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 (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 (https://www.youtube.com/watch?v=UwbuW7oK8rk)
3. https://www.youtube.com/watch?v=qxXRKVompI8 (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.

2. Machine Learning Problem Formulation

2.1. Data

2.1.1. Data Overview

- Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/data (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:
  - training_variants (ID , Gene, Variations, Class)
  - training_text (ID, Text)

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 class class
ification problem
```

2.2.2. Performance Metric

Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation (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 [4]:

```
import pandas as pd
import matplotlib.pyplot as plt
import re
import time
import warnings
import numpy as np
from nltk.corpus import stopwords
from sklearn.decomposition import TruncatedSVD
from sklearn.preprocessing import normalize
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.manifold import TSNE
import seaborn as sns
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics.classification import accuracy_score, log_loss
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.linear_model import SGDClassifier
from imblearn.over_sampling import SMOTE

from collections import Counter
from scipy.sparse import hstack
from sklearn.multiclass import OneVsRestClassifier
from sklearn.svm import SVC
from sklearn.model_selection import StratifiedKFold
from collections import Counter, defaultdict
from sklearn.calibration import CalibratedClassifierCV
from sklearn.naive_bayes import MultinomialNB
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import train_test_split
from sklearn.model_selection import GridSearchCV
import math
from sklearn.metrics import normalized_mutual_info_score
from sklearn.ensemble import RandomForestClassifier
warnings.filterwarnings("ignore")

from mlxtend.classifier import StackingClassifier

from sklearn import model_selection
from sklearn.linear_model import LogisticRegression

```

In [128]:
```
# import dill
# dill.load_session('notebook_env.db')
```

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

In [5]:
```
data = pd.read_csv('training/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[5]:

	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/training_variants is a comma separated file containing the description of the genetic mutations used for training.
Fields are

- **ID :** the id of the row used to link the mutation to the clinical evidence
- **Gene :** the gene where this genetic mutation is located
- **Variation :** the aminoacid change for this mutations
- **Class :** 1-9 the class this genetic mutation has been classified on

3.1.2. Reading Text Data

In [6]:
```
# note the seprator in this file
data_text =pd.read_csv("training/training_text",sep="\|\|",engine="python",names=["ID","TEXT"],skiprows=1)
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[6]:

	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 [7]:
```
# loading stop words from nltk library
stop_words = set(stopwords.words('english'))


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]', ' ', 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
            if not word in stop_words:
                string += word + " "

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

In [8]:
```
#text processing stage.
start_time = time.clock()
for index, row in data_text.iterrows():
    if type(row['TEXT']) is str:
        nlp_preprocessing(row['TEXT'], index, 'TEXT')
    else:
        print("there is no text description for id:",index)
print('Time took for preprocessing the text :',time.clock() - start_time, "seconds")
```

```
there is no text description for id: 1109
there is no text description for id: 1277
there is no text description for id: 1407
there is no text description for id: 1639
there is no text description for id: 2755
Time took for preprocessing the text : 227.813003 seconds
```

In [10]:
```
#merging both gene_variations and text data based on ID
result = pd.merge(data, data_text,on='ID', how='left')
result.head()
```

Out[10]:

	ID	Gene	Variation	Class	TEXT
0	0	FAM58A	Truncating Mutations	1	cyclin dependent kinases cdks regulate variety...
1	1	CBL	W802*	2	abstract background non small cell lung cancer...
2	2	CBL	Q249E	2	abstract background non small cell lung cancer...
3	3	CBL	N454D	3	recent evidence demonstrated acquired uniparen...
4	4	CBL	L399V	4	oncogenic mutations monomeric casitas b lineag...

In [81]:
```
1 result["TEXT"]
```

Out[81]:
```
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...
5       oncogenic mutations monomeric casitas b lineag...
6       oncogenic mutations monomeric casitas b lineag...
7       cbl negative regulator activated receptor tyro...
8       abstract juvenile myelomonocytic leukemia jmml...
9       abstract juvenile myelomonocytic leukemia jmml...
10      oncogenic mutations monomeric casitas b lineag...
11      noonan syndrome autosomal dominant congenital ...
12      noonan syndrome autosomal dominant congenital ...
13      noonan syndrome autosomal dominant congenital ...
14      oncogenic mutations monomeric casitas b lineag...
15      noonan syndrome autosomal dominant congenital ...
16      determine residual cylindrical refractive erro...
17      acquired uniparental disomy aupd common featur...
18      oncogenic mutations monomeric casitas b lineag...
19      acquired uniparental disomy aupd common featur...
20      abstract background non small cell lung cancer...
21      oncogenic mutations monomeric casitas b lineag...
22      oncogenic mutations monomeric casitas b lineag...
23      recent evidence demonstrated acquired uniparen...
24      recent evidence demonstrated acquired uniparen...
25      recent evidence demonstrated acquired uniparen...
26      abstract n myristoylation common form co trans...
27      heterozygous mutations telomerase components t...
28      sequencing studies identified many recurrent c...
29      heterozygous mutations telomerase components t...
                              ...
3291    investigatedthe transformingactivityofthe ret ...
3292    investigatedthe transformingactivityofthe ret ...
3293    ret transmembrane tyrosine kinase participatin...
3294    introduction inherited germ line activating mu...
3295    many missense mutations ret proto oncogene fou...
3296    ret proto oncogene encodes receptor tyrosine k...
3297    aml1 gene known frequent target chromosomal tr...
3298    introduction myelodysplastic syndromes mds het...
```

```
3299    bcr abl fusion protein generated 9 22 q34 q11 ...
3300    frequent mutations associated leukemia recurre...
3301    frequent mutations associated leukemia recurre...
3302    familial platelet disorder predisposition acut...
3303    introduction myelodysplastic syndromes mds het...
3304    familial platelet disorder predisposition acut...
3305    introduction myelodysplastic syndromes mds het...
3306    report two new runx1 mutations one patient con...
3307    runx genes come prominence recently roles esse...
3308    familial platelet disorder propensity acute my...
3309    bcr abl fusion protein generated 9 22 q34 q11 ...
3310    runx proteins belong family metazoan transcrip...
3311    aml1 evi 1 chimeric gene generated 3 21 q26 q2...
3312    balanced chromosomal translocations frequently...
3313    bcr abl fusion protein generated 9 22 q34 q11 ...
3314    introduction myelodysplastic syndromes mds het...
3315    runx gene family includes three evolutionarily...
3316    introduction myelodysplastic syndromes mds het...
3317    introduction myelodysplastic syndromes mds het...
3318    runt related transcription factor 1 gene runx1...
3319    runx1 aml1 gene frequent target chromosomal tr...
3320    frequent mutations associated leukemia recurre...
Name: TEXT, Length: 3321, dtype: object
```

In [11]:
```
result[result.isnull().any(axis=1)]
```

Out[11]:

	ID	Gene	Variation	Class	TEXT
1109	1109	FANCA	S1088F	1	NaN
1277	1277	ARID5B	Truncating Mutations	1	NaN
1407	1407	FGFR3	K508M	6	NaN
1639	1639	FLT1	Amplification	6	NaN
2755	2755	BRAF	G596C	7	NaN

In [12]:
```
result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Variation']
```

In [13]:
```
result[result['ID']==1109]
```

Out[13]:

	ID	Gene	Variation	Class	TEXT
1109	1109	FANCA	S1088F	1	FANCA S1088F

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 [15]:
```
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 varaible 'y_true' [stratify
X_train, test_df, y_train, y_test = train_test_split(result, y_true, stratify=y_true, test_size=0.2)
# split the train data into train and cross validation by maintaining same distribution of output varaible
train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train, stratify=y_train, test_size=0.2)
```

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

In [16]:
```
print('Number of data points in train data:', train_df.shape[0])
print('Number of data points in test data:', test_df.shape[0])
print('Number of data points in cross validation data:', cv_df.shape[0])
```

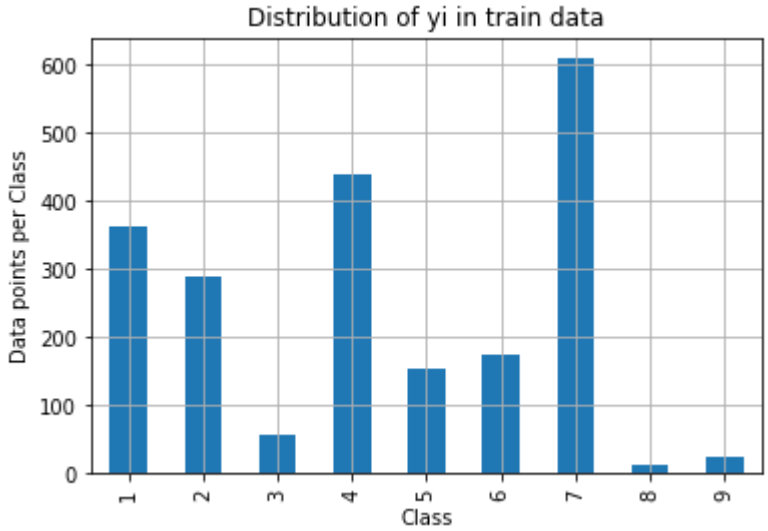
```
Number of data points in train data: 2124
Number of data points in test data: 665
Number of data points in cross validation data: 532
```

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

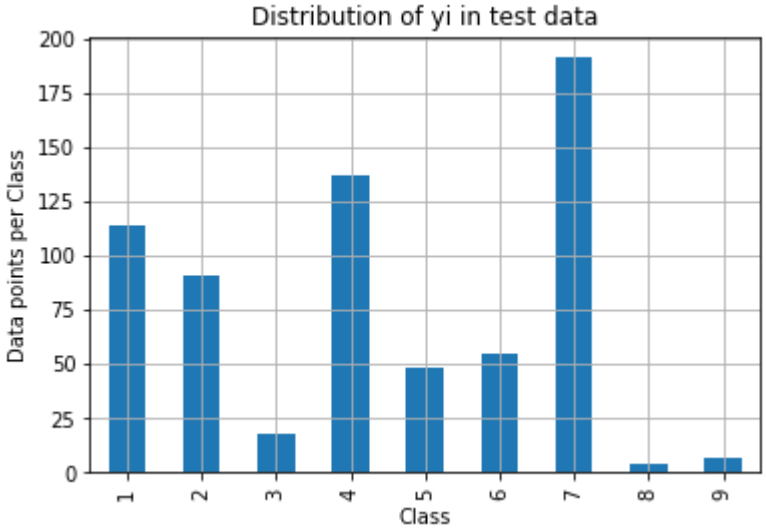
In [17]:

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

my_colors = 'rgbkymc'
train_class_distribution.plot(kind='bar')
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], '(', np.round((tra


print('-'*80)
my_colors = 'rgbkymc'
test_class_distribution.plot(kind='bar')
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], '(', np.round((test_

print('-'*80)
my_colors = 'rgbkymc'
cv_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in cross validation data')
```

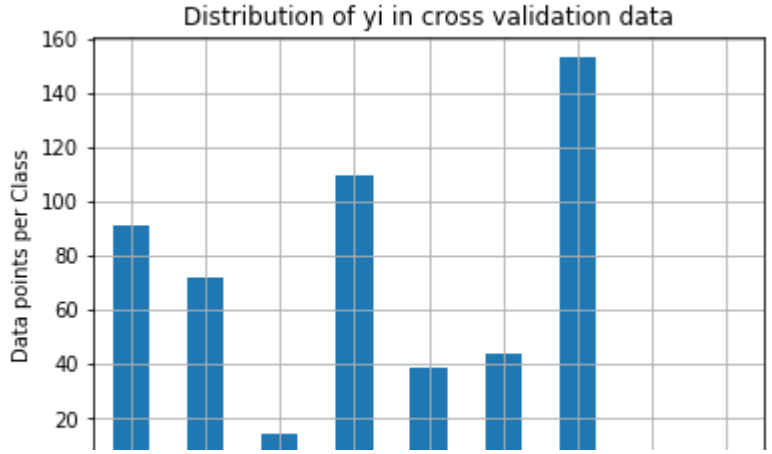
```
plt.grid()
plt.show()

# 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], '(', np.round((cv_cla
```




```
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.

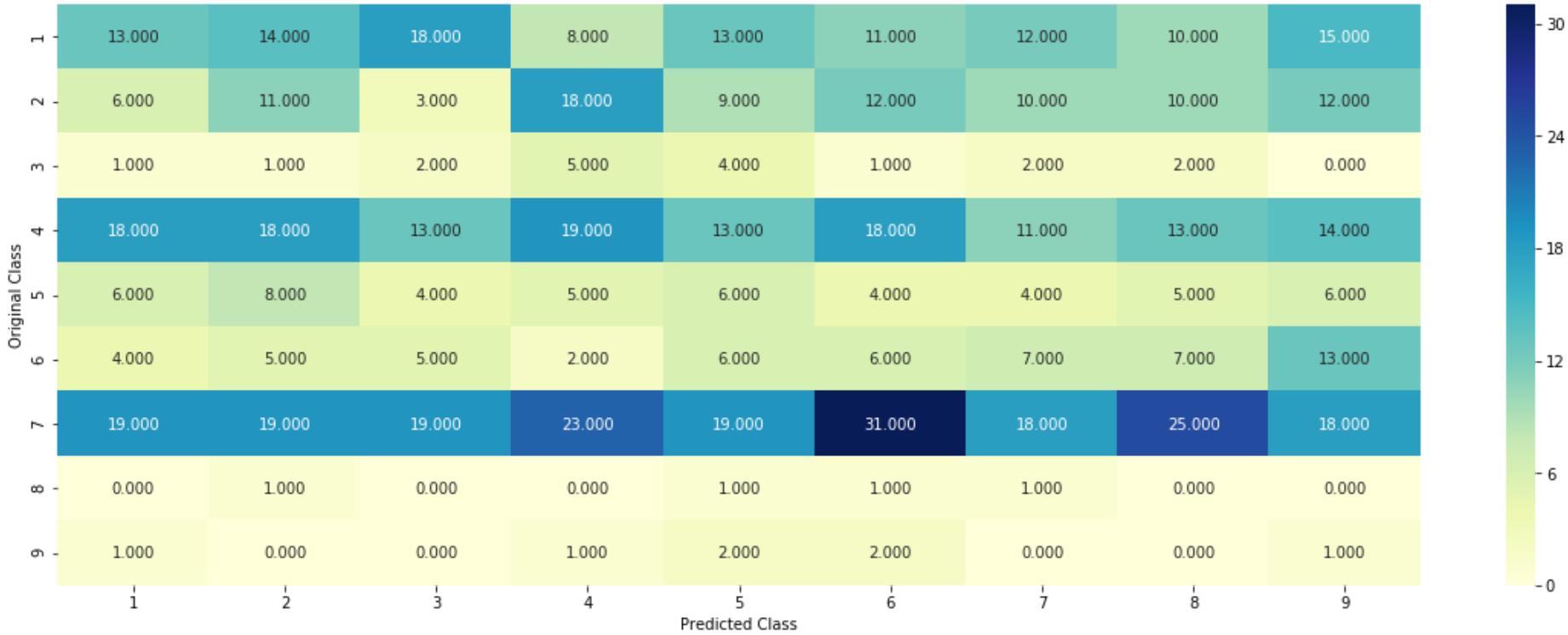
In [18]:

```
# 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 predicted class j

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

    # 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 two diamensional arra
    # 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 two diamensional arra
    # 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, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()

    print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
    plt.figure(figsize=(20,7))
```

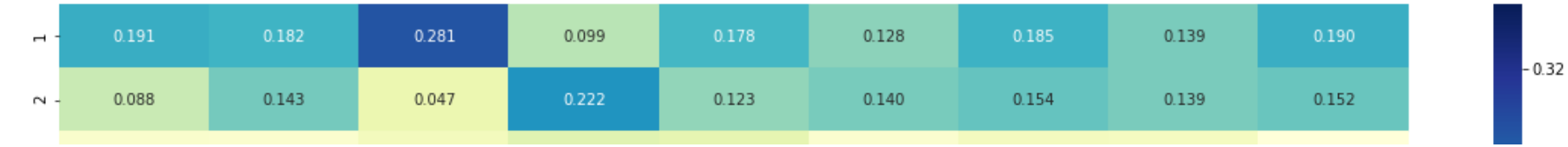
```
    sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()

    # 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, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()
```

In [19]:
```
# 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_predicted_y, eps=1e-15))


# 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=1e-15))

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

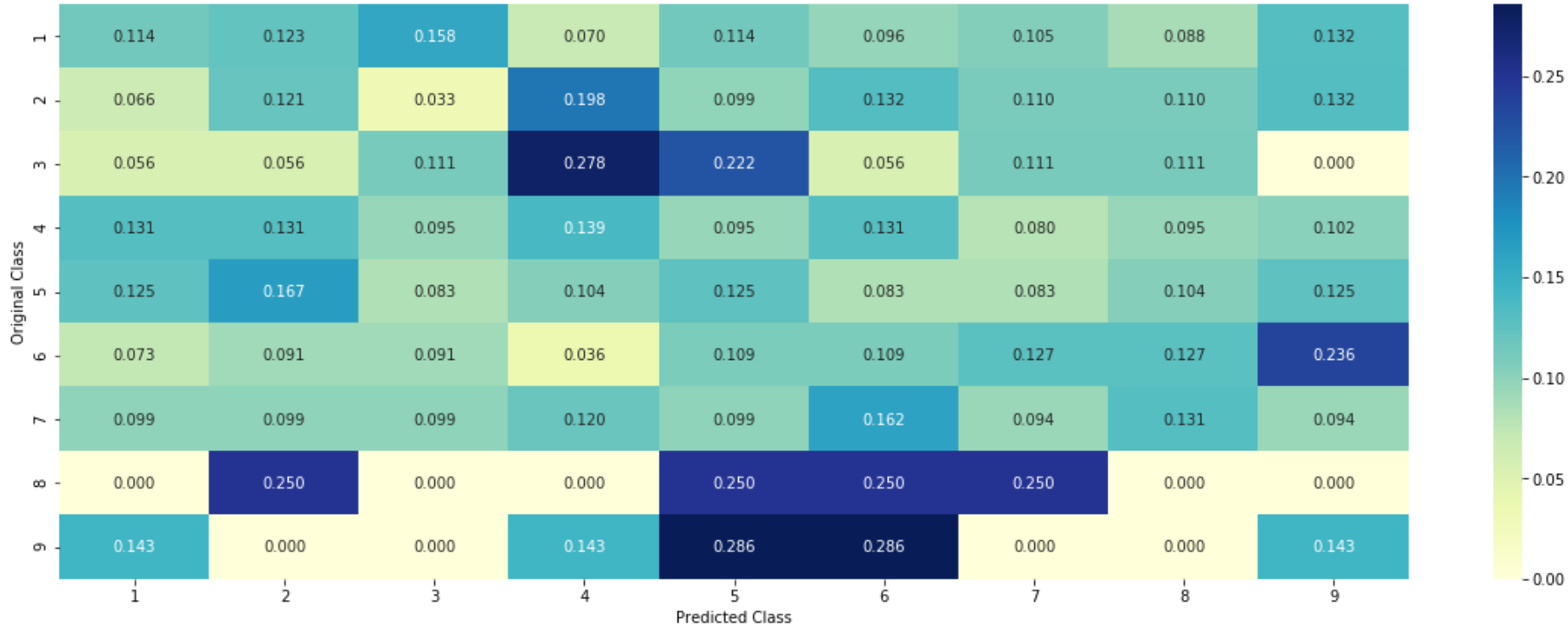
```
Log loss on Cross Validation Data using Random Model 2.4695406766150847
Log loss on Test Data using Random Model 2.475479077789838
-------------------- Confusion matrix --------------------
```



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




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



3.3 Univariate Analysis

In [20]:

```
# 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 data dataframe
# build a vector (1*9) , the first element = (number of times it occured in class1 + 10*alpha / number of t
# gv_dict is like a look up table, for every gene it store a (1*9) representation of it
# 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 gene/variation
    gv_dict = dict()

    # denominator will contain the number of time that particular feature occured in whole data
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticular class
        # 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
            # 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 particular feature occured i
            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, 0.06818181818181818, 0.13636363636363635, 0
    #      'TP53': [0.32142857142857145, 0.06122448979591836, 0.06122448979591836, 0.27040816326530615, 0
    #      'EGFR': [0.05681818181818181, 0.21590909090909091, 0.0625, 0.06818181818181818, 0.06818181818
```

```
    #       'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.060606060606060608, 0.078787878787878782,
    #       'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 0.4654088050314465,
    #       'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.072847682119205295, 0
    #       'BRAF': [0.06666666666666666, 0.17999999999999999, 0.073333333333333334, 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 value in the data
    gv_fea = []
    # for every feature values in the given data frame we will check if it is there in the train data then
    # 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?

