3, 7]]
# ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
#                            [2/3, 4/7]]

# ((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, yticklabe
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, yticklabe
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, yticklabe
plt.xlabel('Predicted Class')
plt.ylabel('Original Class')
plt.show()
```

In [11]:
```
# we need to generate 9 numbers and the sum of numbers should be 1
# one solution is to genarate 9 numbers and divide each of the numbers by their sum
# ref: https://stackoverflow.com/a/18662466/4084039
```

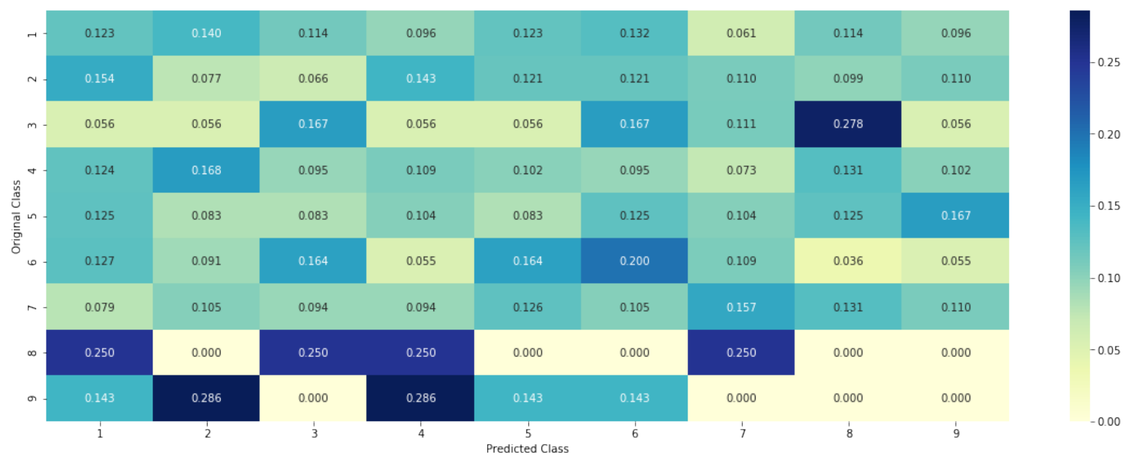
```
test_data_len = test_df.shape[0]
cv_data_len = cv_df.shape[0]

# we create a output array that has exactly same size as the CV data
cv_predicted_y = np.zeros((cv_data_len,9))
for i in range(cv_data_len):
    rand_probs = np.random.rand(1,9)
    cv_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Cross Validation Data using Random Model",log_loss(y_cv,cv_predicte


# Test-Set error.
#we create a output array that has exactly same as the test data
test_predicted_y = np.zeros((test_data_len,9))
for i in range(test_data_len):
    rand_probs = np.random.rand(1,9)
    test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Test Data using Random Model",log_loss(y_test,test_predicted_y, eps

predicted_y =np.argmax(test_predicted_y, axis=1)
plot_confusion_matrix(y_test, predicted_y+1)
```

```
Log loss on Cross Validation Data using Random Model 2.52634639533
Log loss on Test Data using Random Model 2.40777991412
-------------------- Confusion matrix --------------------
```


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




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



3.3 Univariate Analysis

```
In [12]: # code for response coding with Laplace smoothing.
         # alpha : used for laplace smoothing
         # feature: ['gene', 'variation']
         # df: ['train_df', 'test_df', 'cv_df']
         # algorithm
         # ----------
         # Consider all unique values and the number of occurances of given feature in train d
         # build a vector (1*9) , the first element = (number of times it occured in class1 +
         # gv_dict is like a look up table, for every gene it store a (1*9) representation of
         # for a value of feature in df:
         # if it is in train data:
```

```
# we add the vector that was stored in 'gv_dict' look up table to 'gv_fea'
# if it is not there is train:
# we add [1/9, 1/9, 1/9, 1/9,1/9, 1/9, 1/9, 1/9, 1/9] to 'gv_fea'
# return 'gv_fea'
# ----------------------

# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
    # value_count: it contains a dict like
    # print(train_df['Gene'].value_counts())
    # output:
    #        {BRCA1      174
    #         TP53       106
    #         EGFR        86
    #         BRCA2       75
    #         PTEN        69
    #         KIT         61
    #         BRAF        60
    #         ERBB2       47
    #         PDGFRA      46
    #         ...}
    # print(train_df['Variation'].value_counts())
    # output:
    # {
    # Truncating_Mutations                     63
    # Deletion                                 43
    # Amplification                            43
    # Fusions                                  22
    # Overexpression                            3
    # E17K                                      3
    # Q61L                                      3
    # S222D                                     2
    # P130S                                     2
    # ...
    # }
    value_count = train_df[feature].value_counts()

    # gv_dict : Gene Variation Dict, which contains the probability array for each ge
    gv_dict = dict()

    # denominator will contain the number of time that particular feature occured in t
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to pert
        # vec is 9 diamensional vector
        vec = []
        for k in range(1,10):
            # print(train_df.loc[(train_df['Class']==1) & (train_df['Gene']=='BRCA1')
            #         ID   Gene             Variation  Class
```

```python
                # 2470  2470  BRCA1                S1715C      1
                # 2486  2486  BRCA1                S1841R      1
                # 2614  2614  BRCA1                   M1R      1
                # 2432  2432  BRCA1                L1657P      1
                # 2567  2567  BRCA1                T1685A      1
                # 2583  2583  BRCA1                E1660G      1
                # 2634  2634  BRCA1                W1718L      1
                # cls_cnt.shape[0] will return the number of rows

                cls_cnt = train_df.loc[(train_df['Class']==k) & (train_df[feature]==i)]

                # cls_cnt.shape[0](numerator) will contain the number of time that partic
                vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))

            # we are adding the gene/variation to the dict as key and vec as value
            gv_dict[i]=vec
        return gv_dict

    # Get Gene variation feature
    def get_gv_feature(alpha, feature, df):
        # print(gv_dict)
        #     {'BRCA1': [0.20075757575757575, 0.03787878787878788, 0.068181818181818177, 
        #      'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 
        #      'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.06818181818181
        #      'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.060606060606060608, 
        #      'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 
        #      'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0
        #      'BRAF': [0.066666666666666666, 0.17999999999999999, 0.073333333333333334, 
        #      ...
        #     }
        gv_dict = get_gv_fea_dict(alpha, feature, df)
        # value_count is similar in get_gv_fea_dict
        value_count = train_df[feature].value_counts()

        # gv_fea: Gene_variation feature, it will contain the feature for each feature va
        gv_fea = []
        # for every feature values in the given data frame we will check if it is there i
        # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to gv_fea
        for index, row in df.iterrows():
            if row[feature] in dict(value_count).keys():
                gv_fea.append(gv_dict[row[feature]])
            else:
                gv_fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
    #             gv_fea.append([-1,-1,-1,-1,-1,-1,-1,-1,-1])
        return gv_fea
```

when we caculate the probability of a feature belongs to any particular class, we apply laplace smoothing

(numerator + 10*alpha) / (denominator + 90*alpha)
3.2.1 Univariate Analysis on Gene Feature
Q1. Gene, What type of feature it is ?
Ans. Gene is a categorical variable
Q2. How many categories are there and How they are distributed?

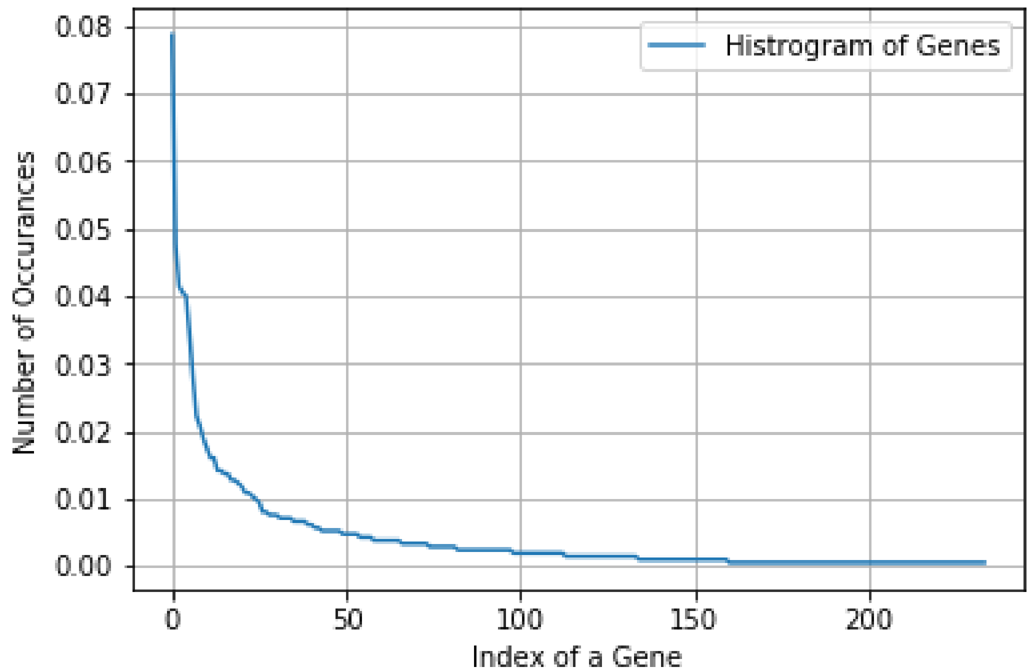
```
In [13]: unique_genes = train_df['Gene'].value_counts()
         print('Number of Unique Genes :', unique_genes.shape[0])
         # the top 10 genes that occured most
         print(unique_genes.head(10))
```

```
Number of Unique Genes : 234
BRCA1     167
TP53      101
PTEN       88
BRCA2      86
EGFR       85
KIT        73
BRAF       59
ERBB2      47
ALK        44
PDGFRA     40
Name: Gene, dtype: int64
```

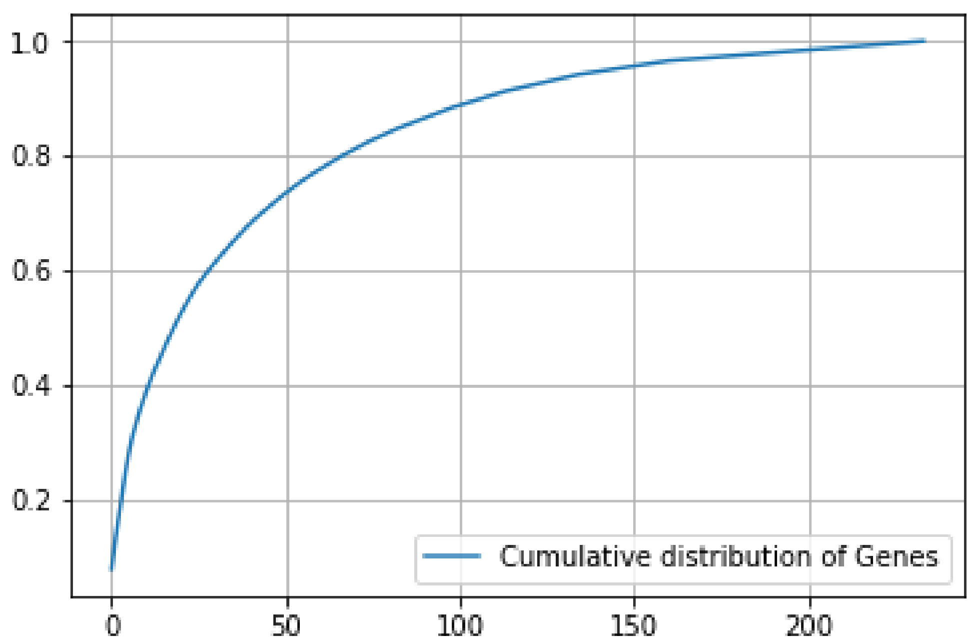
```
In [14]: print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in the t
```

```
Ans: There are 234 different categories of genes in the train data, and they are distibuted as
```

```
In [15]: s = sum(unique_genes.values);
         h = unique_genes.values/s;
         plt.plot(h, label="Histrogram of Genes")
         plt.xlabel('Index of a Gene')
         plt.ylabel('Number of Occurances')
         plt.legend()
         plt.grid()
         plt.show()
```




```
In [16]: c = np.cumsum(h)
         plt.plot(c,label='Cumulative distribution of Genes')
         plt.grid()
         plt.legend()
         plt.show()
```



Q3. How to featurize this Gene feature ?

Ans.there are two ways we can featurize this variable check out this video: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/handling-categorical-and-numerical-features/

One hot Encoding

Response coding

We will choose the appropriate featurization based on the ML model we use. For this problem of multi-class classification with categorical features, one-hot encoding is better for Logistic regression while response coding is better for Random Forests.

In [17]:
```
#response-coding of the Gene feature
# alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", train_df))
# test gene feature
test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", test_df))
# cross validation gene feature
cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", cv_df))
```

In [18]:
```
print("train_gene_feature_responseCoding is converted feature using respone coding me
```

```
train_gene_feature_responseCoding is converted feature using respone coding method. The shape o
```

In [19]:
```
# one-hot encoding of Gene feature.
gene_vectorizer = CountVectorizer()
train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gene'])
test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gene'])
cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
```

In [20]:
```
train_df['Gene'].head()
```

Out[20]:
```
2923    NFE2L2
2468     BRCA1
1802      ARAF
896     PDGFRA
2439     BRCA1
Name: Gene, dtype: object
```

In [21]:
```
gene_vectorizer.get_feature_names()[0:5]
```

Out[21]:
```
['abl1', 'acvr1', 'ago2', 'akt1', 'akt2']
```

In [22]:
```
print("train_gene_feature_onehotCoding is converted feature using one-hot encoding me
```

```
train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape o
```

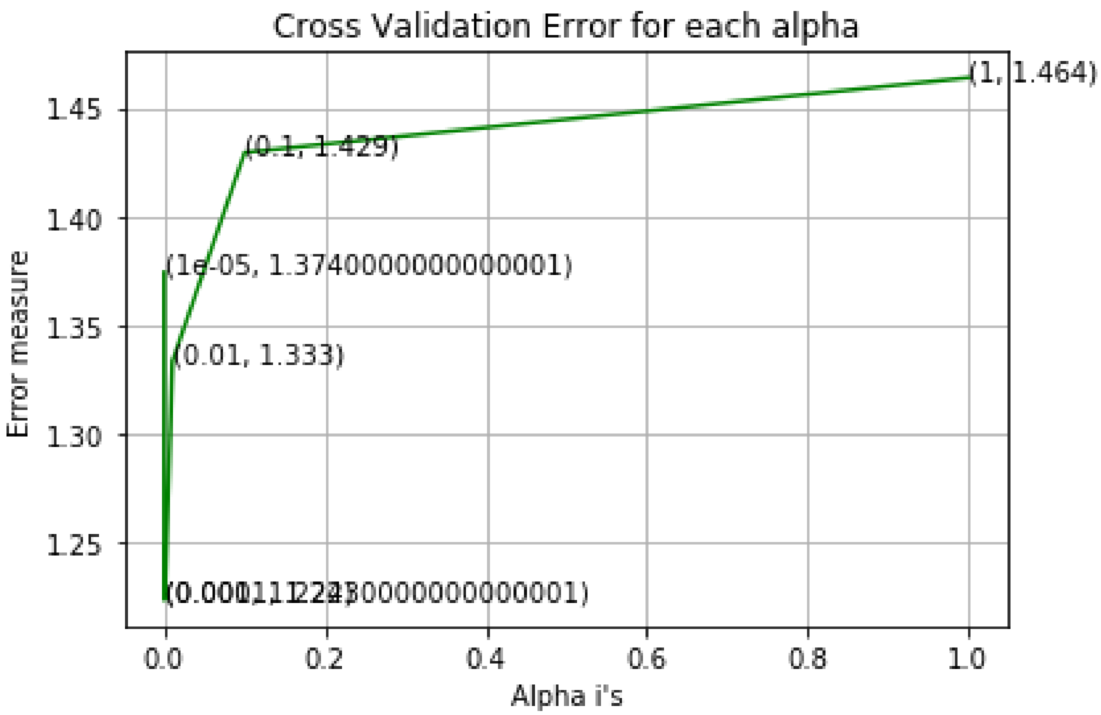
Q4. How good is this gene feature in predicting y_i?

There are many ways to estimate how good a feature is, in predicting y_i. One of the good methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y_i.

In [23]:
```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with Stochastic Gr
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link:
#------------------------------


cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
    clf.fit(train_gene_feature_onehotCoding, y_train)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_gene_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, la

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],np.round(txt,3)), (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=42
clf.fit(train_gene_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
```

```
        sig_clf.fit(train_gene_feature_onehotCoding, y_train)

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

```
For values of alpha =  1e-05 The log loss is: 1.3742007599
For values of alpha =  0.0001 The log loss is: 1.22323106009
For values of alpha =  0.001 The log loss is: 1.22398247133
For values of alpha =  0.01 The log loss is: 1.33311069485
For values of alpha =  0.1 The log loss is: 1.42936500432
For values of alpha =  1 The log loss is: 1.4638331712
```




```
For values of best alpha =  0.0001 The train log loss is: 1.05405500212
For values of best alpha =  0.0001 The cross validation log loss is: 1.22323106009
For values of best alpha =  0.0001 The test log loss is: 1.23765886252
```

Q5. Is the Gene feature stable across all the data sets (Test, Train, Cross validation)?
Ans. Yes, it is. Otherwise, the CV and Test errors would be significantly more than train error.

