Personalized cancer diagnosis

1. Business Problem

1.1. Description

Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/ (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 (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 classification 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 [175]:

```
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, CountVectorizer
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
```

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

In [2]:

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

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

Out[2]:

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

training/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 [3]:

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

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

Out[3]:

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

3.1.3. Preprocessing of text

In [4]:

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


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 [5]:

```
#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 : 306.3311523 seconds
```

In [6]:

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

Out[6]:

	ID	Gene	Variation	Class	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 [7]:

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

Out[7]:

	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 [8]:

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

In [9]:

```
result[result['ID']==1109]
```

Out[9]:

	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 [10]:

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

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

In [11]:

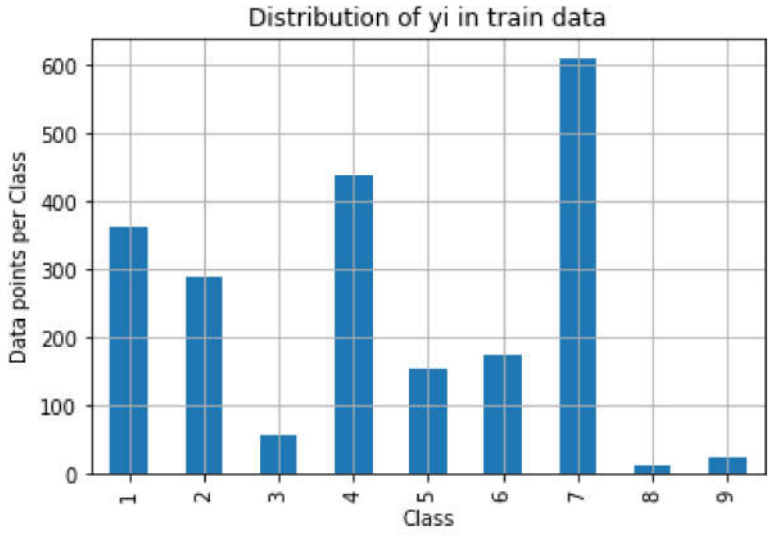
```
print('Number of data points in train data:', train_df.shape[0])
print('Number of data points in test data:', test_df.shape[0])
print('Number of data points in cross validation data:', cv_df.shape[0])
```

```
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
```

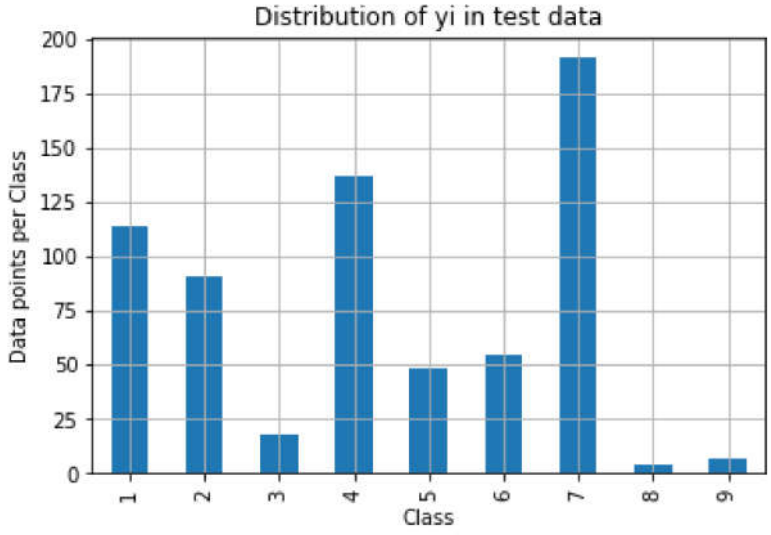
3.1.4.2. Distribution of y_i's in Train, Test and Cross Validation datasets

In [12]:

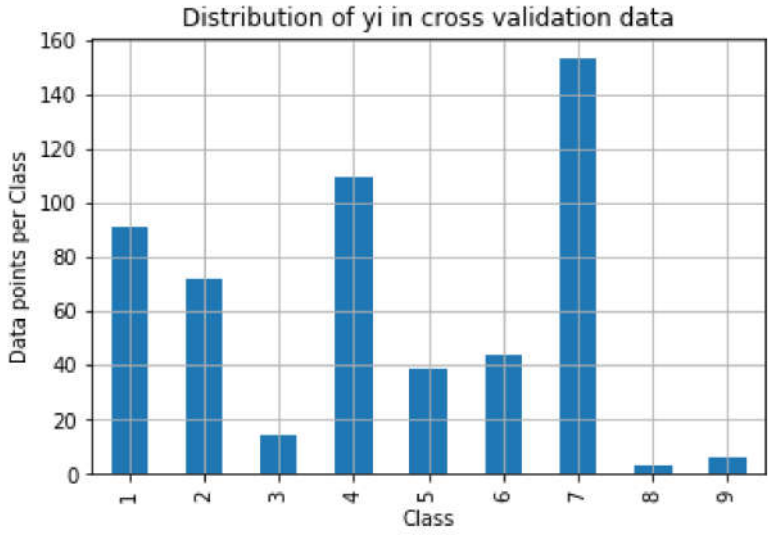
```
# it returns a dict, keys as class labels and values as the number of data points in that c
train_class_distribution = train_df['Class'].value_counts().sort_index()
test_class_distribution = test_df['Class'].value_counts().sort_index()
cv_class_distribution = cv_df['Class'].value_counts().sort_index()

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], '(


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], '('

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], '(',
```




```
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.

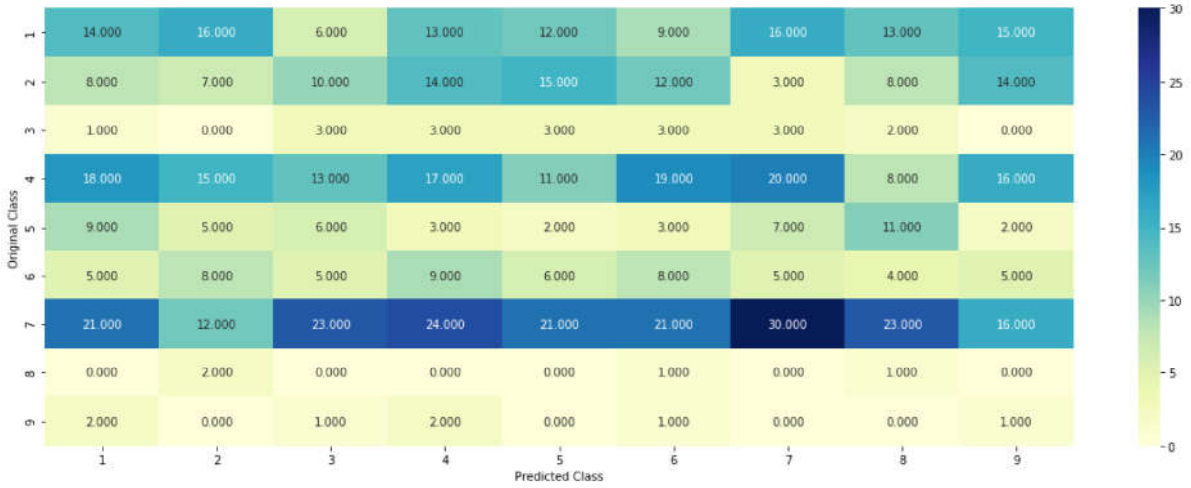
In [13]:

```
# 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

    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 a
    # 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 a
    # 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=la
    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=la
    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=la
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()
```

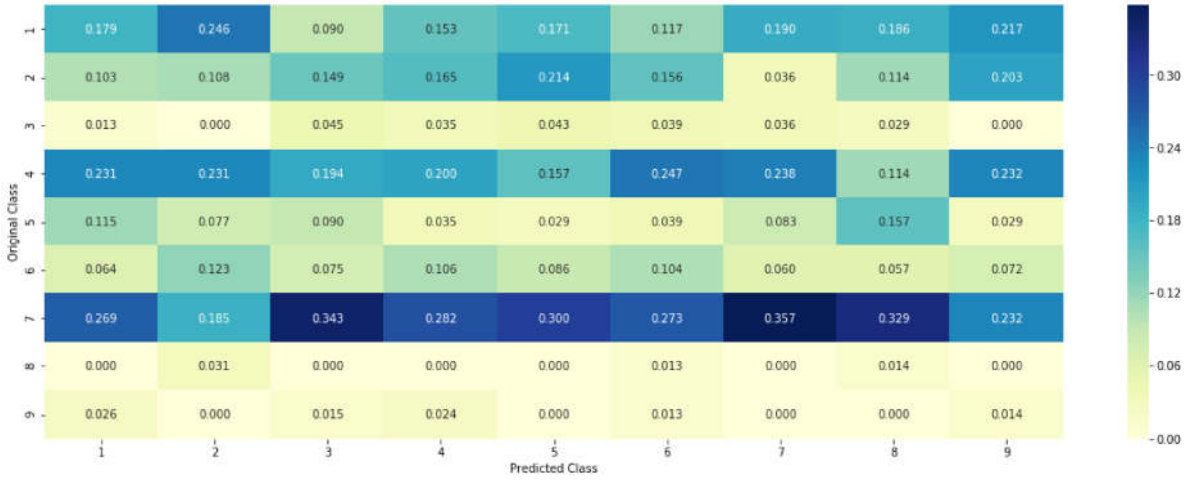
In [14]:

```
# 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,


# 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-1

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

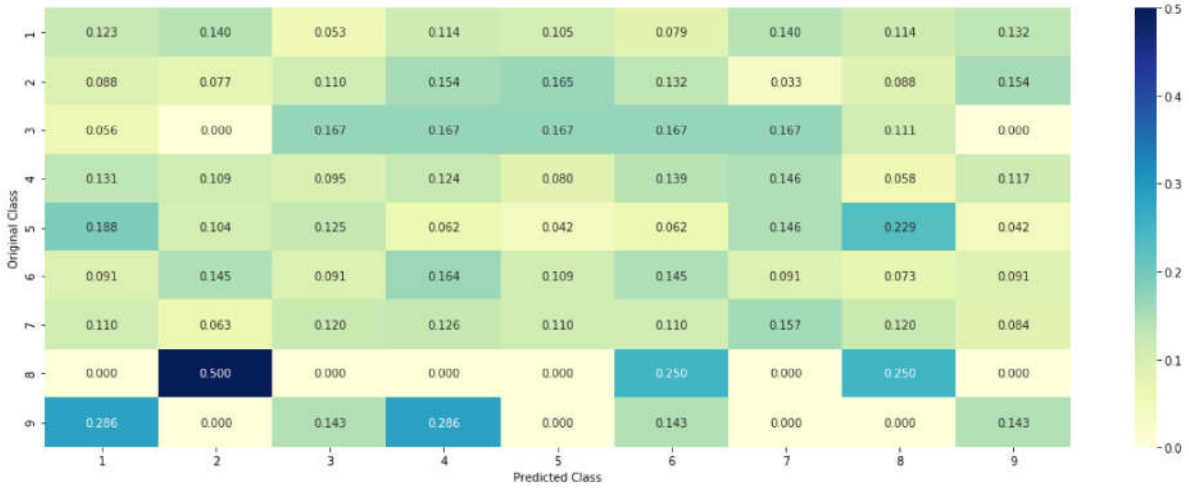
```
Log loss on Cross Validation Data using Random Model 2.5164445887481466
Log loss on Test Data using Random Model 2.518711330495878
-------------------- Confusion matrix --------------------
```




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



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



3.3 Univariate Analysis

In [15]:

```
# 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 da
# build a vector (1*9) , the first element = (number of times it occured in class1 + 10*alp
# 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/var
    gv_dict = dict()

    # denominator will contain the number of time that particular feature occured in whole
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticular
        # 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 f
            vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))

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

# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
    # print(gv_dict)
    #     {'BRCA1': [0.20075757575757575, 0.03787878787878788, 0.068181818181818177, 0.1363
    #      'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 0.2704
    #      'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.068181818181818177
    #      'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.060606060606060608, 0.078
    #      'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 0.465
    #      'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.07284
    #      'BRAF': [0.066666666666666666, 0.17999999999999999, 0.073333333333333334, 0.0733
    #       ...
    #     }
    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
    gv_fea = []
    # for every feature values in the given data frame we will check if it is there in the
    # 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 [16]:

```
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 : 243
BRCA1     167
TP53      109
EGFR       95
PTEN       79
BRCA2      77
KIT        65
BRAF       57
PIK3CA     44
ERBB2      41
ALK        41
Name: Gene, dtype: int64
```

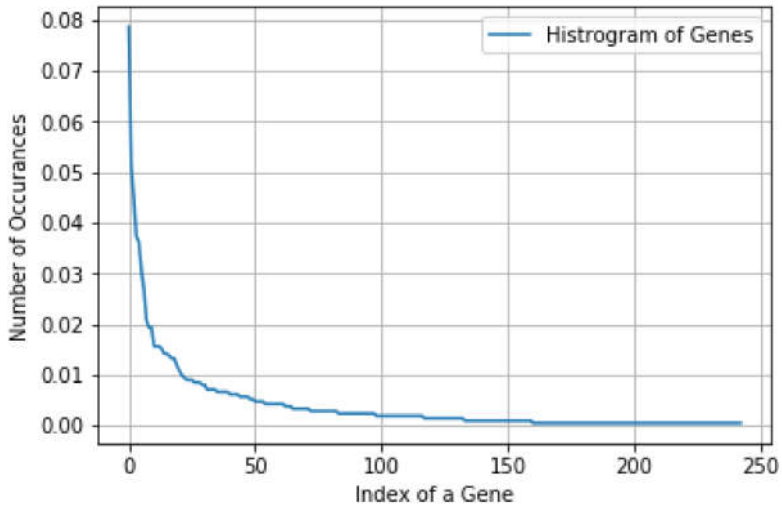
In [17]:

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

```
Ans: There are 243 different categories of genes in the train data, and they
are distibuted as follows
```

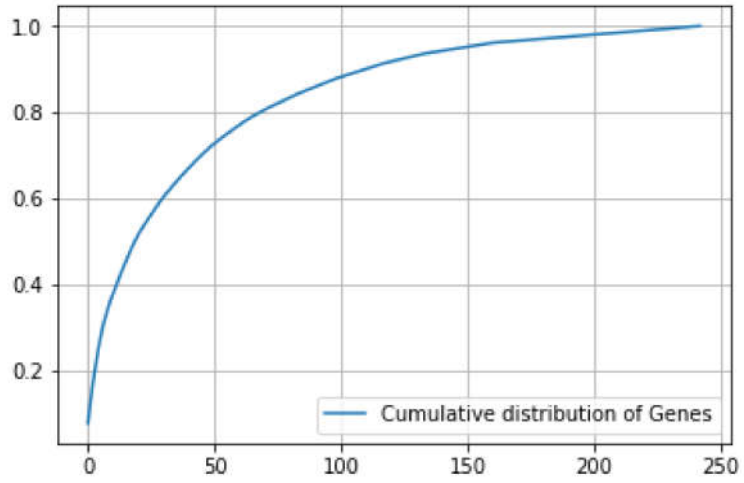
In [18]:

```
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 [19]:

```
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/ (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 [20]:

```
#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 [21]:

```
print("train_gene_feature_responseCoding is converted feature using respone coding method.
```

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

In [22]:

```
# one-hot encoding of Gene feature.
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 [23]:

```
train_df['Gene'].head()
```

Out[23]:

```
1707     PPM1D
252       EGFR
1638     RRAS2
2371    PTPN11
1233      PIM1
Name: Gene, dtype: object
```

In [24]:

```
train_gene_feature_onehotCoding
```

Out[24]:

```
<2124x242 sparse matrix of type '<class 'numpy.float64'>'
        with 2124 stored elements in Compressed Sparse Row format>
```

In [25]:

```
gene_vectorizer.get_feature_names()
```

Out[25]:

```
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
 'akt3',
 'alk',
 'apc',
 'ar',
 'araf',
 'arid1b',
 'arid2',
 'arid5b',
 'asxl1',
 'asxl2',
 'atm',
 'atr',
 'atrx',
```

In [26]:

```
print("train_gene_feature_onehotCoding is converted feature using one-hot encoding method.
```

```
train_gene_feature_onehotCoding is converted feature using one-hot encoding
method. The shape of gene feature: (2124, 242)
```

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

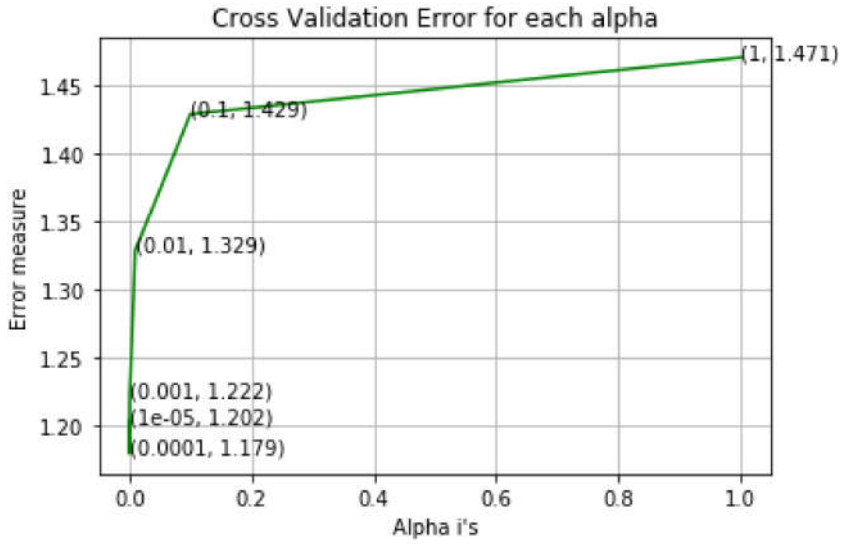
There are many ways to estimate how good a feature is, in predicting y_i. One of the good methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y_i.

In [27]:

```
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/sklea
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal
# 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 Desce
# predict(X)    Predict class labels for samples in X.

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


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

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


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
clf.fit(train_gene_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_gene_feature_onehotCoding, y_train)

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

```
For values of alpha =  1e-05 The log loss is: 1.201921313392381
For values of alpha =  0.0001 The log loss is: 1.1791330653831467
For values of alpha =  0.001 The log loss is: 1.2215086234804406
For values of alpha =  0.01 The log loss is: 1.328720183487397
```

```
For values of alpha =  0.1 The log loss is: 1.4291311026378817
For values of alpha =  1 The log loss is: 1.4706833951979281
```




```
For values of best alpha =  0.0001 The train log loss is: 0.9990278493040442
For values of best alpha =  0.0001 The cross validation log loss is: 1.17913
30653831467
For values of best alpha =  0.0001 The test log loss is: 1.1724574298406922
```

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 [28]:

```
print("Q6. How many data points in Test and CV datasets are covered by the ", unique_genes.

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/t
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_coverage
```

```
Q6. How many data points in Test and CV datasets are covered by the  243  ge
nes in train dataset?
Ans
1. In test data 651 out of 665 : 97.89473684210527
2. In cross validation data 518 out of  532 : 97.36842105263158
```

3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it ?

Ans. Variation is a categorical variable

Q8. How many categories are there?