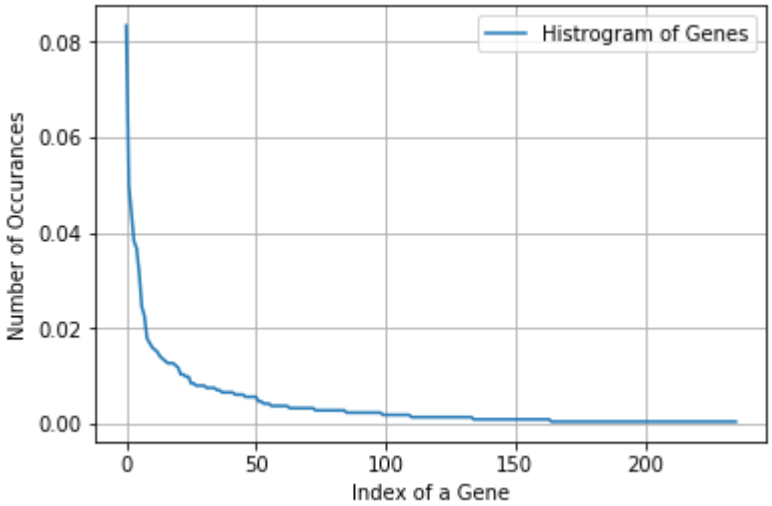
In [21]:
```
unique_genes = train_df['Gene'].value_counts()
print('Number of Unique Genes :', unique_genes.shape[0])
# the top 10 genes that occured most
print(unique_genes.head(10))
```

```
Number of Unique Genes : 236
BRCA1     177
TP53      106
EGFR       94
BRCA2      81
PTEN       78
BRAF       67
KIT        52
ALK        48
ERBB2      38
PIK3CA     36
Name: Gene, dtype: int64
```

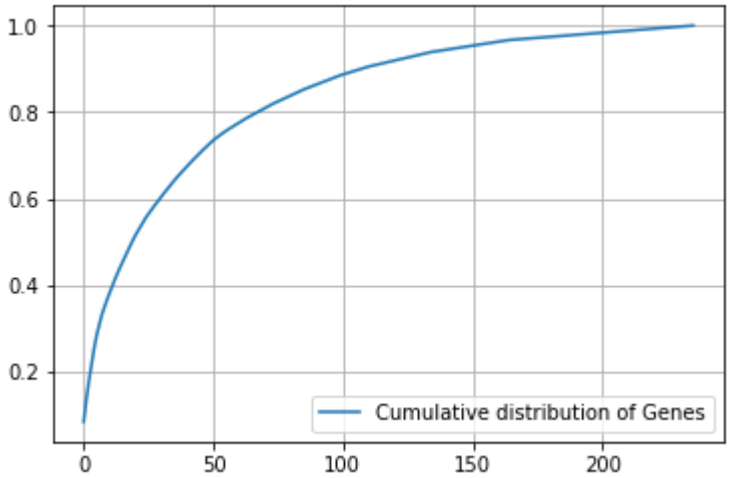
In [22]:
```
print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in the train data, and they a
```

```
Ans: There are 236 different categories of genes in the train data, and they are distibuted as follows
```

In [23]:
```
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 [24]:
```
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/

1. One hot Encoding
2. 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 [25]:
```
#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 [26]:
```
print("train_gene_feature_responseCoding is converted feature using respone coding method. The shape of gen
```

```
train_gene_feature_responseCoding is converted feature using respone coding method. The shape of gene featur
e: (2124, 9)
```

In [27]:
```
# TFIDF
from sklearn.feature_extraction.text import TfidfVectorizer
gene_vectorizer = TfidfVectorizer()
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 [28]:
```
train_df['Gene'].head()
```

Out[28]:
```
116     KMT2D
2513    BRCA1
2693     BRAF
578     SMAD4
3009      KIT
Name: Gene, dtype: object
```

In [29]:
```
1 gene_vectorizer.get_feature_names()
```

Out[29]:
```
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
 'akt3',
 'alk',
 'apc',
 'ar',
 'araf',
 'arid1a',
 'arid1b',
 'arid2',
 'arid5b',
 'asxl1',
 'atm',
 'atr',
 'atrx',
 'aurka',
```

In [30]:
```
1 print("train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gen
```

```
train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene featur
e: (2124, 235)
```

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

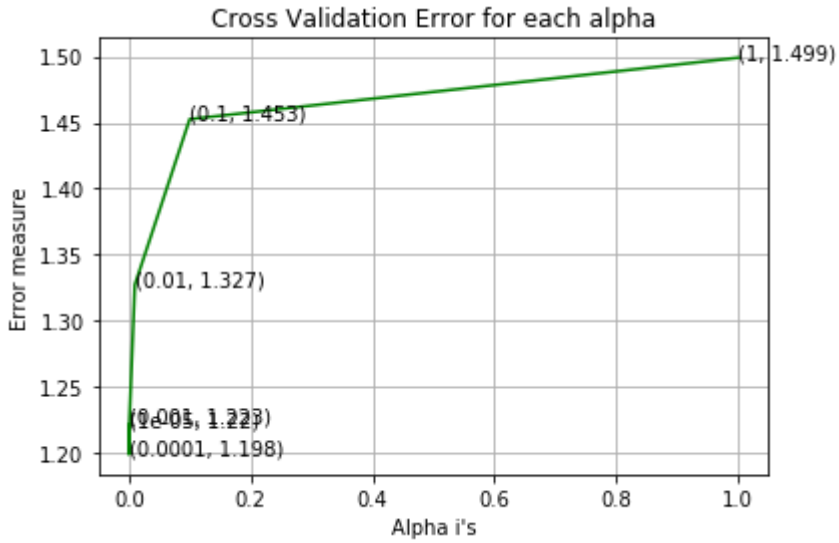
There are many ways to estimate how good a feature is, in predicting y_i. One of the good methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y_i.

In [31]:

```
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/sklearn.linear_model.
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_iter=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0=0.0, pow
# 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 Gradient Descent.
# 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, n_jobs=3)
    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, labels=clf.classes_, ep

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, n_jobs=3)
```

```
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_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
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_loss(y_test, predict_y,

```

```
For values of alpha =  1e-05 The log loss is: 1.2202789742572298
For values of alpha =  0.0001 The log loss is: 1.1982950255130638
For values of alpha =  0.001 The log loss is: 1.222517090954132
For values of alpha =  0.01 The log loss is: 1.3269440830250716
For values of alpha =  0.1 The log loss is: 1.4525111676082707
For values of alpha =  1 The log loss is: 1.499096866060869
```



```
For values of best alpha =  0.0001 The train log loss is: 1.007164617292122
For values of best alpha =  0.0001 The cross validation log loss is: 1.1982950255130638
For values of best alpha =  0.0001 The test log loss is: 1.1654562649337685
```

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 [33]:
```
print("Q6. How many data points in Test and CV datasets are covered by the ", unique_genes.shape[0], " gene

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_coverage/test_df.shape[0])
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_coverage/cv_df.shape[0])
```

```
Q6. How many data points in Test and CV datasets are covered by the  236  genes in train dataset?
Ans
1. In test data 651 out of 665 : 97.89473684210527
2. In cross validation data 514 out of  532 : 96.61654135338345
```

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?

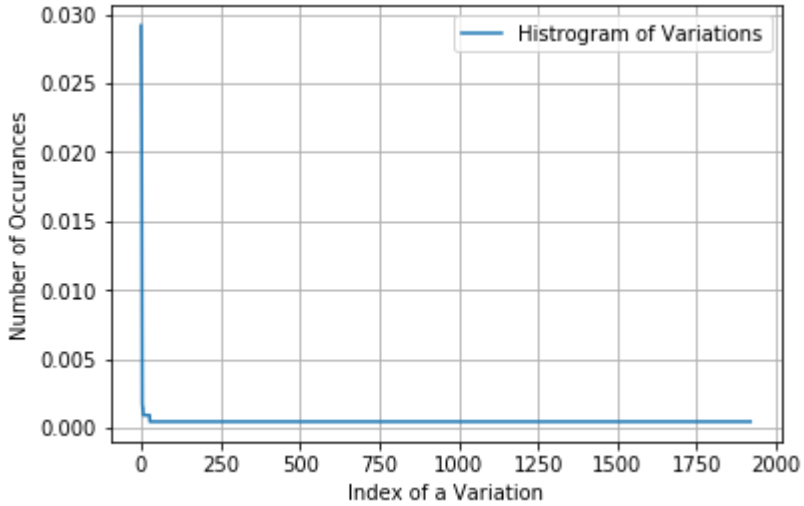
In [34]:
```
unique_variations = train_df['Variation'].value_counts()
print('Number of Unique Variations :', unique_variations.shape[0])
# the top 10 variations that occured most
print(unique_variations.head(10))
```

```
Number of Unique Variations : 1920
Truncating_Mutations    62
Deletion                52
Amplification           45
Fusions                 21
Overexpression           4
G12V                     3
E17K                     3
F28L                     2
T73I                     2
A146T                    2
Name: Variation, dtype: int64
```

In [35]:
```
print("Ans: There are", unique_variations.shape[0] ,"different categories of variations in the train data,
```

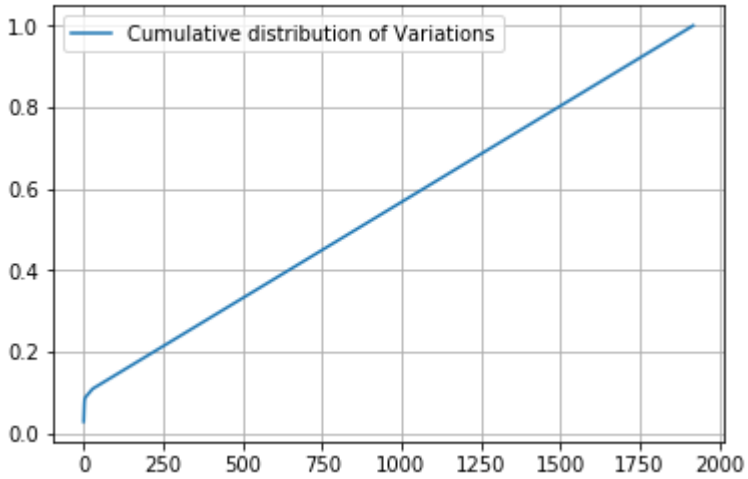
```
Ans: There are 1920 different categories of variations in the train data, and they are distibuted as follows
```

In [36]:
```
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 [37]:
```
c = np.cumsum(h)
print(c)
plt.plot(c,label='Cumulative distribution of Variations')
plt.grid()
plt.legend()
plt.show()
```

```
[0.02919021 0.05367232 0.07485876 ... 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/

1. One hot Encoding
2. Response coding

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

In [0]:
```
# alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train_df))
# test gene feature
test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", test_df))
# cross validation gene feature
cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", cv_df))
```

In [0]:
```
print("train_variation_feature_responseCoding is a converted feature using the response coding method. The
```

```
train_variation_feature_responseCoding is a converted feature using the response coding method. The shape of
Variation feature: (2124, 9)
```

In [38]:
```
# TFIDF
variation_vectorizer = TfidfVectorizer()
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variation'])
test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])
```

In [39]:
```
print("train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method. The s
```

```
train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method. The shape of V
ariation feature: (2124, 1948)
```

Q10. How good is this Variation feature in predicting y_i?

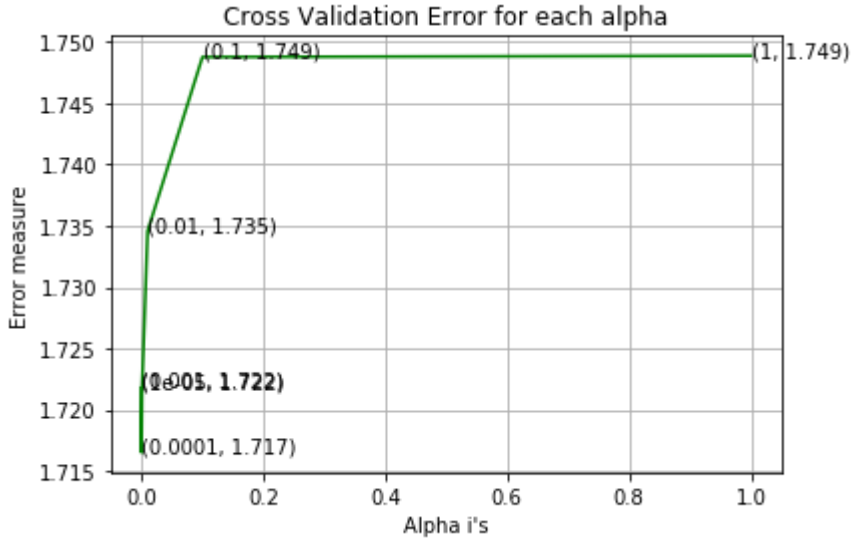
Let's build a model just like the earlier!

In [40]:

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

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_iter=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0=0.0, pow
# 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 Gradient Descent.
# 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, n_jobs=3)
    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, labels=clf.classes_, ep

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, n_jobs=3)
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_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
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_loss(y_test, predict_y,

```

```
For values of alpha =  1e-05 The log loss is: 1.7217921451034903
For values of alpha =  0.0001 The log loss is: 1.716520021064393
For values of alpha =  0.001 The log loss is: 1.7219560644207113
For values of alpha =  0.01 The log loss is: 1.7345769217678837
For values of alpha =  0.1 The log loss is: 1.748764356802458
For values of alpha =  1 The log loss is: 1.748872154328207
```



```
For values of best alpha =  0.0001 The train log loss is: 0.7578118654422595
For values of best alpha =  0.0001 The cross validation log loss is: 1.716520021064393
For values of best alpha =  0.0001 The test log loss is: 1.7176841315254827
```

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 [41]:
```
print("Q12. How many data points are covered by total ", unique_variations.shape[0], " genes in test and cr
test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
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_coverage/test_df.shape[0])
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_coverage/cv_df.shape[0])
```

```
Q12. How many data points are covered by total  1920  genes in test and cross validation data sets?
Ans
1. In test data 70 out of 665 : 10.526315789473683
2. In cross validation data 49 out of  532 : 9.210526315789473
```

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 [0]:
```
# 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 [0]:
```
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(word,0)+90)))
            text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TEXT'].split()))
            row_index += 1
    return text_feature_responseCoding
```

In [82]:
```
# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer = TfidfVectorizer(min_df=3, max_features=1000)
train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*number of features) vect
train_text_fea_counts = train_text_feature_onehotCoding.sum(axis=0).A1

# zip(list(text_features),text_fea_counts) will zip a word with its number of times it occured
text_fea_dict = dict(zip(list(train_text_features),train_text_fea_counts))


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

```
Total number of unique words in train data : 1000
```

In [43]:
```
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)


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

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
<ipython-input-43-6d69a1102340> in <module>
      4     cls_text = train_df[train_df['Class']==i]
      5     # build a word dict based on the words in that class
----> 6     dict_list.append(extract_dictionary_paddle(cls_text))
      7     # append it to dict_list
      8

NameError: name 'extract_dictionary_paddle' is not defined
```

In [0]:
```
#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 [0]:
```
# 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_feature_responseCoding.
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_responseCoding.sum
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.sum(axis=
```

In [83]:
```
# don't forget to normalize every feature
train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding, axis=0)

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

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

In [84]:
```
#https://stackoverflow.com/a/2258273/4084039
sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambda x: x[1] , reverse=True))
sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))
```

In [85]:
```
# Number of words for a given frequency.
print(Counter(sorted_text_occur))
```

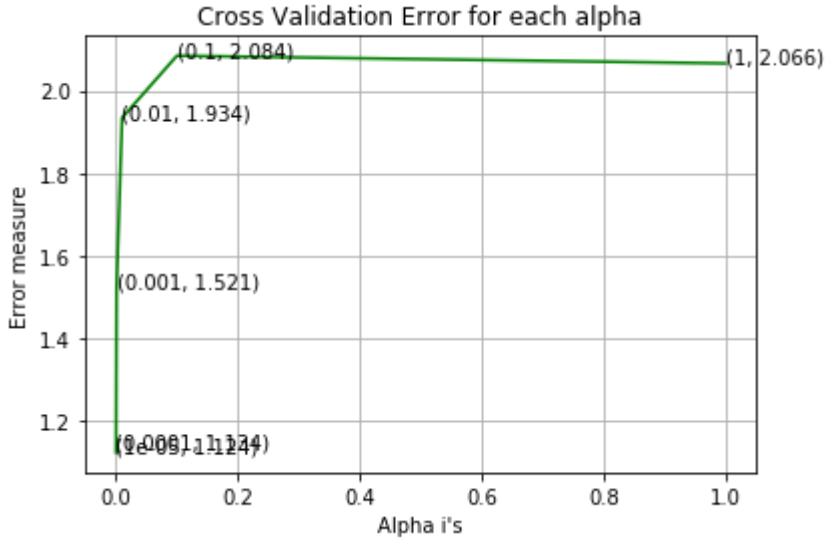
```
Counter({253.45612854557848: 1, 181.8561472374477: 1, 141.81578713152044: 1, 132.4119790600596: 1, 132.248561
3245489: 1, 118.82156729160252: 1, 118.47323464437058: 1, 114.21120064713215: 1, 112.33018004794411: 1, 107.6
71276275327: 1, 107.06482767967276: 1, 89.1263711122647: 1, 88.35227467864152: 1, 86.7254319818862: 1, 81.641
82663564429: 1, 81.46677217209721: 1, 79.43685103101126: 1, 79.33372393634076: 1, 78.82645319750993: 1, 77.99
997212017877: 1, 77.73834725495779: 1, 75.16572289005073: 1, 69.6619948558994: 1, 68.69049717413029: 1, 67.88
022151261575: 1, 67.75392879950992: 1, 67.07620365755038: 1, 65.58130505874054: 1, 65.20226276415035: 1, 63.7
65880603490835: 1, 63.457339760323656: 1, 62.80280020966844: 1, 62.54808981645129: 1, 60.470597635312835: 1,
59.54634341135907: 1, 58.56814084030761: 1, 56.868959718213254: 1, 56.835933427076434: 1, 56.00033536171236:
1, 54.974205192575575: 1, 52.51137471639824: 1, 50.71620160884344: 1, 49.231602410746525: 1, 48.5162219160665
8: 1, 47.34244737784118: 1, 46.46346391448383: 1, 45.89412565164875: 1, 45.61689695648438: 1, 44.560208931307
01: 1, 43.90986592280627: 1, 43.74834766086299: 1, 43.720834052367266: 1, 43.6635037667005: 1, 43.62042213852
648: 1, 42.85457592372548: 1, 42.69494270138875: 1, 42.36474321367222: 1, 42.127512183105054: 1, 41.781929560
19826: 1, 41.58399107872969: 1, 41.124372893441084: 1, 41.05810960675291: 1, 41.00073002392298: 1, 40.5253785
7903626: 1, 39.61881318803275: 1, 39.41481629416075: 1, 39.402334019248535: 1, 39.33721055039442: 1, 38.22811
5566851095: 1, 38.07748568594918: 1, 37.882403866262: 1, 37.870855607768505: 1, 37.161319920779924: 1, 36.717
0867600636: 1, 36.693707887314176: 1, 36.3359922393846: 1, 35.989411003186724: 1, 35.81540382208122: 1, 35.71
451539590343: 1, 35.62467322679815: 1, 35.26610066155905: 1, 34.996741397988245: 1, 34.94013138955001: 1, 34.
63432109591924: 1, 34.50489211328151: 1, 34.3964684020224: 1, 34.283202692168494: 1, 34.08132556614205: 1, 3
4.04406894264587: 1, 33.498236231193: 1, 33.09774659467206: 1, 33.09276623545926: 1, 32.85685527883516: 1, 3
```

In [86]:

```
# Train a Logistic regression+Calibration model using text features whicha re on-hot encoded
alpha = [10 ** x for x in range(-5, 1)]

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_iter=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0=0.0, pow
# 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 Gradient Descent.
# 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, n_jobs=3)
    clf.fit(train_text_feature_onehotCoding, y_train)

    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_text_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_text_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, labels=clf.classes_, ep

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, n_jobs=3)
clf.fit(train_text_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_onehotCoding, y_train)

predict_y = sig_clf.predict_proba(train_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
predict_y = sig_clf.predict_proba(test_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y,

```

```
For values of alpha =  1e-05 The log loss is: 1.1236270404130342
For values of alpha =  0.0001 The log loss is: 1.1339643177809415
For values of alpha =  0.001 The log loss is: 1.5214866424038809
For values of alpha =  0.01 The log loss is: 1.9340658920508387
For values of alpha =  0.1 The log loss is: 2.0844881800102137
For values of alpha =  1 The log loss is: 2.0659298902039547
```




```
For values of best alpha =  1e-05 The train log loss is: 0.7136163056681504
For values of best alpha =  1e-05 The cross validation log loss is: 1.1236270404130342
For values of best alpha =  1e-05 The test log loss is: 1.1432071674613324
```

Q. Is the Text feature stable across all the data sets (Test, Train, Cross validation)?

Ans. Yes, it seems like!

In [87]:
```
def get_intersec_text(df):
    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) & set(df_text_features))
    return len1,len2
```

In [88]:
```
len1,len2 = get_intersec_text(test_df)
print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data")
len1,len2 = get_intersec_text(cv_df)
print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train data")
```

```
3.414 % of word of test data appeared in train data
3.792 % of word of Cross Validation appeared in train data
```

4. Machine Learning Models

In [51]:
```
#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 each class
    print("Log loss :",log_loss(test_y, sig_clf.predict_proba(test_x)))
    # calculating the number of data points that are misclassified
    print("Number of mis-classified points :", np.count_nonzero((pred_y- test_y))/test_y.shape[0])
    plot_confusion_matrix(test_y, pred_y)
```

In [52]:
```
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 [53]:

```
# 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(word,yes_no))
        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 [{}]".format(word,yes_no))
        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(word,yes_no))

    print("Out of the top ",no_features," features ", word_present, "are present in query point")
```

Stacking the three types of features

In [89]:

```
# 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_feature_onehotCoding))
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_onehotCoding))
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehotCoding))

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

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

cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text_feature_onehotCoding)).tocsr()
cv_y = np.array(list(cv_df['Class']))


# train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,train_variation_feature_resp
# test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_feature_respons
# cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature_responseCodin

# train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_responseCoding))
# test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_responseCoding))
# cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding))