In [24]:
```
print("Q6. How many data points in Test and CV datasets are covered by the ", unique_

test_coverage=test_df[test_df['Gene'].isin(list(set(train_df['Gene'])))].shape[0]
cv_coverage=cv_df[cv_df['Gene'].isin(list(set(train_df['Gene'])))].shape[0]

print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_cove
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_co
```

```
Q6. How many data points in Test and CV datasets are covered by the  234  genes in train datas
Ans
1. In test data 640 out of 665 : 96.2406015037594
2. In cross validation data 518 out of  532 : 97.36842105263158
```

3.2.2 Univariate Analysis on Variation Feature
Q7. Variation, What type of feature is it ?
Ans. Variation is a categorical variable
Q8. How many categories are there?

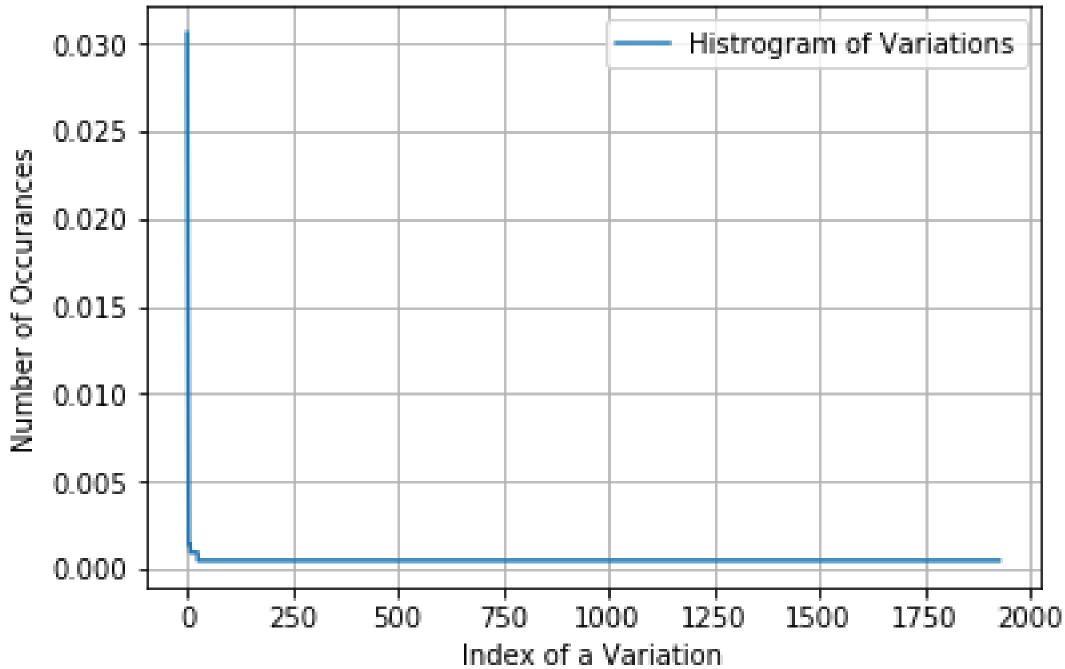
In [25]:
```
unique_variations = train_df['Variation'].value_counts()
print('Number of Unique Variations :', unique_variations.shape[0])
# the top 10 variations that occured most
print(unique_variations.head(10))
```

```
Number of Unique Variations : 1928
Truncating_Mutations    65
Amplification           52
Deletion                39
Fusions                 18
Q61H                     3
Q61L                     3
G12V                     3
Q61R                     3
I31M                     2
G35R                     2
Name: Variation, dtype: int64
```

In [26]:
```
print("Ans: There are", unique_variations.shape[0] ,"different categories of variatio
```

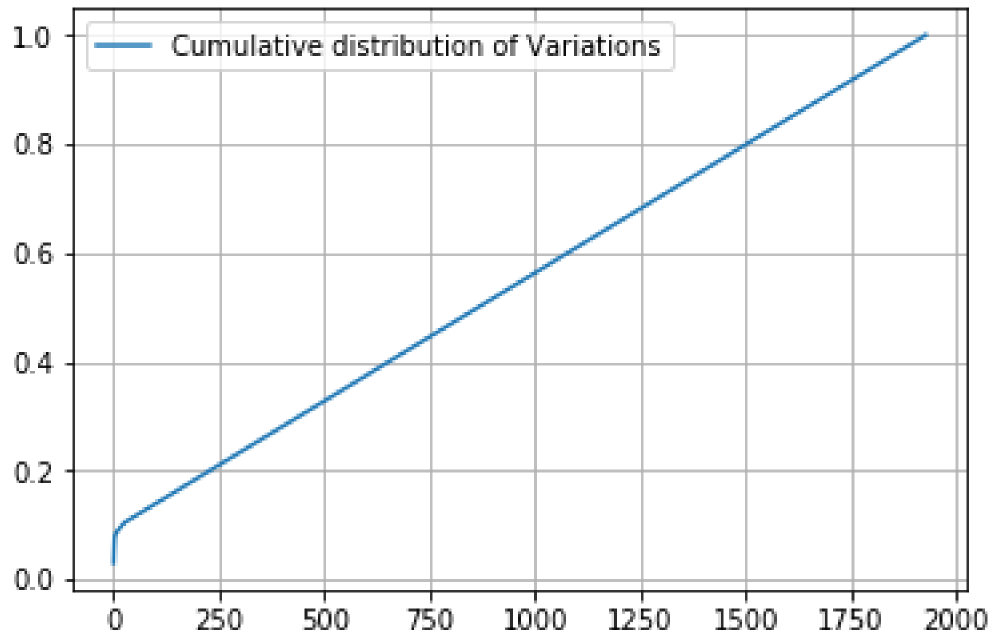
```
Ans: There are 1928 different categories of variations in the train data, and they are distibu
```

In [27]:
```
s = sum(unique_variations.values);
h = unique_variations.values/s;
plt.plot(h, label="Histrogram of Variations")
plt.xlabel('Index of a Variation')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```




```
In [28]: c = np.cumsum(h)
         print(c)
         plt.plot(c,label='Cumulative distribution of Variations')
         plt.grid()
         plt.legend()
         plt.show()
```

```
[ 0.03060264  0.05508475  0.07344633 ...,  0.99905838  0.99952919  1.        ]
```



Q9. How to featurize this Variation feature ?

Ans.There are two ways we can featurize this variable check out this video: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/handling-categorical-and-numerical-features/

One hot Encoding

Response coding

We will be using both these methods to featurize the Variation Feature

```
In [29]: # alpha is used for laplace smoothing
         alpha = 1
         # train gene feature
         train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", t
         # test gene feature
         test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", te
         # cross validation gene feature
         cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", cv_d
```

```
In [30]: print("train_variation_feature_responseCoding is a converted feature using the respons

train_variation_feature_responseCoding is a converted feature using the response coding method
```

```
In [31]: # one-hot encoding of variation feature.
         variation_vectorizer = CountVectorizer()
         train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Va
         test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variatio
         cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation']]
```

```
In [32]: print("train_variation_feature_onehotEncoded is converted feature using the onne-hot e
```

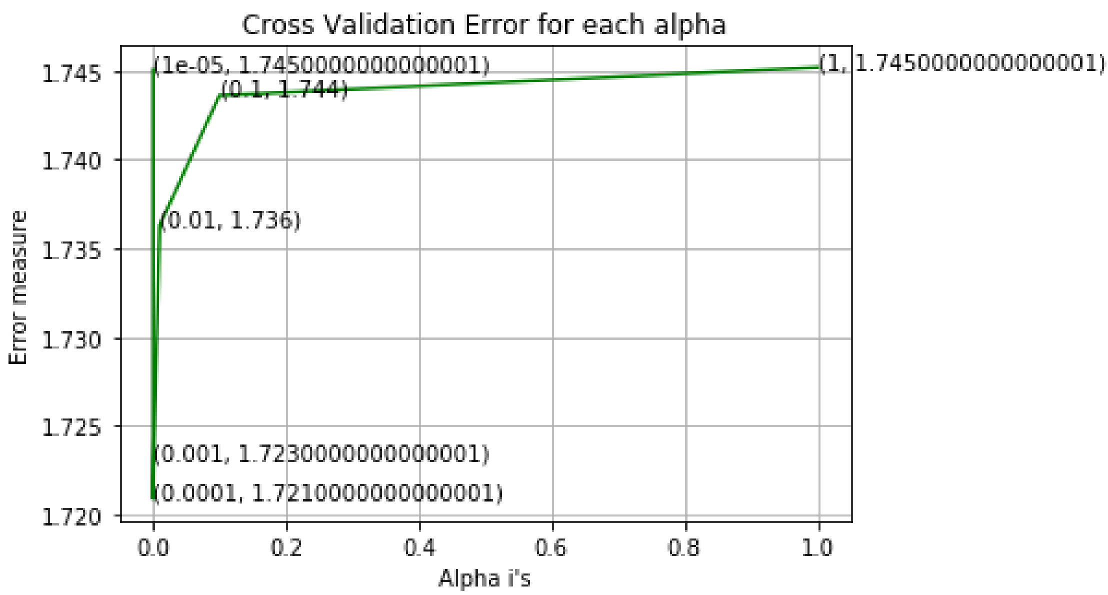
```
train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method.
```

Q10. How good is this Variation feature in predicting y_i?
Let's build a model just like the earlier!

```
In [33]: alpha = [10 ** x for x in range(-5, 1)]

         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # class_weight=None, warm_start=False, average=False, n_iter=None)

         # some of methods
         # fit(X, y[, coef_init, intercept_init, ])        Fit linear model with Stochastic Gr
         # predict(X)        Predict class labels for samples in X.

         #-------------------------------
         # video link:
         #------------------------------


         cv_log_error_array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
             clf.fit(train_variation_feature_onehotCoding, y_train)

             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_variation_feature_onehotCoding, y_train)
             predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)

             cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, la

         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],np.round(txt,3)), (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_variation_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_variation_feature_onehotCoding, y_train)

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

```
For values of alpha =  1e-05 The log loss is: 1.74508539482
For values of alpha =  0.0001 The log loss is: 1.72085302091
For values of alpha =  0.001 The log loss is: 1.72305946667
For values of alpha =  0.01 The log loss is: 1.7362828386
For values of alpha =  0.1 The log loss is: 1.74362826216
For values of alpha =  1 The log loss is: 1.74520569505
```




```
For values of best alpha =  0.0001 The train log loss is: 0.718812331106
For values of best alpha =  0.0001 The cross validation log loss is: 1.72085302091
For values of best alpha =  0.0001 The test log loss is: 1.6830382506
```

Q11. Is the Variation feature stable across all the data sets (Test, Train, Cross validation)?
Ans. Not sure! But lets be very sure using the below analysis.

```
In [34]: print("Q12. How many data points are covered by total ", unique_variations.shape[0], '
         test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))].sha
         cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
         print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_cove
         print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_co
```

```
Q12. How many data points are covered by total  1928  genes in test and cross validation data s
Ans
1. In test data 74 out of 665 : 11.12781954887218
2. In cross validation data 51 out of  532 : 9.586466165413533
```

3.2.3 Univariate Analysis on Text Feature

1. How many unique words are present in train data?
2. How are word frequencies distributed?
3. How to featurize text field?
4. Is the text feature useful in predicitng y_i?
5. Is the text feature stable across train, test and CV datasets?

```
In [35]: # 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 [36]: import math
         #https://stackoverflow.com/a/1602964
         def get_text_responsecoding(df):
             text_feature_responseCoding = np.zeros((df.shape[0],9))
             for i in range(0,9):
                 row_index = 0
                 for index, row in df.iterrows():
                     sum_prob = 0
                     for word in row['TEXT'].split():
                         sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(total_dict.get(w
                     text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TE
                     row_index += 1
             return text_feature_responseCoding
```

```
In [38]: # building a CountVectorizer with all the words that occured minimum 3 times in train
         text_vectorizer_onehotCoding = CountVectorizer(min_df=3)
```

```
train_text_feature_onehotCoding = text_vectorizer_onehotCoding.fit_transform(train_df

#SMUK
# getting all the feature names (words)
train_text_features_1= text_vectorizer_onehotCoding.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*nu
train_text_fea_counts_1 = train_text_feature_onehotCoding.sum(axis=0).A1

# zip(list(text_features),text_fea_counts) will zip a word with its number of times i
text_fea_dict_1 = dict(zip(list(train_text_features_1),train_text_fea_counts_1))

print("Total number of unique words in train data BOW: shape", len(train_text_feature

# building a CountVectorizer with all the words that occured minimum 3 times in train
text_vectorizer_ngram = CountVectorizer(min_df=3,ngram_range=(1,2))
train_text_feature_ngram = text_vectorizer_ngram.fit_transform(train_df['TEXT'])

# getting all the feature names (words)
train_text_features_2= text_vectorizer_ngram.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*nu
train_text_fea_counts_2 = train_text_feature_ngram.sum(axis=0).A1

# zip(list(text_features),text_fea_counts) will zip a word with its number of times i
text_fea_dict_2 = dict(zip(list(train_text_features_2),train_text_fea_counts_2))

print("Total number of unique words in train data ngram: shape", len(train_text_featu


# building a TFIDFVectorizer with all the words that occured minimum 3 times in train
text_vectorizer_tfidf = TfidfVectorizer(min_df=3)
train_text_feature_tfidf = text_vectorizer_tfidf.fit_transform(train_df['TEXT'])

# getting all the feature names (words)
train_text_features_3= text_vectorizer_tfidf.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*nu
train_text_fea_counts_3 = train_text_feature_tfidf.sum(axis=0).A1

# zip(list(text_features),text_fea_counts) will zip a word with its number of times i
text_fea_dict_3 = dict(zip(list(train_text_features_3),train_text_fea_counts_3))

print("Total number of unique words in train data tfidf: shape", len(train_text_featu


# building a TFIDFVectorizer with all the words that occured minimum 3 times in train
text_vectorizer_tfidf1000 = TfidfVectorizer(min_df=3)
```

```
train_text_feature_tfidf = text_vectorizer_tfidf1000.fit_transform(train_df['TEXT'])

#Take top 1000 words start here
indices = np.argsort(text_vectorizer_tfidf1000.idf_)[::-1]
features = text_vectorizer_tfidf1000.get_feature_names()
top_features = [features[i] for i in indices[:1000]]
#add the other feature in stopwords
bottom_features=[features[i] for i in indices[1000:]]
print(top_features[0:10])
#print feature and tfidf score
idf = text_vectorizer_tfidf1000.idf_
#print(dict(zip(text_vectorizer.get_feature_names(), idf)))
text_vectorizer_tfidf1000 = TfidfVectorizer(min_df=3,stop_words=bottom_features)
train_text_feature_tfidf1000 = text_vectorizer_tfidf1000.fit_transform(train_df['TEXT

# getting all the feature names (words)
train_text_features_4 = text_vectorizer_tfidf1000.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*nu

train_text_fea_counts_4 = train_text_feature_tfidf1000.sum(axis=0).A1

# zip(list(text_features),text_fea_counts) will zip a word with its number of times i
text_fea_dict_4 = dict(zip(list(train_text_features_4),train_text_fea_counts_4))

print("Total number of unique words in train data tfidf1000: shape", len(train_text_f
```

```
Total number of unique words in train data BOW: shape 51546 (2124, 51546) (2124,)
Total number of unique words in train data ngram: shape 751379 (2124, 751379)
Total number of unique words in train data tfidf: shape 51546 (2124, 51546)
['seliger', 'disorder89', 'novabiochem', 's41', 's406n', 'mikkelsen', 's3o', 's3k', 'dismantle
Total number of unique words in train data tfidf1000: shape 1000 (2124, 1000)
```