In [29]:

```
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 : 1922
Truncating_Mutations    60
Amplification           54
Deletion                47
Fusions                 23
Overexpression           5
Q61R                     3
Q61L                     3
TMPRSS2-ETV1_Fusion      2
P130S                    2
R173C                    2
Name: Variation, dtype: int64
```

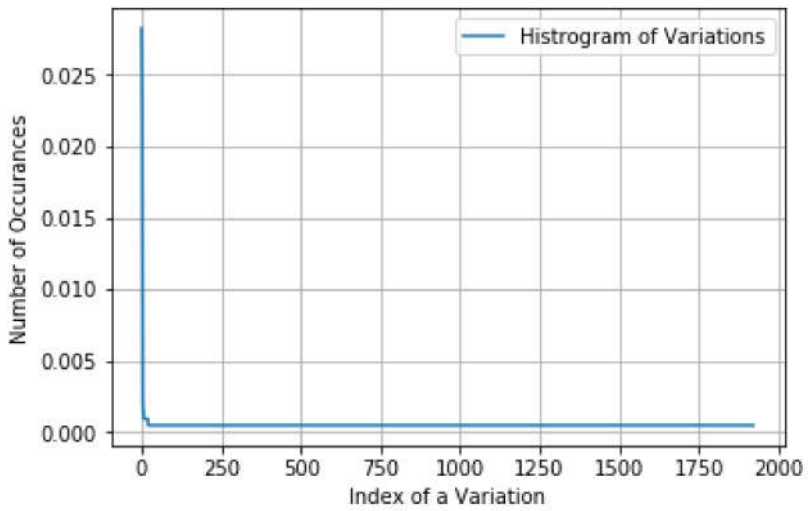
In [30]:

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

```
Ans: There are 1922 different categories of variations in the train data, an
d they are distibuted as follows
```

In [31]:

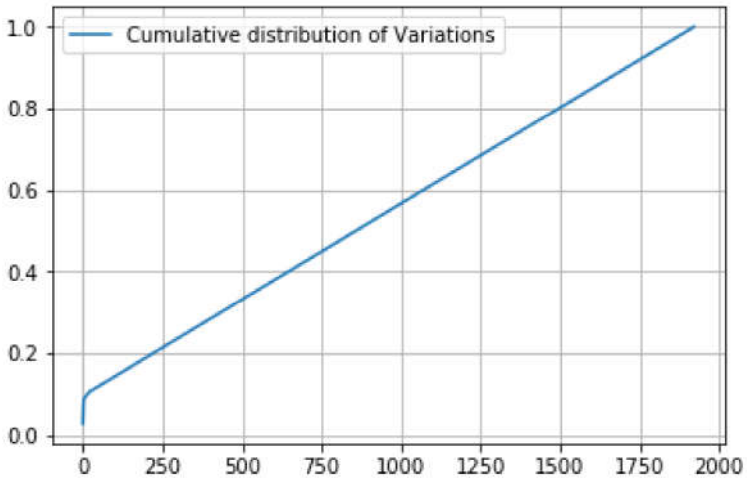
```
s = sum(unique_variations.values);
h = unique_variations.values/s;
plt.plot(h, label="Histrogram of Variations")
plt.xlabel('Index of a Variation')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



In [32]:

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

```
[0.02824859 0.05367232 0.07580038 ... 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/ (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 [33]:

```
# alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train_
# 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 [34]:

```
print("train_variation_feature_responseCoding is a converted feature using the response cod
```

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

In [35]:

```
# one-hot encoding of variation feature.
variation_vectorizer = TfidfVectorizer()
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variati
test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])
```

In [36]:

```
print("train_variation_feature_onehotEncoded is converted feature using the onne-hot encodi
```

```
train_variation_feature_onehotEncoded is converted feature using the onne-ho
t encoding method. The shape of Variation feature: (2124, 1958)
```

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

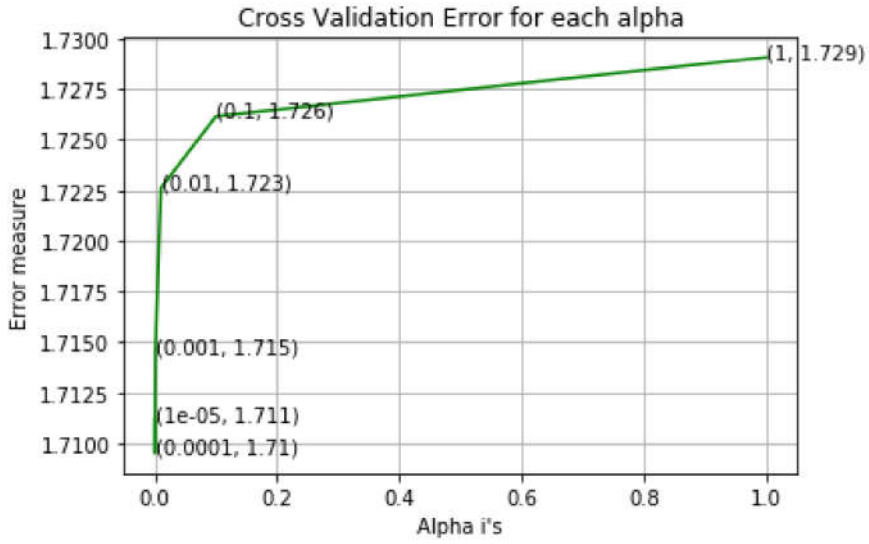
Let's build a model just like the earlier!

In [37]:

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

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

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


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

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

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

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


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
clf.fit(train_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
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:"
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_
```

```
For values of alpha =  1e-05 The log loss is: 1.7111485336443009
For values of alpha =  0.0001 The log loss is: 1.7095044941194737
For values of alpha =  0.001 The log loss is: 1.7145224311737974
```

```
For values of alpha =  0.01 The log loss is: 1.7226140046074891
For values of alpha =  0.1 The log loss is: 1.7261573984424987
For values of alpha =  1 The log loss is: 1.7290792753568696
```




```
For values of best alpha =  0.0001 The train log loss is: 0.7825931880670998
For values of best alpha =  0.0001 The cross validation log loss is: 1.70950
44941194737
For values of best alpha =  0.0001 The test log loss is: 1.714682948943186
```

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 [38]:

```
print("Q12. How many data points are covered by total ", unique_variations.shape[0], " gene
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/t
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_coverage
```

```
Q12. How many data points are covered by total  1922  genes in test and cros
s validation data sets?
Ans
1. In test data 66 out of 665 : 9.924812030075188
2. In cross validation data 51 out of  532 : 9.586466165413533
```

3.2.3 Univariate Analysis on Text Feature

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

In [39]:

```
# 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 [40]:

```
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
            text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TEXT'].s
            row_index += 1
    return text_feature_responseCoding
```

In [41]:

```
train_df['TEXT'].head(4)
```

Out[41]:

```
1707    ppm1d wip1 negatively regulates dephosphorylat...
252     epidermal growth factor receptor egfr overexpr...
1638    abstract approach identify human oncogenes gen...
2371    protein tyrosine phosphatases ptps key positiv...
Name: TEXT, dtype: object
```

In [42]:

```
def top_tfidf_feats(row, features, top_n=25):
    ''' Get top n tfidf values in row and return them with their corresponding feature name
    topn_ids = np.argsort(row)[::-1][:top_n]
    top_feats = [(features[i], row[i]) for i in topn_ids]
    df = pd.DataFrame(top_feats)
    df.columns = ['feature', 'tfidf']
    return df

def top_mean_feats(Xtr, features, min_tfidf=0.1, grp_ids=None, top_n=25):
    ''' Return the top n features that on average are most important amongst documents in r
        indentified by indices in grp_ids. '''
    if grp_ids:
        D = Xtr[grp_ids].toarray()
    else:
        D = Xtr.toarray()

    D[D < min_tfidf] = 0
    tfidf_means = np.mean(D, axis=0)
    return top_tfidf_feats(tfidf_means, features, top_n)
```

In [43]:

```
#building a CountVectorizer with all the words that occured minimum times in train data
text_vectorizer = TfidfVectorizer(min_df=3)
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 o
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 occu
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 : 53084
```

In [44]:

```
train_text_fea_counts
```

Out[44]:

```
array([8.50542282, 8.86859573, 0.02160533, ..., 0.02864126, 0.03927349,
       0.07306987])
```

In [45]:

```
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)
```

In [46]:

```
#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 [47]:

```
# 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
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_re
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_response
```

In [48]:

```
# 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 [49]:

```
#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 [50]:

```
# Number of words for a given frequency.
print(Counter(sorted_text_occur))
```

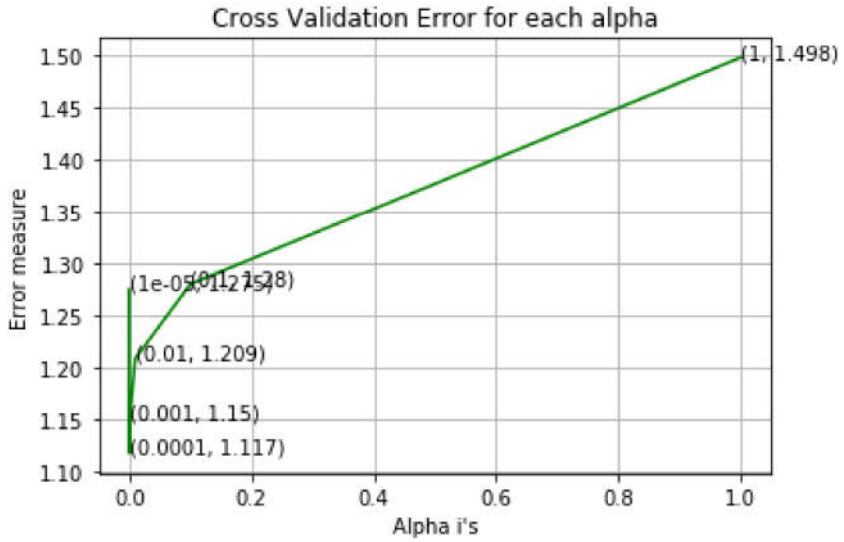
```
Counter({0.01825463012568682: 311, 0.026885358956470595: 233, 0.0586477626
3919755: 197, 0.014163017411216883: 175, 0.3155234186838409: 153, 0.026402
703731809488: 140, 0.0627989523477546: 129, 0.22075384208159432: 126, 0.01
653046035472742: 122, 0.022926121117879217: 116, 0.05155669460244136: 114,
0.05336887404644867: 108, 0.05565523180779691: 106, 0.06756476354641634: 1
05, 0.050652286723839854: 101, 0.12329472035817207: 94, 0.0247994314941133
5: 92, 0.03231118487941169: 91, 0.029196445797497545: 91, 0.01143621616661
665: 87, 0.024039763655583996: 86, 0.026803272240097493: 79, 0.02312927745
5551343: 79, 0.015875512385423236: 79, 0.015199406502918074: 79, 0.0167933
19890310847: 77, 0.041184627298912334: 76, 0.03448601191957191: 73, 0.0322
5251820219677: 71, 0.05691034488382374: 66, 0.04467980376334886: 64, 0.025
857607796780983: 64, 0.012226582245579001: 63, 0.0179100523082097: 62, 0.1
3864857247606216: 60, 0.01196291224387235: 60, 0.04348964093885337: 59, 0.
0332624534218807: 58, 0.015344188682451633: 58, 0.05327115355947187: 57,
0.019632702726497323: 57, 0.017141969036886254: 57, 0.012858392789272019:
57, 0.25170261191975657: 56, 0.014576127656493848: 56, 0.01593977303714456
3: 55, 0.01518593518697746: 55, 0.11713944441039946: 54, 0.121425849731265
6: 53, 0.02361471617105937: 52, 0.01248975378902944: 52, 0.014392204249573
222: 50, 0.020766642903039124: 49, 0.04287204216924623: 48, 0.032117389214
```

In [51]:

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

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

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


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

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


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
clf.fit(train_text_feature_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
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:"
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_
```

```
For values of alpha =  1e-05 The log loss is: 1.2750369752789361
For values of alpha =  0.0001 The log loss is: 1.117498533121457
For values of alpha =  0.001 The log loss is: 1.1498026734310902
```

```
For values of alpha =  0.01 The log loss is: 1.208641149955801
For values of alpha =  0.1 The log loss is: 1.2800110087797332
For values of alpha =  1 The log loss is: 1.4977782747371609
```




```
For values of best alpha =  0.0001 The train log loss is: 0.6517753508893039
For values of best alpha =  0.0001 The cross validation log loss is: 1.11749
8533121457
For values of best alpha =  0.0001 The test log loss is: 1.0599211094859267
```

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

Ans. Yes, it seems like!

In [52]:

```
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 [53]:

```
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")
```

```
96.519 % of word of test data appeared in train data
98.549 % of word of Cross Validation appeared in train data
```

4. Machine Learning Models

In [54]:

```
#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
    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.sh
    plot_confusion_matrix(test_y, pred_y)
```

In [55]:

```
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 [56]:

```
# 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 = TfidfVectorizer()
    var_count_vec = TfidfVectorizer()
    text_count_vec = TfidfVectorizer(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,ye
        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(wo
        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,ye

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

Stacking the three types of features

In [57]:

```
# 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_feat
test_gene_var_onehotCoding  = hstack((test_gene_feature_onehotCoding,test_variation_feature
cv_gene_var_onehotCoding  = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_oneho

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

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

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


train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,train_variatic
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_f
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_respo
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_response
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding
```

In [58]:

```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCoding
print("(number of data points * number of features) in test data = ", test_x_onehotCoding.s
print("(number of data points * number of features) in cross validation data =", cv_x_oneho
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 55284)
(number of data points * number of features) in test data =  (665, 55284)
(number of data points * number of features) in cross validation data = (53
2, 55284)
```

In [59]:

```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_responseCodi
print("(number of data points * number of features) in test data = ", test_x_responseCoding
print("(number of data points * number of features) in cross validation data =", cv_x_respo
```

```
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 27)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data = (53
2, 27)
```

4.1. Base Line Model

4.1.1. Naive Bayes

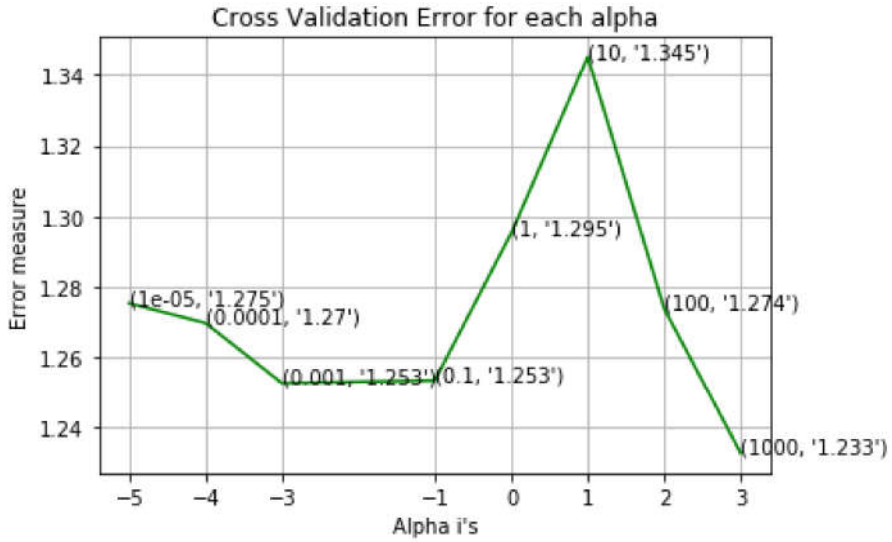
4.1.1.1. Hyper parameter tuning

In [60]:

```
# find more about Multinomial Naive base function here http://scikit-learn.org/stable/modul
# ------------------------
# 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


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


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

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


best_alpha = np.argmin(cv_log_error_array)
clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train_x_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
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:"
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_
```

```
for alpha = 1e-05
Log Loss : 1.2752622356177004
for alpha = 0.0001
Log Loss : 1.269664395462353
for alpha = 0.001
Log Loss : 1.2526392943859541
for alpha = 0.1
Log Loss : 1.253422477372519
for alpha = 1
Log Loss : 1.295172377428481
for alpha = 10
Log Loss : 1.3451704291963553
for alpha = 100
Log Loss : 1.2737632202886557
for alpha = 1000
Log Loss : 1.232804010031772
```



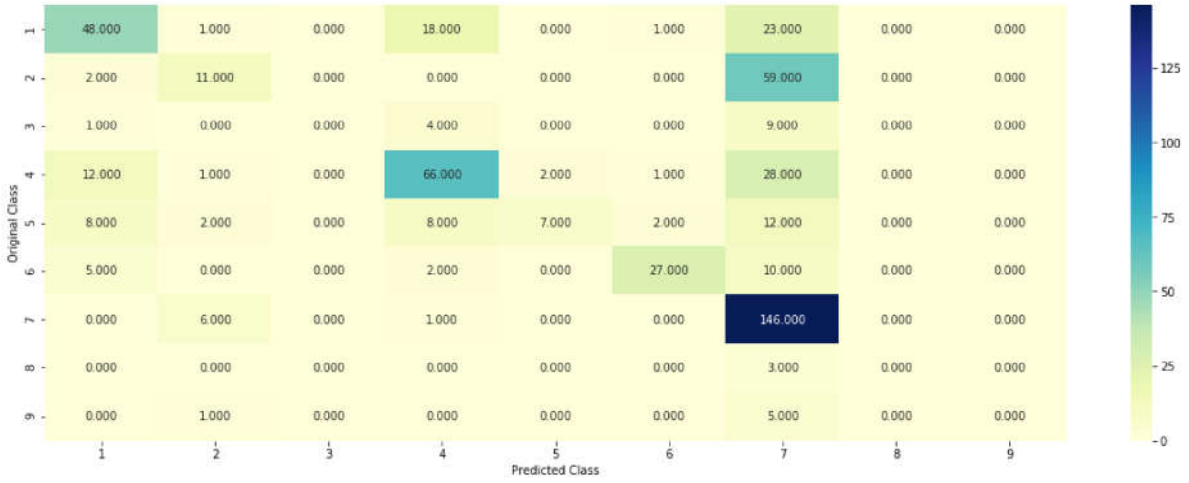

```
For values of best alpha =  1000 The train log loss is: 0.9217499566643759
For values of best alpha =  1000 The cross validation log loss is: 1.2328040
10031772
For values of best alpha =  1000 The test log loss is: 1.194405811390313
```