```

In [90]:
```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCoding.shape)
print("(number of data points * number of features) in test data = ", test_x_onehotCoding.shape)
print("(number of data points * number of features) in cross validation data =", cv_x_onehotCoding.shape)
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 3183)
(number of data points * number of features) in test data =  (665, 3183)
(number of data points * number of features) in cross validation data = (532, 3183)
```

In [56]:
```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_responseCoding.shape)
print("(number of data points * number of features) in test data = ", test_x_responseCoding.shape)
print("(number of data points * number of features) in cross validation data =", cv_x_responseCoding.shape)
```

```
 Response encoding features :

---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
<ipython-input-56-7d7a26188f88> in <module>
      1 print(" Response encoding features :")
----> 2 print("(number of data points * number of features) in train data = ", train_x_responseCoding.shape)
      3 print("(number of data points * number of features) in test data = ", test_x_responseCoding.shape)
      4 print("(number of data points * number of features) in cross validation data =", cv_x_responseCoding.
shape)

NameError: name 'train_x_responseCoding' is not defined
```

4.1. Base Line Model

4.1.1. Naive Bayes

4.1.1.1. Hyper parameter tuning

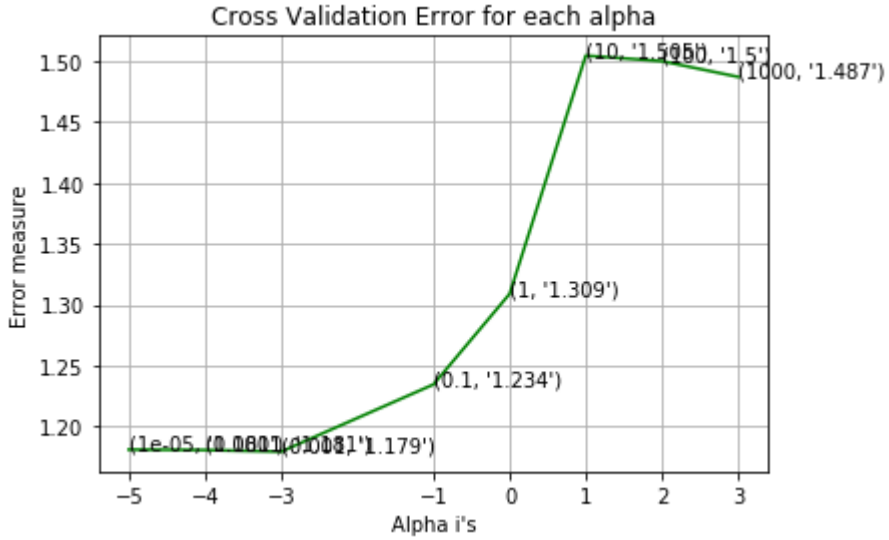
In [91]:

```
# find more about Multinomial Naive base function here http://scikit-learn.org/stable/modules/generated/skl
# ------------------------
# 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/naive-bayes-algorithm
# -----------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.c
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# 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/naive-bayes-algorithm
# -----------------------


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_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
```

```
42
43 fig, ax = plt.subplots()
44 ax.plot(np.log10(alpha), cv_log_error_array,c='g')
45 for i, txt in enumerate(np.round(cv_log_error_array,3)):
46     ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv_log_error_array[i]))
47 plt.grid()
48 plt.xticks(np.log10(alpha))
49 plt.title("Cross Validation Error for each alpha")
50 plt.xlabel("Alpha i's")
51 plt.ylabel("Error measure")
52 plt.show()
53
54
55 best_alpha = np.argmin(cv_log_error_array)
56 clf = MultinomialNB(alpha=alpha[best_alpha])
57 clf.fit(train_x_onehotCoding, train_y)
58 sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
59 sig_clf.fit(train_x_onehotCoding, train_y)
60
61
62 predict_y = sig_clf.predict_proba(train_x_onehotCoding)
63 print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_
64 predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
65 print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
66 predict_y = sig_clf.predict_proba(test_x_onehotCoding)
67 print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y,
68
```

```
for alpha = 1e-05
Log Loss : 1.1808361651709762
for alpha = 0.0001
Log Loss : 1.1805077618041426
for alpha = 0.001
Log Loss : 1.1791699326060952
for alpha = 0.1
Log Loss : 1.2343585317850052
for alpha = 1
Log Loss : 1.3087969709305698
for alpha = 10
Log Loss : 1.5045900910017453
for alpha = 100
Log Loss : 1.5000429623188356
```

```
for alpha = 1000
Log Loss : 1.4871093699387652
```



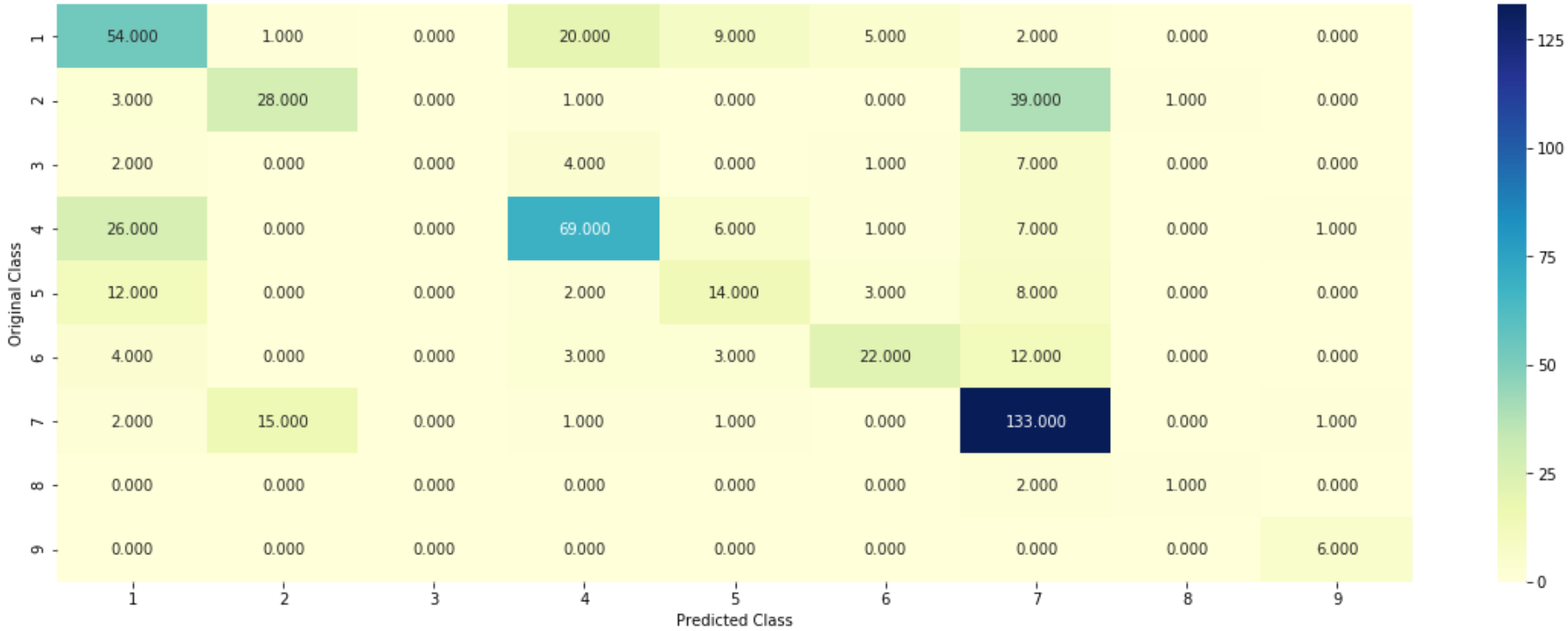

```
For values of best alpha =  0.001 The train log loss is: 0.5142704513553946
For values of best alpha =  0.001 The cross validation log loss is: 1.1791699326060952
For values of best alpha =  0.001 The test log loss is: 1.2041049705163938
```

4.1.1.2. Testing the model with best hyper paramters

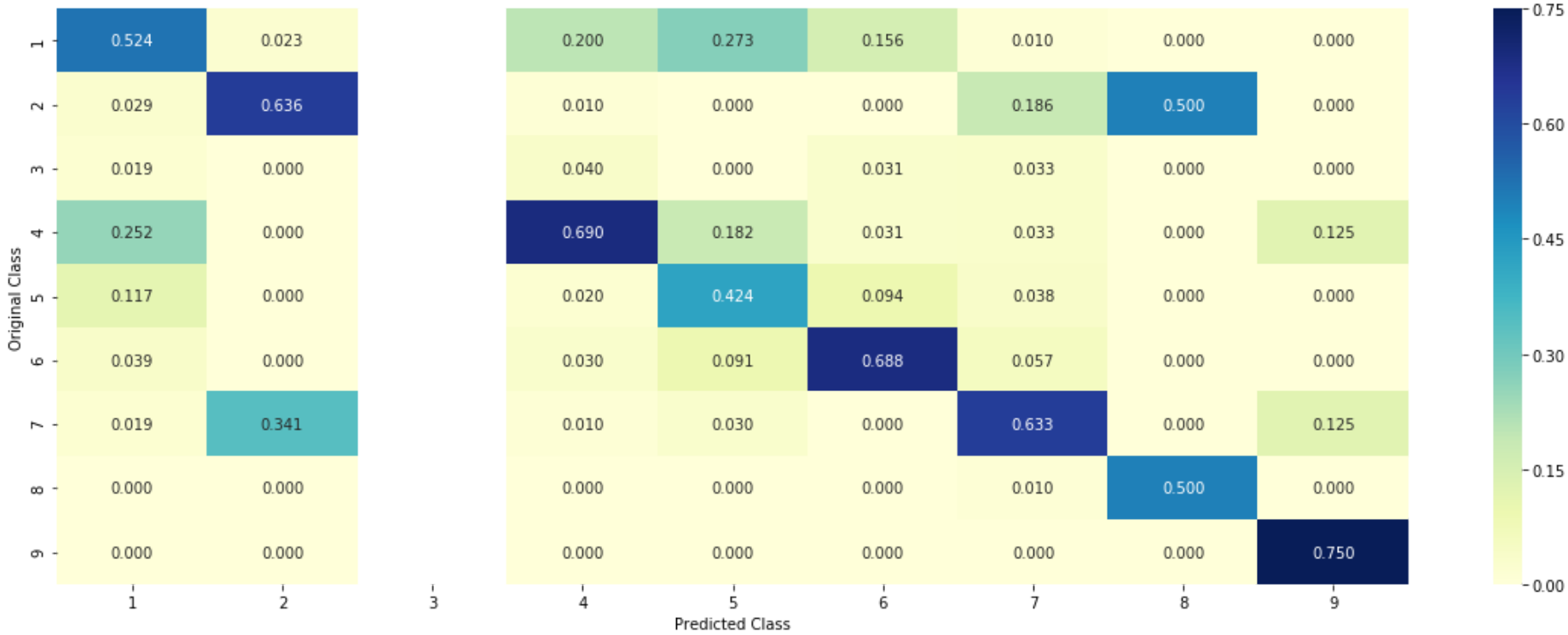
In [92]:

```
# find more about Multinomial Naive base function here http://scikit-learn.org/stable/modules/generated/skl
# ------------------------
# 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/naive-bayes-algorithm
# -----------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.c
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# 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
# ----------------------------

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

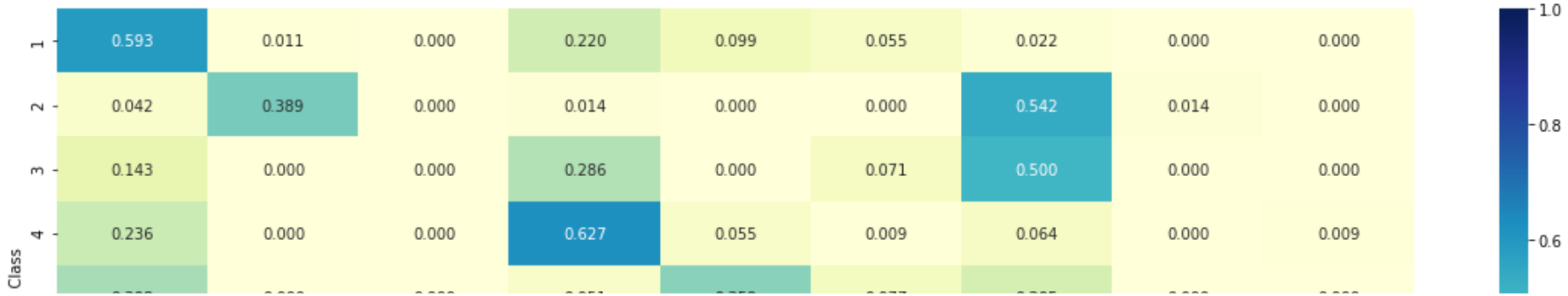
```
Log Loss : 1.1791699326060952
Number of missclassified point : 0.38533834586466165
-------------------- Confusion matrix --------------------
```



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



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



4.1.1.3. Feature Importance, Correctly classified point

In [93]:
```
test_point_index = 1
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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'].iloc[test_point_ind
```

```
Predicted Class : 6
Predicted Class Probabilities: [[0.111  0.0628 0.0172 0.1298 0.1621 0.3874 0.1205 0.0048 0.0045]]
Actual Class : 4
--------------------------------------------------
Out of the top  100  features  0 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

In [94]:
```
test_point_index = 100
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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'].iloc[test_point_ind
```

```
Predicted Class : 8
Predicted Class Probabilities: [[0.2506 0.0746 0.0195 0.1115 0.0526 0.0475 0.1427 0.2909 0.0102]]
Actual Class : 8
--------------------------------------------------
65 Text feature [1000] present in test data point [True]
Out of the top  100  features  1 are present in query point
```

4.2. K Nearest Neighbour Classification

4.2.1. Hyper parameter tuning

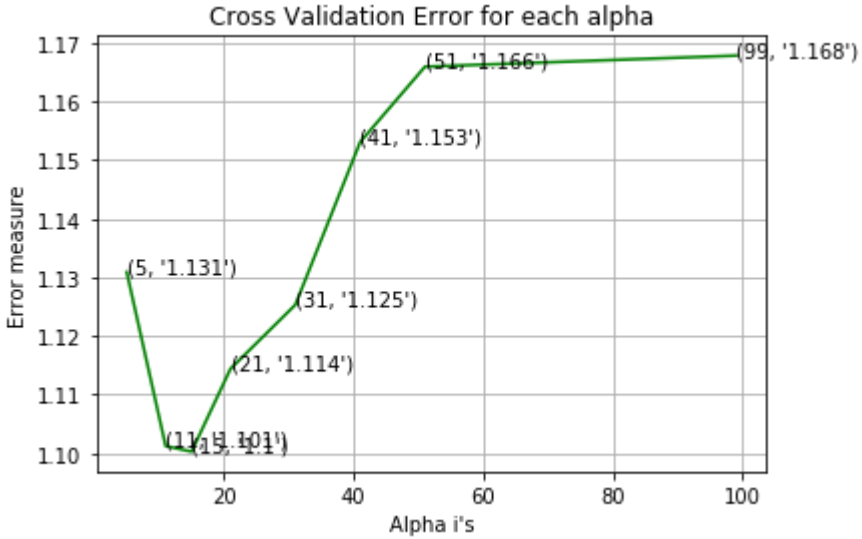
In [0]:

```
# find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/generated/sklearn.neig
# -------------------------
# default parameter
# KNeighborsClassifier(n_neighbors=5, weights='uniform', algorithm='auto', leaf_size=30, p=2,
# 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/k-nearest-neighbors-g
#--------------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.c
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# 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=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
```

```
    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_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y,

```

```
for alpha = 5
Log Loss : 1.1309170126692265
for alpha = 11
Log Loss : 1.1012397762291362
for alpha = 15
Log Loss : 1.1002748803755749
for alpha = 21
Log Loss : 1.1144110925957647
for alpha = 31
Log Loss : 1.1253206995500455
for alpha = 41
Log Loss : 1.1530939773909168
for alpha = 51
Log Loss : 1.1659585643007098

for alpha = 99
```

```
for alpha =  99
Log Loss : 1.1678505034822115
```



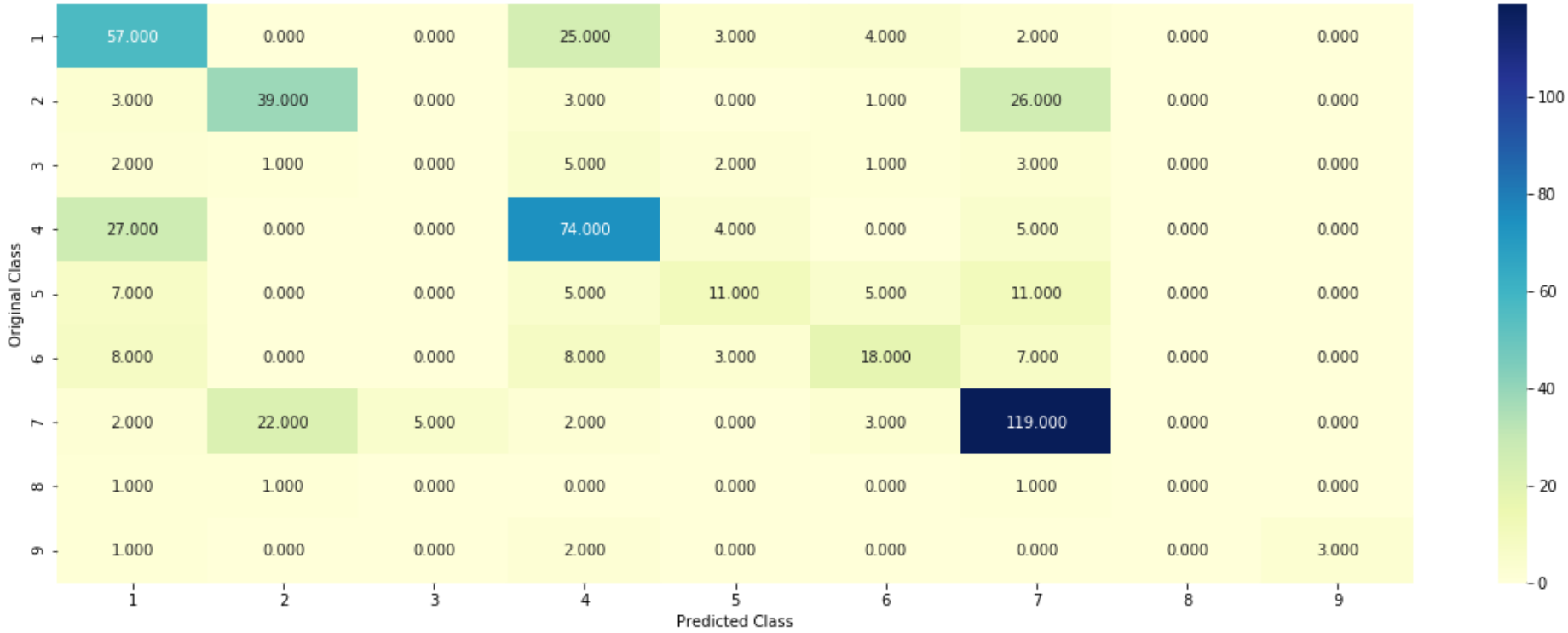

```
For values of best alpha =  15 The train log loss is: 0.7056892871225193
For values of best alpha =  15 The cross validation log loss is: 1.1002748803755749
For values of best alpha =  15 The test log loss is: 1.0911901980302394
```

4.2.2. Testing the model with best hyper paramters

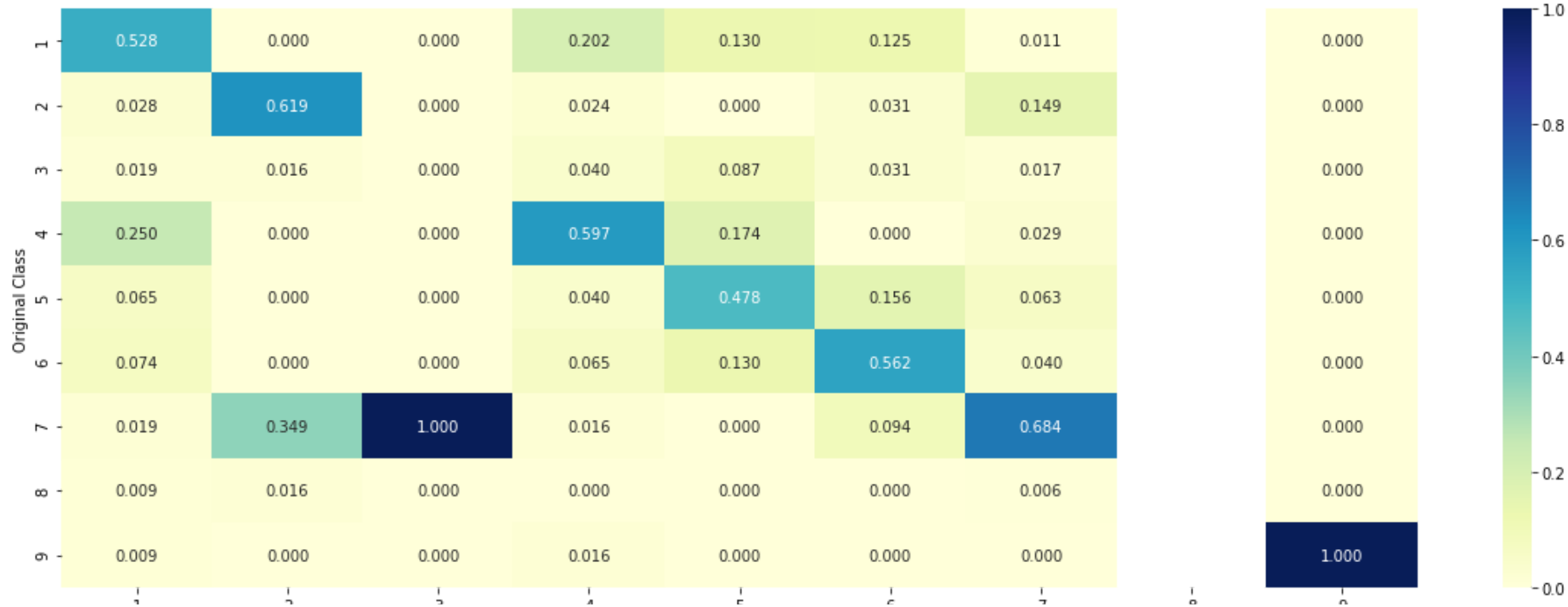
In [0]:

```
# find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/generated/sklearn.neig
# ------------------------
# default parameter
# KNeighborsClassifier(n_neighbors=5, weights='uniform', algorithm='auto', leaf_size=30, p=2,
# 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/k-nearest-neighbors-g
#-------------------------------------
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y, cv_x_responseCoding, cv_y, clf)
```