In [39]:
```
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)

#train_text_features SMUK 1:bow,2:ngram,3:tfidf 4:tfidf1000
confuse_array_1 = []
for i in train_text_features_1:
```

```
        ratios = []
        max_val = -1
        for j in range(0,9):
            ratios.append((dict_list[j][i]+10 )/(total_dict[i]+90))
        confuse_array_1.append(ratios)
    confuse_array_1 = np.array(confuse_array_1)

    confuse_array_2 = []
    for i in train_text_features_2:
        ratios = []
        max_val = -1
        for j in range(0,9):
            ratios.append((dict_list[j][i]+10 )/(total_dict[i]+90))
        confuse_array_2.append(ratios)
    confuse_array_2 = np.array(confuse_array_2)

    confuse_array_3 = []
    for i in train_text_features_3:
        ratios = []
        max_val = -1
        for j in range(0,9):
            ratios.append((dict_list[j][i]+10 )/(total_dict[i]+90))
        confuse_array_3.append(ratios)
    confuse_array_3 = np.array(confuse_array_3)

    confuse_array_4 = []
    for i in train_text_features_4:
        ratios = []
        max_val = -1
        for j in range(0,9):
            ratios.append((dict_list[j][i]+10 )/(total_dict[i]+90))
        confuse_array_4.append(ratios)
    confuse_array_4 = np.array(confuse_array_4)
```

In [40]:
```
#response coding of text features
train_text_feature_responseCoding  = get_text_responsecoding(train_df)
test_text_feature_responseCoding  = get_text_responsecoding(test_df)
cv_text_feature_responseCoding  = get_text_responsecoding(cv_df)
```

In [41]:
```
# https://stackoverflow.com/a/16202486
# we convert each row values such that they sum to 1
train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train_text_fe
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_featu
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_res
```

In [42]:
```
# 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_onehotCoding.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_onehotCoding.transform(cv_df['TEXT'])
# don't forget to normalize every feature
cv_text_feature_onehotCoding = normalize(cv_text_feature_onehotCoding, axis=0)


train_text_feature_ngramg = normalize(train_text_feature_ngram, axis=0)
test_text_feature_ngram = text_vectorizer_ngram.transform(test_df['TEXT'])
test_text_feature_ngram = normalize(test_text_feature_ngram, axis=0)
cv_text_feature_ngram = text_vectorizer_ngram.transform(cv_df['TEXT'])
cv_text_feature_ngram = normalize(cv_text_feature_ngram, axis=0)


train_text_feature_tfidf = normalize(train_text_feature_tfidf, axis=0)
test_text_feature_tfidf = text_vectorizer_tfidf.transform(test_df['TEXT'])
test_text_feature_tfidf = normalize(test_text_feature_tfidf, axis=0)
cv_text_feature_tfidf = text_vectorizer_tfidf.transform(cv_df['TEXT'])
cv_text_feature_tfidf = normalize(cv_text_feature_tfidf, axis=0)

train_text_feature_tfidf1000 = normalize(train_text_feature_tfidf1000, axis=0)
test_text_feature_tfidf1000 = text_vectorizer_tfidf1000.transform(test_df['TEXT'])
test_text_feature_tfidf1000 = normalize(test_text_feature_tfidf1000, axis=0)
cv_text_feature_tfidf1000 = text_vectorizer_tfidf1000.transform(cv_df['TEXT'])
cv_text_feature_tfidf1000 = normalize(cv_text_feature_tfidf1000, axis=0)
```

In [43]:
```
#https://stackoverflow.com/a/2258273/4084039
sorted_text_fea_dict_1 = dict(sorted(text_fea_dict_1.items(), key=lambda x: x[1] , re
sorted_text_occur_1 = np.array(list(sorted_text_fea_dict_1.values()))

sorted_text_fea_dict_2 = dict(sorted(text_fea_dict_2.items(), key=lambda x: x[1] , re
sorted_text_occur_2 = np.array(list(sorted_text_fea_dict_2.values()))

sorted_text_fea_dict_3 = dict(sorted(text_fea_dict_3.items(), key=lambda x: x[1] , re
sorted_text_occur_3 = np.array(list(sorted_text_fea_dict_3.values()))

sorted_text_fea_dict_4 = dict(sorted(text_fea_dict_4.items(), key=lambda x: x[1] , re
sorted_text_occur_4 = np.array(list(sorted_text_fea_dict_4.values()))
```

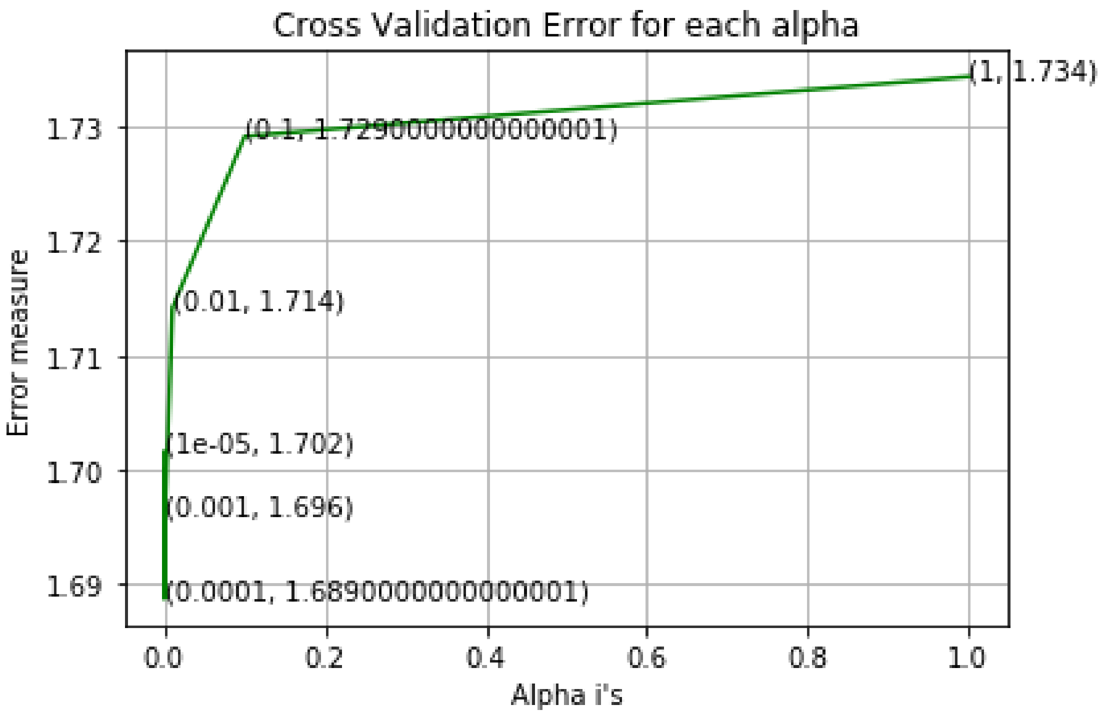
In [44]:
```
# Number of words for a given frequency.
print(Counter(sorted_text_occur_1[0:10]))
print(Counter(sorted_text_occur_2[0:10]))
print(Counter(sorted_text_occur_3[0:10]))
print(Counter(sorted_text_occur_4[0:10]))
print(len(train_df['TEXT']))
```

```
Counter({4832: 1, 754: 1, 52: 1, 5: 1, 4: 1, 106: 1, 412: 1, 61: 1, 158: 1, 95: 1})
Counter({5: 3, 3: 2, 4: 2, 7: 1, 43: 1, 221: 1})
Counter({0.63506617887882777: 1, 1.9271270771001563: 1, 0.26753597927792766: 1, 1.333699780500
Counter({0.57025630761017432: 1, 0.89816473061831248: 1, 2.5153732744155644: 1, 3.0: 1, 2.1213
2124
```

In [45]:
```
# Train a Logistic regression+Calibration model using text features whicha re tfidf e
alpha = [10 ** x for x in range(-5, 1)]

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])       Fit linear model with Stochastic Gr
# predict(X)       Predict class labels for samples in X.

#-------------------------------
# video link:
#------------------------------


cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
    clf.fit(train_text_feature_tfidf1000, y_train)

    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_text_feature_tfidf1000, y_train)
    predict_y = sig_clf.predict_proba(cv_text_feature_tfidf1000)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-1
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, l

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],np.round(txt,3)), (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=42
clf.fit(train_text_feature_tfidf1000, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_tfidf1000, y_train)

predict_y = sig_clf.predict_proba(train_text_feature_tfidf1000)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_l
predict_y = sig_clf.predict_proba(cv_text_feature_tfidf1000)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
predict_y = sig_clf.predict_proba(test_text_feature_tfidf1000)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_lo
```

```
For values of alpha =  1e-05 The log loss is: 1.70155381066
For values of alpha =  0.0001 The log loss is: 1.68864189522
For values of alpha =  0.001 The log loss is: 1.69603762778
For values of alpha =  0.01 The log loss is: 1.71413010336
For values of alpha =  0.1 The log loss is: 1.72919475043
For values of alpha =  1 The log loss is: 1.73441131626
```




```
For values of best alpha =  0.0001 The train log loss is: 1.51889609674
For values of best alpha =  0.0001 The cross validation log loss is: 1.68864189522
For values of best alpha =  0.0001 The test log loss is: 1.69149592263
```

Q. Is the Text feature stable across all the data sets (Test, Train, Cross validation)?
Ans. Yes, it seems like!

In [46]:
```
def get_intersec_text(df,type=1):
    df_text_vec = CountVectorizer(min_df=3)
    if type==2:
        df_text_vec = CountVectorizer(min_df=3,ngram_range=(1,2))
    if type==3:
        df_text_vec = TfidfVectorizer(min_df=3)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

    df_text_fea_counts = df_text_fea.sum(axis=0).A1
    df_text_fea_dict = dict(zip(list(df_text_features),df_text_fea_counts))
    len1 = len(set(df_text_features))
    len2 = len(set(train_text_features_1) & set(df_text_features))
    if type==2:
        len2 = len(set(train_text_features_2) & set(df_text_features))
    if type==3:
        len2 = len(set(train_text_features_2) & set(df_text_features))

    return len1,len2
```

In [47]:
```
len1,len2 = get_intersec_text(test_df,1)
print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data fo
len1,len2 = get_intersec_text(cv_df)
print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train 

len1,len2 = get_intersec_text(test_df,2)
print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data fo
len1,len2 = get_intersec_text(cv_df)
print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train 

len1,len2 = get_intersec_text(test_df,3)
print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data fo
len1,len2 = get_intersec_text(cv_df)
print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train 
```

```
96.356 % of word of test data appeared in train data for bow
96.958 % of word of Cross Validation appeared in train data for bow
92.882 % of word of test data appeared in train data for ngram
96.958 % of word of Cross Validation appeared in train data for ngram
96.356 % of word of test data appeared in train data for tfidf
96.958 % of word of Cross Validation appeared in train data for tfidf
```

4. Machine Learning Models

In [48]:
```
#Data preparation for ML models.
```

```
#Misc. functionns for ML models


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))/tes
    plot_confusion_matrix(test_y, pred_y)
```

In [49]:
```
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 [50]:
```
# 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 [{}]".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
```

Stacking the three types of features

```
In [51]: # merging gene, variance and text features

         # building train, test and cross validation data sets
         # a = [[1, 2],
         #      [3, 4]]
         # b = [[4, 5],
         #      [6, 7]]
         # hstack(a, b) = [[1, 2, 4, 5],
         #                 [ 3, 4, 6, 7]]

         train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,train_variation_
         test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_fea
         cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_o

         train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text_feature_onehotC
         train_y = np.array(list(train_df['Class']))

         test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_feature_onehotCodi
         test_y = np.array(list(test_df['Class']))

         cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text_feature_onehotCoding)).t
         cv_y = np.array(list(cv_df['Class']))

         #apply ngram on text and onehotCoding in gene and variation
         train_x_ngram = hstack((train_gene_var_onehotCoding, train_text_feature_ngram)).tocsr
         test_x_ngram = hstack((test_gene_var_onehotCoding, test_text_feature_ngram)).tocsr()
         cv_x_ngram = hstack((cv_gene_var_onehotCoding, cv_text_feature_ngram)).tocsr()

         #apply tfidf on text and onehotCoding in gene and variation
         train_x_tfidf = hstack((train_gene_var_onehotCoding, train_text_feature_tfidf)).tocsr
         test_x_tfidf = hstack((test_gene_var_onehotCoding, test_text_feature_tfidf)).tocsr()
         cv_x_tfidf = hstack((cv_gene_var_onehotCoding, cv_text_feature_tfidf)).tocsr()
```

```
#apply tfidf(top1000 words) on text and onehotCoding in gene and variation
train_x_tfidf1000 = hstack((train_gene_var_onehotCoding, train_text_feature_tfidf1000)
test_x_tfidf1000 = hstack((test_gene_var_onehotCoding, test_text_feature_tfidf1000)).t
cv_x_tfidf1000 = hstack((cv_gene_var_onehotCoding, cv_text_feature_tfidf1000)).tocsr()


train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,train_var
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variat
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_fe

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_res
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_response
```

In [52]:
```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehot
print("(number of data points * number of features) in test data = ", test_x_onehotCo
print("(number of data points * number of features) in cross validation data =", cv_x_

print("ngram features :")
print("(number of data points * number of features) in train data = ", train_x_ngram.s
print("(number of data points * number of features) in test data = ", test_x_ngram.sha
print("(number of data points * number of features) in cross validation data =", cv_x_

print("tfidf features :")
print("(number of data points * number of features) in train data = ", train_x_tfidf.s
print("(number of data points * number of features) in test data = ", test_x_tfidf.sha
print("(number of data points * number of features) in cross validation data =", cv_x_

print("tfidf to 1000 words features :")
print("(number of data points * number of features) in train data = ", train_x_tfidf1
print("(number of data points * number of features) in test data = ", test_x_tfidf100
print("(number of data points * number of features) in cross validation data =", cv_x_

print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_respons
print("(number of data points * number of features) in test data = ", test_x_response
print("(number of data points * number of features) in cross validation data =", cv_x_
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 53735)
(number of data points * number of features) in test data =  (665, 53735)
(number of data points * number of features) in cross validation data = (532, 53735)
ngram features :
(number of data points * number of features) in train data =  (2124, 753568)
(number of data points * number of features) in test data =  (665, 753568)
(number of data points * number of features) in cross validation data = (532, 753568)
tfidf features :
```