4.1.1.2. Testing the model with best hyper paramters

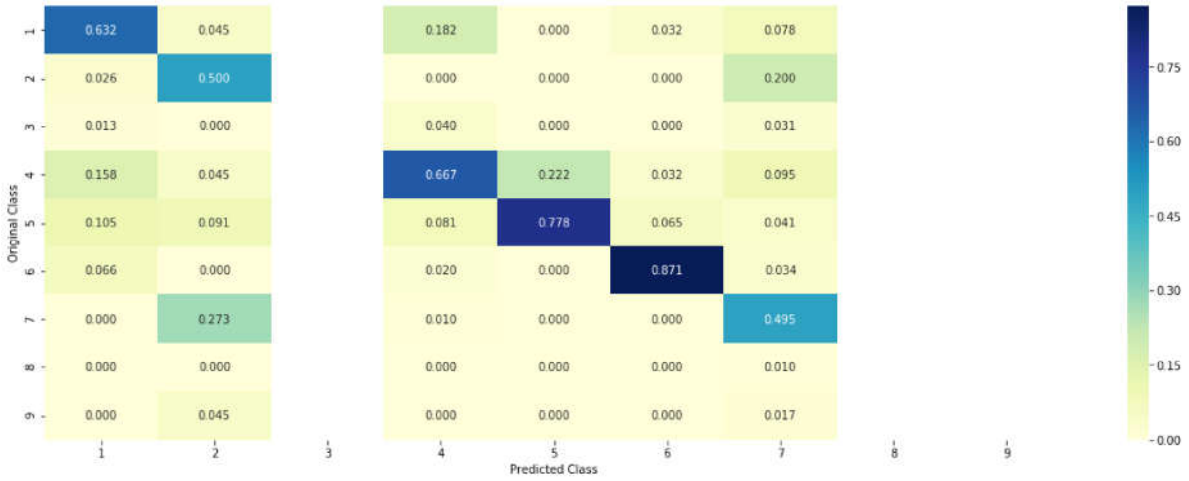
In [61]:

```
# find more about Multinomial Naive base function here http://scikit-learn.org/stable/modul
# ------------------------
# 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
# -----------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# ----------------------------
# 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_onehotCodi
plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray()))
```

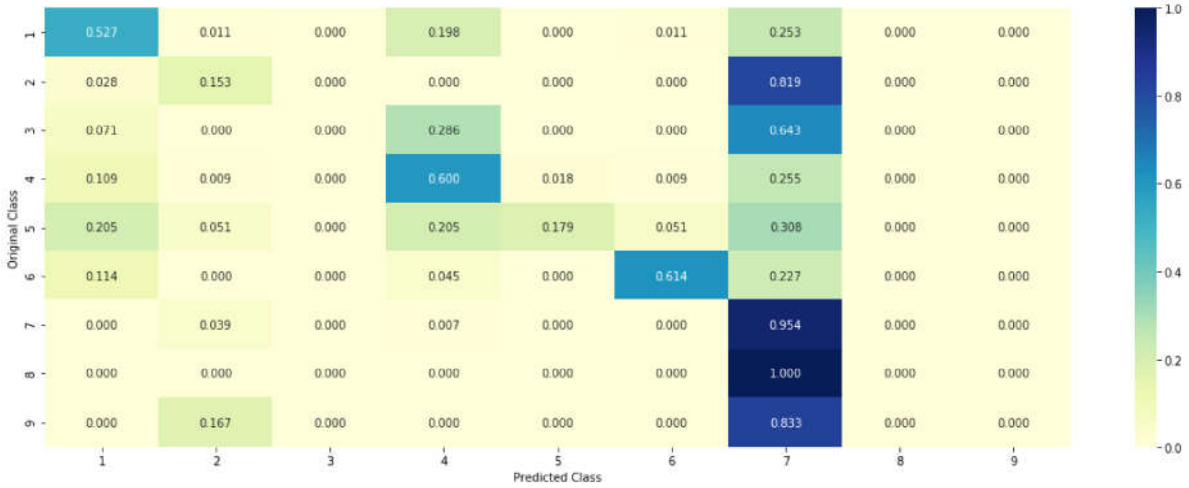
```
Log Loss : 1.232804010031772
Number of missclassified point : 0.4266917293233083
-------------------- Confusion matrix --------------------
```




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



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



4.1.1.3. Feature Importance, Correctly classified point

In [62]:

```
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[
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'].ilc
```

```
Predicted Class : 7
Predicted Class Probabilities: [[5.690e-02 6.300e-02 1.900e-03 4.800e-02 9.1
50e-02 2.130e-02 7.164e-01
  6.000e-04 4.000e-04]]
Actual Class : 5
--------------------------------------------------
14 Text feature [cells] present in test data point [True]
15 Text feature [downstream] present in test data point [True]
17 Text feature [kinase] present in test data point [True]
18 Text feature [cell] present in test data point [True]
19 Text feature [activation] present in test data point [True]
23 Text feature [phosphorylation] present in test data point [True]
25 Text feature [contrast] present in test data point [True]
27 Text feature [expressing] present in test data point [True]
28 Text feature [shown] present in test data point [True]
29 Text feature [also] present in test data point [True]
30 Text feature [inhibitor] present in test data point [True]
31 Text feature [signaling] present in test data point [True]
32 Text feature [growth] present in test data point [True]
33 Text feature [however] present in test data point [True]
34 Text feature [suggest] present in test data point [True]
35 Text feature [independent] present in test data point [True]
37 Text feature [previously] present in test data point [True]
38 Text feature [increased] present in test data point [True]
39 Text feature [compared] present in test data point [True]
40 Text feature [10] present in test data point [True]
41 Text feature [addition] present in test data point [True]
42 Text feature [similar] present in test data point [True]
43 Text feature [found] present in test data point [True]
45 Text feature [1a] present in test data point [True]
46 Text feature [higher] present in test data point [True]
47 Text feature [mechanism] present in test data point [True]
48 Text feature [potential] present in test data point [True]
49 Text feature [enhanced] present in test data point [True]
50 Text feature [figure] present in test data point [True]
52 Text feature [well] present in test data point [True]
53 Text feature [activating] present in test data point [True]
54 Text feature [mutations] present in test data point [True]
56 Text feature [mutant] present in test data point [True]
57 Text feature [tyrosine] present in test data point [True]
58 Text feature [3b] present in test data point [True]
59 Text feature [consistent] present in test data point [True]
61 Text feature [treatment] present in test data point [True]
62 Text feature [described] present in test data point [True]
66 Text feature [interestingly] present in test data point [True]
67 Text feature [may] present in test data point [True]
68 Text feature [using] present in test data point [True]
69 Text feature [demonstrated] present in test data point [True]
```

```
72 Text feature [various] present in test data point [True]
75 Text feature [inhibitors] present in test data point [True]
76 Text feature [followed] present in test data point [True]
77 Text feature [lines] present in test data point [True]
78 Text feature [including] present in test data point [True]
79 Text feature [proliferation] present in test data point [True]
81 Text feature [3a] present in test data point [True]
82 Text feature [furthermore] present in test data point [True]
84 Text feature [report] present in test data point [True]
86 Text feature [reported] present in test data point [True]
87 Text feature [observed] present in test data point [True]
90 Text feature [mutation] present in test data point [True]
91 Text feature [expression] present in test data point [True]
93 Text feature [two] present in test data point [True]
94 Text feature [identified] present in test data point [True]
95 Text feature [obtained] present in test data point [True]
96 Text feature [increase] present in test data point [True]
97 Text feature [examined] present in test data point [True]
Out of the top  100  features  60 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

In [63]:

```
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[
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'].ilc
```

```
Predicted Class : 4
Predicted Class Probabilities: [[1.136e-01 9.000e-03 3.790e-02 6.822e-01 5.9
80e-02 4.940e-02 4.750e-02
  4.000e-04 2.000e-04]]
Actual Class : 6
--------------------------------------------------
10 Text feature [proteins] present in test data point [True]
11 Text feature [activity] present in test data point [True]
12 Text feature [protein] present in test data point [True]
14 Text feature [experiments] present in test data point [True]
15 Text feature [loss] present in test data point [True]
16 Text feature [acid] present in test data point [True]
18 Text feature [determined] present in test data point [True]
19 Text feature [whereas] present in test data point [True]
20 Text feature [whether] present in test data point [True]
21 Text feature [shown] present in test data point [True]
23 Text feature [indicated] present in test data point [True]
25 Text feature [described] present in test data point [True]
26 Text feature [function] present in test data point [True]
27 Text feature [missense] present in test data point [True]
28 Text feature [two] present in test data point [True]
29 Text feature [important] present in test data point [True]
30 Text feature [results] present in test data point [True]
35 Text feature [type] present in test data point [True]
36 Text feature [amino] present in test data point [True]
38 Text feature [bind] present in test data point [True]
39 Text feature [also] present in test data point [True]
40 Text feature [mutations] present in test data point [True]
41 Text feature [functions] present in test data point [True]
42 Text feature [expressed] present in test data point [True]
45 Text feature [vitro] present in test data point [True]
48 Text feature [wild] present in test data point [True]
50 Text feature [thus] present in test data point [True]
52 Text feature [indicate] present in test data point [True]
53 Text feature [levels] present in test data point [True]
54 Text feature [purified] present in test data point [True]
55 Text feature [partially] present in test data point [True]
56 Text feature [reduced] present in test data point [True]
57 Text feature [suppressor] present in test data point [True]
58 Text feature [related] present in test data point [True]
59 Text feature [transfected] present in test data point [True]
60 Text feature [determine] present in test data point [True]
61 Text feature [containing] present in test data point [True]
62 Text feature [tagged] present in test data point [True]
63 Text feature [may] present in test data point [True]
64 Text feature [either] present in test data point [True]
65 Text feature [see] present in test data point [True]
66 Text feature [lower] present in test data point [True]
```

```
67 Text feature [three] present in test data point [True]
68 Text feature [analyzed] present in test data point [True]
70 Text feature [although] present in test data point [True]
71 Text feature [30] present in test data point [True]
73 Text feature [standard] present in test data point [True]
74 Text feature [mm] present in test data point [True]
75 Text feature [effects] present in test data point [True]
83 Text feature [except] present in test data point [True]
86 Text feature [made] present in test data point [True]
87 Text feature [critical] present in test data point [True]
90 Text feature [result] present in test data point [True]
92 Text feature [using] present in test data point [True]
93 Text feature [suggest] present in test data point [True]
Out of the top  100  features  55 are present in query point
```

4.2. K Nearest Neighbour Classification

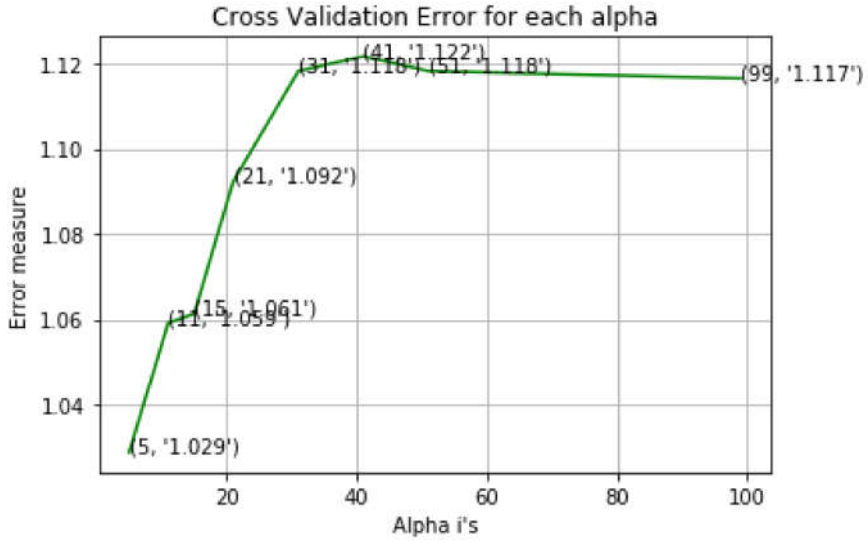
4.2.1. Hyper parameter tuning

In [64]:

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

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


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# ----------------------------
# 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 estimat
    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
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:"
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_
```

```
for alpha = 5
Log Loss : 1.0287617628155055
for alpha = 11
Log Loss : 1.0591593928899152
for alpha = 15
Log Loss : 1.0612819158060707
for alpha = 21
Log Loss : 1.0923449041197113
for alpha = 31
Log Loss : 1.1182542439970928
for alpha = 41
Log Loss : 1.121808887531119
for alpha = 51
Log Loss : 1.1182624339938598
for alpha = 99
Log Loss : 1.1165451019710568
```



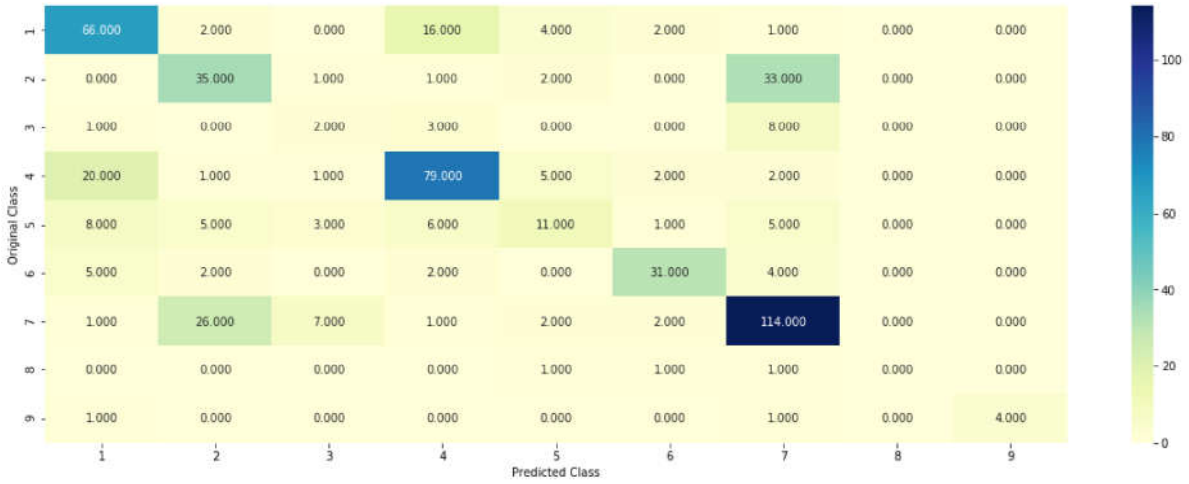

```
For values of best alpha =  5 The train log loss is: 0.47188162335748696
For values of best alpha =  5 The cross validation log loss is: 1.0287617628
155055
For values of best alpha =  5 The test log loss is: 1.0301971131023804
```

4.2.2. Testing the model with best hyper paramters

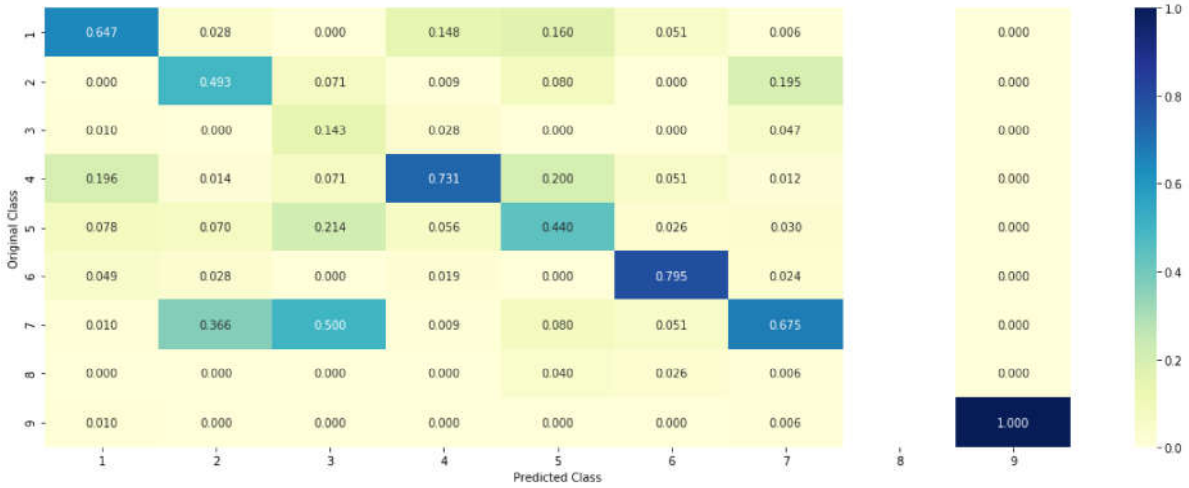
In [65]:

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

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

```
Log loss : 1.0287617628155055
Number of mis-classified points : 0.35714285714285715
-------------------- Confusion matrix --------------------
```




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




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

4.2.3.Sample Query point -1

In [66]:

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

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

```
Predicted Class : 7
Actual Class : 5
The  5  nearest neighbours of the test points belongs to classes [1 2 7 5 5]
Fequency of nearest points : Counter({5: 2, 1: 1, 2: 1, 7: 1})
```

4.2.4. Sample Query Point-2

In [67]:

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

```
Predicted Class : 4
Actual Class : 6
the k value for knn is 5 and the nearest neighbours of the test points belon
gs to classes [3 4 3 4 4]
Fequency of nearest points : Counter({4: 3, 3: 2})
```

4.3. Logistic Regression

4.3.1. With Class balancing

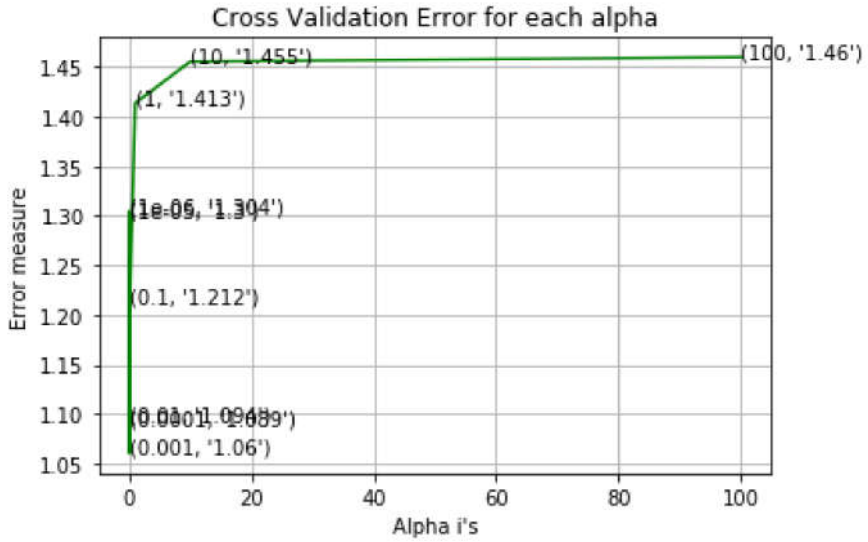
4.3.1.1. Hyper paramter tuning

In [68]:

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

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


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# ----------------------------
# 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_
    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 estimat
    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='l
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
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:"
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_
```