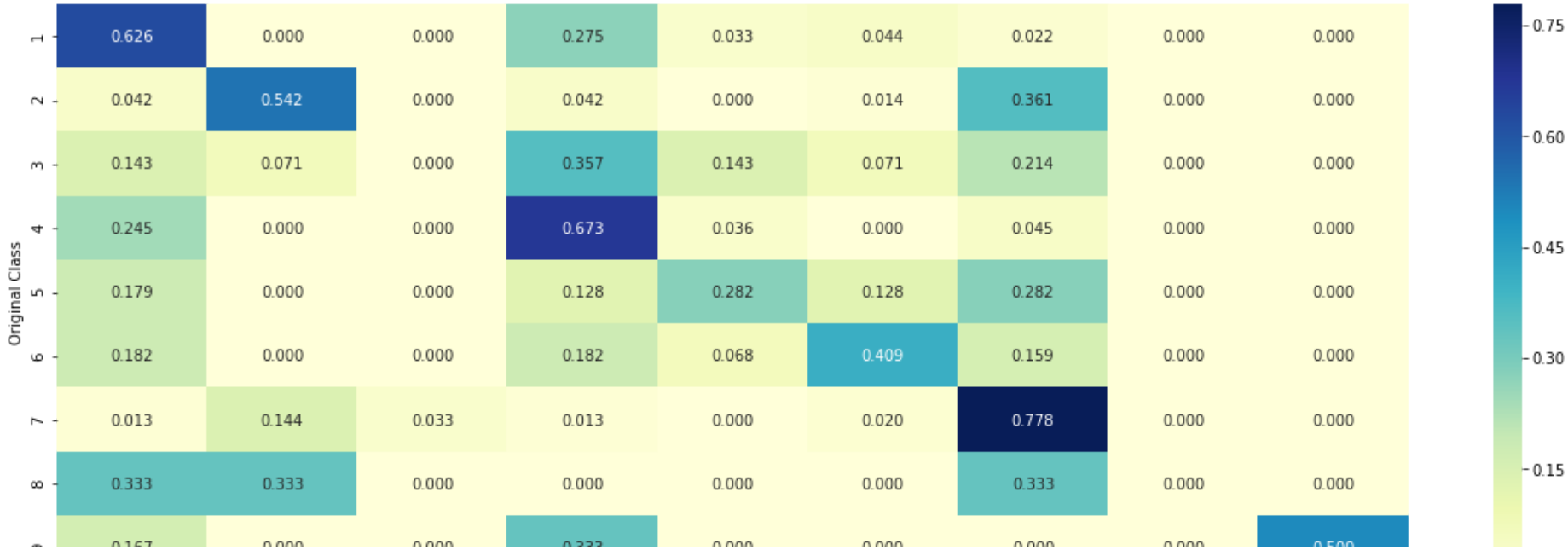
```
Log loss : 1.1002748803755749
Number of mis-classified points : 0.3966165413533835
-------------------- Confusion matrix --------------------
```



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



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



4.2.3.Sample Query point -1

In [0]:

```
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), alpha[best_alpha])
print("The ",alpha[best_alpha]," nearest neighbours of the test points belongs to classes",train_y[neighbor
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

```
Predicted Class : 6
Actual Class : 7
The  15  nearest neighbours of the test points belongs to classes [7 7 7 6 6 7 6 7 6 7 7 7 7 7 6]
Fequency of nearest points : Counter({7: 10, 6: 5})
```

4.2.4. Sample Query Point-2

In [0]:
```
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), alpha[best_alpha])
print("the k value for knn is",alpha[best_alpha],"and the nearest neighbours of the test points belongs to
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

```
Predicted Class : 7
Actual Class : 7
the k value for knn is 15 and the nearest neighbours of the test points belongs to classes [2 7 5 7 7 2 7 7 7
2 7 7 7 7 7]
Fequency of nearest points : Counter({7: 11, 2: 3, 5: 1})
```

4.3. Logistic Regression

4.3.1. With Class balancing

4.3.1.1. Hyper paramter tuning

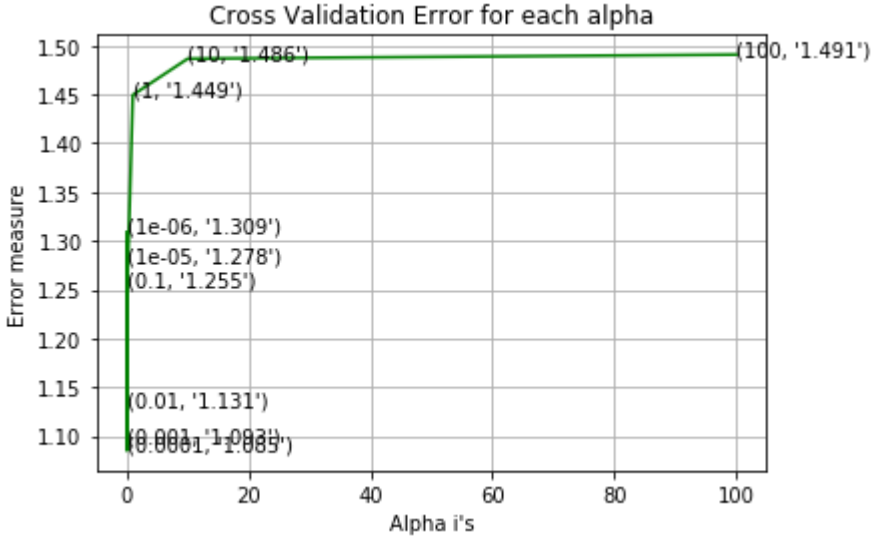
In [61]:

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_iter=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0=0.0, pow
# 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 Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1
#-------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.c
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# 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, 3)]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='log', random_state=42, n_jobs
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
```

```
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    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', loss='log', random_stat
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y,
```

```
for alpha = 1e-06
Log Loss : 1.3088182435952065
for alpha = 1e-05
Log Loss : 1.2776692006389703
for alpha = 0.0001
Log Loss : 1.08501525947154
for alpha = 0.001
Log Loss : 1.093454308037274
for alpha = 0.01
Log Loss : 1.1313606853109164
for alpha = 0.1
Log Loss : 1.2545938717297804
for alpha = 1
Log Loss : 1.449333904723763
for alpha = 10
```

```
Log Loss : 1.4864632116895264
for alpha = 100
Log Loss : 1.4906691508630068
```



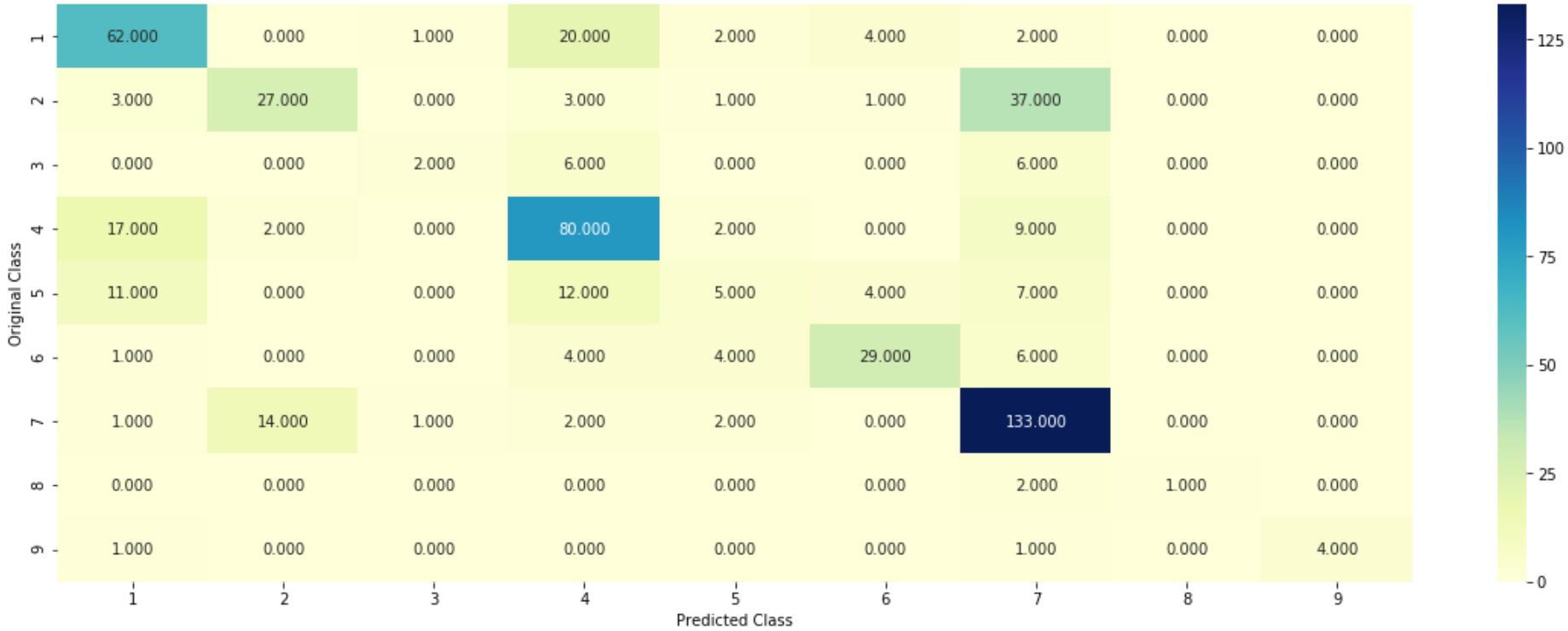

```
For values of best alpha =  0.0001 The train log loss is: 0.5563652337873516
For values of best alpha =  0.0001 The cross validation log loss is: 1.08501525947154
For values of best alpha =  0.0001 The test log loss is: 1.1115249520602726
```

4.3.1.2. Testing the model with best hyper paramters

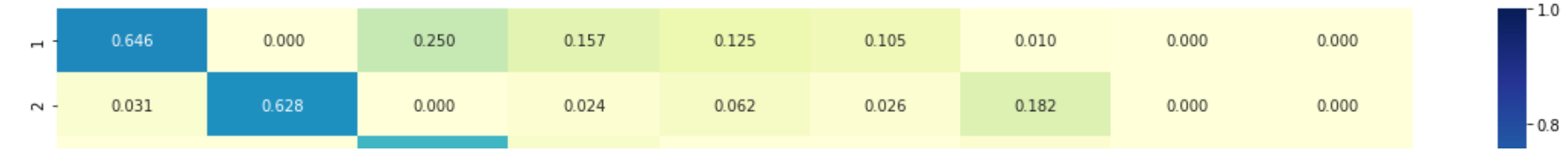
In [62]:

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_iter=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0=0.0, pow
# 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 Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1
#-------------------------------
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='log', random_stat
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, clf)
```

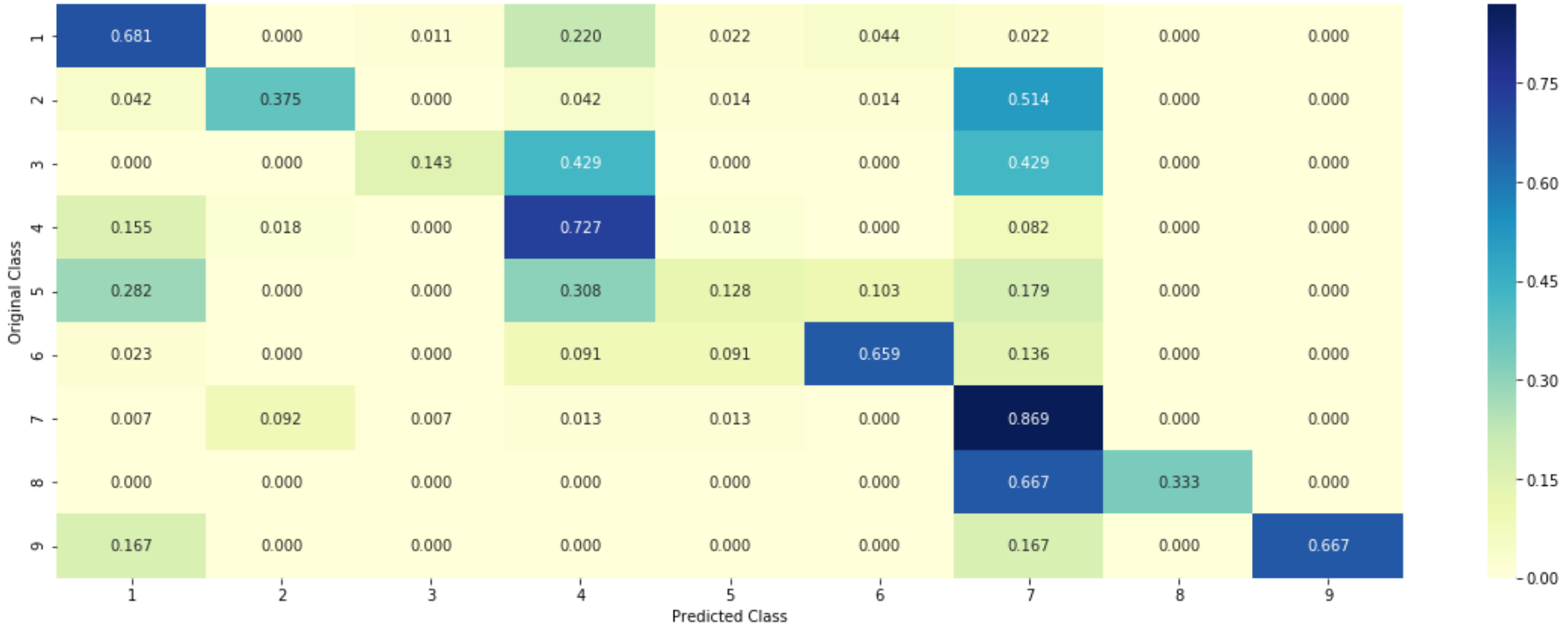
```
Log loss : 1.08501525947154
Number of mis-classified points : 0.35526315789473684
-------------------- Confusion matrix --------------------
```



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



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



4.3.1.3. Feature Importance

In [63]:
```
def get_imp_feature_names(text, indices, removed_ind = []):
    word_present = 0
    tabulte_list = []
    incresingorder_ind = 0
    for i in indices:
        if i < train_gene_feature_onehotCoding.shape[1]:
            tabulte_list.append([incresingorder_ind, "Gene", "Yes"])
        elif i< 18:
            tabulte_list.append([incresingorder_ind,"Variation", "Yes"])
        if ((i > 17) & (i not in removed_ind)) :
            word = train_text_features[i]
            yes_no = True if word in text.split() else False
            if yes_no:
                word_present += 1
            tabulte_list.append([incresingorder_ind,train_text_features[i], yes_no])
        incresingorder_ind += 1
    print(word_present, "most importent features are present in our query point")
    print("-"*50)
    print("The features that are most importent of the ",predicted_cls[0]," class:")
    print (tabulate(tabulte_list, headers=["Index",'Feature name', 'Present or Not']))
```

4.3.1.3.1. Correctly Classified point

In [64]:
```
# from tabulate import tabulate
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='log', random_stat
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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'].iloc[test_point_ind
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.161  0.0456 0.0365 0.5917 0.0637 0.0146 0.0478 0.0292 0.0099]]
Actual Class : 4
--------------------------------------------------
150 Text feature [382] present in test data point [True]
236 Text feature [truncate] present in test data point [True]
244 Text feature [adapted] present in test data point [True]
284 Text feature [inactivation] present in test data point [True]
393 Text feature [instability] present in test data point [True]
436 Text feature [chenevix] present in test data point [True]
437 Text feature [hereditary] present in test data point [True]
439 Text feature [germline] present in test data point [True]
440 Text feature [deficiencies] present in test data point [True]
452 Text feature [inactivating] present in test data point [True]
473 Text feature [pms2] present in test data point [True]
485 Text feature [material] present in test data point [True]
Out of the top  500  features  12 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

In [65]:
```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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'].iloc[test_point_ind
```

```
Predicted Class : 8
Predicted Class Probabilities: [[0.107  0.1074 0.0566 0.0831 0.0171 0.002  0.2638 0.3446 0.0185]]
Actual Class : 8
--------------------------------------------------
23 Text feature [g34v] present in test data point [True]
28 Text feature [schiffman] present in test data point [True]
30 Text feature [paediatric] present in test data point [True]
33 Text feature [k27] present in test data point [True]
34 Text feature [schwartzentruber] present in test data point [True]
35 Text feature [h3f3a] present in test data point [True]
38 Text feature [somers] present in test data point [True]
47 Text feature [permissiveness] present in test data point [True]
49 Text feature [g34r] present in test data point [True]
53 Text feature [thalamic] present in test data point [True]
59 Text feature [1004] present in test data point [True]
64 Text feature [wake] present in test data point [True]
66 Text feature [extensions] present in test data point [True]
71 Text feature [wolffe] present in test data point [True]
73 Text feature [foxg1] present in test data point [True]
```

4.3.2. Without Class balancing

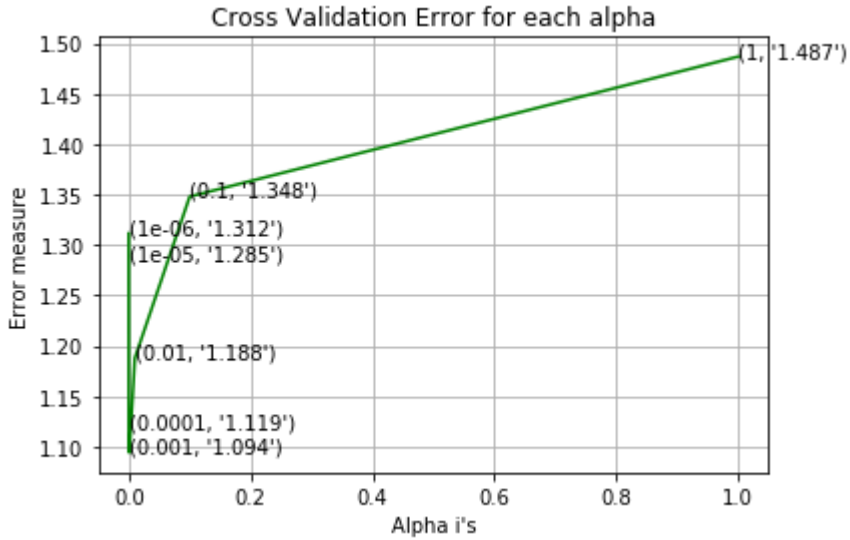
4.3.2.1. Hyper paramter tuning

In [66]:

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_iter=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0=0.0, pow
# 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 Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1
#-------------------------------



# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.c
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# 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, n_jobs=3)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
```

```
    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, n_jobs=3)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y,
```

```
for alpha = 1e-06
Log Loss : 1.3115387654652857
for alpha = 1e-05
Log Loss : 1.28525478407198
for alpha = 0.0001
Log Loss : 1.1185234997053703
for alpha = 0.001
Log Loss : 1.0941479320488363
for alpha = 0.01
Log Loss : 1.1878002654430508
for alpha = 0.1
Log Loss : 1.3480381452471564
for alpha = 1
Log Loss : 1.4867946160872978
```