```
(number of data points * number of features) in train data =  (2124, 53735)
(number of data points * number of features) in test data =  (665, 53735)
(number of data points * number of features) in cross validation data = (532, 53735)
tfidf to 1000 words features :
(number of data points * number of features) in train data =  (2124, 3189)
(number of data points * number of features) in test data =  (665, 3189)
(number of data points * number of features) in cross validation data = (532, 3189)
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 27)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data = (532, 27)
```

In [56]:
```
#Try feature engineering technique to use log of train_gene_var_onehotCoding
print(train_gene_var_onehotCoding.shape)
#first make same variable as without feature transformation
train_gene_var_feature=train_gene_var_onehotCoding
test_gene_var_feature=test_gene_var_onehotCoding
cv_gene_var_feature=cv_gene_var_onehotCoding

train_gene_var_feature.data=np.log(train_gene_var_onehotCoding.data+1)
test_gene_var_feature.data=np.log(test_gene_var_onehotCoding.data+1)
cv_gene_var_feature.data=np.log(cv_gene_var_onehotCoding.data+1)
print(train_gene_var_onehotCoding.shape)
print(train_gene_var_onehotCoding.data)

#apply ngram on text and onehotCoding+log transform in gene and variation
train_x_feature = hstack((train_gene_var_feature, train_text_feature_tfidf1000)).tocs
test_x_feature = hstack((test_gene_var_feature, test_text_feature_tfidf1000)).tocsr()
cv_x_feature = hstack((cv_gene_var_feature, cv_text_feature_tfidf1000)).tocsr()

print(" After log transformation on gene and variation features :")
print("(number of data points * number of features) in train data = ", train_x_featur
print("(number of data points * number of features) in test data = ", test_x_feature.
print("(number of data points * number of features) in cross validation data =", cv_x
```

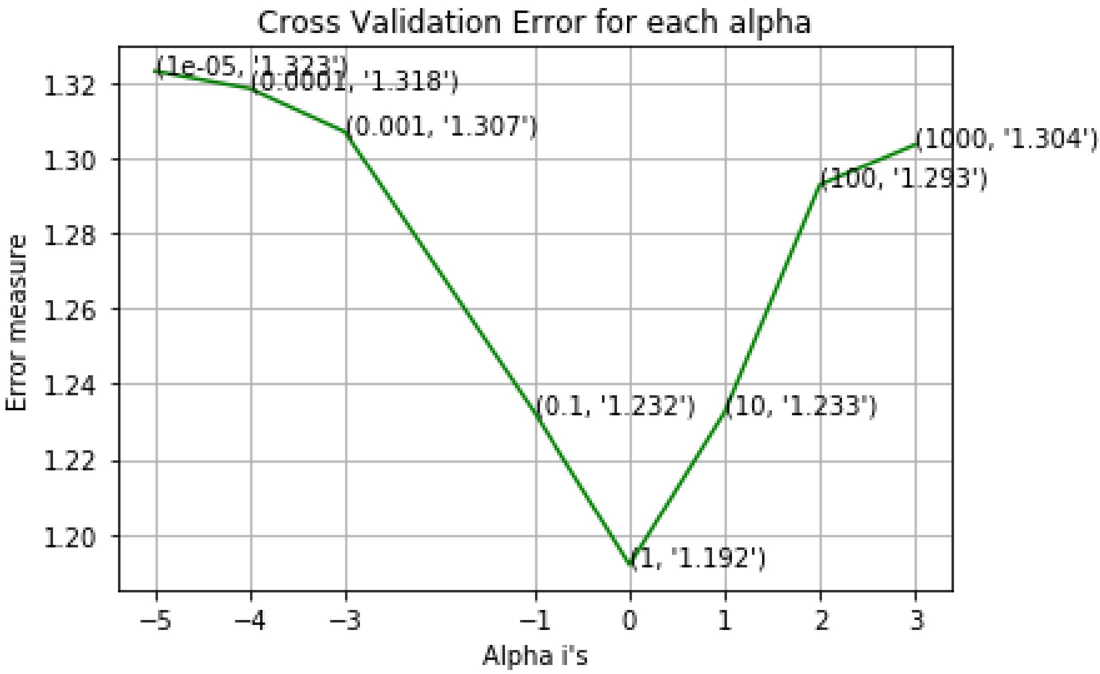
```
(2124, 2189)
(2124, 2189)
[ 0.52658903  0.52658903  0.52658903 ...,  0.52658903  0.52658903
  0.52658903]
 After log transformation on gene and variation features :
(number of data points * number of features) in train data =  (2124, 3189)
(number of data points * number of features) in test data =  (665, 3189)
(number of data points * number of features) in cross validation data = (532, 3189)
```

4.1. Base Line Model
4.1.1. Naive Bayes
4.1.1.1. Hyper parameter tuning

In [59]:
```
# find more about Multinomial Naive base function here http://scikit-learn.org/stable/
# -------------------------
# default paramters
# sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_prior=None)

# some of methods of MultinomialNB()
# fit(X, y[, sample_weight])        Fit Naive Bayes classifier according to X, y
# predict(X)        Perform classification on an array of test vectors X.
# predict_log_proba(X)        Return log-probability estimates for the test vector X.
# -----------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
# -----------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/module
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
# ----------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
# -----------------------

#any dataset can be applied here like bow,tfidf,featurized,response coding
#train_x_onehotCoding/train_x_ngram/train_x_tfidf/train_x_tfidf1000/train_x_feature(f

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_x_tfidf1000, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_tfidf1000, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_tfidf1000)
    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_x_tfidf1000, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_tfidf1000, train_y)


predict_y = sig_clf.predict_proba(train_x_tfidf1000)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_l
predict_y = sig_clf.predict_proba(cv_x_tfidf1000)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
predict_y = sig_clf.predict_proba(test_x_tfidf1000)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_lo
```

```
for alpha = 1e-05
Log Loss : 1.32305552865
for alpha = 0.0001
Log Loss : 1.31849656247
for alpha = 0.001
Log Loss : 1.30700804357
for alpha = 0.1
Log Loss : 1.23232503907
for alpha = 1
Log Loss : 1.19190853658
for alpha = 10
Log Loss : 1.23252672978
for alpha = 100
Log Loss : 1.29280385569
for alpha = 1000
Log Loss : 1.3035253399
```



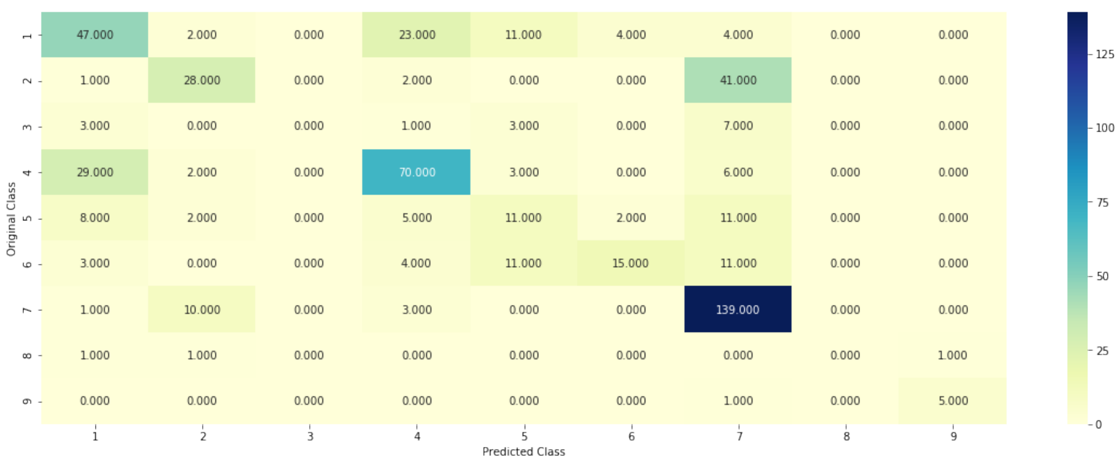

```
For values of best alpha =  1 The train log loss is: 0.748579218365
For values of best alpha =  1 The cross validation log loss is: 1.19190853658
For values of best alpha =  1 The test log loss is: 1.1728574778
```

4.1.1.2. Testing the model with best hyper paramters

In [60]:
```
# find more about Multinomial Naive base function here http://scikit-learn.org/stable/
# -------------------------
# default paramters
# sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_prior=None)

# some of methods of MultinomialNB()
# fit(X, y[, sample_weight])        Fit Naive Bayes classifier according to X, y
# predict(X)        Perform classification on an array of test vectors X.
# predict_log_proba(X)        Return log-probability estimates for the test vector X.
# -----------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
# -----------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
```

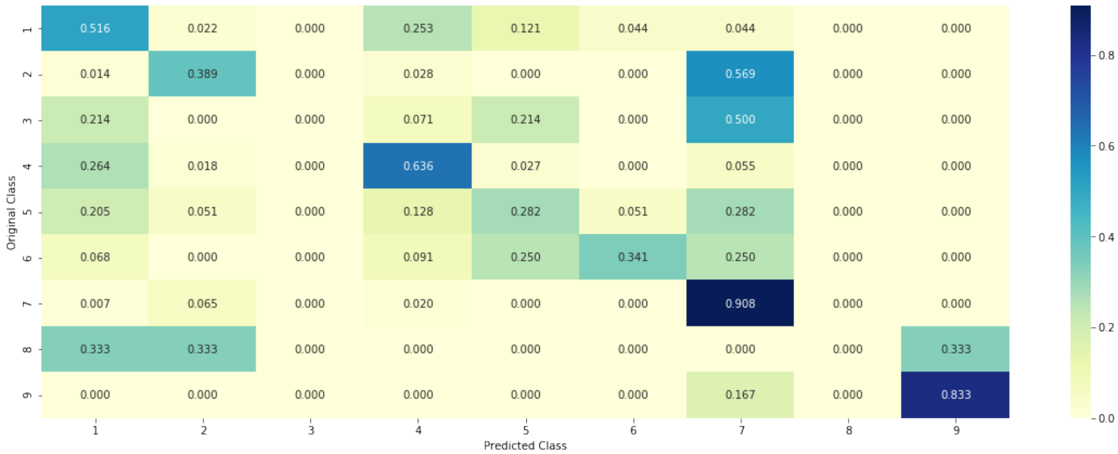
```
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
# ----------------------------

#any dataset can be applied here like bow,tfidf,featurized,response coding
#train_x_onehotCoding/train_x_ngram/train_x_tfidf/train_x_tfidf1000/train_x_feature(f

clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train_x_tfidf1000, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_tfidf1000, train_y)
sig_clf_probs = sig_clf.predict_proba(cv_x_tfidf1000)
# 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_x_tfid
plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_tfidf1000.toarray()))
```

```
Log Loss : 1.19190853658
Number of missclassified point : 0.40789473684210525
-------------------- Confusion matrix --------------------
```




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


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



4.1.1.3. Feature Importance, Correctly classified point

```
In [61]: test_point_index = 1
         no_feature = 100
         predicted_cls = sig_clf.predict(test_x_tfidf1000[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf100
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.0663  0.0752  0.0265  0.6544  0.0396  0.0475  0.0769  0.00
```

```
Actual Class : 4
--------------------------------------------------
55 Text feature [005] present in test data point [True]
Out of the top  100  features  1 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

In [62]:
```
test_point_index = 100
no_feature = 100
predicted_cls = sig_clf.predict(test_x_tfidf1000[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf10
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.7782  0.0445  0.0132  0.0593  0.0213  0.0341  0.0398  0.00
Actual Class : 1
--------------------------------------------------
Out of the top  100  features  0 are present in query point
```

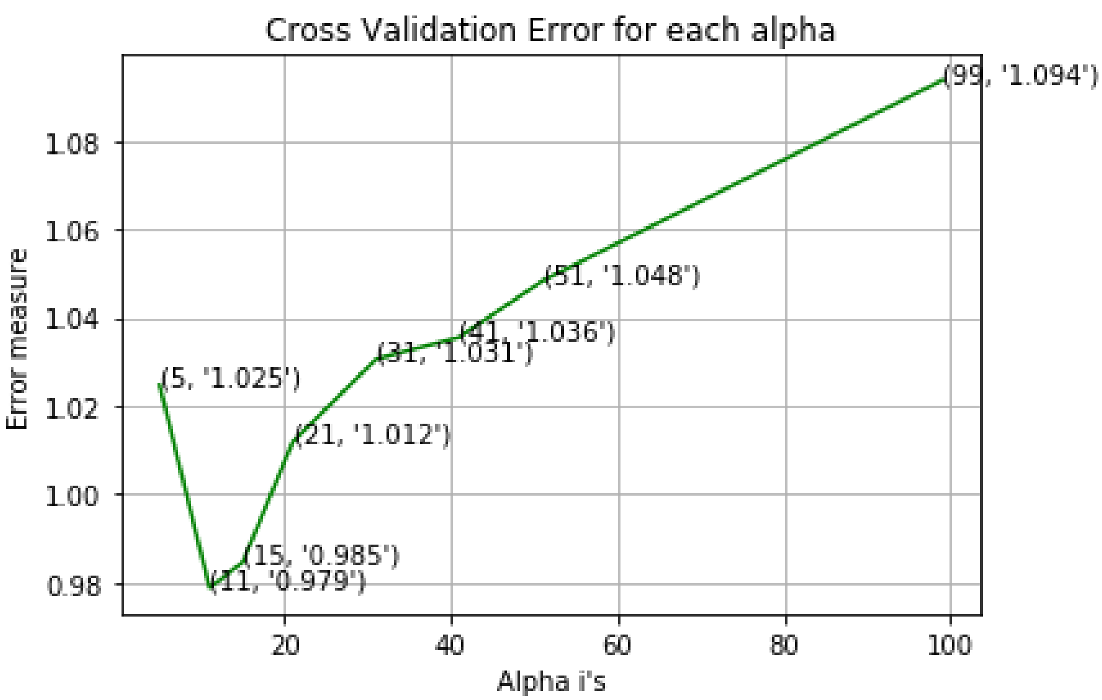
4.2. K Nearest Neighbour Classification
4.2.1. Hyper parameter tuning

In [63]:
```
# find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/
# -------------------------
# default parameter
# KNeighborsClassifier(n_neighbors=5, weights=uniform, algorithm=auto, leaf_size=30, 
# metric=minkowski, metric_params=None, n_jobs=1, **kwargs)

# methods of
# fit(X, y) : Fit the model using X as training data and y as target values
# predict(X):Predict the class labels for the provided data
# predict_proba(X):Return probability estimates for the test data X.
#--------------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons
#--------------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
#
# some of the methods of CalibratedClassifierCV()
```

```
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
#-------------------------------------
# video link:
#-------------------------------------


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_x_responseCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_responseCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
    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_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

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

```
for alpha = 5
Log Loss : 1.02475889632
```

```
for alpha = 11
Log Loss : 0.978824227639
for alpha = 15
Log Loss : 0.984707188713
for alpha = 21
Log Loss : 1.01189740329
for alpha = 31
Log Loss : 1.03055503801
for alpha = 41
Log Loss : 1.03557372372
for alpha = 51
Log Loss : 1.04829411825
for alpha = 99
Log Loss : 1.09363939709
```