```
for alpha = 1e-06
Log Loss : 1.3042815707526412
for alpha = 1e-05
Log Loss : 1.2998182904486122
for alpha = 0.0001
Log Loss : 1.0894281825665182
for alpha = 0.001
Log Loss : 1.0601647505037206
for alpha = 0.01
Log Loss : 1.093890891832136
for alpha = 0.1
Log Loss : 1.2115862539200877
for alpha = 1
Log Loss : 1.413384028448876
for alpha = 10
Log Loss : 1.4552120861811846
for alpha = 100
Log Loss : 1.460117203415138
```



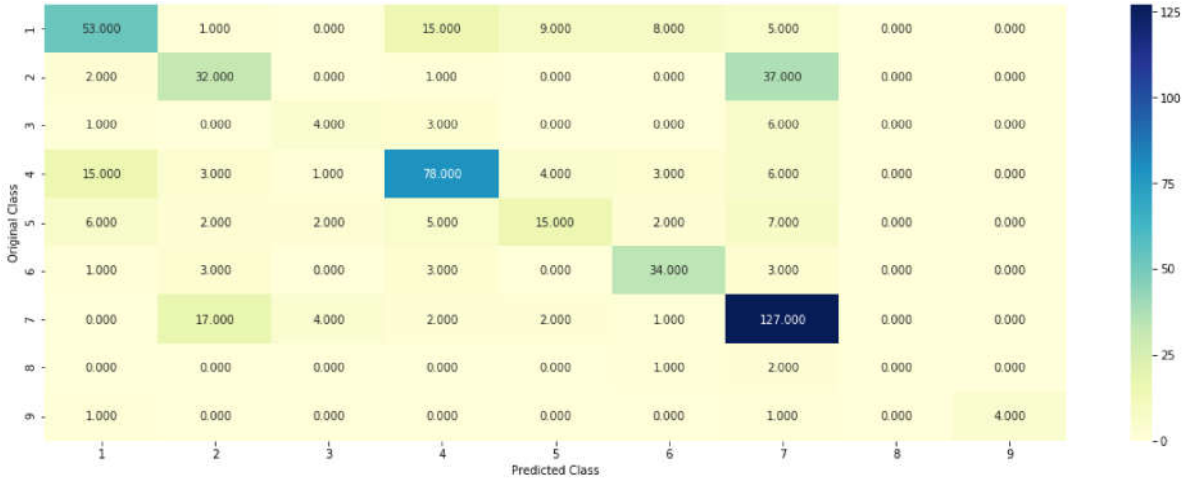

```
For values of best alpha =  0.001 The train log loss is: 0.5215763162424594
For values of best alpha =  0.001 The cross validation log loss is: 1.060164
7505037206
For values of best alpha =  0.001 The test log loss is: 1.0071251506052734
```

4.3.1.2. Testing the model with best hyper paramters

In [69]:

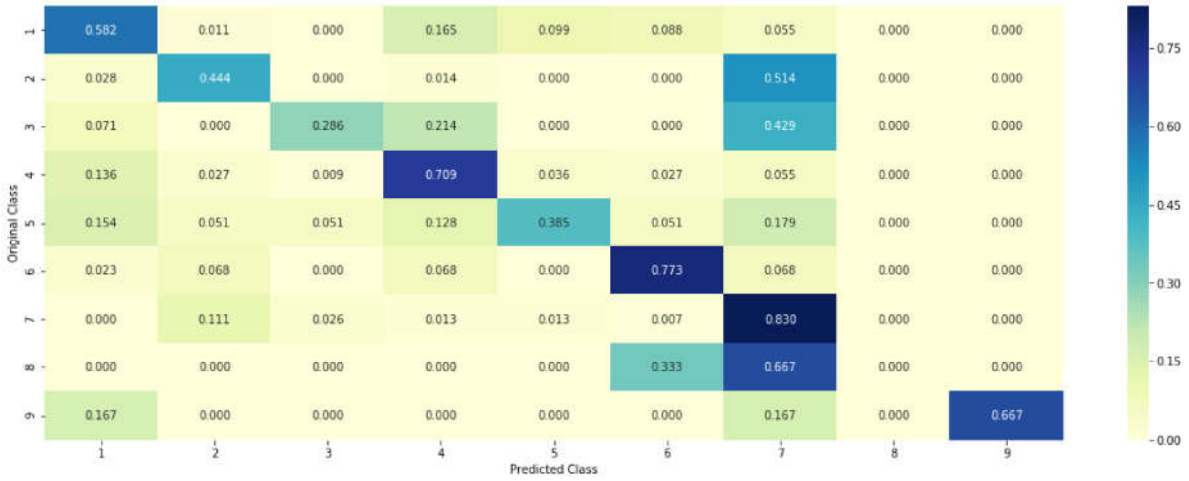
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklea
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,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

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

```
Log loss : 1.0601647505037206
Number of mis-classified points : 0.34774436090225563
-------------------- Confusion matrix --------------------
```




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


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



4.3.1.3. Feature Importance

In [70]:

```
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 [71]:

```
# from tabulate import tabulate
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='l
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[
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'].ilc
```

```
Predicted Class : 5
Predicted Class Probabilities: [[0.0753 0.1092 0.0033 0.0083 0.5285 0.0122
0.2596 0.0015 0.002 ]]
Actual Class : 5
--------------------------------------------------
270 Text feature [figure22] present in test data point [True]
Out of the top  500  features  1 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

In [72]:

```
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[
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'].ilc
```

```
Predicted Class : 4
Predicted Class Probabilities: [[2.400e-03 2.400e-03 4.854e-01 5.001e-01 3.3
00e-03 5.000e-03 8.000e-04
  3.000e-04 3.000e-04]]
Actual Class : 6
--------------------------------------------------
44 Text feature [cys61gly] present in test data point [True]
126 Text feature [fluorescing] present in test data point [True]
129 Text feature [gcuccucucacucuucagu] present in test data point [True]
130 Text feature [jdp] present in test data point [True]
131 Text feature [t37k] present in test data point [True]
132 Text feature [uaaauuuggacauaaggaguccucc] present in test data point [Tru
e]
133 Text feature [dr13] present in test data point [True]
134 Text feature [asterisked] present in test data point [True]
135 Text feature [ay273801] present in test data point [True]
136 Text feature [c27a] present in test data point [True]
137 Text feature [cbas] present in test data point [True]
152 Text feature [pdr] present in test data point [True]
155 Text feature [osu] present in test data point [True]
164 Text feature [dilemma] present in test data point [True]
168 Text feature [decrements] present in test data point [True]
208 Text feature [fourths] present in test data point [True]
230 Text feature [suppressor] present in test data point [True]
232 Text feature [immunoaffinity] present in test data point [True]
300 Text feature [adapted] present in test data point [True]
301 Text feature [nonsense] present in test data point [True]
307 Text feature [magnitudes] present in test data point [True]
335 Text feature [claes] present in test data point [True]
338 Text feature [truncate] present in test data point [True]
363 Text feature [ionizing] present in test data point [True]
377 Text feature [monolayers] present in test data point [True]
392 Text feature [deficiencies] present in test data point [True]
397 Text feature [germline] present in test data point [True]
428 Text feature [302] present in test data point [True]
495 Text feature [neoplasias] present in test data point [True]
Out of the top  500  features  29 are present in query point
```

4.3.2. Without Class balancing

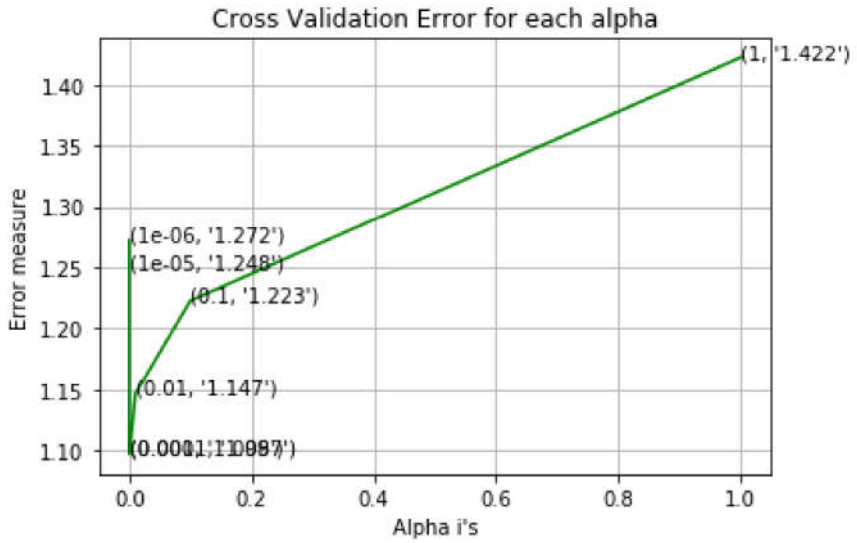
4.3.2.1. Hyper paramter tuning

In [73]:

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

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



# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# ----------------------------
# 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)
    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)
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
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:"
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_
```

```
for alpha = 1e-06
Log Loss : 1.2721582907725741
for alpha = 1e-05
Log Loss : 1.2482753265185487
for alpha = 0.0001
Log Loss : 1.0973509608941066
for alpha = 0.001
Log Loss : 1.0980745627243476
for alpha = 0.01
Log Loss : 1.146519582987
for alpha = 0.1
Log Loss : 1.2226600891460393
for alpha = 1
Log Loss : 1.422323509881528
```



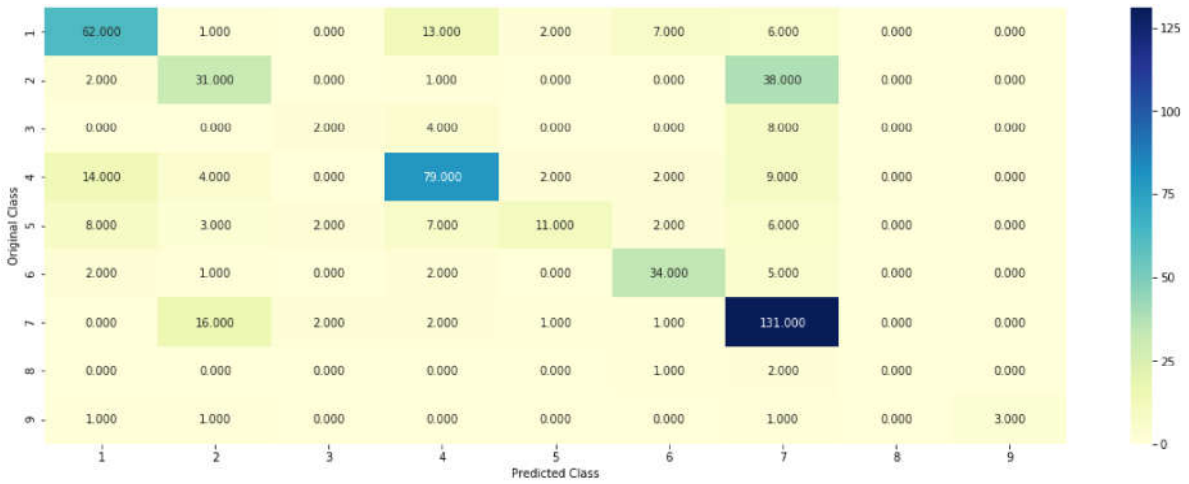

```
For values of best alpha =  0.0001 The train log loss is: 0.516129615400089
For values of best alpha =  0.0001 The cross validation log loss is: 1.09735
09608941066
For values of best alpha =  0.0001 The test log loss is: 1.0187249180666924
```

4.3.2.2. Testing model with best hyper parameters

In [74]:

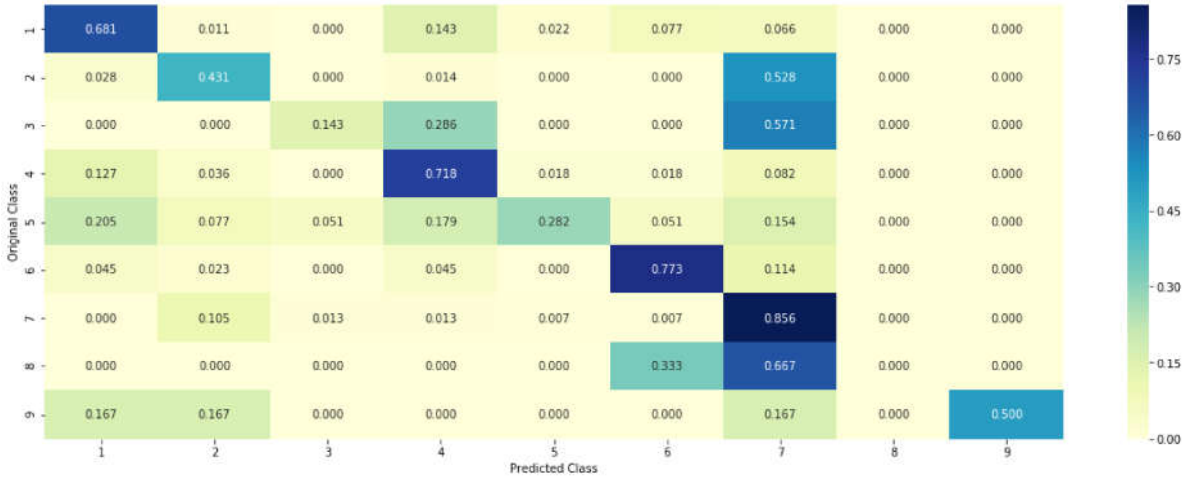
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklea
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,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

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

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

```
Log loss : 1.0973509608941066
Number of mis-classified points : 0.33646616541353386
-------------------- Confusion matrix --------------------
```




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


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



4.3.2.3. Feature Importance, Correctly Classified point

In [75]:

```
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
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[
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'].ilc
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.1321 0.1186 0.0024 0.0142 0.2964 0.0123
0.4204 0.0023 0.0014]]
Actual Class : 5
--------------------------------------------------
239 Text feature [transformation] present in test data point [True]
256 Text feature [activation] present in test data point [True]
274 Text feature [phosphorylation] present in test data point [True]
282 Text feature [downstream] present in test data point [True]
283 Text feature [overexpression] present in test data point [True]
390 Text feature [phospho] present in test data point [True]
473 Text feature [responding] present in test data point [True]
Out of the top  500  features  7 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

In [76]:

```
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[
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'].ilc
```

```
Predicted Class : 4
Predicted Class Probabilities: [[4.700e-03 1.040e-02 3.682e-01 5.998e-01
3.100e-03 3.300e-03 9.300e-03
  9.000e-04 4.000e-04]]
Actual Class : 6
--------------------------------------------------
157 Text feature [cys61gly] present in test data point [True]
164 Text feature [cbas] present in test data point [True]
165 Text feature [c27a] present in test data point [True]
166 Text feature [asterisked] present in test data point [True]
167 Text feature [dr13] present in test data point [True]
168 Text feature [gcuccucucacucuucagu] present in test data point [True]
169 Text feature [t37k] present in test data point [True]
170 Text feature [jdp] present in test data point [True]
171 Text feature [uaaauuuggacauaaggaguccucc] present in test data point [T
rue]
172 Text feature [ay273801] present in test data point [True]
179 Text feature [pdr] present in test data point [True]
186 Text feature [fluorescing] present in test data point [True]
```

4.4. Linear Support Vector Machines

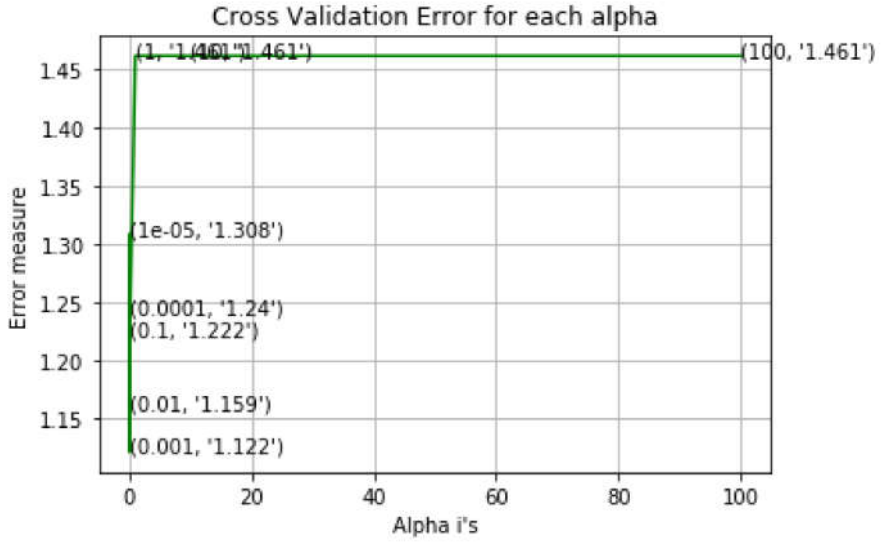
4.4.1. Hyper paramter tuning

In [77]:

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

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

# 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/mathe
# --------------------------------



# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# ----------------------------
# 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', rand
    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='h
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
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:"
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_
```

```
for C = 1e-05
Log Loss : 1.308425202952882
for C = 0.0001
Log Loss : 1.2401831076206464
for C = 0.001
Log Loss : 1.1217251801897135
for C = 0.01
Log Loss : 1.1585454249452924
for C = 0.1
Log Loss : 1.2221690495249855
for C = 1
Log Loss : 1.4611226682070682
for C = 10
Log Loss : 1.4610616839040127
for C = 100
Log Loss : 1.4610609215510388
```



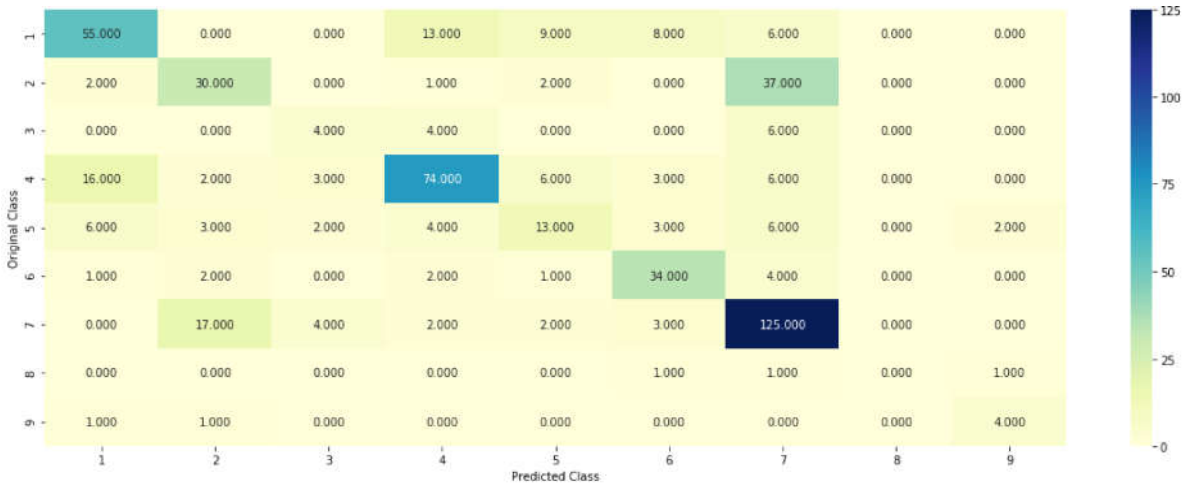

```
For values of best alpha =  0.001 The train log loss is: 0.5671580307946241
For values of best alpha =  0.001 The cross validation log loss is: 1.121725
1801897135
For values of best alpha =  0.001 The test log loss is: 1.034955350080306
```

4.4.2. Testing model with best hyper parameters

In [78]:

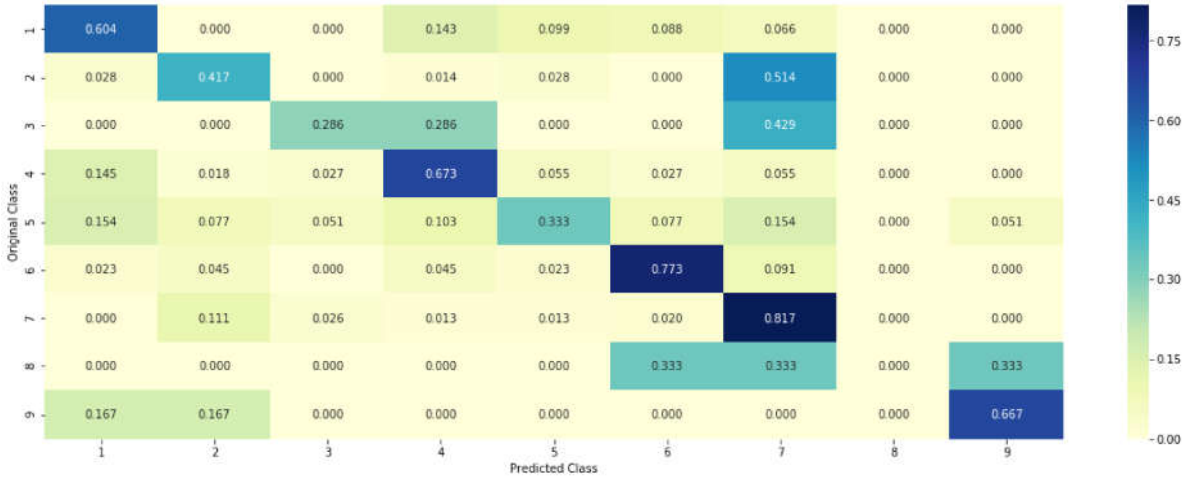
```
# read more about support vector machines with linear kernals here http://scikit-learn.org/

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

# 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/mathe
# --------------------------------


# 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,cl
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf
```

```
Log loss : 1.1217251801897135
Number of mis-classified points : 0.36278195488721804
-------------------- 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 [79]:

```
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[
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'].ilc
```

```
Predicted Class : 5
Predicted Class Probabilities: [[0.099  0.1166 0.0127 0.078  0.5022 0.0277
0.1522 0.003  0.0086]]
Actual Class : 5
--------------------------------------------------
297 Text feature [figure22] present in test data point [True]
307 Text feature [outcomes] present in test data point [True]
442 Text feature [limitations] present in test data point [True]
Out of the top  500  features  3 are present in query point
```

4.3.3.2. For Incorrectly classified point

In [80]:

```
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[
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'].ilc
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.0156 0.02   0.4597 0.4739 0.0022 0.0033
0.0201 0.0015 0.0036]]
Actual Class : 6
--------------------------------------------------
134 Text feature [c27a] present in test data point [True]
135 Text feature [cbas] present in test data point [True]
136 Text feature [t37k] present in test data point [True]
137 Text feature [ay273801] present in test data point [True]
138 Text feature [gcuccucucacucuucagu] present in test data point [True]
139 Text feature [uaaauuuggacauaaggaguccucc] present in test data point [Tru
e]
140 Text feature [asterisked] present in test data point [True]
141 Text feature [jdp] present in test data point [True]
142 Text feature [dr13] present in test data point [True]
144 Text feature [pdr] present in test data point [True]
156 Text feature [dilemma] present in test data point [True]
160 Text feature [fluorescing] present in test data point [True]
162 Text feature [decrements] present in test data point [True]
168 Text feature [fourths] present in test data point [True]
209 Text feature [osu] present in test data point [True]
211 Text feature [magnitudes] present in test data point [True]
218 Text feature [cys61gly] present in test data point [True]
257 Text feature [adapted] present in test data point [True]
298 Text feature [immunoaffinity] present in test data point [True]
311 Text feature [i21v] present in test data point [True]
399 Text feature [recombined] present in test data point [True]
410 Text feature [302] present in test data point [True]
443 Text feature [ionizing] present in test data point [True]
444 Text feature [1292] present in test data point [True]
452 Text feature [monolayers] present in test data point [True]
453 Text feature [guiding] present in test data point [True]
484 Text feature [798] present in test data point [True]
Out of the top  500  features  27 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

In [81]:

```
# ------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# 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/rando
# ------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# ----------------------------
# 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_
        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
        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_a
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_d
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:"
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross validation lo
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:",
```

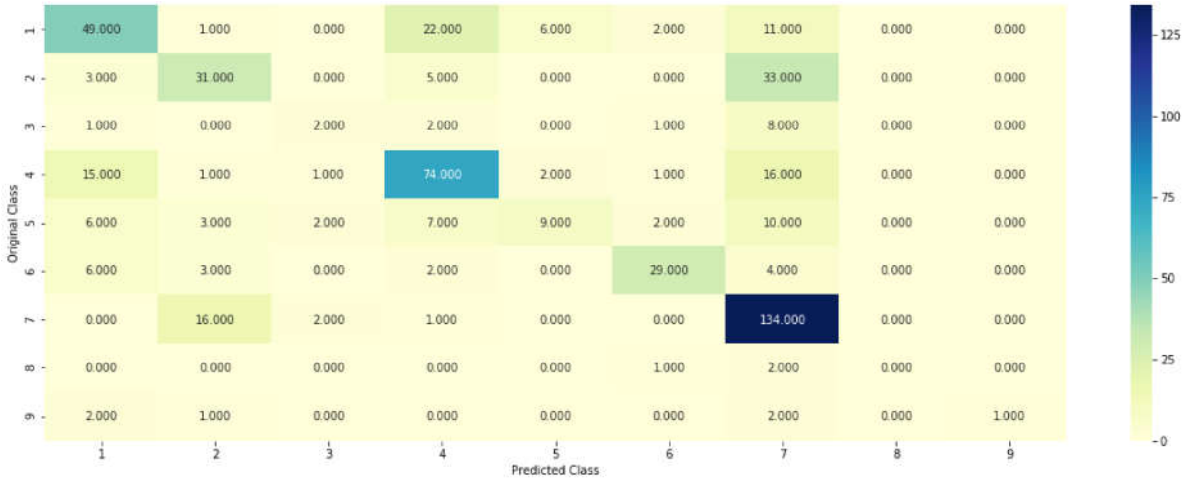
```
for n_estimators = 100 and max depth =  5
Log Loss : 1.1927150731927265
for n_estimators = 100 and max depth =  10
Log Loss : 1.167893323525949
for n_estimators = 200 and max depth =  5
Log Loss : 1.1809069441947004
for n_estimators = 200 and max depth =  10
Log Loss : 1.1506606079557182
for n_estimators = 500 and max depth =  5
Log Loss : 1.1664947074027054
for n_estimators = 500 and max depth =  10
Log Loss : 1.1446997931033098
for n_estimators = 1000 and max depth =  5
Log Loss : 1.171247356853659
for n_estimators = 1000 and max depth =  10
Log Loss : 1.1451307725487907
for n_estimators = 2000 and max depth =  5
Log Loss : 1.169172266154061
for n_estimators = 2000 and max depth =  10
Log Loss : 1.1455971669668354
For values of best estimator =  500 The train log loss is: 0.650748846844593
7
For values of best estimator =  500 The cross validation log loss is: 1.1446
997931033096
For values of best estimator =  500 The test log loss is: 1.154552185659132
```

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

In [82]:

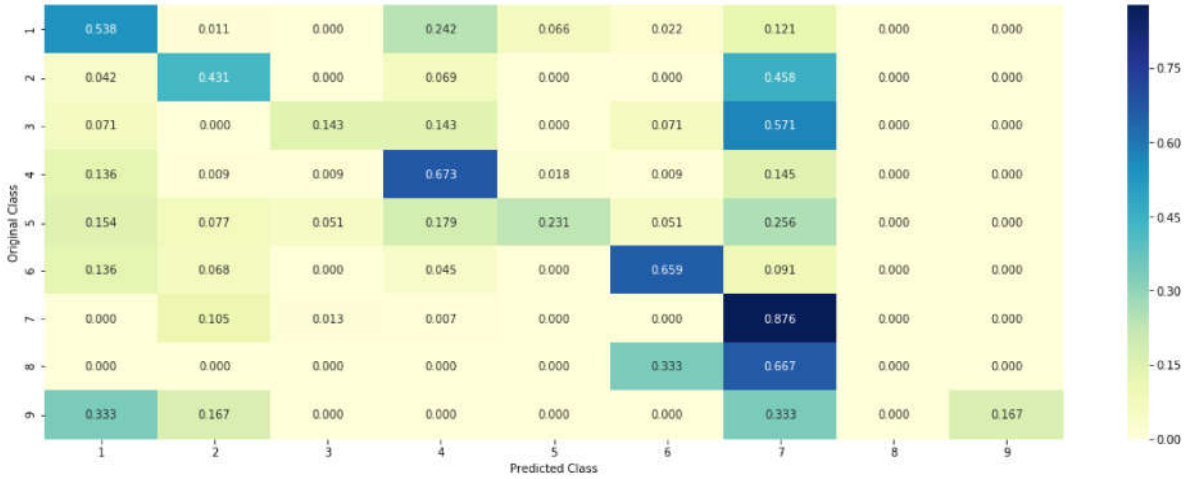
```
# ------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# 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/rando
# ------------------------------

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

```
Log loss : 1.1446997931033098
Number of mis-classified points : 0.3815789473684211
-------------------- 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 [83]:

```
# test_point_index = 10
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_c
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[
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['
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.1159 0.1735 0.0195 0.0716 0.1946 0.0582
0.3529 0.0051 0.0088]]
Actual Class : 5
--------------------------------------------------
0 Text feature [kinase] present in test data point [True]
1 Text feature [activation] present in test data point [True]
2 Text feature [inhibitor] present in test data point [True]
3 Text feature [inhibitors] present in test data point [True]
6 Text feature [phosphorylation] present in test data point [True]
7 Text feature [tyrosine] present in test data point [True]
8 Text feature [treatment] present in test data point [True]
9 Text feature [activating] present in test data point [True]
10 Text feature [missense] present in test data point [True]
11 Text feature [oncogenic] present in test data point [True]
15 Text feature [resistance] present in test data point [True]
17 Text feature [signaling] present in test data point [True]
18 Text feature [function] present in test data point [True]
20 Text feature [growth] present in test data point [True]
21 Text feature [therapy] present in test data point [True]
22 Text feature [extracellular] present in test data point [True]
23 Text feature [drug] present in test data point [True]
27 Text feature [phospho] present in test data point [True]
28 Text feature [transforming] present in test data point [True]
29 Text feature [loss] present in test data point [True]
32 Text feature [receptor] present in test data point [True]
34 Text feature [cells] present in test data point [True]
35 Text feature [therapeutic] present in test data point [True]
36 Text feature [advanced] present in test data point [True]
37 Text feature [efficacy] present in test data point [True]
38 Text feature [downstream] present in test data point [True]
39 Text feature [cell] present in test data point [True]
40 Text feature [trials] present in test data point [True]
46 Text feature [pathogenic] present in test data point [True]
48 Text feature [variants] present in test data point [True]
51 Text feature [functional] present in test data point [True]
52 Text feature [effective] present in test data point [True]
53 Text feature [stability] present in test data point [True]
55 Text feature [lines] present in test data point [True]
57 Text feature [harboring] present in test data point [True]
58 Text feature [kinases] present in test data point [True]
59 Text feature [clinical] present in test data point [True]
```

```
61 Text feature [phosphorylated] present in test data point [True]
64 Text feature [protein] present in test data point [True]
65 Text feature [inactivation] present in test data point [True]
66 Text feature [variant] present in test data point [True]
69 Text feature [tkis] present in test data point [True]
71 Text feature [proliferation] present in test data point [True]
72 Text feature [expressing] present in test data point [True]
73 Text feature [amplification] present in test data point [True]
77 Text feature [likely] present in test data point [True]
82 Text feature [responses] present in test data point [True]
84 Text feature [assay] present in test data point [True]
86 Text feature [potential] present in test data point [True]
87 Text feature [sensitivity] present in test data point [True]
95 Text feature [ring] present in test data point [True]
97 Text feature [functions] present in test data point [True]
Out of the top  100  features  52 are present in query point
```

4.5.3.2. Inorrectly Classified point

In [84]:

```
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[
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['
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.1136 0.0387 0.2864 0.3797 0.0754 0.0685
0.026  0.0046 0.0071]]
Actuall Class : 6
--------------------------------------------------
1 Text feature [activation] present in test data point [True]
4 Text feature [suppressor] present in test data point [True]
10 Text feature [missense] present in test data point [True]
14 Text feature [nonsense] present in test data point [True]
15 Text feature [resistance] present in test data point [True]
18 Text feature [function] present in test data point [True]
24 Text feature [treated] present in test data point [True]
28 Text feature [transforming] present in test data point [True]
29 Text feature [loss] present in test data point [True]
32 Text feature [receptor] present in test data point [True]
33 Text feature [brca1] present in test data point [True]
34 Text feature [cells] present in test data point [True]
38 Text feature [downstream] present in test data point [True]
39 Text feature [cell] present in test data point [True]
46 Text feature [pathogenic] present in test data point [True]
48 Text feature [variants] present in test data point [True]
49 Text feature [classify] present in test data point [True]
51 Text feature [functional] present in test data point [True]
55 Text feature [lines] present in test data point [True]
59 Text feature [clinical] present in test data point [True]
64 Text feature [protein] present in test data point [True]
66 Text feature [variant] present in test data point [True]
70 Text feature [frameshift] present in test data point [True]
72 Text feature [expressing] present in test data point [True]
74 Text feature [mutants] present in test data point [True]
75 Text feature [patients] present in test data point [True]
76 Text feature [factor] present in test data point [True]
77 Text feature [likely] present in test data point [True]
79 Text feature [membranes] present in test data point [True]
80 Text feature [deleterious] present in test data point [True]
81 Text feature [defective] present in test data point [True]
84 Text feature [assay] present in test data point [True]
86 Text feature [potential] present in test data point [True]
89 Text feature [database] present in test data point [True]
95 Text feature [ring] present in test data point [True]
96 Text feature [patient] present in test data point [True]
97 Text feature [functions] present in test data point [True]
98 Text feature [resistant] present in test data point [True]
Out of the top  100  features  38 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

In [85]:

```
# ------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# 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/rando
# ------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# ----------------------------
# 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_
        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
        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_a
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_d
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
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The cross validation log lo
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_
```

```
for n_estimators = 10 and max depth =  2
Log Loss : 1.9486622409397882
for n_estimators = 10 and max depth =  3
Log Loss : 1.4907936910889927
for n_estimators = 10 and max depth =  5
Log Loss : 1.5852770855785963
for n_estimators = 10 and max depth =  10
Log Loss : 1.6793600896699592
for n_estimators = 50 and max depth =  2
Log Loss : 1.7281234592499115
for n_estimators = 50 and max depth =  3
Log Loss : 1.3754404025704692
for n_estimators = 50 and max depth =  5
Log Loss : 1.3450240748584454
for n_estimators = 50 and max depth =  10
Log Loss : 1.5806884017329255
for n_estimators = 100 and max depth =  2
Log Loss : 1.6188344722355248
for n_estimators = 100 and max depth =  3
Log Loss : 1.42605906849819
for n_estimators = 100 and max depth =  5
Log Loss : 1.3071470065512318
for n_estimators = 100 and max depth =  10
Log Loss : 1.5962872636991463
for n_estimators = 200 and max depth =  2
Log Loss : 1.6397260550043664
for n_estimators = 200 and max depth =  3
Log Loss : 1.4200257625767485
for n_estimators = 200 and max depth =  5
Log Loss : 1.308526547861796
for n_estimators = 200 and max depth =  10
Log Loss : 1.6541913031563706
for n_estimators = 500 and max depth =  2
Log Loss : 1.6591453540682177
for n_estimators = 500 and max depth =  3
Log Loss : 1.5050668971902854
for n_estimators = 500 and max depth =  5
Log Loss : 1.3306255586784295
for n_estimators = 500 and max depth =  10
Log Loss : 1.680413522370788
for n_estimators = 1000 and max depth =  2
Log Loss : 1.610037876760534
for n_estimators = 1000 and max depth =  3
Log Loss : 1.4734393642535262
for n_estimators = 1000 and max depth =  5
Log Loss : 1.3218422287061997
```

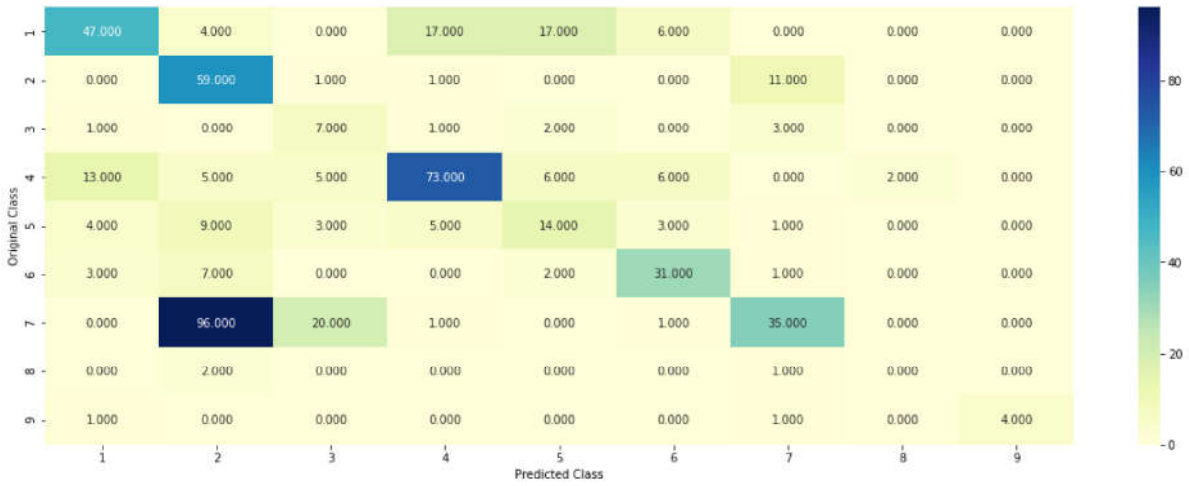
```
for n_estimators = 1000 and max depth =  10
Log Loss : 1.648580122707394
For values of best alpha =  100 The train log loss is: 0.06425748890616
For values of best alpha =  100 The cross validation log loss is: 1.30714700
65512318
For values of best alpha =  100 The test log loss is: 1.317529213672818
```

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

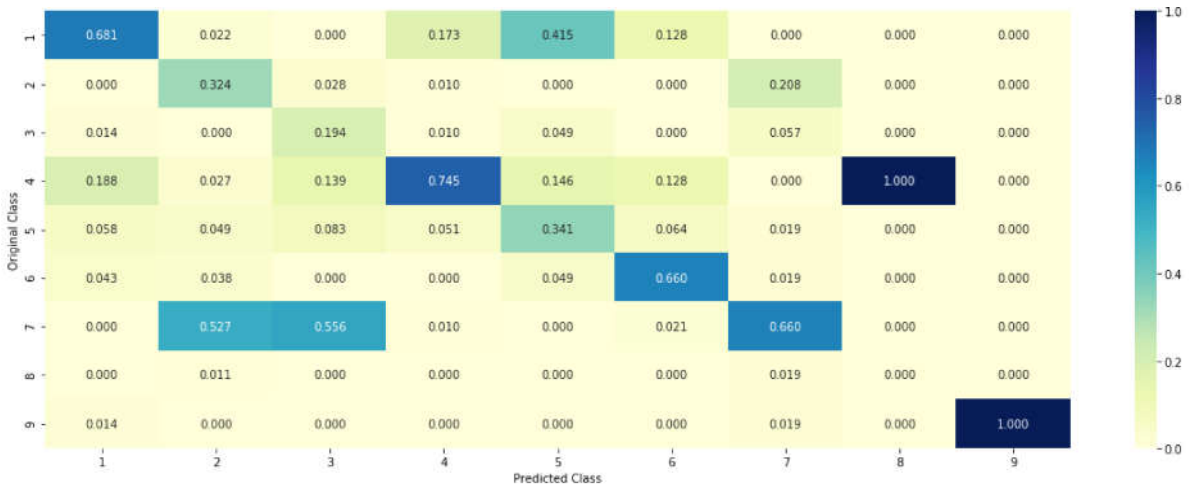
In [86]:

```
# ------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# 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/rando
# ------------------------------

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

```
Log loss : 1.3071470065512318
Number of mis-classified points : 0.4924812030075188
-------------------- 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 [87]:

```
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gini', max_c
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_responseCodir
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: [[0.0163 0.4061 0.1024 0.0239 0.0863 0.0516
0.2856 0.0137 0.014 ]]
Actual Class : 5
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation 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
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Gene is important feature
Text 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 [88]:

```
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_responseCodir
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 : 5
Predicted Class Probabilities: [[0.0449 0.0065 0.2397 0.0818 0.4828 0.1291
0.0041 0.0046 0.0065]]
Actual Class : 6
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation 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
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Gene is important feature
Text 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 [89]:

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

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


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

# 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/mathe
# ---------------------------------


# read more about support vector machines with linear kernals here http://scikit-learn.org/
# ---------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# 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/rando
# ---------------------------------


clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class_weight='balanced', random
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_s
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_
sig_clf2.fit(train_x_onehotCoding, train_y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf2.predict_proba(
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_onehotC
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=l
    sclf.fit(train_x_onehotCoding, train_y)
    print("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" % (i, log_loss(
    log_error =log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    if best_alpha > log_error:
        best_alpha = log_error
```

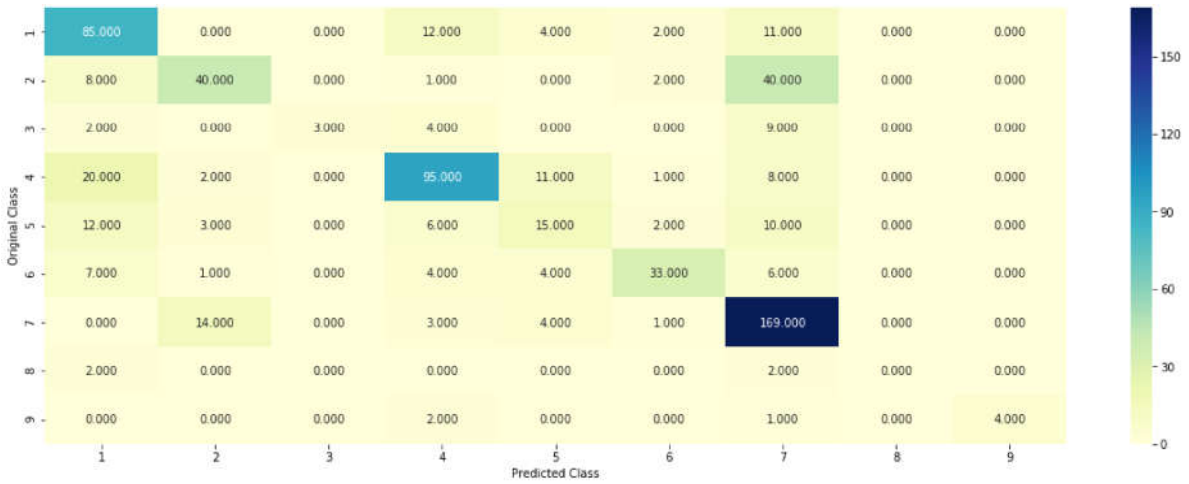
```
Logistic Regression :  Log Loss: 1.06
Support vector machines : Log Loss: 1.46
Naive Bayes : Log Loss: 1.25
--------------------------------------------------
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 2.177
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 2.030
Stacking Classifer : for the value of alpha: 0.010000 Log Loss: 1.489
Stacking Classifer : for the value of alpha: 0.100000 Log Loss: 1.119
Stacking Classifer : for the value of alpha: 1.000000 Log Loss: 1.235
Stacking Classifer : for the value of alpha: 10.000000 Log Loss: 1.566
```

4.7.2 testing the model with the best hyper parameters

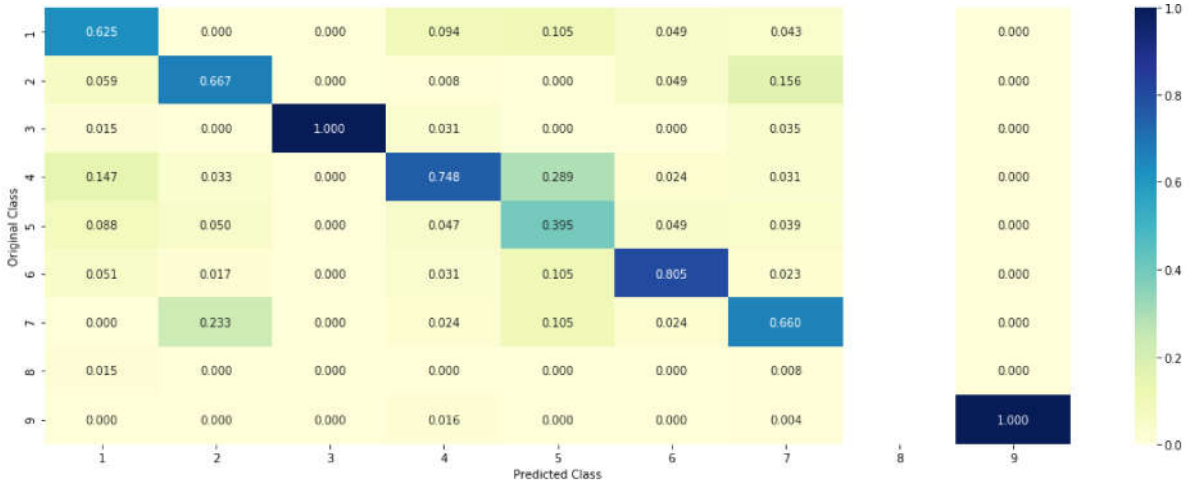
In [90]:

```
lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=lr, u
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_onehotCodir
plot_confusion_matrix(test_y=test_y, predict_y=sclf.predict(test_x_onehotCoding))
```

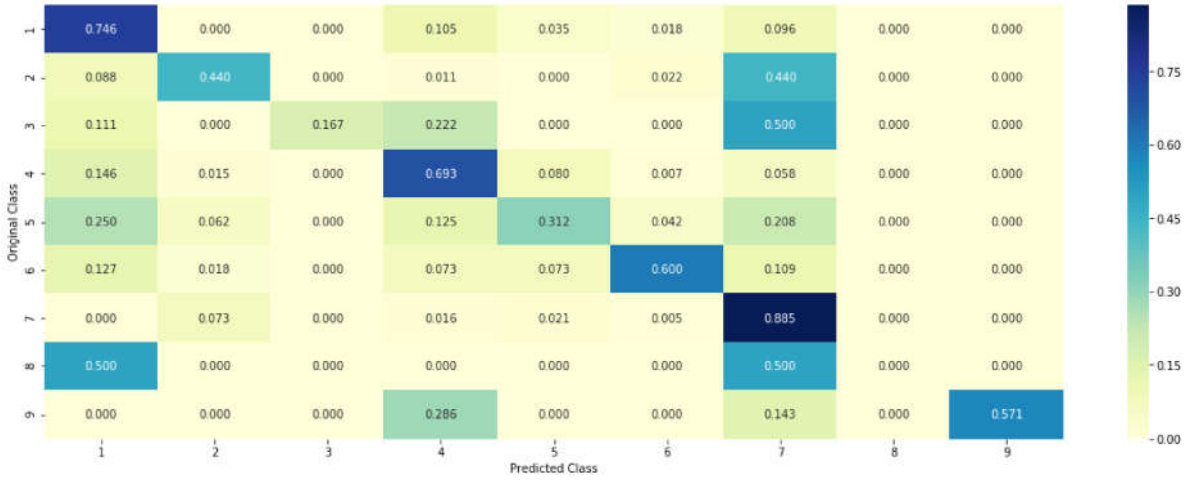
```
Log loss (train) on the stacking classifier : 0.610040141357214
Log loss (CV) on the stacking classifier : 1.1191471782009077
Log loss (test) on the stacking classifier : 1.084215456193397
Number of missclassified point : 0.3323308270676692
-------------------- Confusion matrix --------------------
```




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




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

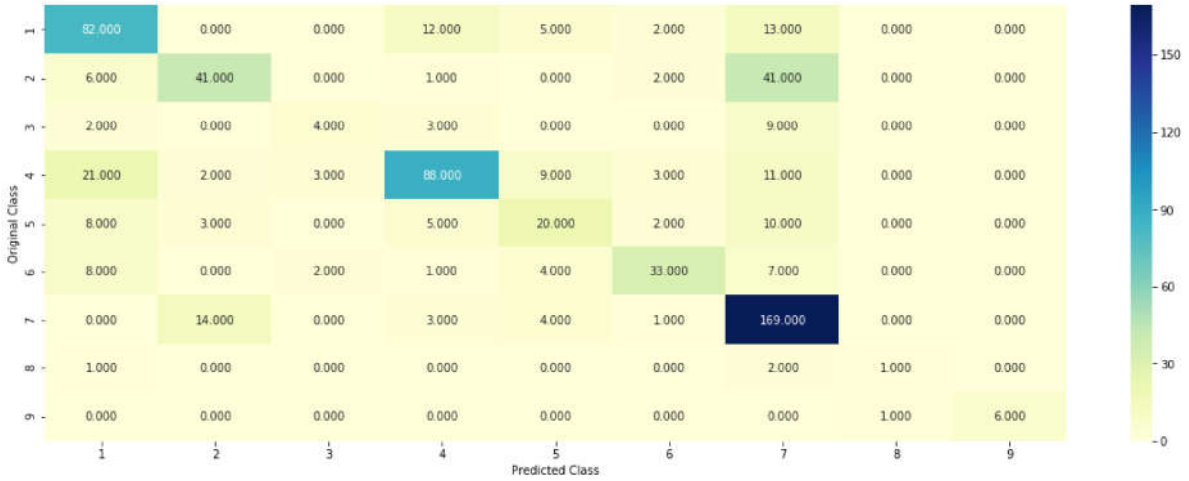


4.7.3 Maximum Voting classifier

In [91]:

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

```
Log loss (train) on the VotingClassifier : 0.8282366920273875
Log loss (CV) on the VotingClassifier : 1.1263915231839183
Log loss (test) on the VotingClassifier : 1.1143193824417803
Number of missclassified point : 0.3323308270676692
-------------------- Confusion matrix --------------------
```




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


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

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

In [92]:

```
#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 [93]:

```
# one-hot encoding of Gene feature.
gene_vectorizer = CountVectorizer(ngram_range=(1, 2))
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'])

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

Variation Feature

In [94]:

```
# alpha is used for laplace smoothing
alpha = 1

# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train_

# 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 [95]:

```
# one-hot encoding of variation feature.
variation_vectorizer = CountVectorizer(ngram_range=(1, 2))
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variati
test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])


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

Text Feature

In [96]:

```


# 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 = 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 o
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 occu
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 : 776987
```

In [97]:

```
#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)

# 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
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_re
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_response
```

In [98]:

```
# 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)
```

Stack above three features

In [99]:

```
# 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_featu
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehot

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

test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_feature_onehotCoding)).
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_variatic
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_f
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_respc
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_response
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding
```

In [100]:

```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCoding
print("(number of data points * number of features) in test data = ", test_x_onehotCoding.s
print("(number of data points * number of features) in cross validation data =", cv_x_oneho
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 779288)
(number of data points * number of features) in test data =  (665, 779288)
(number of data points * number of features) in cross validation data = (53
2, 779288)
```

In [101]:

```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_responseCodi
print("(number of data points * number of features) in test data = ", test_x_responseCoding
print("(number of data points * number of features) in cross validation data =", cv_x_respc
```

```
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 27)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data = (53
2, 27)
```

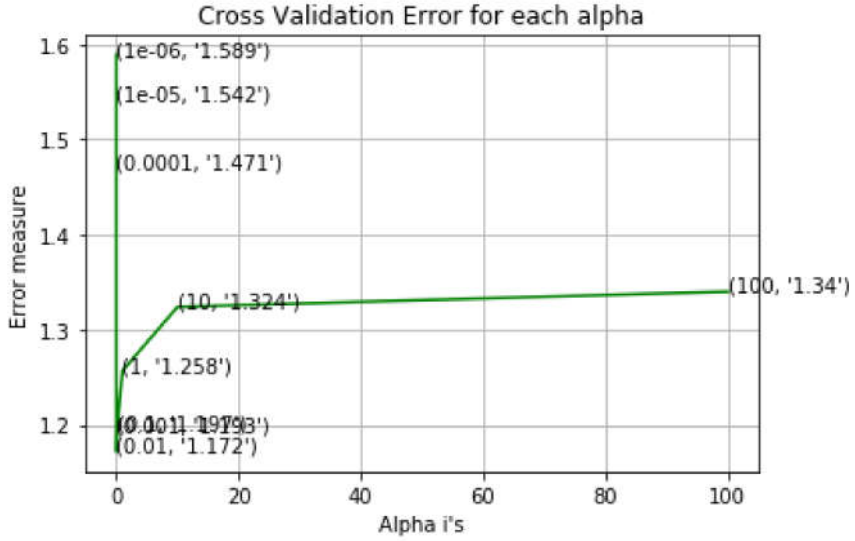
Logistic Regression

In [102]:

```
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_
    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 estimat
    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='l
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_y, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.5888878065123857
for alpha = 1e-05
Log Loss : 1.5423532119912036
for alpha = 0.0001
Log Loss : 1.4709323256653155
for alpha = 0.001
Log Loss : 1.1933233102008804
for alpha = 0.01
Log Loss : 1.1719492128354452
for alpha = 0.1
Log Loss : 1.1966895193122504
for alpha = 1
Log Loss : 1.2576540959113942
```

```
for alpha = 10
Log Loss : 1.3242734239822405
for alpha = 100
Log Loss : 1.3402567752899845
```



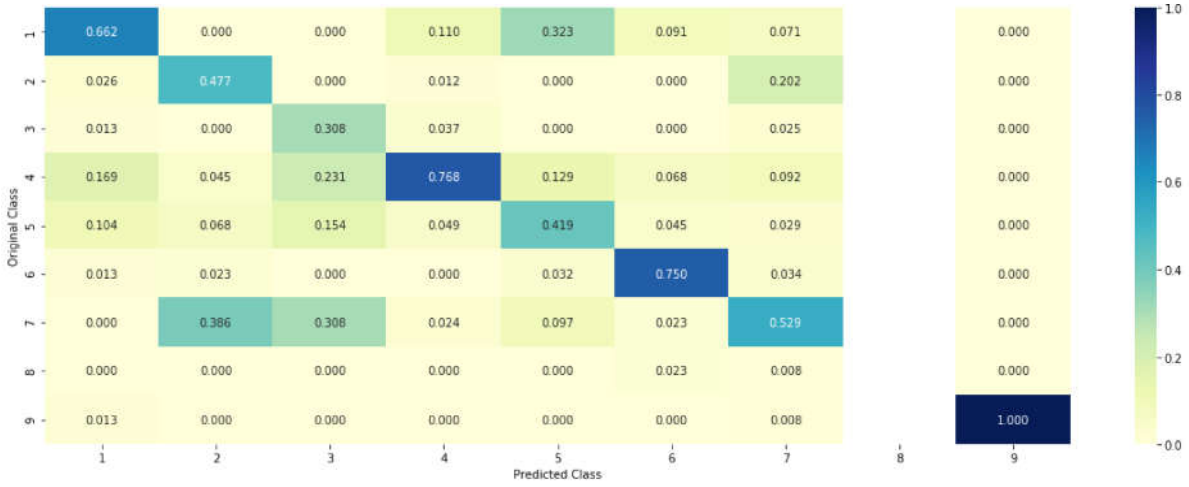

```
For values of best alpha =  0.01 The train log loss is: 0.7162500668498496
For values of best alpha =  0.01 The cross validation log loss is: 1.1719492
128354452
For values of best alpha =  0.01 The test log loss is: 1.1339179938706174
```

In [103]:

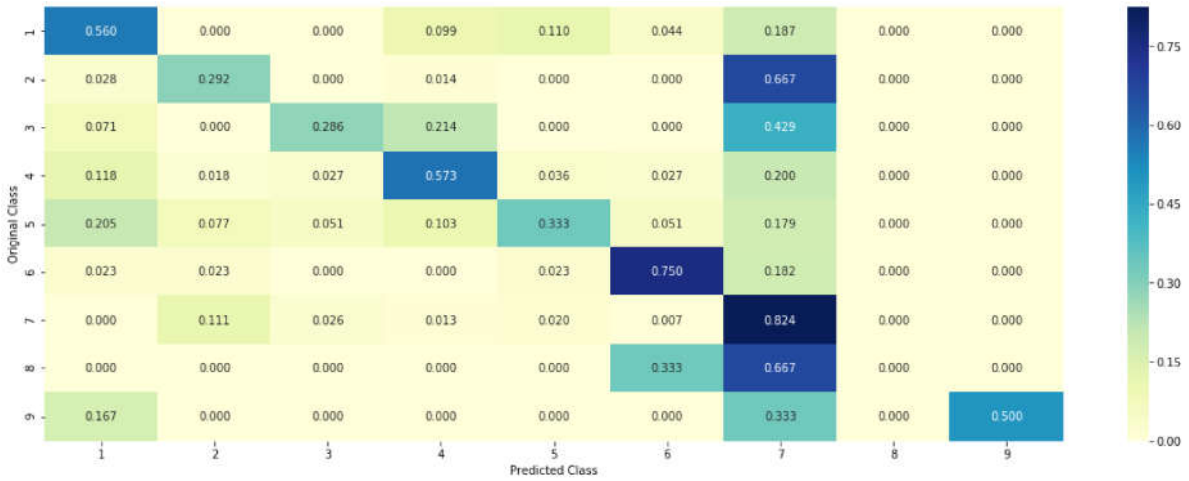
```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='l
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, c
```

```
Log loss : 1.1719492128354452
Number of mis-classified points : 0.40977443609022557
-------------------- Confusion matrix --------------------
```


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




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



Still model does not decreases log loss values after using unigram and bigram features

Apply Logistic regression with CountVectorizer Features, including both unigrams and Quatergrams

Gene features

In [108]:

```
#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 [109]:

```

# one-hot encoding of Gene feature.
gene_vectorizer = CountVectorizer(ngram_range=(1, 4))
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'])

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

Variation Feature

In [110]:

```
# alpha is used for laplace smoothing
alpha = 1

# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train_

# 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 [111]:

```
# one-hot encoding of variation feature.
variation_vectorizer = CountVectorizer(ngram_range=(1, 4))
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variati
test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])


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

Text Feature

In [114]:

```
# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer = CountVectorizer(min_df=3,ngram_range=(1, 4))
train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])

# getting all the feature names (words)
# getting top 2000 feature names (words)
#train_text_features = top_mean_feats(train_text_feature_onehotCoding,
                                                #text_vectorizer.get_feature_names(),
                                                #top_n=2000)['feature'].tolist()
train_text_features= text_vectorizer.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*number o
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 occu
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 : 2968930
```

In [115]:

```
#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)

# 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
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_re
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_response
```

In [116]:

```
# 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)
```

Stack above three features

In [118]:

```
# 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_featu
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehot

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

test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_feature_onehotCoding)).
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_variatic
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_f
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_respo
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_response
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding
```

In [119]:

```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCoding
print("(number of data points * number of features) in test data = ", test_x_onehotCoding.s
print("(number of data points * number of features) in cross validation data =", cv_x_oneho
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 297121
7)
(number of data points * number of features) in test data =  (665, 2971217)
(number of data points * number of features) in cross validation data = (53
2, 2971217)
```

In [120]:

```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_responseCodi
print("(number of data points * number of features) in test data = ", test_x_responseCoding
print("(number of data points * number of features) in cross validation data =", cv_x_respo
```

```
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 27)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data = (53
2, 27)
```

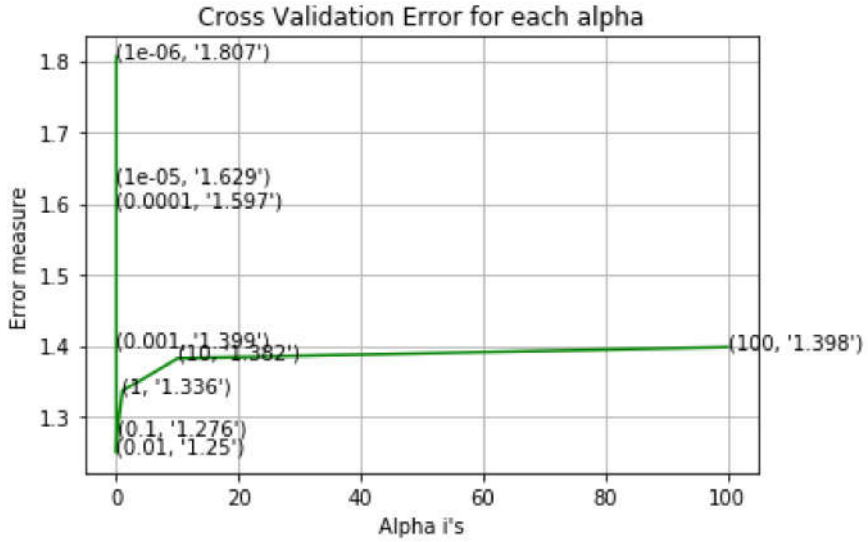
Logistic Regression

In [121]:

```
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_
    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 estimat
    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='l
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_y, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.8066316539448797
for alpha = 1e-05
Log Loss : 1.6294875917407785
for alpha = 0.0001
Log Loss : 1.5972869998570707
for alpha = 0.001
Log Loss : 1.3986384646613301
for alpha = 0.01
Log Loss : 1.2497237169616435
for alpha = 0.1
Log Loss : 1.276333987473048
for alpha = 1
```

```
Log Loss : 1.3362297460847055
for alpha = 10
Log Loss : 1.3823747150482502
for alpha = 100
Log Loss : 1.3981015542348065
```




```
For values of best alpha =  0.01 The train log loss is: 0.7771611922961507
For values of best alpha =  0.01 The cross validation log loss is: 1.2497237
169616435
For values of best alpha =  0.01 The test log loss is: 1.2784499657581352
```

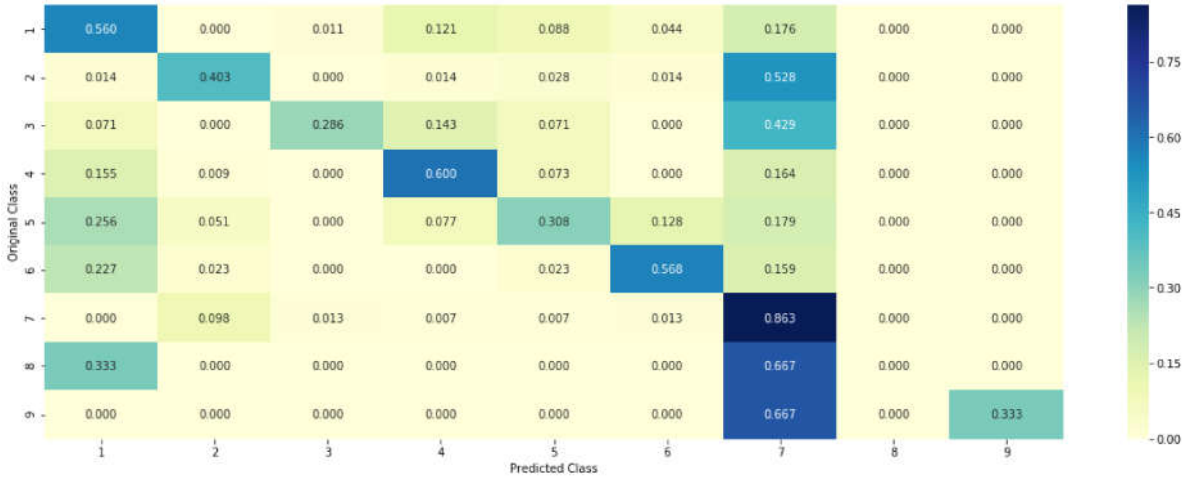
In [122]:

```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='l
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, c
```

```
Log loss : 1.2497237169616435
Number of mis-classified points : 0.3966165413533835
-------------------- Confusion matrix --------------------
```


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


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



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

Lets merge gene and variation data into one list and apply TFidfVectorizer on top of it.

Gene Feature

In [123]:

```
result = pd.merge(data, data_text,on='ID', how='left')
result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Variation']
y_true = result['Class'].values
result.Gene = result.Gene.str.replace('\s+', '_')
result.Variation = result.Variation.str.replace('\s+', '_')

x_train, test_df, y_train, y_test = train_test_split(result, y_true, stratify=y_true, test_

train_df, cv_df, y_train, y_cv = train_test_split(x_train, y_train, stratify=y_train, test_
```

In [124]:

```
# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
    value_count = train_df[feature].value_counts()
    gv_dict = dict()
    for i, denominator in value_count.items():
        vec = []
        for k in range(1,10):
            cls_cnt = train_df.loc[(train_df['Class']==k) & (train_df[feature]==i)]
            vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
        gv_dict[i]=vec
    return gv_dict

# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
    gv_dict = get_gv_fea_dict(alpha, feature, df)
    value_count = train_df[feature].value_counts()
    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])
    return gv_fea
```

In [125]:

```
#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 [126]:

```
# one-hot encoding of Gene feature.
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'])
```

Variation Feature

In [127]:

```
# alpha is used for laplace smoothing
alpha = 1

# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train_

# 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 [128]:

```
# one-hot encoding of variation feature.
variation_vectorizer = TfidfVectorizer()
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variati
test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])
```

Text Feature

In [129]:

```
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


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
            text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TEXT'].s
            row_index += 1
    return text_feature_responseCoding
```

In [130]:

```
# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer = TfidfVectorizer()
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 o
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 occu
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 : 125275
```

In [131]:

```
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)
```

In [132]:

```
#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)

# 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
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_re
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_response
```

In [133]:

```
test_text_feature_onehotCoding = text_vectorizer.transform(test_df['TEXT'])
cv_text_feature_onehotCoding = text_vectorizer.transform(cv_df['TEXT'])
```

Features after feature engineering

In [134]:

```
# Collecting all the genes and variations data into a single list
gene_variation = []

for gene in data['Gene'].values:
    gene_variation.append(gene)

for variation in data['Variation'].values:
    gene_variation.append(variation)
```

In [135]:

```
tfidfVectorizer = TfidfVectorizer(max_features=1000)
text2 = tfidfVectorizer.fit_transform(gene_variation)
gene_variation_features = tfidfVectorizer.get_feature_names()

train_text = tfidfVectorizer.transform(train_df['TEXT'])
test_text = tfidfVectorizer.transform(test_df['TEXT'])
cv_text = tfidfVectorizer.transform(cv_df['TEXT'])
```

Stack above three features

In [136]:

```
train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,train_variation_featu
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehot

# Adding the train_text feature
train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text))
train_x_onehotCoding = hstack((train_x_onehotCoding, train_text_feature_onehotCoding)).tocs
train_y = np.array(list(train_df['Class']))

# Adding the test_text feature
test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text))
test_x_onehotCoding = hstack((test_x_onehotCoding, test_text_feature_onehotCoding)).tocsr()
test_y = np.array(list(test_df['Class']))

# Adding the cv_text feature
cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text))
cv_x_onehotCoding = hstack((cv_x_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_variatic
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_f
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_respo
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_response
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding
```

In [137]:

```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCoding
print("(number of data points * number of features) in test data = ", test_x_onehotCoding.s
print("(number of data points * number of features) in cross validation data =", cv_x_oneho
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 128461)
(number of data points * number of features) in test data =  (665, 128461)
(number of data points * number of features) in cross validation data = (53
2, 128461)
```

In [138]:

```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_responseCodi
print("(number of data points * number of features) in test data = ", test_x_responseCoding
print("(number of data points * number of features) in cross validation data =", cv_x_respo
```

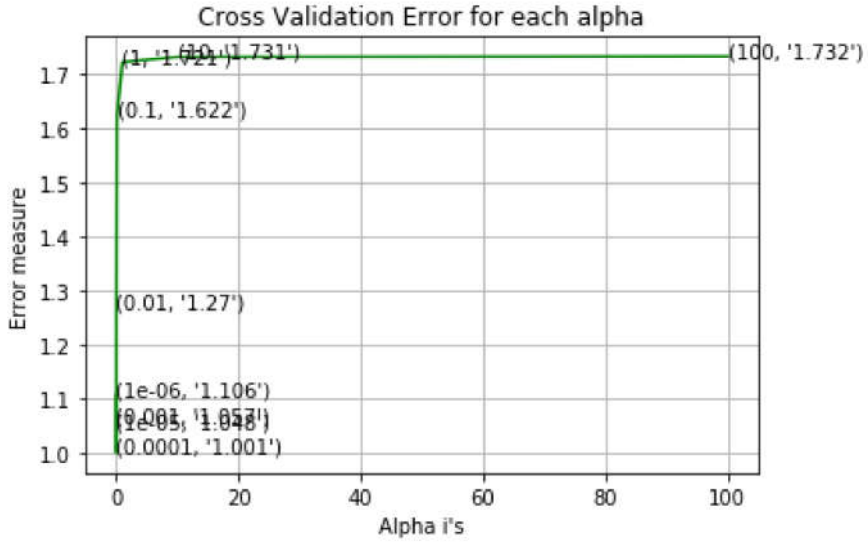
```
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 27)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data = (53
2, 27)
```

In [139]:

```
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_
    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 estimat
    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='l
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_y, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.105527446324402
for alpha = 1e-05
Log Loss : 1.0477104228840888
for alpha = 0.0001
Log Loss : 1.0011576044702446
for alpha = 0.001
Log Loss : 1.0573274038173124
for alpha = 0.01
Log Loss : 1.2699878622635565
for alpha = 0.1
Log Loss : 1.62245317287363
for alpha = 1
```

```
Log Loss : 1.7205552001995568
for alpha = 10
Log Loss : 1.7307834952612375
for alpha = 100
Log Loss : 1.7318319240228155
```

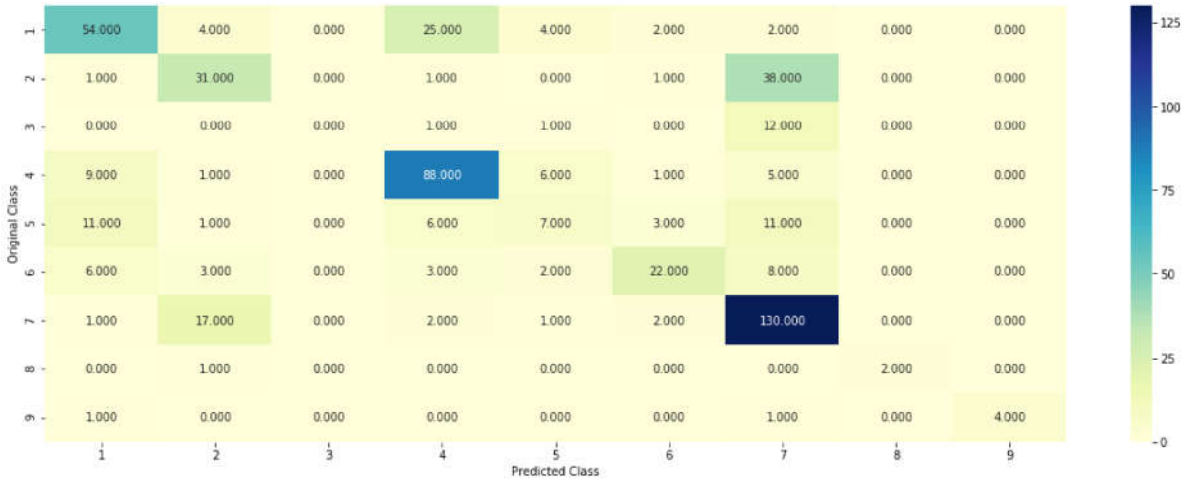



```
For values of best alpha =  0.0001 The train log loss is: 0.4375377376630504
3
For values of best alpha =  0.0001 The cross validation log loss is: 1.00115
76044702446
For values of best alpha =  0.0001 The test log loss is: 1.002581386661197
```

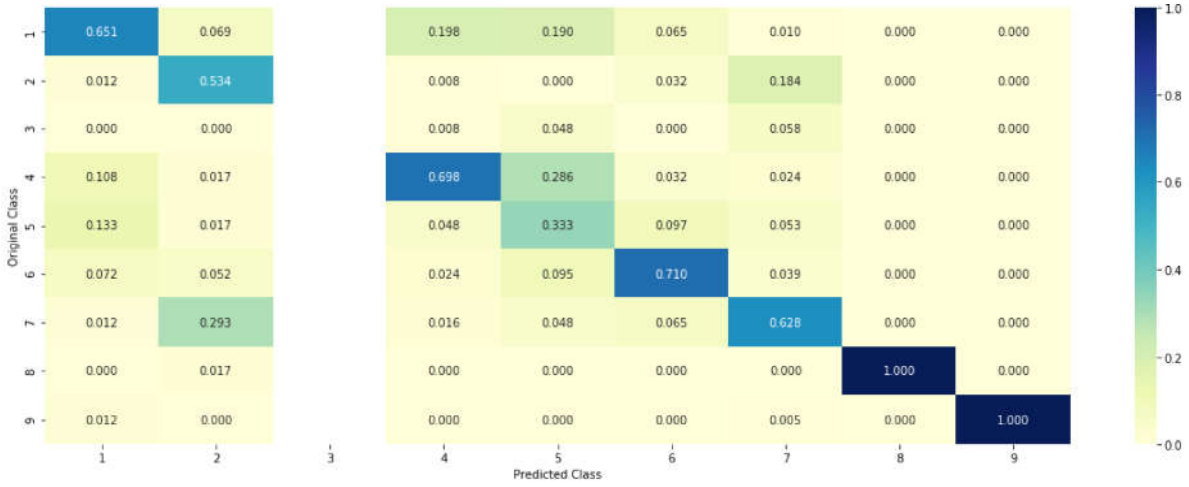
In [140]:

```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='l
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, c
```

```
Log loss : 1.0011576044702446
Number of mis-classified points : 0.36466165413533835
-------------------- Confusion matrix --------------------
```




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




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

Logistic regression + feature engineering+unigrams

and bigrams

merging gene and variation data into one list and apply TFidfVectorizer on top of it

Gene Feature

In [144]:

```
result = pd.merge(data, data_text,on='ID', how='left')
result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Variation']
y_true = result['Class'].values
result.Gene = result.Gene.str.replace('\s+', '_')
result.Variation = result.Variation.str.replace('\s+', '_')

x_train, test_df, y_train, y_test = train_test_split(result, y_true, stratify=y_true, test_

train_df, cv_df, y_train, y_cv = train_test_split(x_train, y_train, stratify=y_train, test_
```

In [146]:

```
# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
    value_count = train_df[feature].value_counts()
    gv_dict = dict()
    for i, denominator in value_count.items():
        vec = []
        for k in range(1,10):
            cls_cnt = train_df.loc[(train_df['Class']==k) & (train_df[feature]==i)]
            vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
        gv_dict[i]=vec
    return gv_dict

# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
    gv_dict = get_gv_fea_dict(alpha, feature, df)
    value_count = train_df[feature].value_counts()
    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])
    return gv_fea
```

In [147]:

```
#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 [149]:

```
# one-hot encoding of Gene feature.
gene_vectorizer = TfidfVectorizer(ngram_range=(1, 2))
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 [150]:

```
print(train_gene_feature_onehotCoding.shape)
print(test_gene_feature_onehotCoding.shape)
print(cv_gene_feature_onehotCoding.shape)
```

```
(2124, 226)
(665, 226)
(532, 226)
```

Variation Feature

In [152]:

```
# alpha is used for laplace smoothing
alpha = 1

# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train_

# 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 [153]:

```
# one-hot encoding of variation feature.
variation_vectorizer = TfidfVectorizer(ngram_range=(1, 2))
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variati
test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])
```

In [154]:

```
print(train_variation_feature_onehotCoding.shape)
print(test_variation_feature_onehotCoding.shape)
print(cv_variation_feature_onehotCoding.shape)
```

```
(2124, 2048)
(665, 2048)
(532, 2048)
```

Text Feature

In [155]:

```
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


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
            text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TEXT'].s
            row_index += 1
    return text_feature_responseCoding
```

In [156]:

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

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*number o
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 occu
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 : 2353896
```

In [157]:

```
print(train_text_feature_onehotCoding.shape)
```

```
(2124, 2353896)
```

In [158]:

```
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)
```

In [159]:

```
#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)

# 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
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_re
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_response
```

Features after feature engineering

In [161]:

```
# Collecting all the genes and variations data into a single list
gene_variation = []

for gene in data['Gene'].values:
    gene_variation.append(gene)

for variation in data['Variation'].values:
    gene_variation.append(variation)
```

In [162]:

```
tfidfVectorizer = TfidfVectorizer(max_features=1000)
text2 = tfidfVectorizer.fit_transform(gene_variation)
gene_variation_features = tfidfVectorizer.get_feature_names()

train_text = tfidfVectorizer.transform(train_df['TEXT'])
test_text = tfidfVectorizer.transform(test_df['TEXT'])
cv_text = tfidfVectorizer.transform(cv_df['TEXT'])
```

In [163]:

```
print(train_text.shape)
print(test_text.shape)
print(cv_text.shape)
```

```
(2124, 1000)
(665, 1000)
(532, 1000)
```