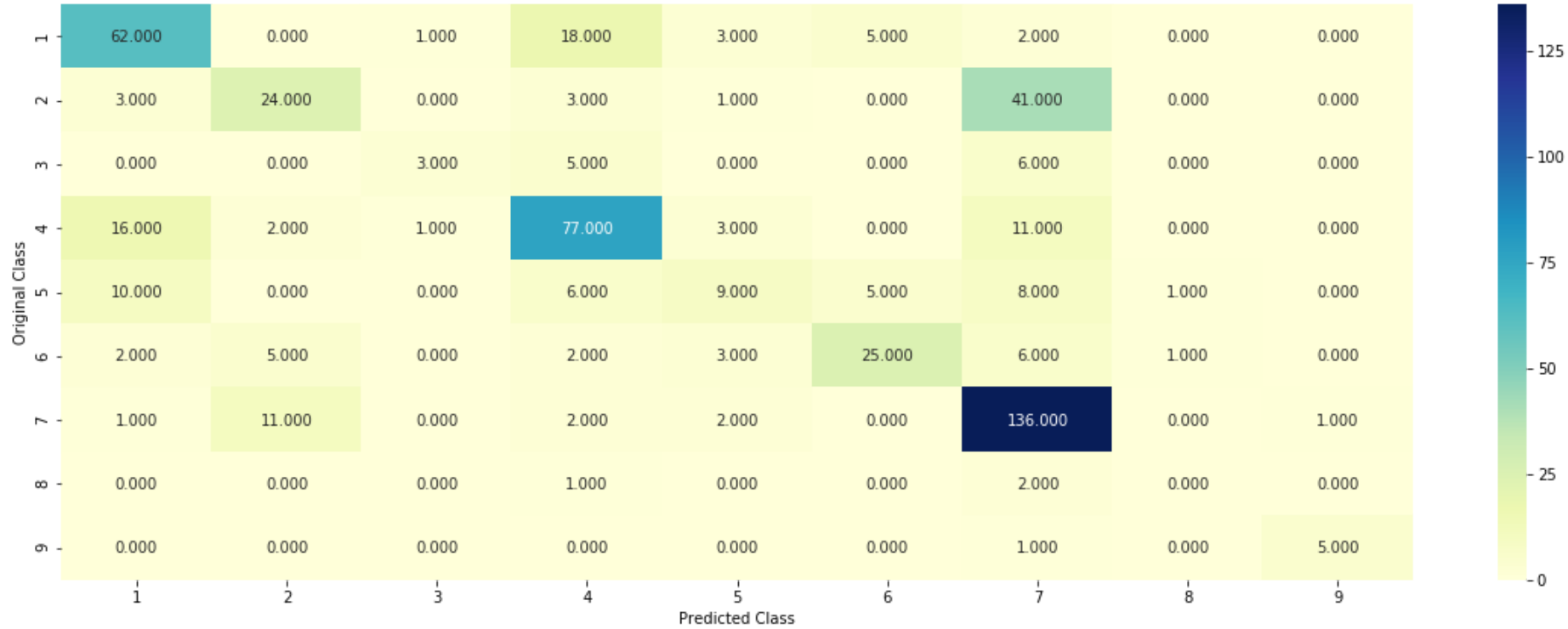

```
For values of best alpha =  0.001 The train log loss is: 0.5492333718423743
For values of best alpha =  0.001 The cross validation log loss is: 1.0941479320488363
For values of best alpha =  0.001 The test log loss is: 1.0838709350672702
```

4.3.2.2. Testing model with best hyper parameters

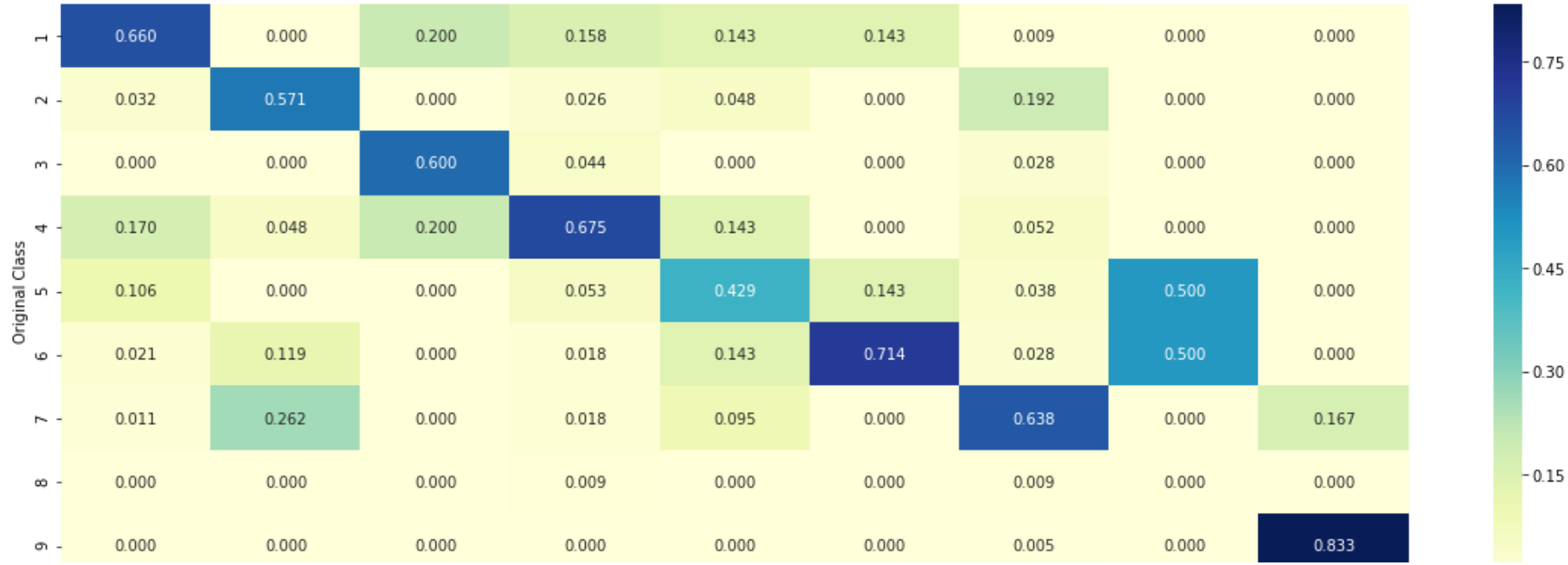
In [67]:

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_iter=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0=0.0, pow
# 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 Gradient Descent.
# predict(X)    Predict class labels for samples in X.

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

clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42, n_jobs=3)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, clf)
```

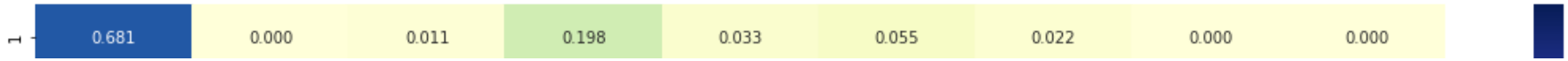
```
Log loss : 1.0941479320488363
Number of mis-classified points : 0.35902255639097747
--------------------- Confusion matrix --------------------
```



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



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



4.3.2.3. Feature Importance, Correctly Classified point

In [68]:
```
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42, n_jobs=3)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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'].iloc[test_point_ind
```

```
Predicted Class : 4
Predicted Class Probabilities: [[1.509e-01 1.410e-02 1.000e-02 6.896e-01 7.280e-02 1.370e-02 1.460e-02
  3.420e-02 1.000e-04]]
Actual Class : 4
--------------------------------------------------
99 Text feature [382] present in test data point [True]
144 Text feature [truncate] present in test data point [True]
177 Text feature [inactivation] present in test data point [True]
207 Text feature [adapted] present in test data point [True]
242 Text feature [deficiencies] present in test data point [True]
273 Text feature [instability] present in test data point [True]
333 Text feature [germline] present in test data point [True]
373 Text feature [pms2] present in test data point [True]
376 Text feature [hereditary] present in test data point [True]
407 Text feature [material] present in test data point [True]
412 Text feature [carriers] present in test data point [True]
489 Text feature [inactivating] present in test data point [True]
Out of the top  500  features  12 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

In [69]:
```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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'].iloc[test_point_ind
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.1685 0.099  0.003  0.1324 0.0099 0.0032 0.3391 0.2445 0.0004]]
Actual Class : 8
--------------------------------------------------
45 Text feature [activated] present in test data point [True]
58 Text feature [constitutive] present in test data point [True]
99 Text feature [activation] present in test data point [True]
113 Text feature [constitutively] present in test data point [True]
114 Text feature [expressing] present in test data point [True]
120 Text feature [recurrence] present in test data point [True]
138 Text feature [transformation] present in test data point [True]
142 Text feature [downstream] present in test data point [True]
240 Text feature [agar] present in test data point [True]
243 Text feature [serum] present in test data point [True]
297 Text feature [conventional] present in test data point [True]
335 Text feature [hazards] present in test data point [True]
379 Text feature [oncogenesis] present in test data point [True]
381 Text feature [transform] present in test data point [True]
455 Text feature [phosphorylation] present in test data point [True]
```

4.4. Linear Support Vector Machines

4.4.1. Hyper paramter tuning

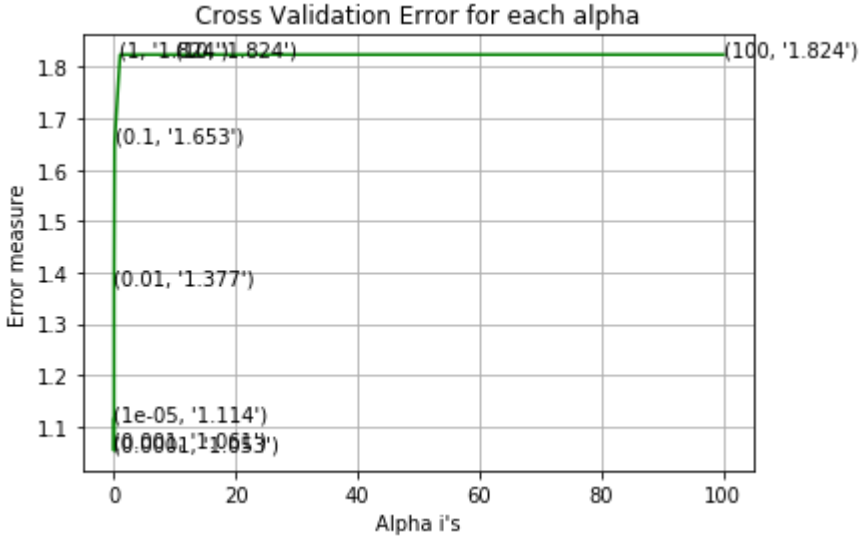
In [95]:

```
# read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/g

# --------------------------------
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001,
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_shape='ovr', random_stat

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



# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.c
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# 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', random_state=42, n_j
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
```

```
    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', loss='hinge', random_st
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y,
```

```
for C = 1e-05
Log Loss : 1.1142159368824716
for C = 0.0001
Log Loss : 1.0530701415497956
for C = 0.001
Log Loss : 1.0607930820778635
for C = 0.01
Log Loss : 1.3770671358668958
for C = 0.1
Log Loss : 1.6533655406696115
for C = 1
Log Loss : 1.8243564312423943
for C = 10
Log Loss : 1.824353879737443

for C = 100
```

```
for C = 100
Log Loss : 1.8243536192153422
```



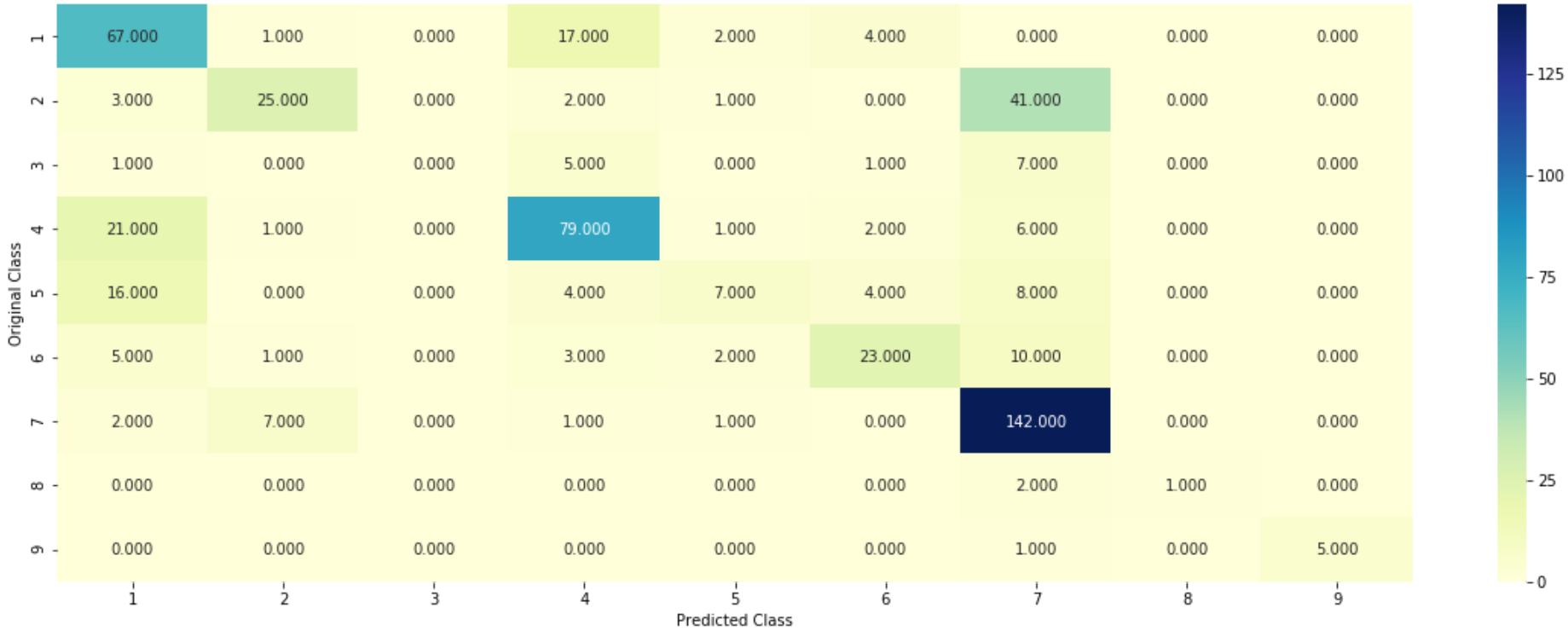

```
For values of best alpha =  0.0001 The train log loss is: 0.3836468326570109
For values of best alpha =  0.0001 The cross validation log loss is: 1.0530701415497956
For values of best alpha =  0.0001 The test log loss is: 1.0328584955264182
```

4.4.2. Testing model with best hyper parameters

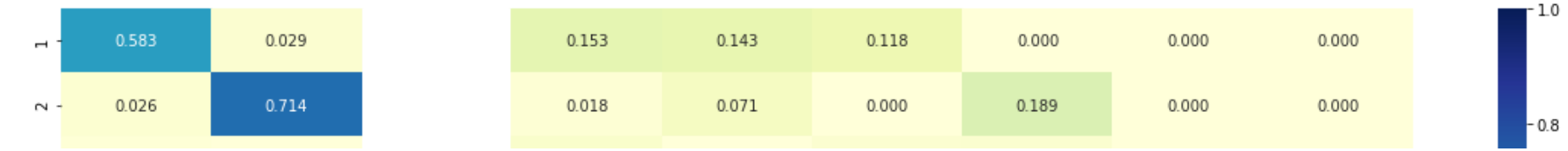
In [96]:

```
# read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/g

# --------------------------------
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001,
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_shape='ovr', random_stat

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


# clf = SVC(C=alpha[best_alpha],kernel='linear',probability=True, class_weight='balanced')
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge', random_state=42,class_weight='bala
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf)
```

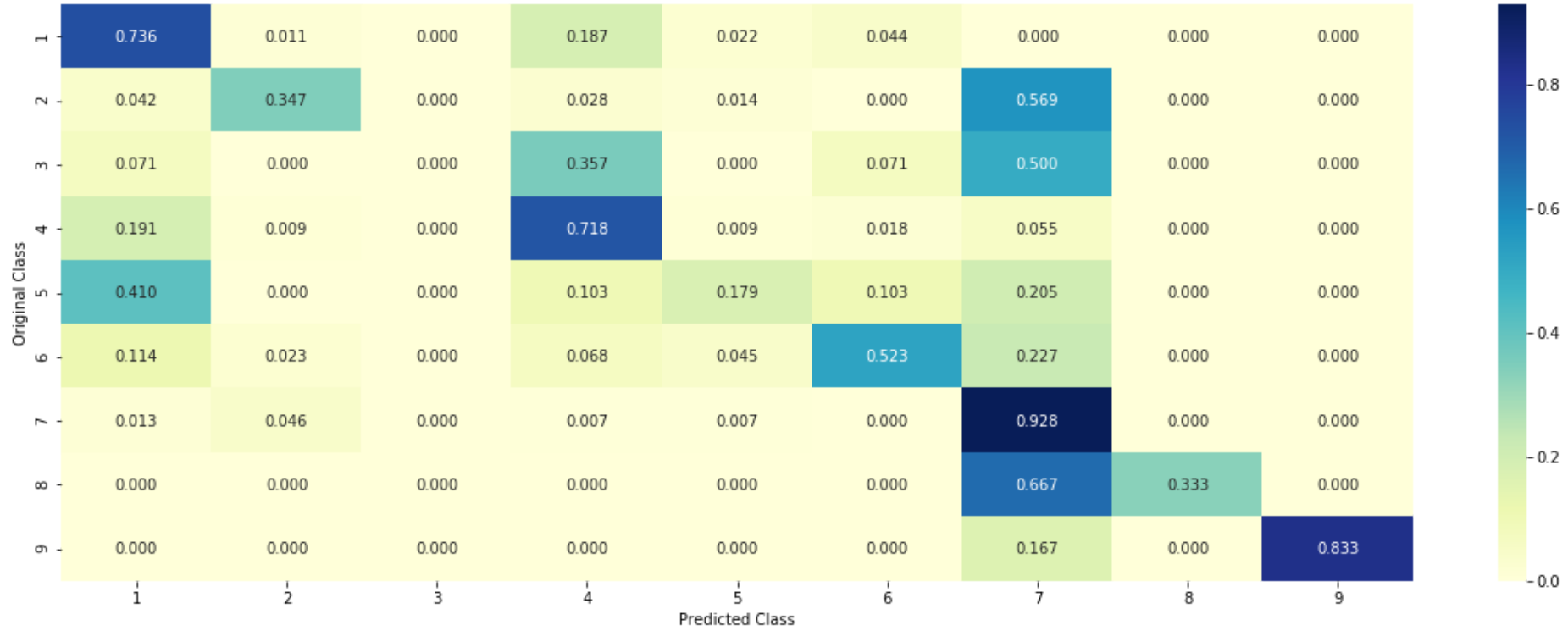
```
Log loss : 1.0530701415497956
Number of mis-classified points : 0.34398496240601506
-------------------- Confusion matrix --------------------
```



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



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



4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

In [97]:
```
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge', random_state=42)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
# test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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'].iloc[test_point_ind
```

```
Predicted Class : 6
Predicted Class Probabilities: [[0.1798 0.0563 0.0237 0.1681 0.1823 0.3664 0.0152 0.0047 0.0035]]
Actual Class : 4
--------------------------------------------------
112 Text feature [119] present in test data point [True]
284 Text feature [006] present in test data point [True]
287 Text feature [111] present in test data point [True]
379 Text feature [000249] present in test data point [True]
492 Text feature [05] present in test data point [True]
Out of the top  500  features  5 are present in query point
```

4.3.3.2. For Incorrectly classified point

In [98]:
```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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'].iloc[test_point_ind
```

```
Predicted Class : 8
Predicted Class Probabilities: [[0.1644 0.0823 0.0055 0.1492 0.0165 0.0088 0.0933 0.4707 0.0094]]
Actual Class : 8
--------------------------------------------------
54 Text feature [100] present in test data point [True]
56 Text feature [1000] present in test data point [True]
246 Text feature [120] present in test data point [True]
312 Text feature [0016] present in test data point [True]
367 Text feature [10] present in test data point [True]
374 Text feature [113] present in test data point [True]
Out of the top  500  features  6 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

In [0]:

```
# ------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None, min_samples_sp
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_impurity_
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, verbose=0, warm_st
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])    Fit the SVM model according to the given training data.
# 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/random-forest-and-the
# ------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.c
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# 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 = [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, random_state=42, n_jobs
        clf.fit(train_x_onehotCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_onehotCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
        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_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 = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max_depth[i
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The train log loss is:",log_loss(y_trai
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross validation log loss is:",log_
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss is:",log_loss(y_test,
```