```
For values of best alpha =  11 The train log loss is: 0.624293086675
For values of best alpha =  11 The cross validation log loss is: 0.978824227639
For values of best alpha =  11 The test log loss is: 1.05665993724
```

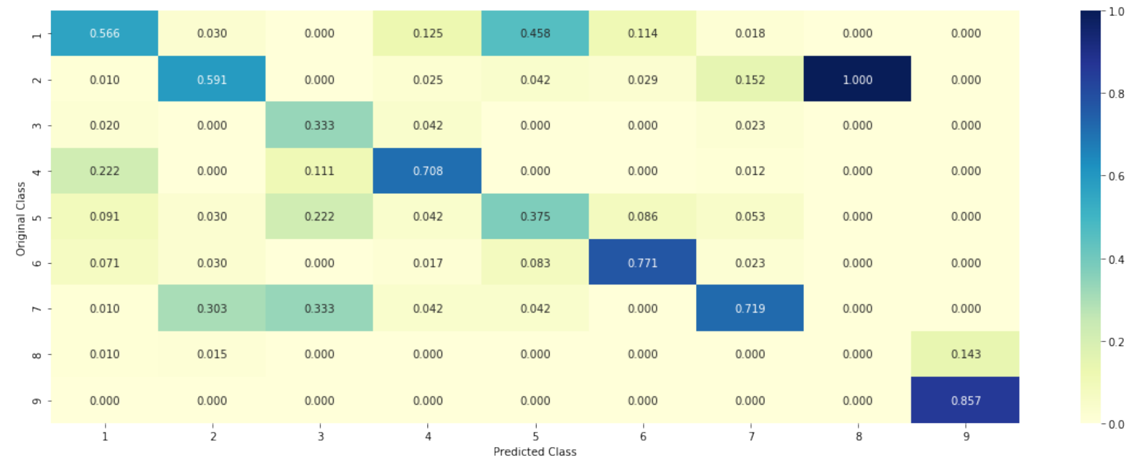
4.2.2. Testing the model with best hyper paramters

```
In [64]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/
         # -------------------------
```

```
# default parameter
# KNeighborsClassifier(n_neighbors=5, weights=uniform, algorithm=auto, leaf_size=30, p
# metric=minkowski, metric_params=None, n_jobs=1, **kwargs)

# methods of
# fit(X, y) : Fit the model using X as training data and y as target values
# predict(X):Predict the class labels for the provided data
# predict_proba(X):Return probability estimates for the test data X.
#-------------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
#-------------------------------------
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y, cv_x_responseCoding
```

```
Log loss : 0.978824227639
Number of mis-classified points : 0.3458646616541353
-------------------- Confusion matrix --------------------
```


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




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

4.2.3.Sample Query point -1

In [65]:
```
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

test_point_index = 1
predicted_cls = sig_clf.predict(test_x_responseCoding[0].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Actual Class :", test_y[test_point_index])
neighbors = clf.kneighbors(test_x_responseCoding[test_point_index].reshape(1, -1), al
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 : 7
Actual Class : 4
The  11  nearest neighbours of the test points belongs to classes [4 4 4 4 3 4 4 5 4 4 4]
Fequency of nearest points : Counter({4: 9, 3: 1, 5: 1})
```

4.2.4. Sample Query Point-2

```
In [66]: clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
         clf.fit(train_x_responseCoding, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_x_responseCoding, train_y)

         test_point_index = 100

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

```
Predicted Class : 1
Actual Class : 1
the k value for knn is 11 and the nearest neighbours of the test points belongs to classes [1 
Fequency of nearest points : Counter({1: 10, 4: 1})
```

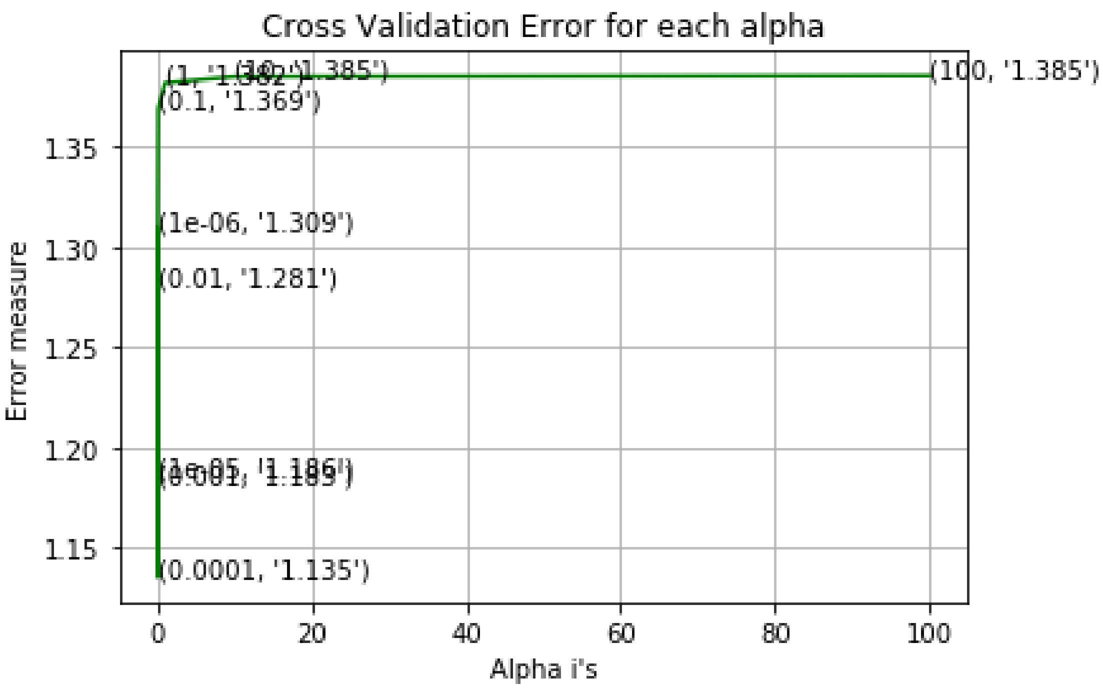
4.3. Logistic Regression
4.3.1. With Class balancing
4.3.1.1. Hyper paramter tuning

```
In [67]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # class_weight=None, warm_start=False, average=False, n_iter=None)

         # some of methods
         # fit(X, y[, coef_init, intercept_init, ])       Fit linear model with Stochastic Gr
         # predict(X)       Predict class labels for samples in X.

         #-------------------------------
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons
         #------------------------------


         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
```

```
# -----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
#-------------------------------------
# video link:
#-------------------------------------
#any dataset can be applied here like bow,tfidf,featurized,response coding
#train_x_onehotCoding/train_x_ngram/train_x_tfidf/train_x_tfidf1000/train_x_feature(f


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_x_feature, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_feature, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_feature)
    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_x_feature, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_feature, train_y)

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

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

```
for alpha = 1e-06
Log Loss : 1.30926370153
for alpha = 1e-05
Log Loss : 1.18584662095
for alpha = 0.0001
Log Loss : 1.13543288575
for alpha = 0.001
Log Loss : 1.18300458344
for alpha = 0.01
Log Loss : 1.28135572921
for alpha = 0.1
Log Loss : 1.36920026153
for alpha = 1
Log Loss : 1.38197229662
for alpha = 10
Log Loss : 1.38502633482
for alpha = 100
Log Loss : 1.38545887595
```

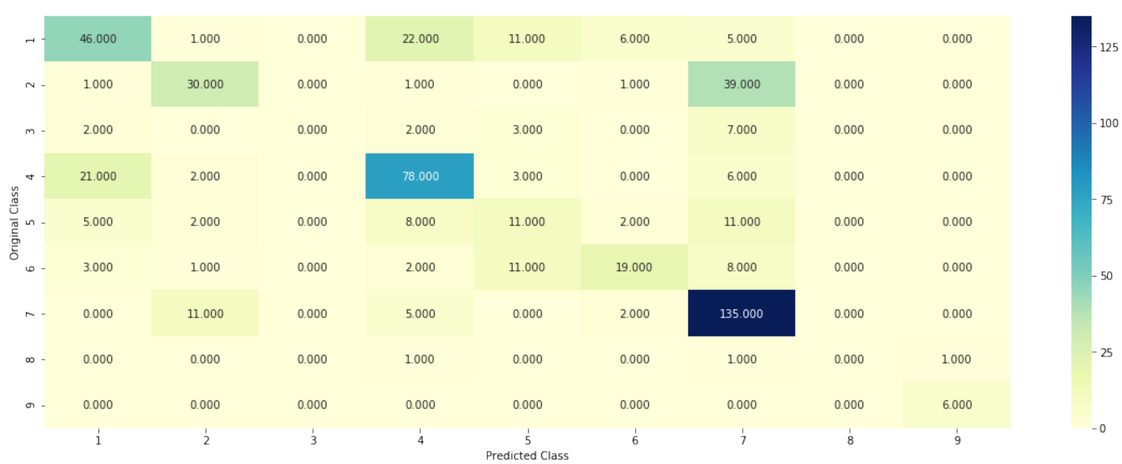


```
For values of best alpha =  0.0001 The train log loss is: 0.624076019615
For values of best alpha =  0.0001 The cross validation log loss is: 1.13543288575
For values of best alpha =  0.0001 The test log loss is: 1.12230429858
```

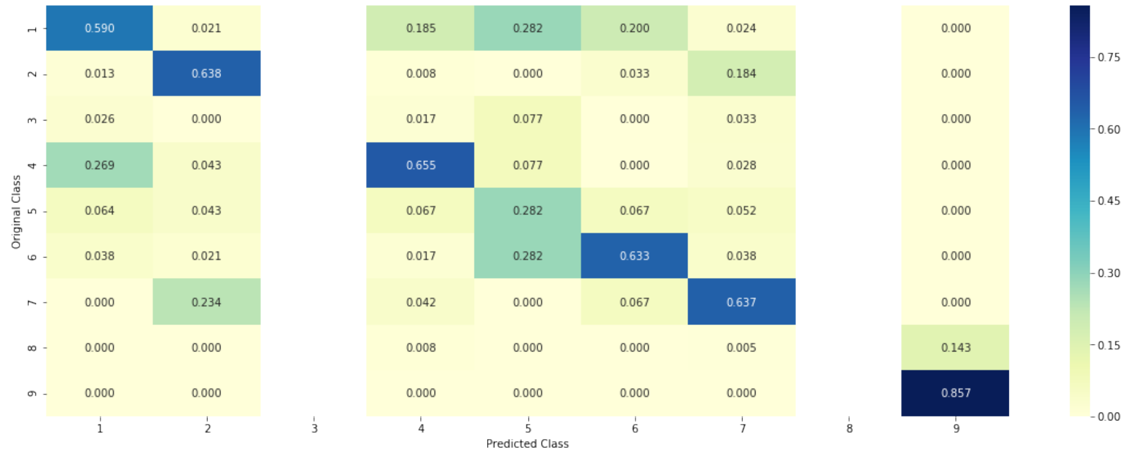
4.3.1.2. Testing the model with best hyper paramters

```
In [68]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # class_weight=None, warm_start=False, average=False, n_iter=None)

         # some of methods
         # fit(X, y[, coef_init, intercept_init, ])       Fit linear model with Stochastic Gr
         # predict(X)        Predict class labels for samples in X.

         #-------------------------------
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
         #------------------------------
         clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', lo
         predict_and_plot_confusion_matrix(train_x_feature, train_y, cv_x_feature, cv_y, clf)
```

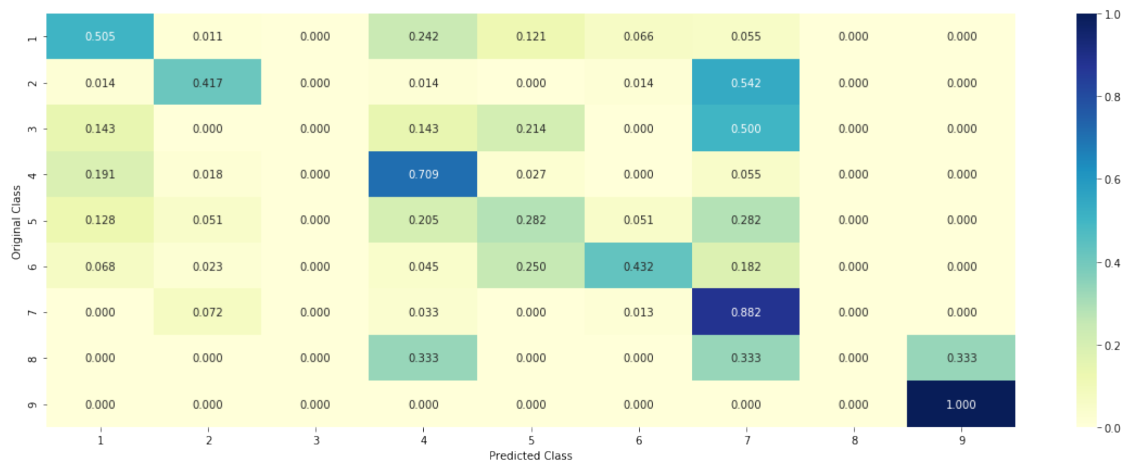
```
Log loss : 1.13543288575
Number of mis-classified points : 0.3890977443609023
-------------------- Confusion matrix --------------------
```




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




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



4.3.1.3. Feature Importance

```
In [69]: 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_feature.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']))
```

4.3.1.3.1. Correctly Classified point

```
In [70]: # from tabulate import tabulate
         clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', lo
         clf.fit(train_x_feature,train_y)
         test_point_index = 1
         no_feature = 500
         predicted_cls = sig_clf.predict(test_x_feature[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_feature
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.0624  0.0574  0.0108  0.7183  0.0276  0.0303  0.0813  0.005
Actual Class : 4
--------------------------------------------------
56 Text feature [005] present in test data point [True]
Out of the top  500  features  1 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

```
In [71]: test_point_index = 100
         no_feature = 500
         predicted_cls = sig_clf.predict(test_x_feature[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_feature
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.7319  0.0605  0.0046  0.0616  0.0117  0.1009  0.0191  0.005
Actual Class : 1
--------------------------------------------------
```

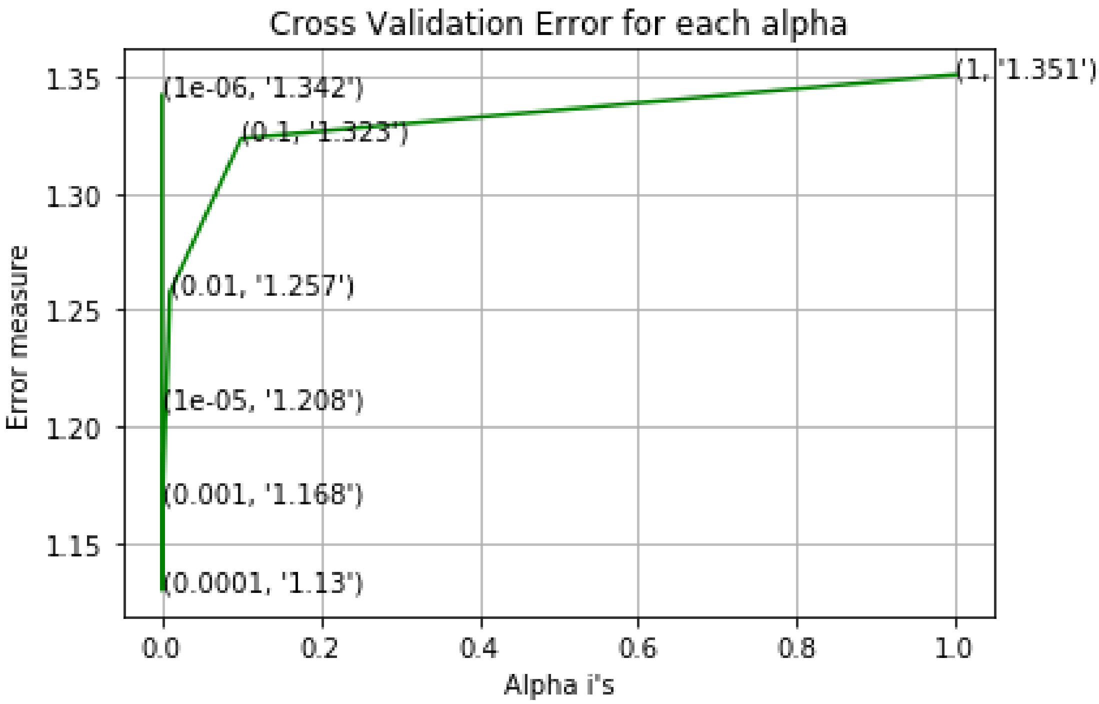
```
23 Text feature [002] present in test data point [True]
268 Text feature [109] present in test data point [True]
318 Text feature [09] present in test data point [True]
439 Text feature [003] present in test data point [True]
459 Text feature [10] present in test data point [True]
Out of the top  500  features  5 are present in query point
```