In [164]:

```
test_text_feature_onehotCoding = text_vectorizer.transform(test_df['TEXT'])
cv_text_feature_onehotCoding = text_vectorizer.transform(cv_df['TEXT'])
```

In [165]:

```
print(train_text_feature_onehotCoding.shape )
print(test_text_feature_onehotCoding.shape )
print(cv_text_feature_onehotCoding.shape )
```

```
(2124, 2353896)
(665, 2353896)
(532, 2353896)
```

Stack above three features

In [166]:

```
train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,train_variation_featu
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehot

# Adding the train_text feature
train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text))
train_x_onehotCoding = hstack((train_x_onehotCoding, train_text_feature_onehotCoding)).tocs
train_y = np.array(list(train_df['Class']))

# Adding the test_text feature
test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text))
test_x_onehotCoding = hstack((test_x_onehotCoding, test_text_feature_onehotCoding)).tocsr()
test_y = np.array(list(test_df['Class']))

# Adding the cv_text feature
cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text))
cv_x_onehotCoding = hstack((cv_x_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_variatic
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_f
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_respc
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_response
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding
```

In [167]:

```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCoding
print("(number of data points * number of features) in test data = ", test_x_onehotCoding.s
print("(number of data points * number of features) in cross validation data =", cv_x_oneho
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 235717
0)
(number of data points * number of features) in test data =  (665, 2357170)
(number of data points * number of features) in cross validation data = (53
2, 2357170)
```

In [168]:

```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_responseCodi
print("(number of data points * number of features) in test data = ", test_x_responseCoding
print("(number of data points * number of features) in cross validation data =", cv_x_respc
```

```
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 27)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data = (53
2, 27)
```

In [169]:

```
cv_x_onehotCoding.shape
```

Out[169]:

```
(532, 2357170)
```

In [170]:

```
print(train_x_onehotCoding.shape)
test_x_onehotCoding.shape
```

```
(2124, 2357170)
```

Out[170]:

```
(665, 2357170)
```

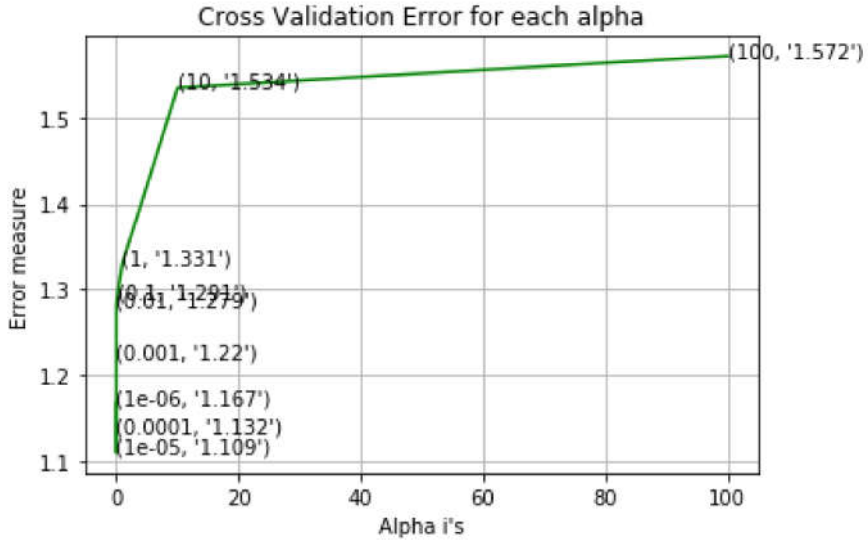
LR + FE + Response coding

In [171]:

```
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_
    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 estimat
    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='l
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_y, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.166615377941956
for alpha = 1e-05
Log Loss : 1.108949698481365
for alpha = 0.0001
Log Loss : 1.1319978949685288
for alpha = 0.001
Log Loss : 1.2200980363200777
for alpha = 0.01
Log Loss : 1.279240571838944
for alpha = 0.1
Log Loss : 1.2908105447756197
```

```
for alpha = 1
Log Loss : 1.3305357199221168
for alpha = 10
Log Loss : 1.5344923112657416
for alpha = 100
Log Loss : 1.571581129875967
```

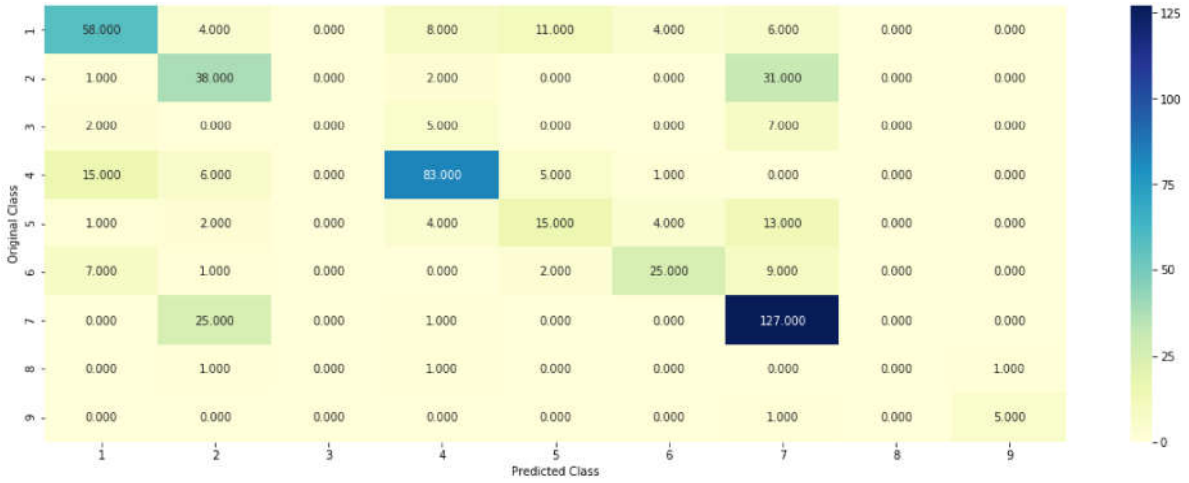



```
For values of best alpha =  1e-05 The train log loss is: 0.6159240484249302
For values of best alpha =  1e-05 The cross validation log loss is: 1.108949
698481365
For values of best alpha =  1e-05 The test log loss is: 1.1037071899186286
```

In [172]:

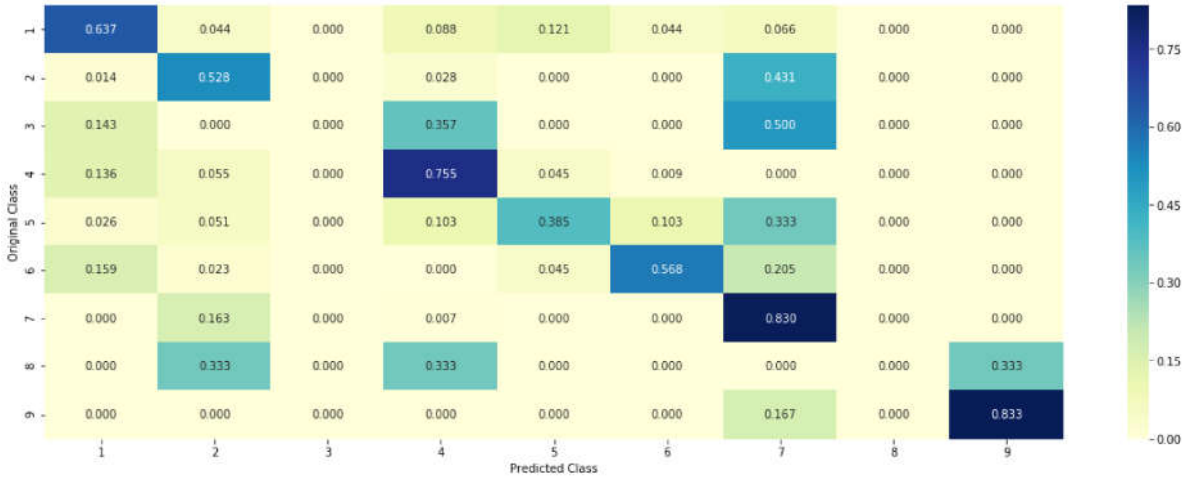
```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='l
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y, cv_x_responseCoding, cv_
```

```
Log loss : 1.108949698481365
Number of mis-classified points : 0.34022556390977443
-------------------- Confusion matrix --------------------
```




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


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



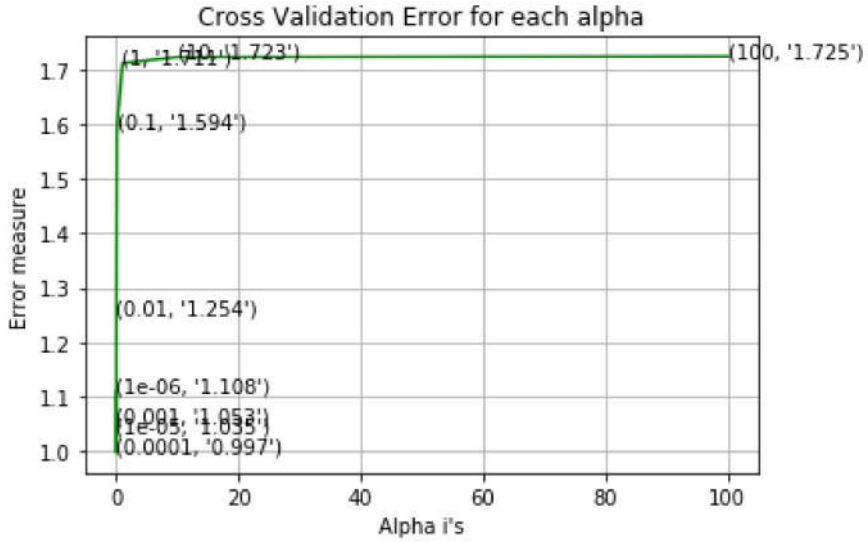
LR + FE + Tfidf

In [173]:

```
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_
    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 estimat
    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='l
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_y, labels=clf.classes_, eps=1e-15))
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, labels=clf.classes_, eps=1e-15))

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, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.1075287259590694
for alpha = 1e-05
Log Loss : 1.0350873487835524
for alpha = 0.0001
Log Loss : 0.9969212115686542
for alpha = 0.001
Log Loss : 1.053306564221487
for alpha = 0.01
Log Loss : 1.2536572910934247
for alpha = 0.1
Log Loss : 1.5936442310422554
for alpha = 1
```

```
Log Loss : 1.7113381715545082
for alpha = 10
Log Loss : 1.723327353998306
for alpha = 100
Log Loss : 1.7246019205915866
```

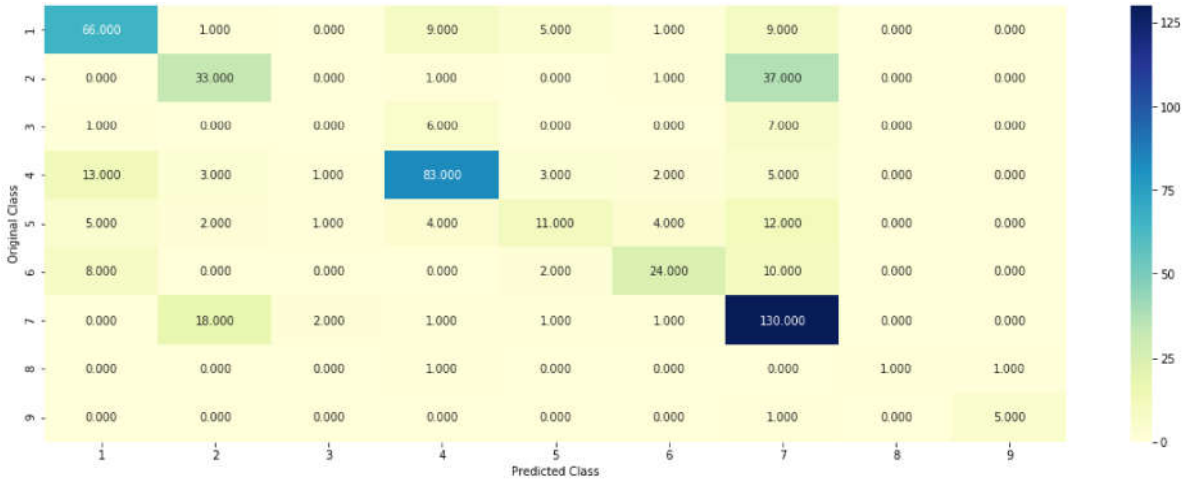



```
For values of best alpha =  0.0001 The train log loss is: 0.4066870708103957
3
For values of best alpha =  0.0001 The cross validation log loss is: 0.99692
12115686542
For values of best alpha =  0.0001 The test log loss is: 1.0556962301711788
```

In [174]:

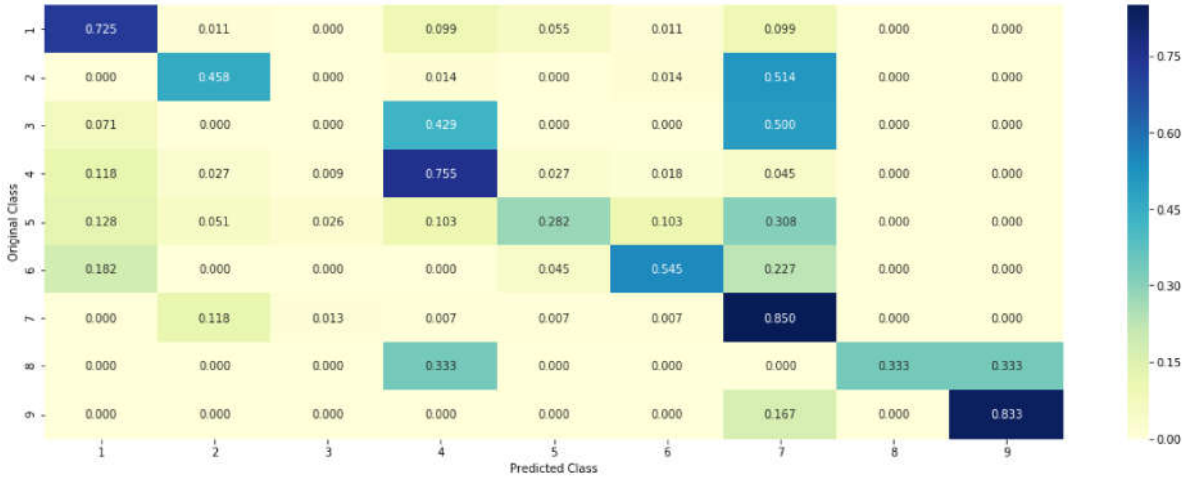
```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='l
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, c
```

```
Log loss : 0.9969212115686542
Number of mis-classified points : 0.33646616541353386
-------------------- Confusion matrix --------------------
```




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


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



Conclusion

without Feature Engineering

In [176]:

```
print()
from prettytable import PrettyTable
ptable = PrettyTable()
ptable.title = "*** Model Summary *** [Performance Metric: Log-Loss]"
ptable.field_names=["Model Name","Train","CV","Test","% Misclassified Points"]
ptable.add_row(["Naive Bayes","0.92","1.23","1.19","42"])
ptable.add_row(["KNN","0.47","1.02","1.03","35"])
ptable.add_row(["Logistic Regression With Class balancing","0.52","1.06","1.00","34"])
ptable.add_row(["Logistic Regression Without Class balancing","0.51","1.09","1.01","33"])
ptable.add_row(["Linear SVM","0.56","1.12","1.03","36"])
ptable.add_row(["Random Forest Classifier With One hot Encoding","0.65","1.14","1.15","38"]
ptable.add_row(["Random Forest Classifier With Response Coding","0.064","1.30","1.31","49"]
ptable.add_row(["Stack Models:LR+NB+SVM","1.06","1.46","1.25","33"])
ptable.add_row(["Maximum Voting classifier","0.82","1.12","1.11","33"])
print(ptable)
print()
```

```
+-------------------------------------------------+-------+------+------+----
--------------------+
|                   Model Name                    | Train |  CV  | Test | % M
isclassified Points |
+-------------------------------------------------+-------+------+------+----
--------------------+
|                  Naive Bayes                    |  0.92 | 1.23 | 1.19 |
42           |
|                      KNN                        |  0.47 | 1.02 | 1.03 |
35           |
|    Logistic Regression With Class balancing     |  0.52 | 1.06 | 1.00 |
34           |
|  Logistic Regression Without Class balancing    |  0.51 | 1.09 | 1.01 |
33           |
|                   Linear SVM                    |  0.56 | 1.12 | 1.03 |
36           |
| Random Forest Classifier With One hot Encoding  |  0.65 | 1.14 | 1.15 |
38           |
| Random Forest Classifier With Response Coding   | 0.064 | 1.30 | 1.31 |
49           |
|             Stack Models:LR+NB+SVM              |  1.06 | 1.46 | 1.25 |
33           |
|           Maximum Voting classifier             |  0.82 | 1.12 | 1.11 |
33           |
+-------------------------------------------------+-------+------+------+----
--------------------+
```

With Feature Engineering

In [177]:

```
from prettytable import PrettyTable
ptable1 = PrettyTable()
ptable1.field_names=["Model Name","Train Log-Loss","CV Log-Loss","Test Log-Loss","% Misclas
ptable1.add_row(["LR with Response Coding(unigrams and bigrams)","0.71","1.17","1.13","40"]
ptable1.add_row(["LR with Response Coding(unigrams and quatergram)","0.77","1.24","1.27","3
ptable1.add_row(["LR with one hot encoding + feature engineering","0.43","1.00","1.0","36"]
ptable1.add_row(["LR with one hot encodin+unigram-quatergram+feature engineering","0.61","1
ptable1.add_row(["LR with Response coding+unigram-quatergram+feature engineering","0.40","0
print(ptable1)
```

```
+-------------------------------------------------------------------+----------
------+------------+--------------+-----------------------+
|                          Model Name                               | Train Log
-Loss | CV Log-Loss | Test Log-Loss | % Misclassified Points |
+-------------------------------------------------------------------+----------
------+------------+--------------+-----------------------+
|         LR with Response Coding(unigrams and bigrams)             |      0.71
|     1.17     |      1.13     |           40           |
|        LR with Response Coding(unigrams and quatergram)           |      0.77
|     1.24     |      1.27     |           39           |
|         LR with one hot encoding + feature engineering            |      0.43
|     1.00     |      1.0      |           36           |
| LR with one hot encodin+unigram-quatergram+feature engineering    |      0.61
|     1.1      |      1.1      |           36           |
| LR with Response coding+unigram-quatergram+feature engineering    |      0.40
|     0.99     |      1.0      |           33           |
+-------------------------------------------------------------------+----------
------+------------+--------------+-----------------------+
```

- We have applied some feature engineering like merging gene and variation and length of text as a new feature but it's difficult to decrease the test logloss to less than 1.
- In our logistic Regression(without class balancing) model the train log loss is great but the difference between train log loss and test/cv log loss is high here so, model may overfits.
- In terms of train log loss our logistic regression(without class balancing) model is good but overall logistic regression(with class balancing) is out best model because test/cv logloss are comparatively low as compared to others and the difference between train and test/cv logloss is also low.