```
for n_estimators = 100 and max depth =  5
Log Loss : 1.2572535683354957
for n_estimators = 100 and max depth =  10
Log Loss : 1.1868414223711878
for n_estimators = 200 and max depth =  5
Log Loss : 1.2378734502517341
for n_estimators = 200 and max depth =  10
Log Loss : 1.1811031780258958
for n_estimators = 500 and max depth =  5
```

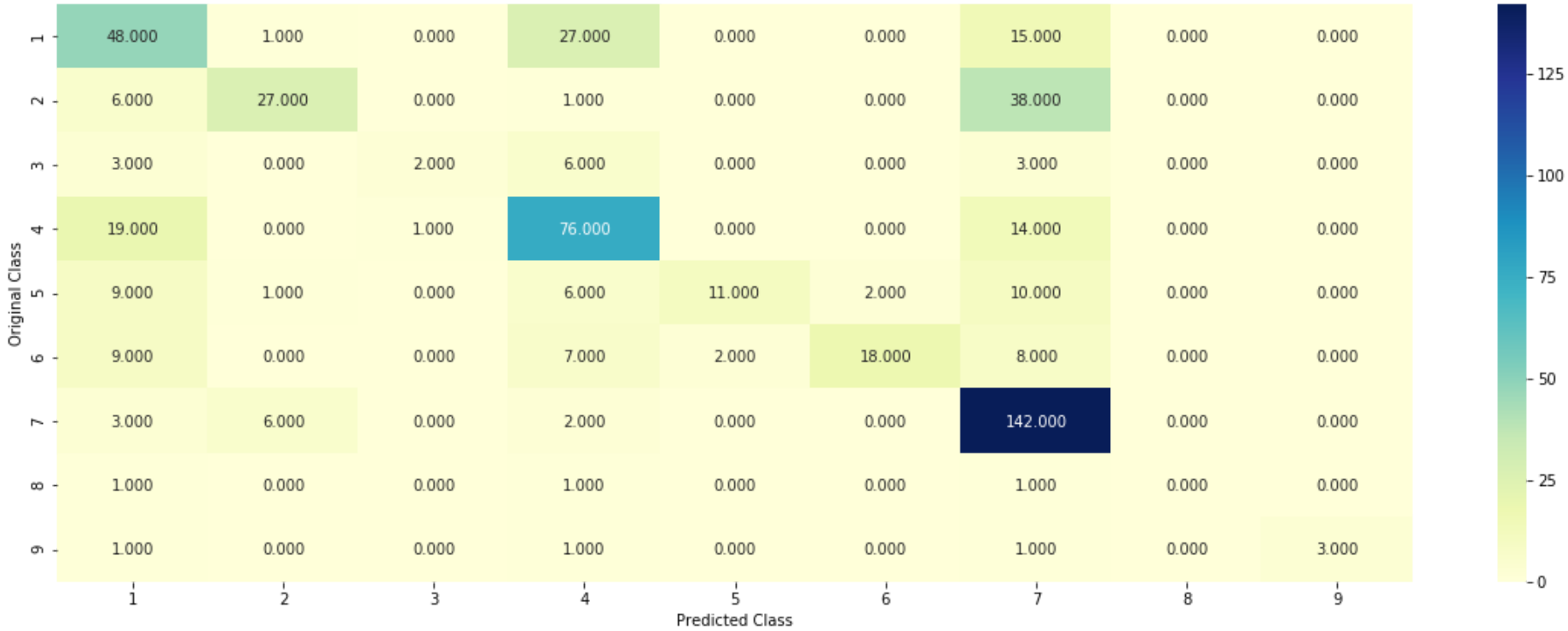
```
Log Loss : 1.2368241894319212
for n_estimators = 500 and max depth =  10
Log Loss : 1.176754594516683
for n_estimators = 1000 and max depth =  5
Log Loss : 1.2357829533963691
for n_estimators = 1000 and max depth =  10
Log Loss : 1.174993079576866
for n_estimators = 2000 and max depth =  5
Log Loss : 1.236042392554891
for n_estimators = 2000 and max depth =  10
Log Loss : 1.1759745074379755
For values of best estimator =  1000 The train log loss is: 0.7095396732082752
For values of best estimator =  1000 The cross validation log loss is: 1.174993079576866
For values of best estimator =  1000 The test log loss is: 1.1630923149103904
```

4.5.2. Testing model with best hyper parameters (One Hot Encoding)

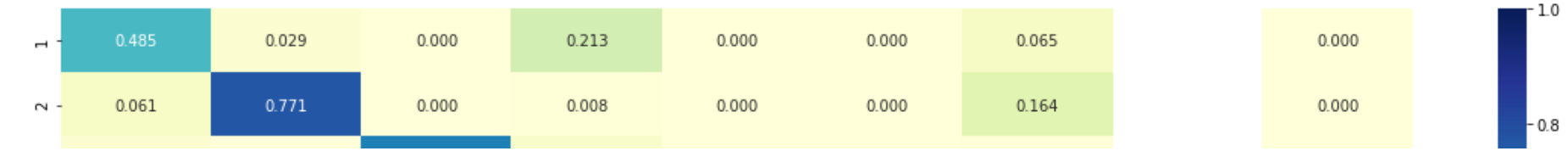
In [0]:

```
# --------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None, min_samples_sp
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_impurity_
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, verbose=0, warm_st
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])    Fit the SVM model according to the given training data.
# 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/random-forest-and-the
# --------------------------------

clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max_depth[i
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf)
```

```
Log loss : 1.174993079576866
Number of mis-classified points : 0.38533834586466165
-------------------- 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 [0]:
```
# test_point_index = 10
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max_depth[i
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

test_point_index = 1
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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],test_df['Gene'].iloc[test
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0454 0.1404 0.0133 0.029  0.036  0.0294 0.6977 0.005  0.004 ]]
Actual Class : 7
--------------------------------------------------
0 Text feature [inhibitors] present in test data point [True]
1 Text feature [kinase] present in test data point [True]
2 Text feature [activating] present in test data point [True]
3 Text feature [tyrosine] present in test data point [True]
4 Text feature [missense] present in test data point [True]
5 Text feature [inhibitor] present in test data point [True]
7 Text feature [treatment] present in test data point [True]
8 Text feature [oncogenic] present in test data point [True]
9 Text feature [suppressor] present in test data point [True]
10 Text feature [activation] present in test data point [True]
11 Text feature [phosphorylation] present in test data point [True]
12 Text feature [kinases] present in test data point [True]
13 Text feature [nonsense] present in test data point [True]
14 Text feature [akt] present in test data point [True]
15 Text feature [function] present in test data point [True]
17 Text feature [erk] present in test data point [True]
19 Text feature [growth] present in test data point [True]
20 Text feature [variants] present in test data point [True]
22 Text feature [frameshift] present in test data point [True]
24 Text feature [therapeutic] present in test data point [True]
25 Text feature [functional] present in test data point [True]
```

```
28 Text feature [signaling] present in test data point [True]
30 Text feature [patients] present in test data point [True]
31 Text feature [cells] present in test data point [True]
32 Text feature [constitutively] present in test data point [True]
34 Text feature [trials] present in test data point [True]
35 Text feature [therapy] present in test data point [True]
37 Text feature [erk1] present in test data point [True]
38 Text feature [activate] present in test data point [True]
39 Text feature [downstream] present in test data point [True]
41 Text feature [efficacy] present in test data point [True]
42 Text feature [protein] present in test data point [True]
43 Text feature [loss] present in test data point [True]
44 Text feature [inhibited] present in test data point [True]
45 Text feature [expressing] present in test data point [True]
46 Text feature [pten] present in test data point [True]
48 Text feature [lines] present in test data point [True]
49 Text feature [treated] present in test data point [True]
50 Text feature [proliferation] present in test data point [True]
51 Text feature [drug] present in test data point [True]
57 Text feature [mek] present in test data point [True]
59 Text feature [inhibition] present in test data point [True]
61 Text feature [repair] present in test data point [True]
62 Text feature [sensitivity] present in test data point [True]
64 Text feature [receptor] present in test data point [True]
66 Text feature [assays] present in test data point [True]
68 Text feature [survival] present in test data point [True]
69 Text feature [cell] present in test data point [True]
71 Text feature [ligand] present in test data point [True]
73 Text feature [expression] present in test data point [True]
74 Text feature [variant] present in test data point [True]
75 Text feature [oncogene] present in test data point [True]
78 Text feature [extracellular] present in test data point [True]
79 Text feature [doses] present in test data point [True]
80 Text feature [mapk] present in test data point [True]
81 Text feature [hours] present in test data point [True]
84 Text feature [information] present in test data point [True]
86 Text feature [harboring] present in test data point [True]
90 Text feature [dna] present in test data point [True]
91 Text feature [concentrations] present in test data point [True]
92 Text feature [likelihood] present in test data point [True]
93 Text feature [months] present in test data point [True]
94 Text feature [binding] present in test data point [True]
```

```
96 Text feature [imatinib] present in test data point [True]
98 Text feature [preclinical] present in test data point [True]
Out of the top  100  features  65 are present in query point
```

4.5.3.2. Inorrectly Classified point

In [0]:
```
test_point_index = 100
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index
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],test_df['Gene'].iloc[test
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.1337 0.116  0.0224 0.1773 0.0674 0.0545 0.4156 0.0071 0.0059]]
Actuall Class : 7
--------------------------------------------------
0 Text feature [inhibitors] present in test data point [True]
1 Text feature [kinase] present in test data point [True]
2 Text feature [activating] present in test data point [True]
3 Text feature [tyrosine] present in test data point [True]
6 Text feature [activated] present in test data point [True]
8 Text feature [oncogenic] present in test data point [True]
10 Text feature [activation] present in test data point [True]
11 Text feature [phosphorylation] present in test data point [True]
12 Text feature [kinases] present in test data point [True]
14 Text feature [akt] present in test data point [True]
15 Text feature [function] present in test data point [True]
19 Text feature [growth] present in test data point [True]
21 Text feature [constitutive] present in test data point [True]
25 Text feature [functional] present in test data point [True]
28 Text feature [signaling] present in test data point [True]
31 Text feature [cells] present in test data point [True]
32 Text feature [constitutively] present in test data point [True]
38 Text feature [activate] present in test data point [True]
39 Text feature [downstream] present in test data point [True]
42 Text feature [protein] present in test data point [True]
43 Text feature [loss] present in test data point [True]
44 Text feature [inhibited] present in test data point [True]
46 Text feature [pten] present in test data point [True]
47 Text feature [transforming] present in test data point [True]
48 Text feature [lines] present in test data point [True]
50 Text feature [proliferation] present in test data point [True]
53 Text feature [neutral] present in test data point [True]
```

```
55 Text feature [transform] present in test data point [True]
56 Text feature [stability] present in test data point [True]
58 Text feature [transformation] present in test data point [True]
59 Text feature [inhibition] present in test data point [True]
62 Text feature [sensitivity] present in test data point [True]
64 Text feature [receptor] present in test data point [True]
66 Text feature [assays] present in test data point [True]
69 Text feature [cell] present in test data point [True]
75 Text feature [oncogene] present in test data point [True]
84 Text feature [information] present in test data point [True]
90 Text feature [dna] present in test data point [True]
94 Text feature [binding] present in test data point [True]
Out of the top  100  features  39 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

In [0]:

```
# ---------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None, min_samples_sp
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_impurity_
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, verbose=0, warm_st
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])    Fit the SVM model according to the given training data.
# 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/random-forest-and-the
# ---------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.c
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# 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 = [10,50,100,200,500,1000]
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, random_state=42, n_jobs=
        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=1e-15))
        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_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 = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gini', max_depth=max_depth[i
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:",log_loss(y_train, p
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The cross validation log loss is:",log_loss
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:",log_loss(y_test, pre
```

```
for n_estimators = 10 and max depth =  2
Log Loss : 2.2657048897349608
for n_estimators = 10 and max depth =  3
Log Loss : 1.7459205010556096
for n_estimators = 10 and max depth =  5
Log Loss : 1.4368353925512503
for n_estimators = 10 and max depth =  10
Log Loss : 1.904597809032912
for n_estimators = 50 and max depth =  2
```

```
Log Loss : 1.7221951095007484
for n_estimators = 50 and max depth =  3
Log Loss : 1.4984825877845531
for n_estimators = 50 and max depth =  5
Log Loss : 1.4593628982873716
for n_estimators = 50 and max depth =  10
Log Loss : 1.8434939703555409
for n_estimators = 100 and max depth =  2
Log Loss : 1.6182209245331227
for n_estimators = 100 and max depth =  3
Log Loss : 1.5199297988828253
for n_estimators = 100 and max depth =  5
Log Loss : 1.4177501184246677
for n_estimators = 100 and max depth =  10
Log Loss : 1.8227504417195126
for n_estimators = 200 and max depth =  2
Log Loss : 1.6622571648074496
for n_estimators = 200 and max depth =  3
Log Loss : 1.4800771339141767
for n_estimators = 200 and max depth =  5
Log Loss : 1.4412060242341358
for n_estimators = 200 and max depth =  10
Log Loss : 1.7892406351442258
for n_estimators = 500 and max depth =  2
Log Loss : 1.715950314170445
for n_estimators = 500 and max depth =  3
Log Loss : 1.5658682738699774
for n_estimators = 500 and max depth =  5
Log Loss : 1.4445360301518217
for n_estimators = 500 and max depth =  10
Log Loss : 1.8421097596928397
for n_estimators = 1000 and max depth =  2
Log Loss : 1.6834927870864949
for n_estimators = 1000 and max depth =  3
Log Loss : 1.5631973035931377
for n_estimators = 1000 and max depth =  5
Log Loss : 1.4449980792724129
for n_estimators = 1000 and max depth =  10
Log Loss : 1.85233132619749
For values of best alpha =  100 The train log loss is: 0.060702709444608406
For values of best alpha =  100 The cross validation log loss is: 1.417750118424668
For values of best alpha =  100 The test log loss is: 1.3806278998341923
```

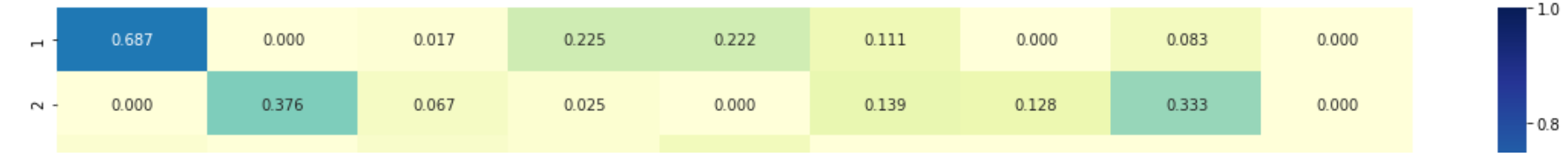
4.5.4. Testing model with best hyper parameters (Response Coding)

In [0]:

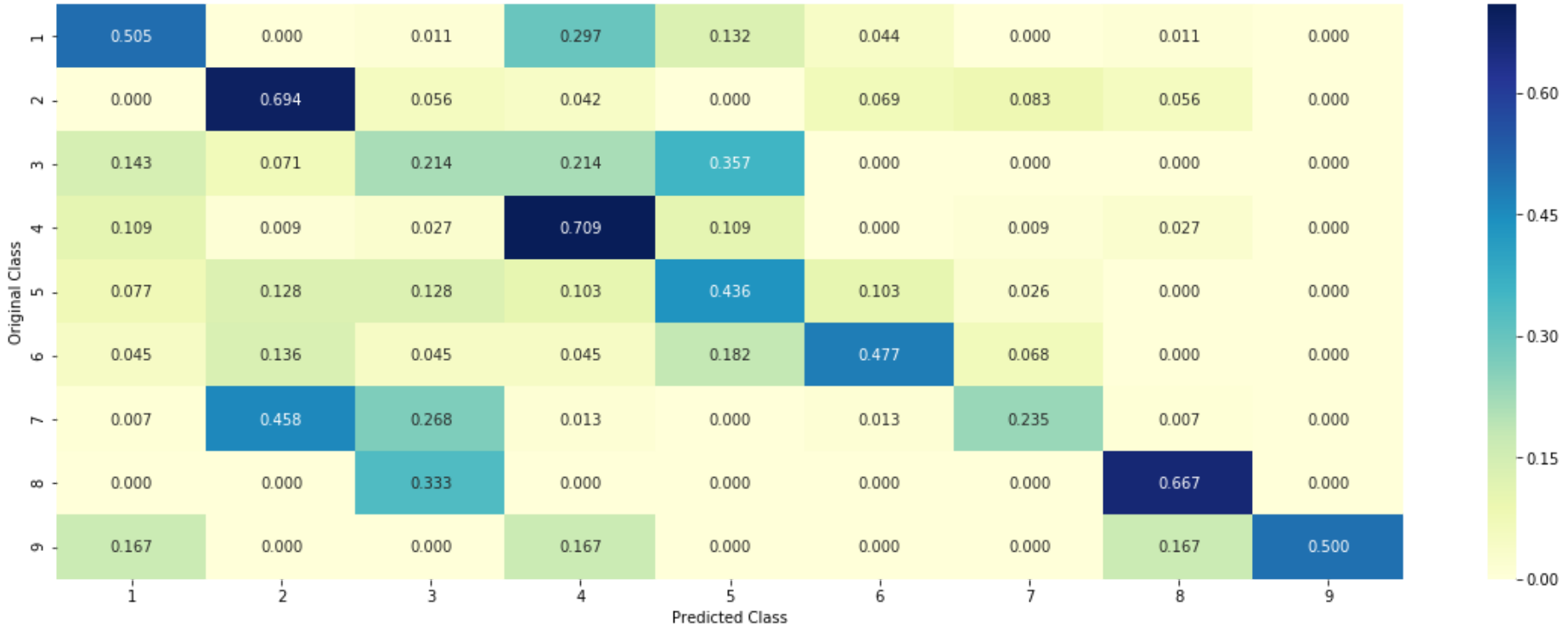
```
# --------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None, min_samples_sp
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_impurity_
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, verbose=0, warm_st
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])    Fit the SVM model according to the given training data.
# 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/random-forest-and-the
# --------------------------------

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

```
Log loss : 1.4177501184246677
Number of mis-classified points : 0.518796992481203
-------------------- 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 [0]:
```
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gini', max_depth=max_depth[i
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_responseCoding[test_point_ind
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 : 2
Predicted Class Probabilities: [[0.0143 0.5044 0.1471 0.0191 0.0245 0.065  0.1724 0.039  0.0142]]
Actual Class : 7
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Text is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene 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
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.5.5.2. Incorrectly Classified point

In [0]:
```
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_responseCoding[test_point_ind
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 : 7
Predicted Class Probabilities: [[0.0281 0.2006 0.203  0.0857 0.0626 0.0906 0.2249 0.0676 0.0369]]
Actual Class : 7
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Text is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene 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
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
```

```
Text is important feature
Gene 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 [0]:

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_iter=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0=0.0, pow
# 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 Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1
#-------------------------------


# read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/g
# ---------------------------------
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001,
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_shape='ovr', random_stat

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


# read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/g
# ---------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None, min_samples_sp
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_impurity_
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, verbose=0, warm_st
# class_weight=None)

# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])    Fit the SVM model according to the given training data.
# 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/random-forest-and-the
# --------------------------------


clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class_weight='balanced', random_state=0)
clf1.fit(train_x_onehotCoding, train_y)
sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")

clf2 = SGDClassifier(alpha=1, penalty='l2', loss='hinge', class_weight='balanced', random_state=0)
clf2.fit(train_x_onehotCoding, train_y)
sig_clf2 = CalibratedClassifierCV(clf2, method="sigmoid")


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

sig_clf1.fit(train_x_onehotCoding, train_y)
print("Logistic Regression :  Log Loss: %0.2f" % (log_loss(cv_y, sig_clf1.predict_proba(cv_x_onehotCoding))
sig_clf2.fit(train_x_onehotCoding, train_y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf2.predict_proba(cv_x_onehotCodin
sig_clf3.fit(train_x_onehotCoding, train_y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba(cv_x_onehotCoding))))
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_classifier=lr, use_probas=Tr
    sclf.fit(train_x_onehotCoding, train_y)
    print("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" % (i, log_loss(cv_y, sclf.predi
    log_error =log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    if best_alpha > log_error:
        best_alpha = log_error
```

Logistic Regression : Log Loss: 1.24

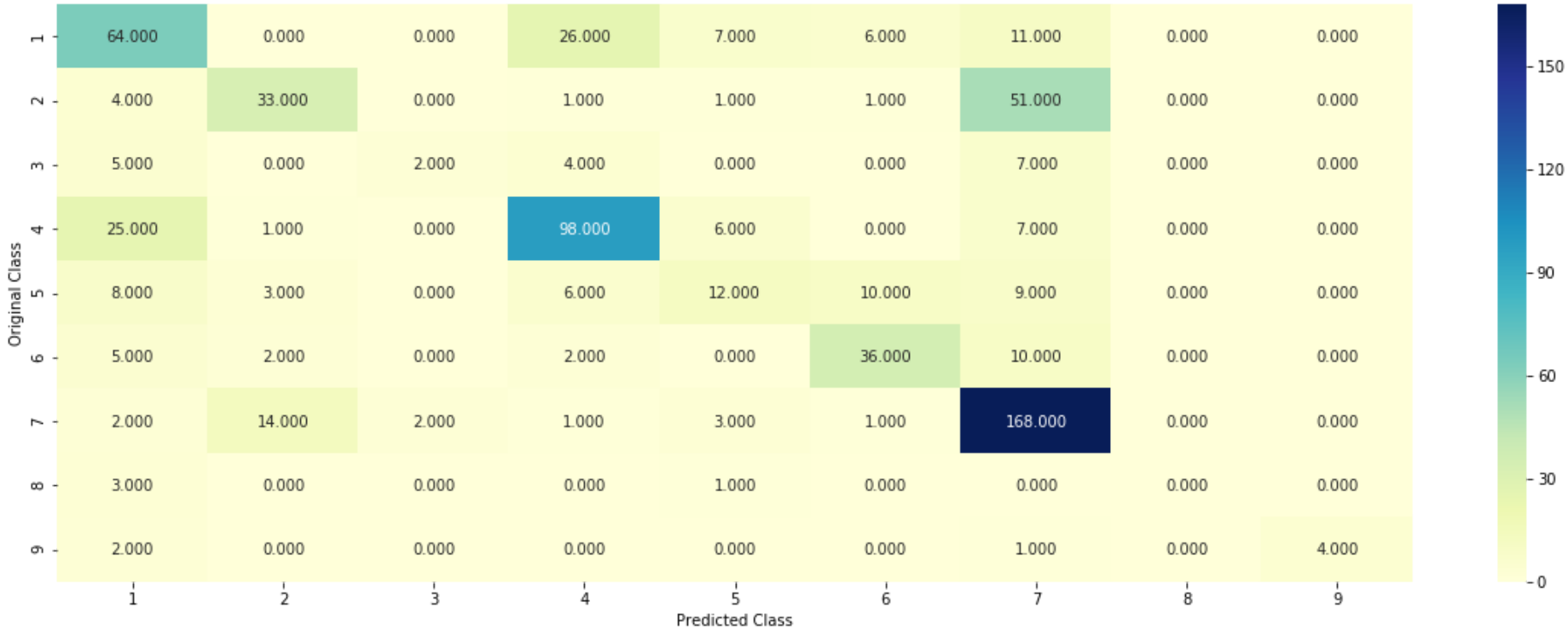
```
Logistic Regression :  Log Loss: 1.24
Support vector machines : Log Loss: 1.72
Naive Bayes : Log Loss: 1.37
--------------------------------------------------
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 2.179
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 2.049
Stacking Classifer : for the value of alpha: 0.010000 Log Loss: 1.577
Stacking Classifer : for the value of alpha: 0.100000 Log Loss: 1.224
Stacking Classifer : for the value of alpha: 1.000000 Log Loss: 1.366
Stacking Classifer : for the value of alpha: 10.000000 Log Loss: 1.690
```