4.3.2. Without Class balancing
4.3.2.1. Hyper paramter tuning

In [72]:
```python
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with Stochastic Gr
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
#------------------------------



# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
#-------------------------------------
# video link:
#-------------------------------------

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_x_feature, train_y)
```

```
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_feature, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_feature)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1
        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=42
    clf.fit(train_x_feature, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_feature, train_y)

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

```
for alpha = 1e-06
Log Loss : 1.341916996
for alpha = 1e-05
Log Loss : 1.20806817496
for alpha = 0.0001
Log Loss : 1.13003733371
for alpha = 0.001
Log Loss : 1.16847707184
for alpha = 0.01
Log Loss : 1.25748907304
for alpha = 0.1
Log Loss : 1.32344709287
for alpha = 1
Log Loss : 1.35074580546
```

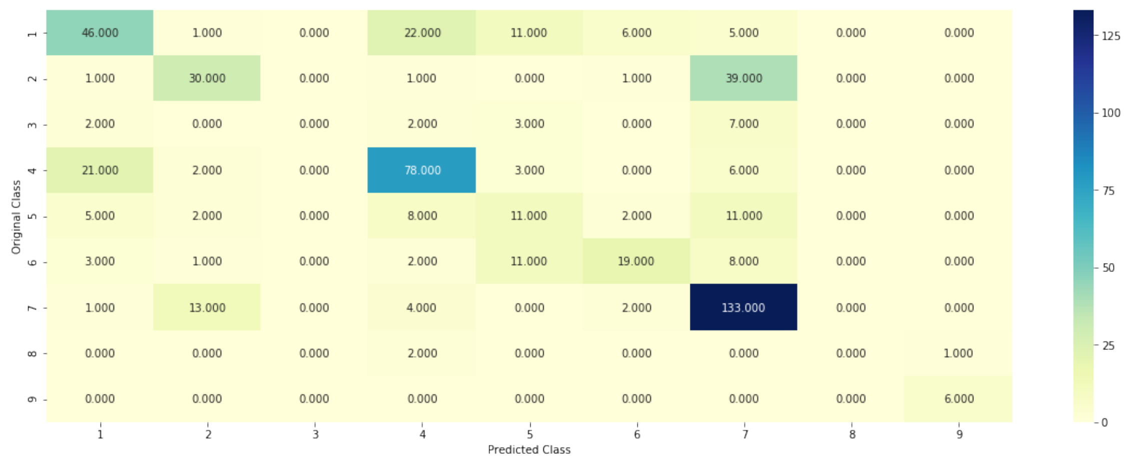



```
For values of best alpha =  0.0001 The train log loss is: 0.600026495389
For values of best alpha =  0.0001 The cross validation log loss is: 1.13003733371
For values of best alpha =  0.0001 The test log loss is: 1.12105540404
```

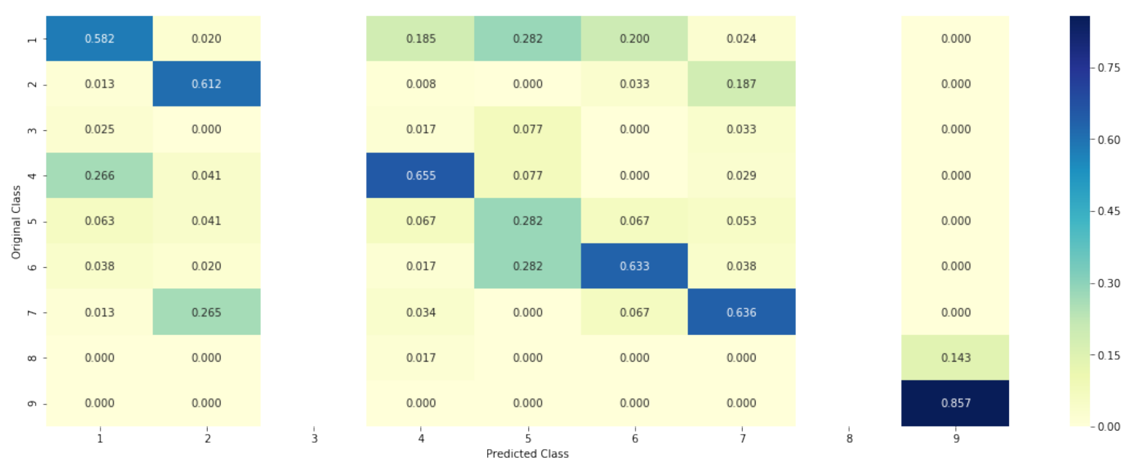
4.3.2.2. Testing model with best hyper parameters

In [73]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with Stochastic Gr
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link:
#------------------------------

clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42
predict_and_plot_confusion_matrix(train_x_feature, train_y, cv_x_feature, cv_y, clf)
```

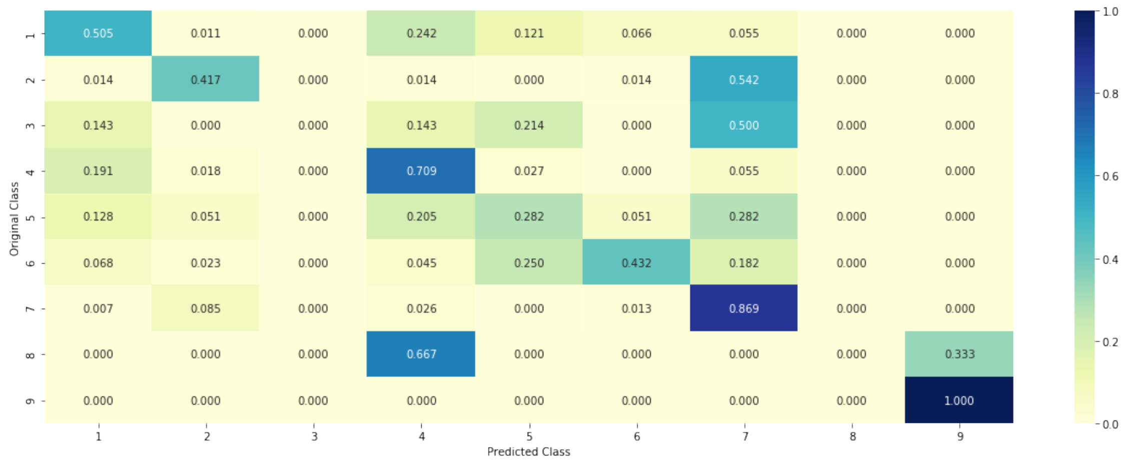
Log loss : 1.13003733371
Number of mis-classified points : 0.39285714285714285
-------------------- Confusion matrix --------------------



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



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



4.3.2.3. Feature Importance, Correctly Classified point

```
In [74]: clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42
         clf.fit(train_x_feature,train_y)
         test_point_index = 1
         no_feature = 500
         predicted_cls = sig_clf.predict(test_x_feature[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_feature
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.057   0.0562  0.0123  0.732   0.0287  0.031   0.071   0.006
Actual Class : 4
--------------------------------------------------
141 Text feature [005] present in test data point [True]
Out of the top  500  features  1 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

```
In [75]: test_point_index = 100
         no_feature = 500
         predicted_cls = sig_clf.predict(test_x_feature[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_feature
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.7323  0.0633  0.0056  0.0672  0.0129  0.0966  0.0154  0.004
Actual Class : 1
--------------------------------------------------
24 Text feature [002] present in test data point [True]
251 Text feature [109] present in test data point [True]
342 Text feature [09] present in test data point [True]
441 Text feature [003] present in test data point [True]
471 Text feature [10] present in test data point [True]
Out of the top  500  features  5 are present in query point
```

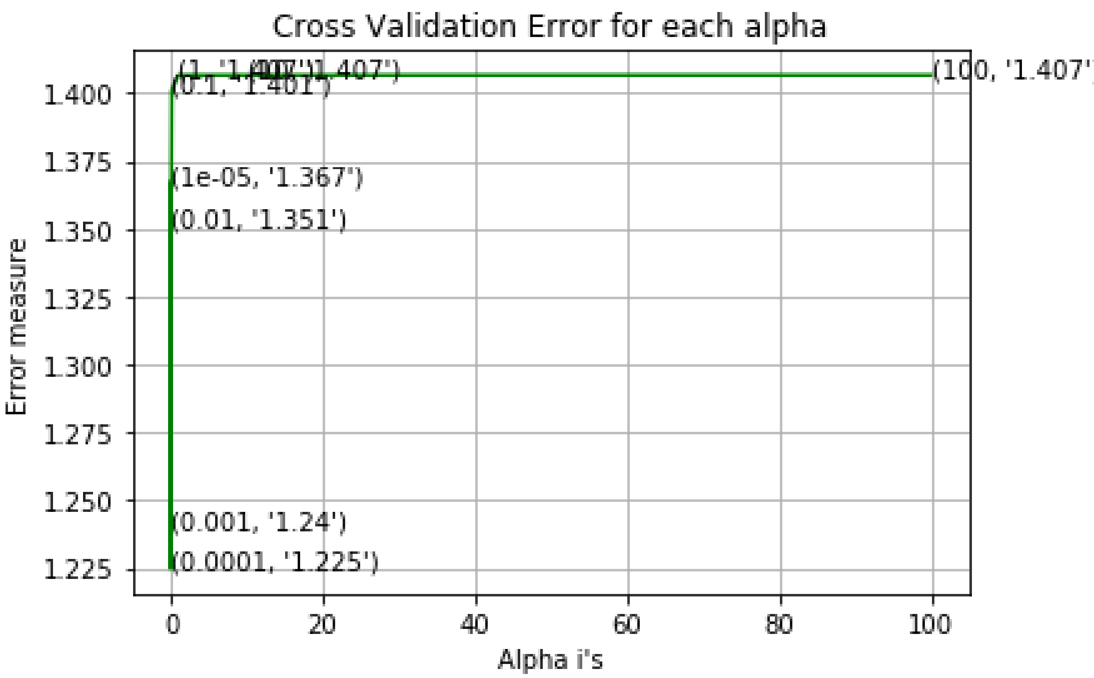
4.4. Linear Support Vector Machines
4.4.1. Hyper paramter tuning

In [76]:
```
# read more about support vector machines with linear kernals here http://scikit-lear

# --------------------------------
# default parameters
# SVC(C=1.0, kernel=rbf, degree=3, gamma=auto, coef0=0.0, shrinking=True, probability
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_sh

# Some of methods of SVM()
# fit(X, y, [sample_weight])        Fit the SVM model according to the given training
# predict(X)        Perform classification on samples in X.
# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons
# --------------------------------



# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
#-------------------------------------
# video link:
#-------------------------------------

alpha = [10 ** x for x in range(-5, 3)]
cv_log_error_array = []
for i in alpha:
```

```
        print("for C =", i)
#       clf = SVC(C=i,kernel='linear',probability=True, class_weight='balanced')
        clf = SGDClassifier( class_weight='balanced', alpha=i, penalty='l2', loss='hinge'
        clf.fit(train_x_tfidf1000, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_tfidf1000, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_tfidf1000)
        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 = SVC(C=i,kernel='linear',probability=True, class_weight='balanced')
    clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', lo
    clf.fit(train_x_tfidf1000, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_tfidf1000, train_y)

    predict_y = sig_clf.predict_proba(train_x_tfidf1000)
    print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_
    predict_y = sig_clf.predict_proba(cv_x_tfidf1000)
    print('For values of best alpha = ', alpha[best_alpha], "The cross validation log los
    predict_y = sig_clf.predict_proba(test_x_tfidf1000)
    print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l
```

```
for C = 1e-05
Log Loss : 1.36714423513
for C = 0.0001
Log Loss : 1.22466412582
for C = 0.001
Log Loss : 1.23980066418
for C = 0.01
Log Loss : 1.35106072077
for C = 0.1
Log Loss : 1.40120509147
for C = 1
Log Loss : 1.40667869955
for C = 10
```

```
Log Loss : 1.40667868093
for C = 100
Log Loss : 1.40667865999
```



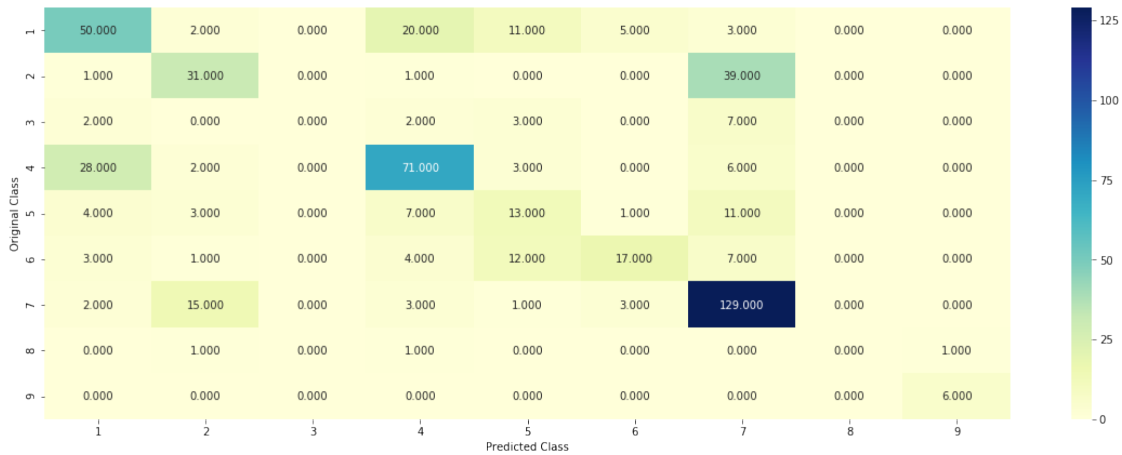