4.7.2 testing the model with the best hyper parameters

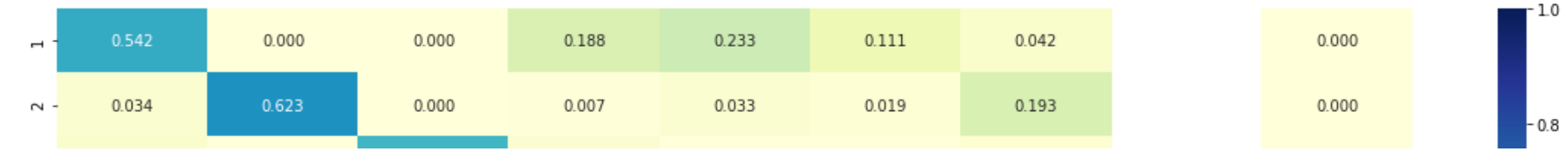
In [0]:

```
lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=lr, use_probas=True)
sclf.fit(train_x_onehotCoding, train_y)

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

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

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

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

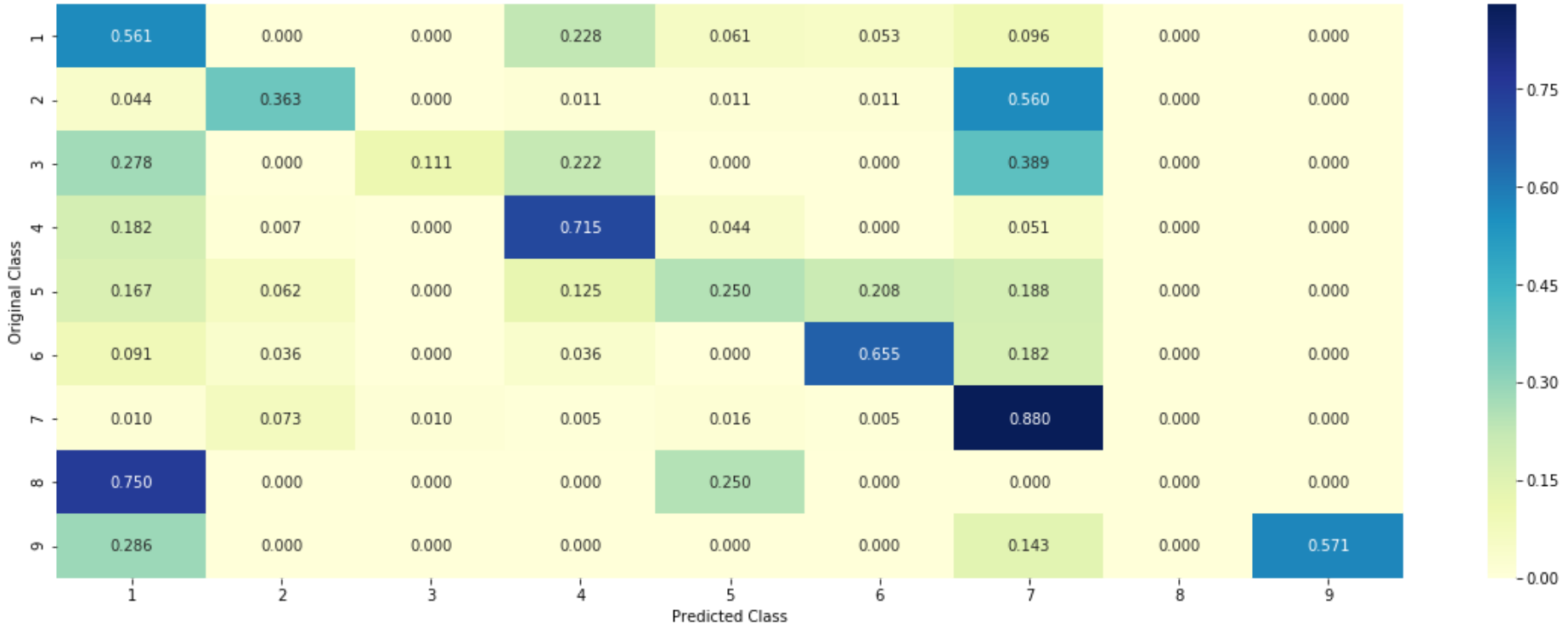
```
Log loss (train) on the stacking classifier : 0.6760284396805781
Log loss (CV) on the stacking classifier : 1.2243084610674686
Log loss (test) on the stacking classifier : 1.1562525475350196
Number of missclassified point : 0.37293233082706767
-------------------- Confusion matrix --------------------
```



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



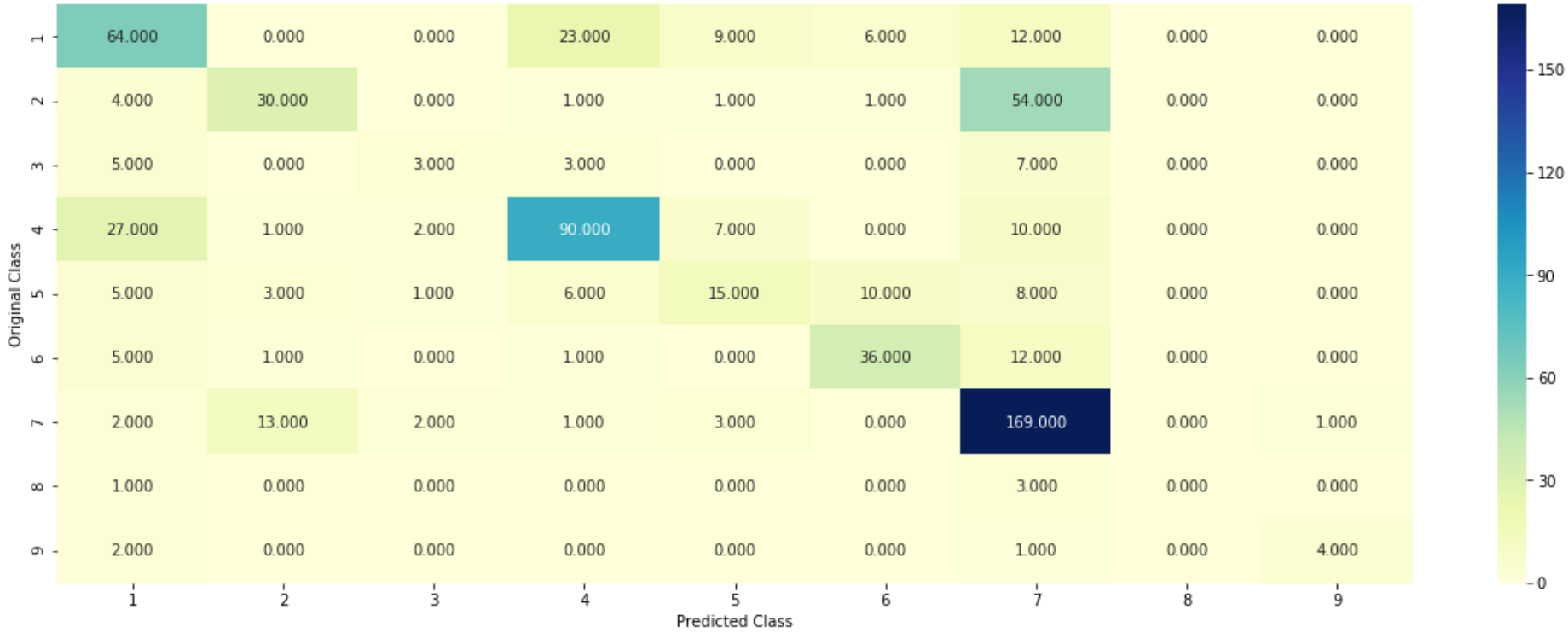

```
-------------------- Recall matrix (Row sum=1) --------------------
```



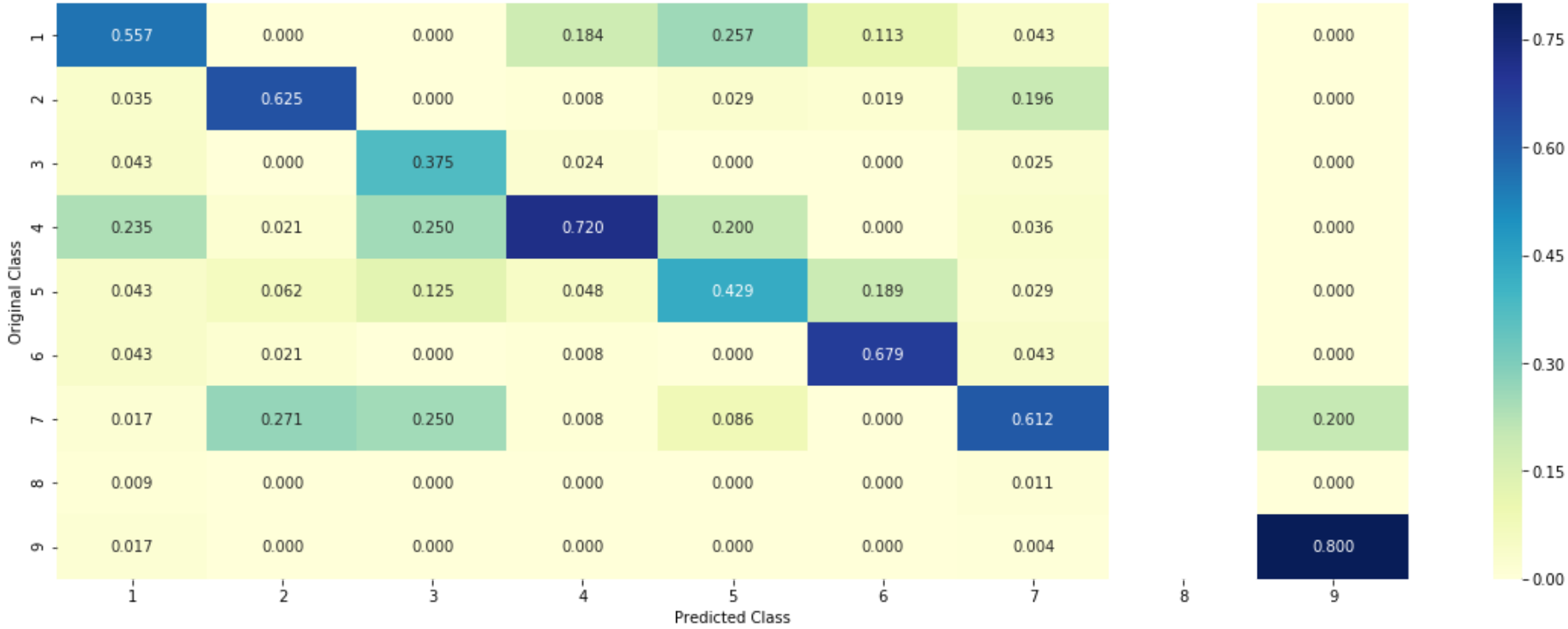
4.7.3 Maximum Voting classifier

In [0]:
```
#Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassifier.html
from sklearn.ensemble import VotingClassifier
vclf = VotingClassifier(estimators=[('lr', sig_clf1), ('svc', sig_clf2), ('rf', sig_clf3)], voting='soft')
vclf.fit(train_x_onehotCoding, train_y)
print("Log loss (train) on the VotingClassifier :", log_loss(train_y, vclf.predict_proba(train_x_onehotCodi
print("Log loss (CV) on the VotingClassifier :", log_loss(cv_y, vclf.predict_proba(cv_x_onehotCoding)))
print("Log loss (test) on the VotingClassifier :", log_loss(test_y, vclf.predict_proba(test_x_onehotCoding)
print("Number of missclassified point :", np.count_nonzero((vclf.predict(test_x_onehotCoding)- test_y))/tes
plot_confusion_matrix(test_y=test_y, predict_y=vclf.predict(test_x_onehotCoding))
```

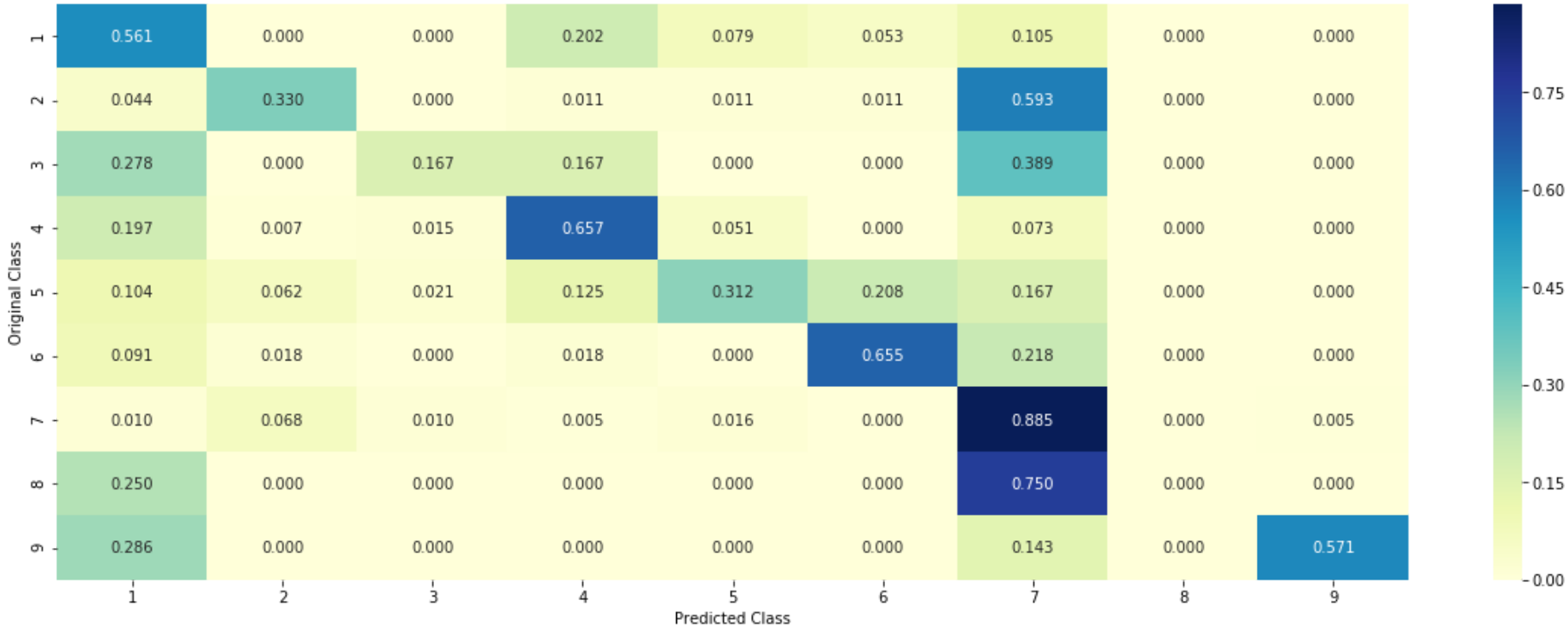
```
Log loss (train) on the VotingClassifier : 0.9407598679043604
Log loss (CV) on the VotingClassifier : 1.2835402100341697
Log loss (test) on the VotingClassifier : 1.223278167176945
Number of missclassified point : 0.3819548872180451
-------------------- Confusion matrix --------------------
```



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




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



5. Assignments

1. Apply All the models with tf-idf features (Replace CountVectorizer with tfidfVectorizer and run the same cells)
2. Instead of using all the words in the dataset, use only the top 1000 words based of tf-idf values
3. Apply Logistic regression with CountVectorizer Features, including both unigrams and bigrams
4. Try any of the feature engineering techniques discussed in the course to reduce the CV and test log-loss to a value less than 1.0

In [99]:
```
feature_array = np.array(text_vectorizer.get_feature_names())
tfidf_sorting = np.argsort(train_text_feature_onehotCoding.toarray()).flatten()[::-1]

n = 1000
top_n = feature_array[tfidf_sorting][:n]
```

In [104]:
```
train_text_feature_tfidf_top_1000 = train_text_feature_onehotCoding[:, np.argsort(text_vectorizer.idf_)[:10
```

In [106]:
```
train_text_feature_tfidf_top_1000 = normalize(train_text_feature_tfidf_top_1000)
```

In [107]:
```
train_text_feature_tfidf_top_1000
```

Out[107]:
```
<2124x1000 sparse matrix of type '<class 'numpy.float64'>'
        with 1130862 stored elements in Compressed Sparse Row format>
```

In [109]:
```
test_text_feature_tfidf_top_1000 = text_vectorizer.transform(test_df['TEXT'])[:, np.argsort(text_vectorizer
test_text_feature_tfidf_top_1000 = normalize(test_text_feature_tfidf_top_1000)

cv_text_feature_tfidf_top_1000 = text_vectorizer.transform(cv_df['TEXT'])[:, np.argsort(text_vectorizer.idf
cv_text_feature_tfidf_top_1000 = normalize(cv_text_feature_tfidf_top_1000)
```

In [110]:
```
test_text_feature_tfidf_top_1000
```

Out[110]:
```
<665x1000 sparse matrix of type '<class 'numpy.float64'>'
        with 349459 stored elements in Compressed Sparse Row format>
```

In [126]:
```

cv_text_feature_tfidf_top_1000
```

Out[126]:
```
<532x1000 sparse matrix of type '<class 'numpy.float64'>'
        with 284687 stored elements in Compressed Sparse Row format>
```

In [112]:
```
# Stack gene, variation and text features horizontally
train_x_onehotCoding_tfidf_top_1000 = hstack([train_gene_var_onehotCoding, train_text_feature_tfidf_top_100

test_x_onehotCoding_tfidf_top_1000 = hstack((test_gene_var_onehotCoding, test_text_feature_tfidf_top_1000))

cv_x_onehotCoding_tfidf_top_1000 = hstack((cv_gene_var_onehotCoding, cv_text_feature_tfidf_top_1000))
```

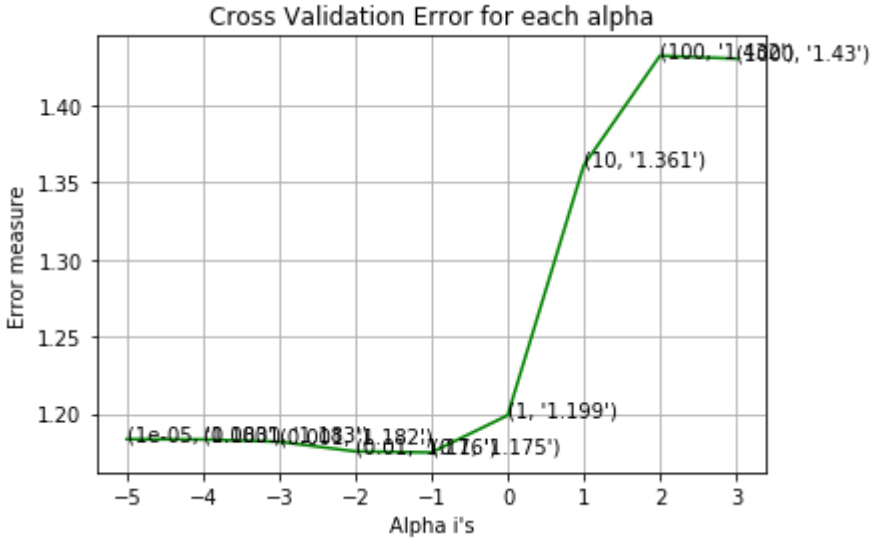
In [113]:
```
train_y = np.array(list(train_df['Class']))
test_y=np.array(list(test_df['Class']))
cv_y=np.array(list(cv_df['Class']))
```

In [114]:

```
alpha = [0.00001, 0.0001, 0.001, 0.01, 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_onehotCoding_tfidf_top_1000, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding_tfidf_top_1000, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding_tfidf_top_1000)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs, eps=1e-15))

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_onehotCoding_tfidf_top_1000, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding_tfidf_top_1000, train_y)


predict_y = sig_clf.predict_proba(train_x_onehotCoding_tfidf_top_1000)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_x_onehotCoding_tfidf_top_1000)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv,
predict_y = sig_clf.predict_proba(test_x_onehotCoding_tfidf_top_1000)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y,

```