```
For values of best alpha =  0.0001 The train log loss is: 0.56446873178
For values of best alpha =  0.0001 The cross validation log loss is: 1.22466412582
For values of best alpha =  0.0001 The test log loss is: 1.24459492014
```

4.4.2. Testing model with best hyper parameters

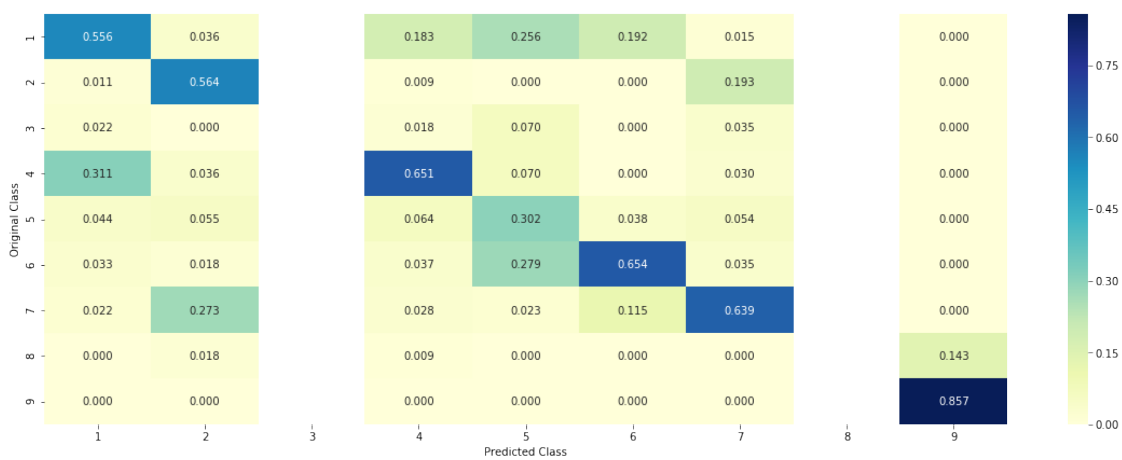
In [77]:
```
# read more about support vector machines with linear kernals here http://scikit-lear

# --------------------------------
# default parameters
# SVC(C=1.0, kernel=rbf, degree=3, gamma=auto, coef0=0.0, shrinking=True, probability
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_sh

# Some of methods of SVM()
# fit(X, y, [sample_weight])        Fit the SVM model according to the given training
# predict(X)        Perform classification on samples in X.
# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
# --------------------------------
```

```
# clf = SVC(C=alpha[best_alpha],kernel='linear',probability=True, class_weight='balan
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge', random_state=
predict_and_plot_confusion_matrix(train_x_tfidf1000, train_y,cv_x_tfidf1000,cv_y, clf)
```

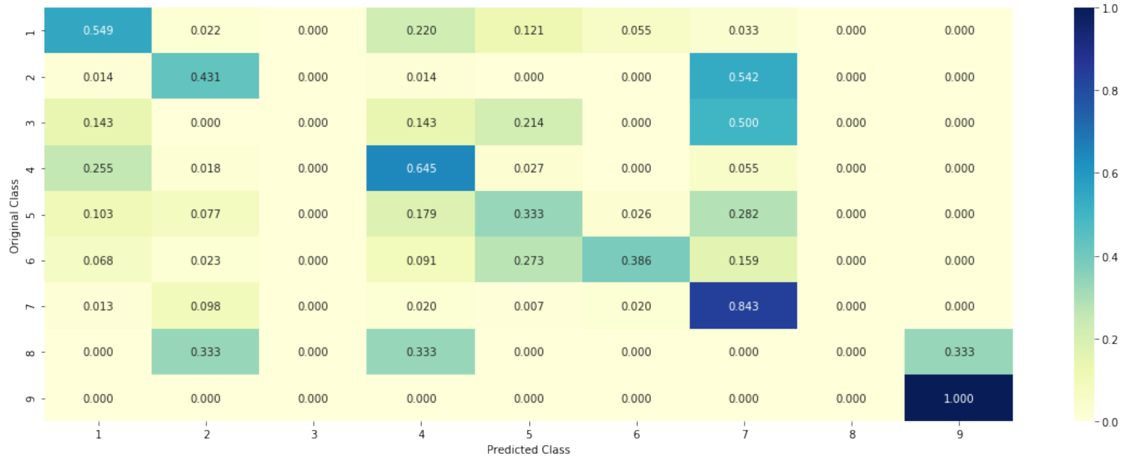
```
Log loss : 1.22466412582
Number of mis-classified points : 0.4041353383458647
-------------------- Confusion matrix --------------------
```




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




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



4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

```
In [78]: clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge', random_state=
         clf.fit(train_x_tfidf1000,train_y)
         test_point_index = 1
         # test_point_index = 100
         no_feature = 500
         predicted_cls = sig_clf.predict(test_x_tfidf1000[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf100
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.0361  0.0811  0.0243  0.591   0.0458  0.0536  0.1585  0.004
Actual Class : 4
--------------------------------------------------
220 Text feature [005] present in test data point [True]
Out of the top  500  features  1 are present in query point
```

4.3.3.2. For Incorrectly classified point

```
In [79]: test_point_index = 100
         no_feature = 500
         predicted_cls = sig_clf.predict(test_x_tfidf1000[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf100
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
```

```
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.7786  0.0475  0.0175  0.056   0.0034  0.0708  0.0187  0.004
Actual Class : 1
--------------------------------------------------
199 Text feature [002] present in test data point [True]
385 Text feature [007] present in test data point [True]
386 Text feature [09] present in test data point [True]
398 Text feature [109] present in test data point [True]
Out of the top  500  features  4 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

In [80]:
```
# --------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion=gini, max_depth=
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features=auto, max_leaf_nodes
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=No
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])        Fit the SVM model according to the given training
# predict(X)        Perform classification on samples in X.
# predict_proba (X)        Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons
# --------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
```

```python
#--------------------------------------
# video link:
#--------------------------------------

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_x_tfidf1000, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_tfidf1000, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_tfidf1000)
        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_x_tfidf1000, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_tfidf1000, train_y)

predict_y = sig_clf.predict_proba(train_x_tfidf1000)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The train log loss
predict_y = sig_clf.predict_proba(cv_x_tfidf1000)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross validati
predict_y = sig_clf.predict_proba(test_x_tfidf1000)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss
```

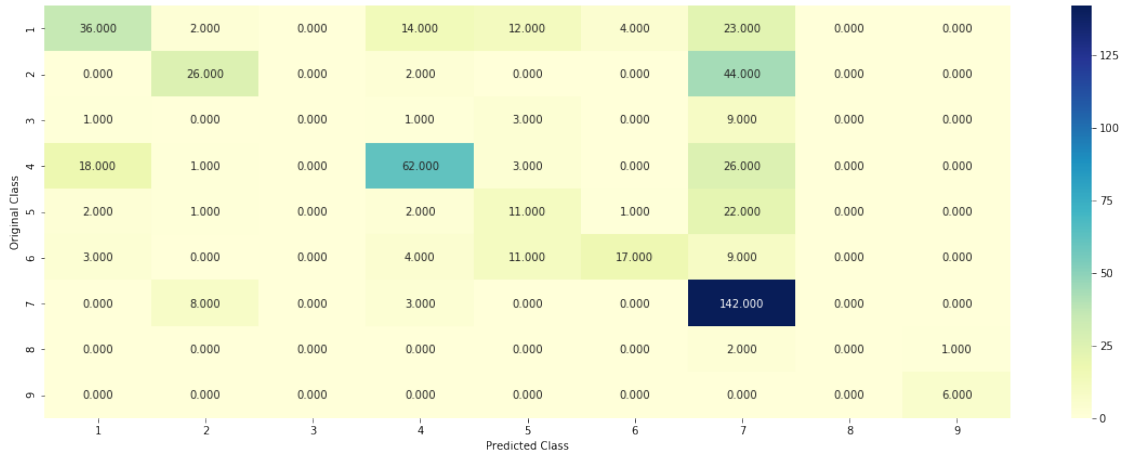
```
for n_estimators = 100 and max depth =  5
Log Loss : 1.26887541702
for n_estimators = 100 and max depth =  10
Log Loss : 1.25083701218
for n_estimators = 200 and max depth =  5
```

```
Log Loss : 1.26595912041
for n_estimators = 200 and max depth =  10
Log Loss : 1.25115525545
for n_estimators = 500 and max depth =  5
Log Loss : 1.25971989533
for n_estimators = 500 and max depth =  10
Log Loss : 1.24559832315
for n_estimators = 1000 and max depth =  5
Log Loss : 1.25634402309
for n_estimators = 1000 and max depth =  10
Log Loss : 1.2451946738
for n_estimators = 2000 and max depth =  5
Log Loss : 1.25284644197
for n_estimators = 2000 and max depth =  10
Log Loss : 1.24652038243
For values of best estimator =  1000 The train log loss is: 1.00332223395
For values of best estimator =  1000 The cross validation log loss is: 1.2451946738
For values of best estimator =  1000 The test log loss is: 1.2363790979
```

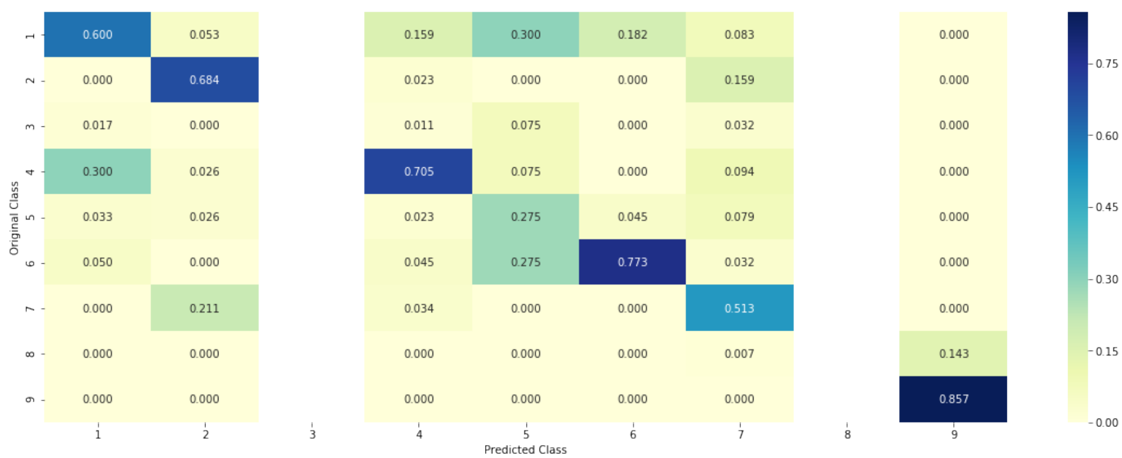
4.5.2. Testing model with best hyper parameters (TFIDF top 1000 words)

In [81]:
```
# --------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion=gini, max_depth=N
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features=auto, max_leaf_nodes=
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=Non
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])        Fit the SVM model according to the given training
# predict(X)        Perform classification on samples in X.
# predict_proba (X)        Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
# --------------------------------

clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini',
predict_and_plot_confusion_matrix(train_x_tfidf1000, train_y,cv_x_tfidf1000,cv_y, clf)
```

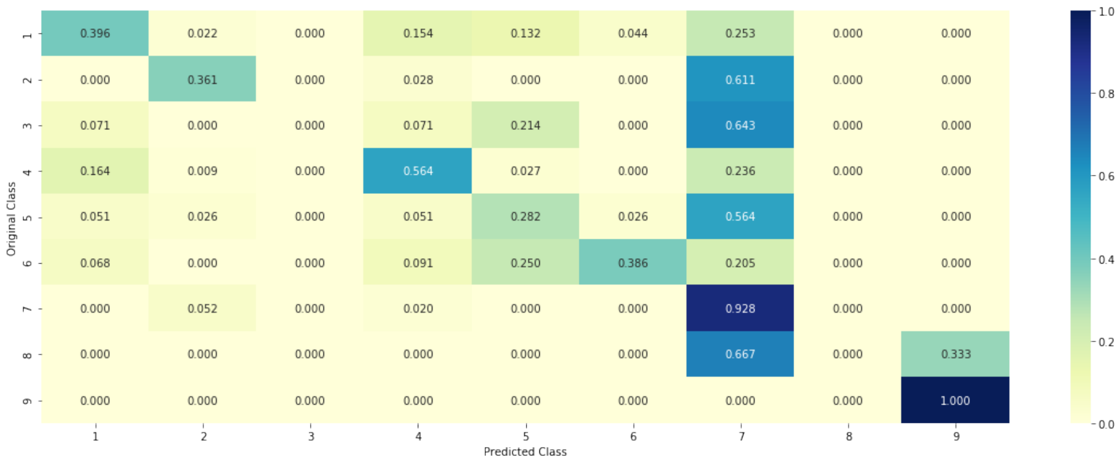
```
Log loss : 1.2451946738
Number of mis-classified points : 0.43609022556390975
-------------------- Confusion matrix --------------------
```



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



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



4.5.3. Feature Importance
4.5.3.1. Correctly Classified point

```
In [82]: # test_point_index = 10
         clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini',
         clf.fit(train_x_tfidf1000, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_x_tfidf1000, train_y)

         test_point_index = 1
         no_feature = 100
         predicted_cls = sig_clf.predict(test_x_tfidf1000[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf100
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.feature_importances_)
         print("-"*50)
         get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],tes

Predicted Class : 4
Predicted Class Probabilities: [[ 0.1412  0.1208  0.0233  0.2871  0.0578  0.0675  0.2862  0.00
Actual Class : 4
--------------------------------------------------
Out of the top  100  features  0 are present in query point
```

4.5.3.2. Inorrectly Classified point

```
In [83]: test_point_index = 100
         no_feature = 100
         predicted_cls = sig_clf.predict(test_x_tfidf1000[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf10
```

```
        print("Actuall Class :", test_y[test_point_index])
        indices = np.argsort(-clf.feature_importances_)
        print("-"*50)
        get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],tes
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.739   0.0335  0.011   0.1133  0.0229  0.036   0.0342  0.00
Actuall Class : 1
--------------------------------------------------
72 Text feature [03] present in test data point [True]
Out of the top  100  features  1 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

```
In [84]: # --------------------------------
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion=gini, max_depth=
         # min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features=auto, max_leaf_nodes
         # min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=No
         # class_weight=None)

         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample_weight])        Fit the SVM model according to the given training
         # predict(X)        Perform classification on samples in X.
         # predict_proba (X)        Perform classification on samples in X.

         # some of attributes of  RandomForestClassifier()
         # feature_importances_ : array of shape = [n_features]
         # The feature importances (the higher, the more important the feature).