```
for alpha = 1e-05
```

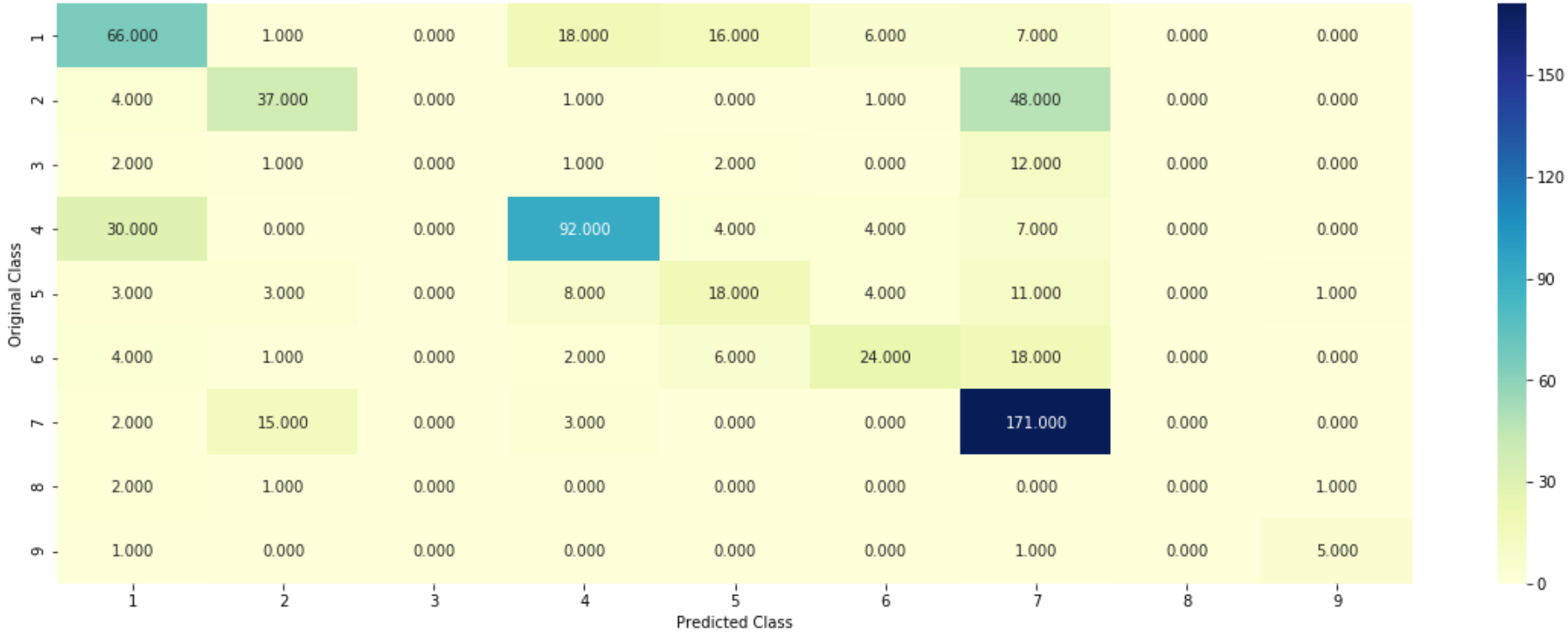
```
Log Loss : 1.1834303887673983
for alpha = 0.0001
Log Loss : 1.183267843927018
for alpha = 0.001
Log Loss : 1.181819646655514
for alpha = 0.01
Log Loss : 1.175509324129162
for alpha = 0.1
Log Loss : 1.1748243948287305
for alpha = 1
Log Loss : 1.1988744136473353
for alpha = 10
Log Loss : 1.3609421484837234
for alpha = 100
Log Loss : 1.4319274865409584
for alpha = 1000
Log Loss : 1.430027611678733
```




```
For values of best alpha =  0.1 The train log loss is: 0.6900123099128517
For values of best alpha =  0.1 The cross validation log loss is: 1.1748243948287305
For values of best alpha =  0.1 The test log loss is: 1.173064487909269
```

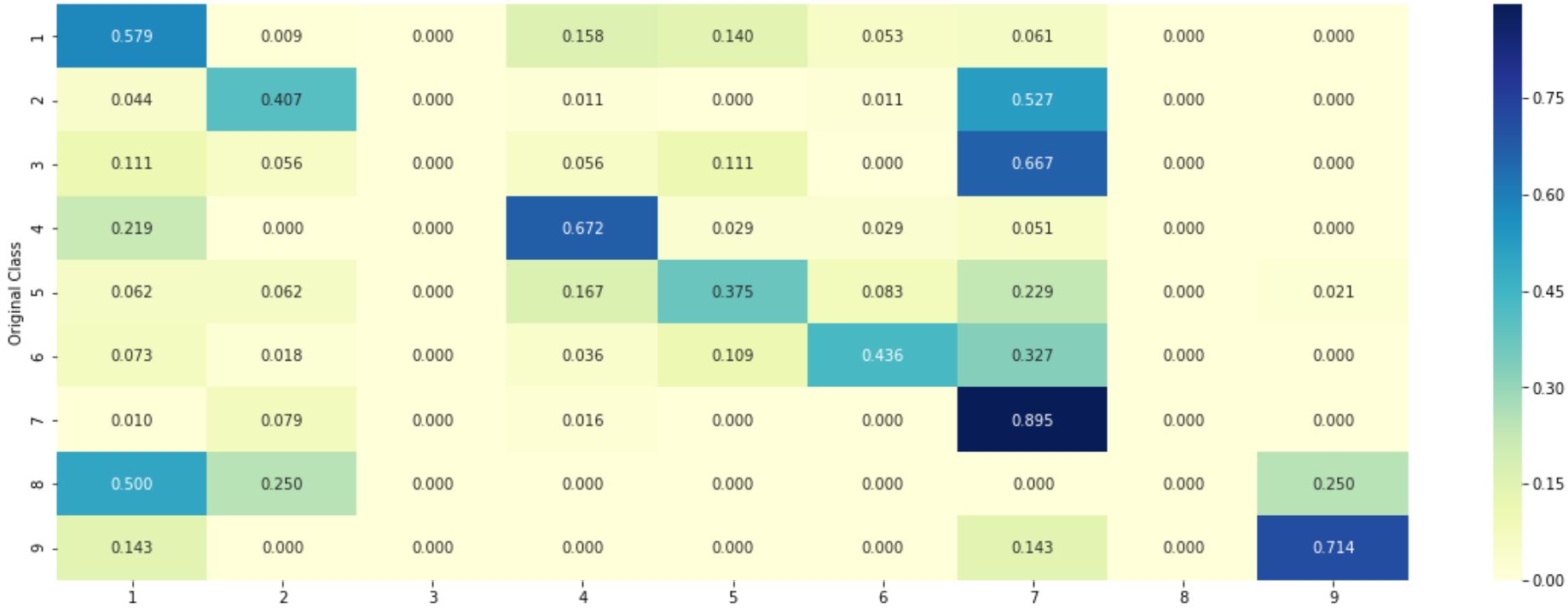
In [115]:
```
clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train_x_onehotCoding_tfidf_top_1000, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding_tfidf_top_1000, train_y)
sig_clf_probs = sig_clf.predict_proba(test_x_onehotCoding_tfidf_top_1000)
# to avoid rounding error while multiplying probabilites we use log-probability estimates
print("Log Loss :",log_loss(test_y, sig_clf_probs))
print("Number of missclassified point :", np.count_nonzero((sig_clf.predict(test_x_onehotCoding_tfidf_top_1
plot_confusion_matrix(test_y, sig_clf.predict(test_x_onehotCoding_tfidf_top_1000))
```

```
Log Loss : 1.173064487909269
Number of missclassified point : 0.37894736842105264
-------------------- Confusion matrix --------------------
```



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

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



In [116]:
```
1 # Just Like this perform on various models
```

In [117]:
```
1 # TASK 3
```

In [118]:
```
# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer = CountVectorizer(min_df=3, ngram_range=(1,2))
train_text_feature_onehotCoding_bigrams = text_vectorizer.fit_transform(train_df['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*number of features) vect
train_text_fea_counts = train_text_feature_onehotCoding_bigrams.sum(axis=0).A1

# zip(list(text_features),text_fea_counts) will zip a word with its number of times it occured
text_fea_dict = dict(zip(list(train_text_features),train_text_fea_counts))


print("Total number of unique 1-grams and 2-grams in train data :", len(train_text_features))
```

```
Total number of unique 1-grams and 2-grams in train data : 787757
```

In [120]:
```
cv_text_onehotCoding_bigrams=text_vectorizer.transform(cv_df['TEXT'])
test_text_onehotCoding_bigrams=text_vectorizer.transform(test_df['TEXT'])
```

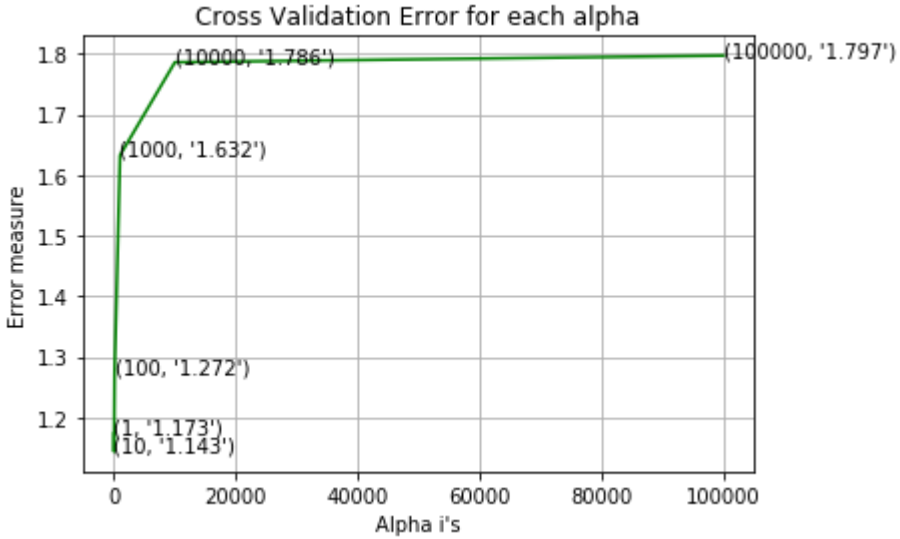
In [121]:
```
train_x_onehotCoding_bigrams = hstack([train_gene_var_onehotCoding, train_text_feature_onehotCoding_bigrams

test_x_onehotCoding_bigrams = hstack((test_gene_var_onehotCoding, test_text_onehotCoding_bigrams))

cv_x_onehotCoding_bigrams = hstack((cv_gene_var_onehotCoding, cv_text_onehotCoding_bigrams))
```

In [123]:

```
alpha = [10 ** x for x in range(0, 6)]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='log', random_state=42, n_jobs
    clf.fit(train_x_onehotCoding_bigrams, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding_bigrams, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding_bigrams)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    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', loss='log', random_stat
clf.fit(train_x_onehotCoding_bigrams, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding_bigrams, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding_bigrams)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_
predict_y = sig_clf.predict_proba(cv_x_onehotCoding_bigrams)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, 
predict_y = sig_clf.predict_proba(test_x_onehotCoding_bigrams)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y,
```

```
for alpha = 1
Log Loss : 1.1732603879951011
for alpha = 10
Log Loss : 1.143466339743986
```

```
for alpha = 100
Log Loss : 1.2717856739723545
for alpha = 1000
Log Loss : 1.6324919602788461
for alpha = 10000
Log Loss : 1.7858845090446755
for alpha = 100000
Log Loss : 1.7968406884272987
```

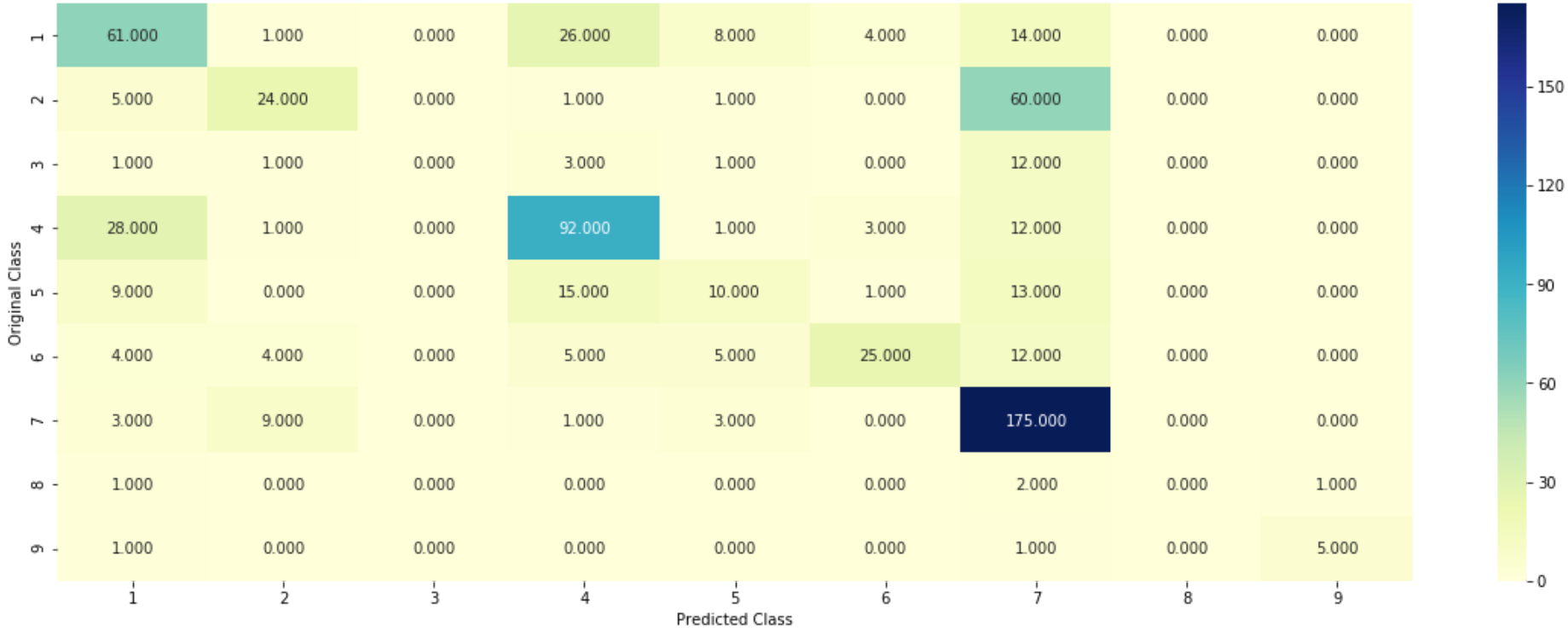



```
For values of best alpha =  10 The train log loss is: 0.8812540858048751
```

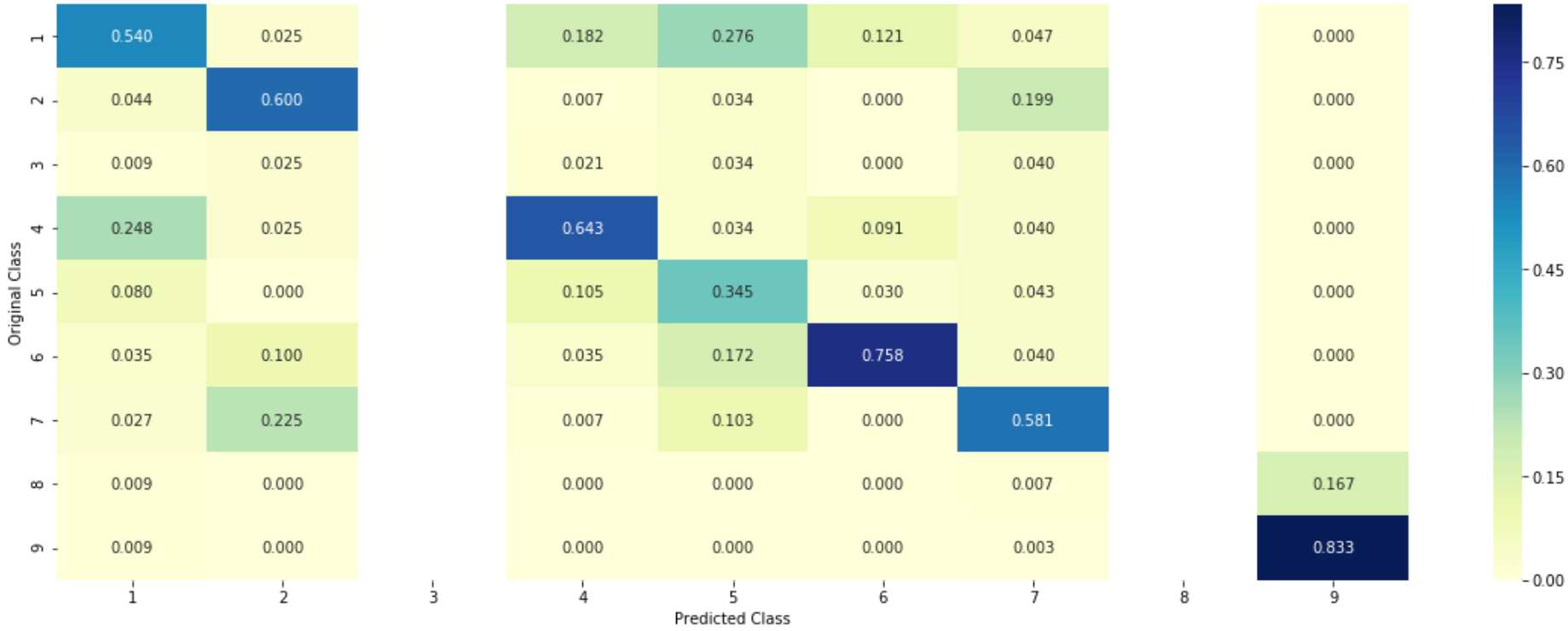
```
For values of best alpha =  10 The cross validation log loss is: 1.143466339743986
For values of best alpha =  10 The test log loss is: 1.1868654202322484
```

In [125]:
```
clf=SGDClassifier(class_weight='balanced', random_state=42, loss='log', alpha=10, n_jobs=3)
clf.fit(train_x_onehotCoding_bigrams, y_train)
predict_and_plot_confusion_matrix(train_x_onehotCoding_bigrams, train_y, test_x_onehotCoding_bigrams, test_
```

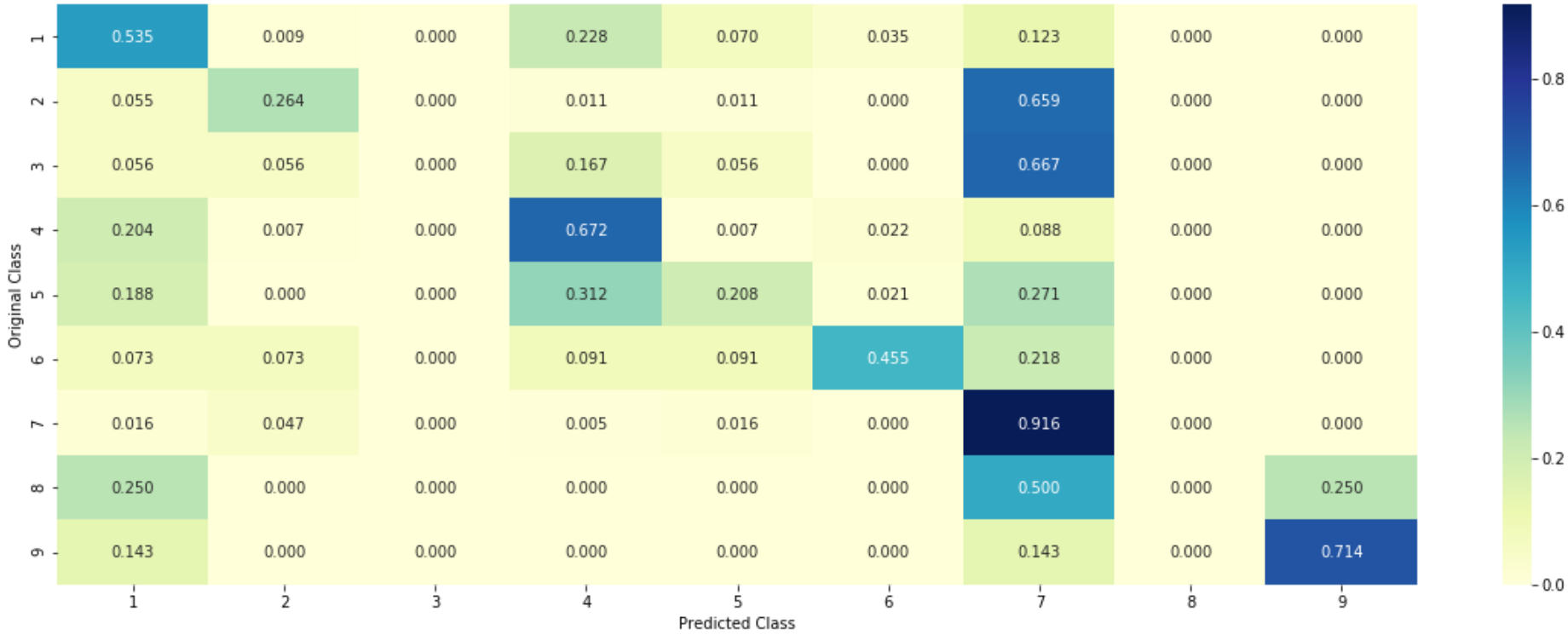
```
Log loss : 1.1868654202322484
Number of mis-classified points : 0.4105263157894737
--------------------- Confusion matrix ---------------------
```




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



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



In [119]:
```
1 #Task 4
```

In [127]:
```
1 import dill
2 dill.dump_session('cancer.db')
```

In [ ]:
```
1
```