         # --------------------------------
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons
         # --------------------------------


         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
         # ----------------------------
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
         #
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample_weight])        Fit the calibrated model
         # get_params([deep])        Get parameters for this estimator.
         # predict(X)        Predict the target of new samples.
         # predict_proba(X)        Posterior probabilities of classification
         #-----------------------------------
         # video link:
```

```python
#--------------------------------------

alpha = [10,50,100,200,500,1000]
max_depth = [2,3,5,10]
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_x_responseCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_responseCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
        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/4)],max_depth[int(i%4)],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/4)], criterion='gini',
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The train log loss is
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The cross validation l
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The test log loss is:"
```

```
for n_estimators = 10 and max depth =  2
Log Loss : 2.23007767376
for n_estimators = 10 and max depth =  3
Log Loss : 1.6863169631
for n_estimators = 10 and max depth =  5
Log Loss : 1.56046238856
for n_estimators = 10 and max depth =  10
```

```
Log Loss : 1.81762449838
for n_estimators = 50 and max depth =  2
Log Loss : 1.72749208996
for n_estimators = 50 and max depth =  3
Log Loss : 1.48445478763
for n_estimators = 50 and max depth =  5
Log Loss : 1.46891693372
for n_estimators = 50 and max depth =  10
Log Loss : 1.92418110972
for n_estimators = 100 and max depth =  2
Log Loss : 1.55066384388
for n_estimators = 100 and max depth =  3
Log Loss : 1.49483768615
for n_estimators = 100 and max depth =  5
Log Loss : 1.3648316752
for n_estimators = 100 and max depth =  10
Log Loss : 1.87095387485
for n_estimators = 200 and max depth =  2
Log Loss : 1.62363956949
for n_estimators = 200 and max depth =  3
Log Loss : 1.52747379064
for n_estimators = 200 and max depth =  5
Log Loss : 1.39743020551
for n_estimators = 200 and max depth =  10
Log Loss : 1.92544620554
for n_estimators = 500 and max depth =  2
Log Loss : 1.75665039964
for n_estimators = 500 and max depth =  3
Log Loss : 1.61394888493
for n_estimators = 500 and max depth =  5
Log Loss : 1.42716183365
for n_estimators = 500 and max depth =  10
Log Loss : 1.9488337181
for n_estimators = 1000 and max depth =  2
Log Loss : 1.71491710203
for n_estimators = 1000 and max depth =  3
Log Loss : 1.64119361873
for n_estimators = 1000 and max depth =  5
Log Loss : 1.43649851311
for n_estimators = 1000 and max depth =  10
Log Loss : 1.92243188562
For values of best alpha =  100 The train log loss is: 0.0589554800667
For values of best alpha =  100 The cross validation log loss is: 1.3648316752
For values of best alpha =  100 The test log loss is: 1.36160585204
```

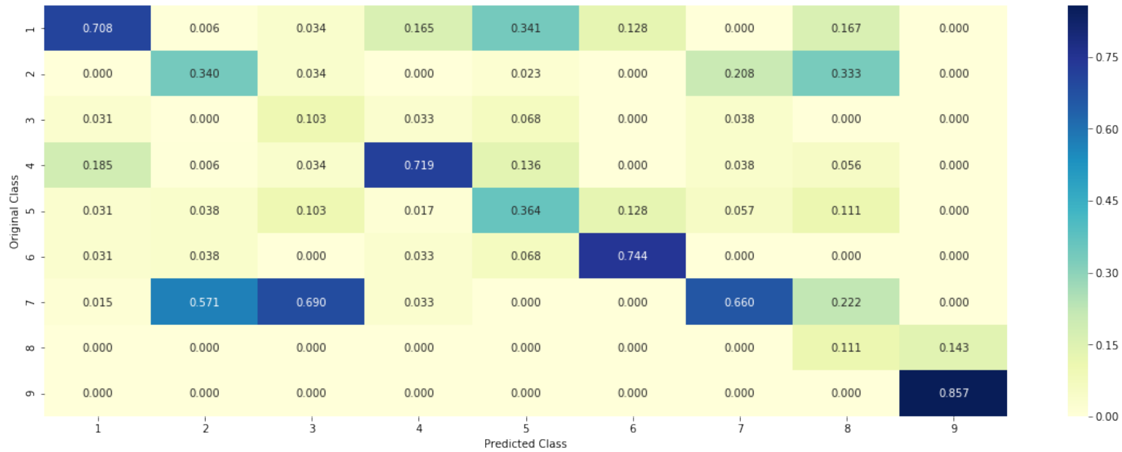
4.5.4. Testing model with best hyper parameters (Response Coding)

```
In [85]: # --------------------------------
```

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion=gini, max_depth=
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features=auto, max_leaf_nodes
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=No
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])        Fit the SVM model according to the given training
# predict(X)        Perform classification on samples in X.
# predict_proba (X)        Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons
# --------------------------------

clf = RandomForestClassifier(max_depth=max_depth[int(best_alpha%4)], n_estimators=alp
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_responseCoding
```

```
Log loss : 1.3648316752
Number of mis-classified points : 0.4793233082706767
-------------------- Confusion matrix --------------------
```


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




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

4.5.5. Feature Importance

4.5.5.1. Correctly Classified point

```
In [86]: clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gini',
         clf.fit(train_x_responseCoding, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_x_responseCoding, train_y)


         test_point_index = 1
         no_feature = 27
         predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
         print("Predicted Class :", predicted_cls[0])
```

```
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_response
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:
        print("Text is important feature")
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.111   0.0251  0.1411  0.4642  0.0888  0.0582  0.0083  0.05
Actual Class : 4
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Variation is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Variation is important feature
Gene is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.5.5.2. Incorrectly Classified point

```
In [87]: test_point_index = 100
         predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
```

```
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_respons
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:
        print("Text is important feature")
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.9751  0.0016  0.0015  0.0115  0.001   0.0037  0.0014  0.00
Actual Class : 1
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Variation is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Variation is important feature
Gene is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.7 Stack the models
4.7.1 testing with hyper parameter tuning

In [88]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
# -------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with Stochastic Gr
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
#------------------------------


# read more about support vector machines with linear kernals here http://scikit-lear
# --------------------------------
# default parameters
# SVC(C=1.0, kernel=rbf, degree=3, gamma=auto, coef0=0.0, shrinking=True, probability
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_sh

# Some of methods of SVM()
# fit(X, y, [sample_weight])        Fit the SVM model according to the given training
# predict(X)        Perform classification on samples in X.
# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
# --------------------------------


# read more about support vector machines with linear kernals here http://scikit-lear
# --------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion=gini, max_depth=
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features=auto, max_leaf_nodes
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=No
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])        Fit the SVM model according to the given training
# predict(X)        Perform classification on samples in X.
# predict_proba (X)        Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# --------------------------------
```

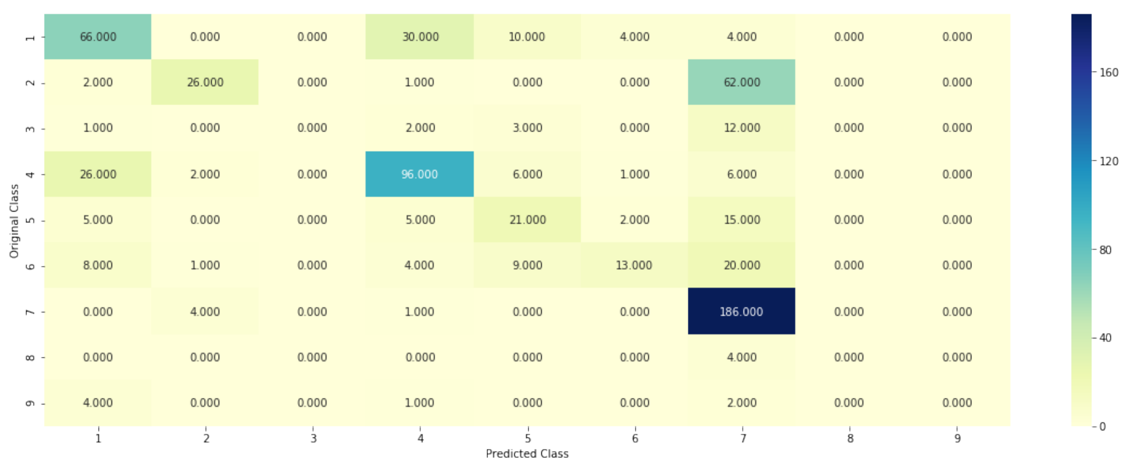
```
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/
# --------------------------------


clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class_weight='balanced', r
clf1.fit(train_x_tfidf1000, train_y)
sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")

clf2 = SGDClassifier(alpha=1, penalty='l2', loss='hinge', class_weight='balanced', ran
clf2.fit(train_x_tfidf1000, train_y)
sig_clf2 = CalibratedClassifierCV(clf2, method="sigmoid")


clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train_x_tfidf1000, train_y)
sig_clf3 = CalibratedClassifierCV(clf3, method="sigmoid")

sig_clf1.fit(train_x_tfidf1000, train_y)
print("Logistic Regression :  Log Loss: %0.2f" % (log_loss(cv_y, sig_clf1.predict_prob
sig_clf2.fit(train_x_tfidf1000, train_y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf2.predict_p
sig_clf3.fit(train_x_tfidf1000, train_y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba(cv_x_tf
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_classif
    sclf.fit(train_x_tfidf1000, 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_x_tfidf1000))
    if best_alpha > log_error:
        best_alpha = log_error
```

```
Logistic Regression :  Log Loss: 1.14
Support vector machines : Log Loss: 1.41
Naive Bayes : Log Loss: 1.31
--------------------------------------------------
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 2.186
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 2.104
Stacking Classifer : for the value of alpha: 0.010000 Log Loss: 1.770
Stacking Classifer : for the value of alpha: 0.100000 Log Loss: 1.290
Stacking Classifer : for the value of alpha: 1.000000 Log Loss: 1.185
Stacking Classifer : for the value of alpha: 10.000000 Log Loss: 1.418
```

4.7.2 testing the model with the best hyper parameters

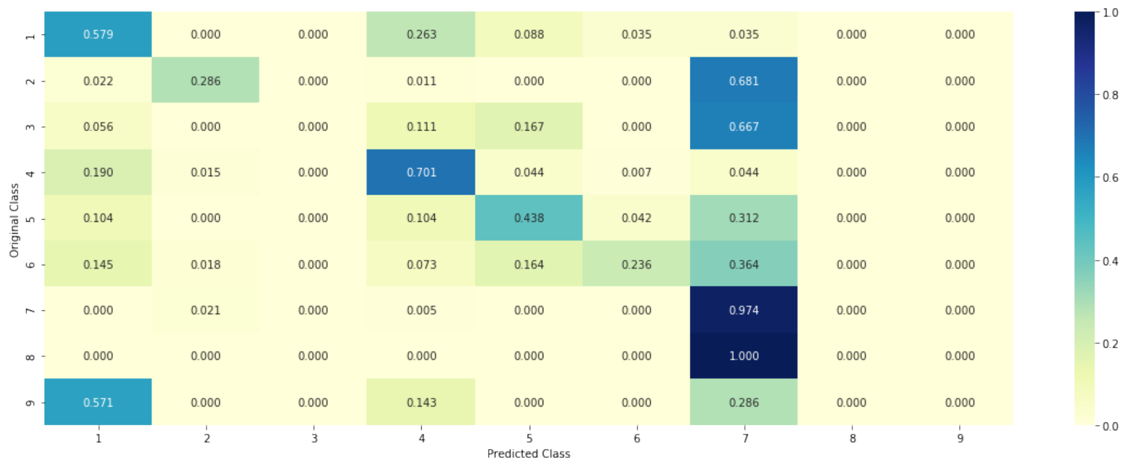
```
In [89]: lr = LogisticRegression(C=0.1)
         sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=
         sclf.fit(train_x_tfidf1000, train_y)

         log_error = log_loss(train_y, sclf.predict_proba(train_x_tfidf1000))
         print("Log loss (train) on the stacking classifier :",log_error)

         log_error = log_loss(cv_y, sclf.predict_proba(cv_x_tfidf1000))
         print("Log loss (CV) on the stacking classifier :",log_error)

         log_error = log_loss(test_y, sclf.predict_proba(test_x_tfidf1000))
         print("Log loss (test) on the stacking classifier :",log_error)

         print("Number of missclassified point :", np.count_nonzero((sclf.predict(test_x_tfidf
         plot_confusion_matrix(test_y=test_y, predict_y=sclf.predict(test_x_tfidf1000))
```

```
Log loss (train) on the stacking classifier : 0.973158330809
Log loss (CV) on the stacking classifier : 1.29020464866
Log loss (test) on the stacking classifier : 1.29367900561
Number of missclassified point : 0.38646616541353385
-------------------- Confusion matrix --------------------
```




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

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

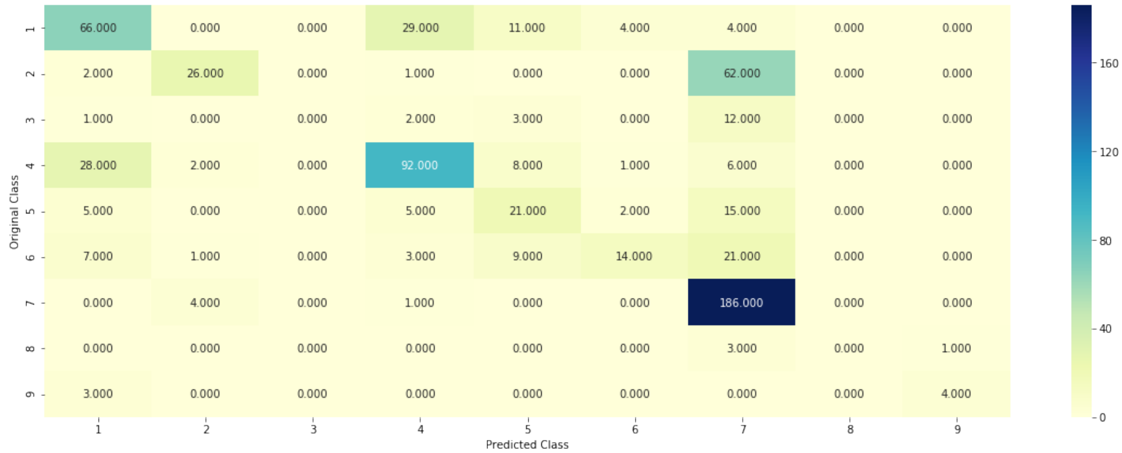


4.7.3 Maximum Voting classifier

```
In [90]: #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_x_tfidf1000, 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_x_tfidf
         plot_confusion_matrix(test_y=test_y, predict_y=vclf.predict(test_x_tfidf1000))
```

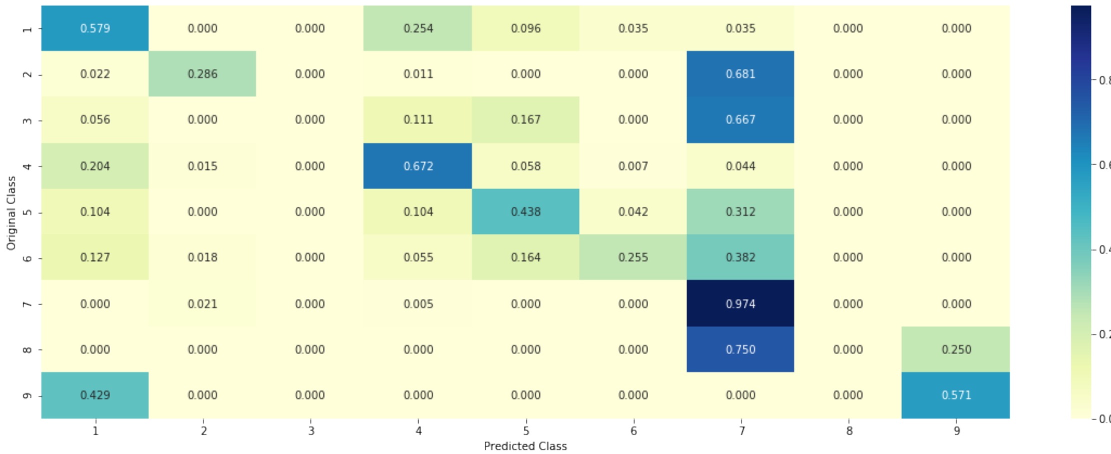
```
Log loss (train) on the VotingClassifier : 0.812105791214
Log loss (CV) on the VotingClassifier : 1.22875608441
```

```
Log loss (test) on the VotingClassifier : 1.22986969181
Number of missclassified point : 0.3849624060150376
-------------------- Confusion matrix --------------------
```




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


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


Original Class
Predicted Class
1 2 3 4 5 6 7 8 9
1: 0.579 0.000 0.000 0.254 0.096 0.035 0.035 0.000 0.000
2: 0.022 0.286 0.000 0.011 0.000 0.000 0.681 0.000 0.000
3: 0.056 0.000 0.000 0.111 0.167 0.000 0.667 0.000 0.000
4: 0.204 0.015 0.000 0.672 0.058 0.007 0.044 0.000 0.000
5: 0.104 0.000 0.000 0.104 0.438 0.042 0.312 0.000 0.000
6: 0.127 0.018 0.000 0.055 0.164 0.255 0.382 0.000 0.000
7: 0.000 0.021 0.000 0.005 0.000 0.000 0.974 0.000 0.000
8: 0.000 0.000 0.000 0.000 0.000 0.000 0.750 0.000 0.250
9: 0.429 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.571
0.8
0.6
0.4
0.2
0.0

5. End