Personalized cancer diagnosis

Here I am using TfidfVectorizer and I am Taking top 1000 features over here...

1. Business Problem

1.1. Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training_variants.zip and training_text.zip from Kaggle.

Context:

Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/discussion/35336#198462

Problem statement :

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

1.2. Source/Useful Links

Some articles and reference blogs about the problem statement

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

1.3. Real-world/Business objectives and constraints.

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

2. Machine Learning Problem Formulation

2.1. Data

2.1.1. Data Overview

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

Metric(s):

- Multi class log-loss
- Confusion matrix

2.2.3. Machine Learing Objectives and Constraints

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

Constraints:

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

2.3. Train, CV and Test Datasets

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

3. Exploratory Data Analysis

In [1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import re
import time
import warnings
import numpy as np
from nltk.corpus import stopwords
from sklearn.decomposition import TruncatedSVD
from sklearn.preprocessing import normalize
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.manifold import TSNE
import seaborn as sns
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics.classification import accuracy_score, log_loss
from sklearn.feature_extraction.text import TfidfVectorizer
```

```
from sklearn.linear_model import SGDClassifier
from imblearn.over_sampling import SMOTE
from collections import Counter
from scipy.sparse import hstack
from sklearn.multiclass import OneVsRestClassifier
from sklearn.svm import SVC
from sklearn.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"],skiprows=1)
print('Number of data points : ', data_text.shape[0])
print('Number of features : ', data_text.shape[1])
print('Features : ', data_text.columns.values)
data_text.head()
```

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

Out[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 t
he 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_tim
e, "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 : 156.29501786521365 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

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

```
train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train, str
atify=y_train, test_size=0.2)
```

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

In [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
])
```

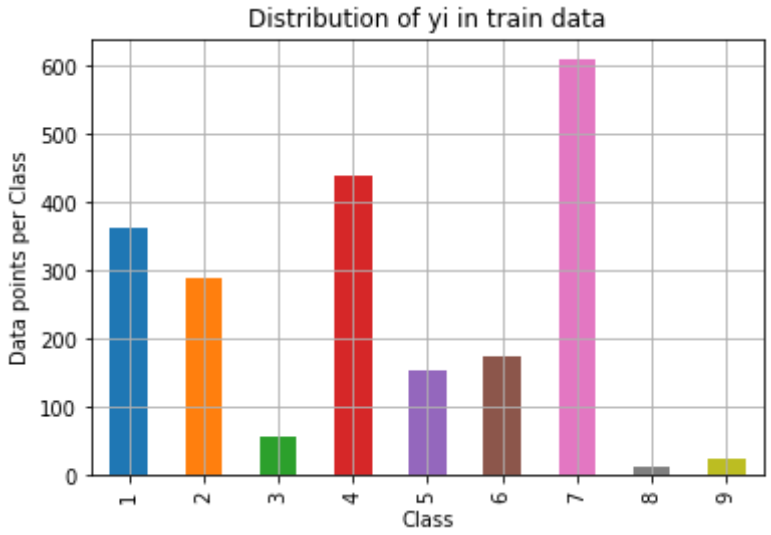
```
Number of data points in train data: 2124
Number of data points in test data: 665
Number of data points in cross validation data: 532
```

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

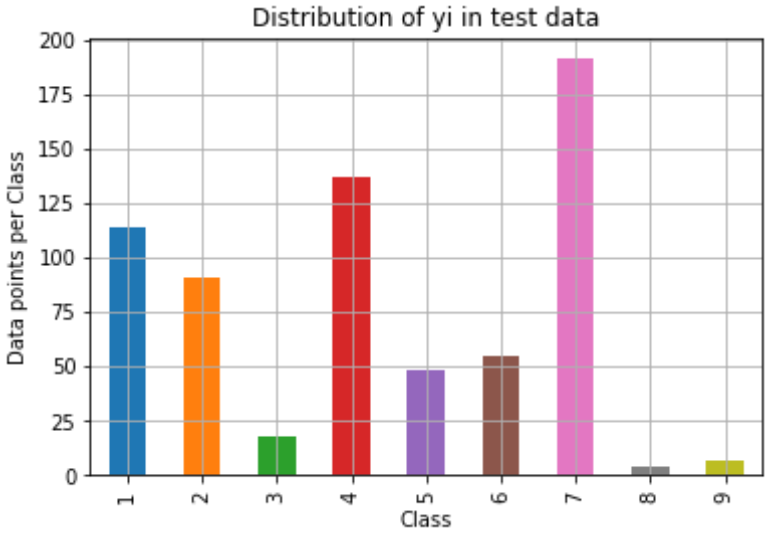
In [12]:
```
# it returns a dict, keys as class labels and values as the number of d
ata points in that class
train_class_distribution = train_df['Class'].value_counts().sortlevel()
test_class_distribution = test_df['Class'].value_counts().sortlevel()
cv_class_distribution = cv_df['Class'].value_counts().sortlevel()

my_colors = '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/num
py.argsort.html
# -(train_class_distribution.values): the minus sign will give us in de
creasing 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_distri
bution.values[i], '(', np.round((train_class_distribution.values[i]/tra
in_df.shape[0]*100), 3), '%)')


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/num
py.argsort.html
# -(train_class_distribution.values): the minus sign will give us in de
creasing 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_distrib
ution.values[i], '(', np.round((test_class_distribution.values[i]/test_
df.shape[0]*100), 3), '%)')

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/num
py.argsort.html
# -(train_class_distribution.values): the minus sign will give us in de
creasing order
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
```

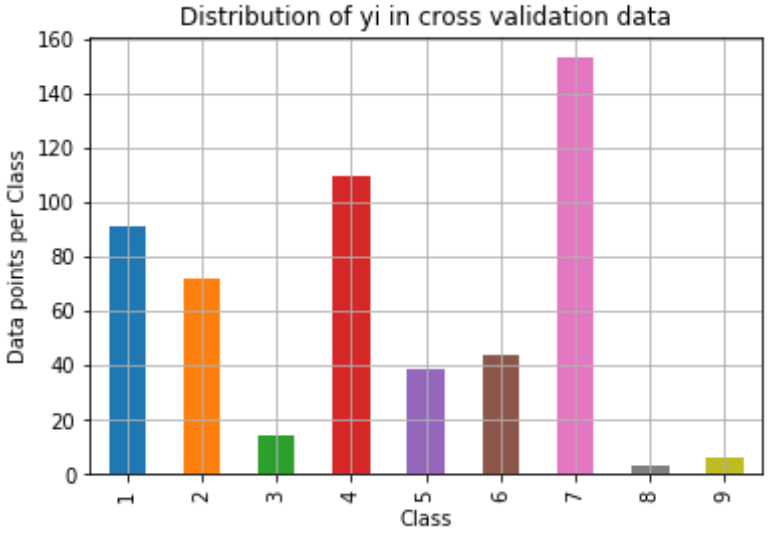
```
    print('Number of data points in class', i+1, ':',cv_class_distribut
ion.values[i], '(', np.round((cv_class_distribution.values[i]/cv_df.sha
pe[0]*100), 3), '%)')
```




```
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 cl
ass i are predicted class j

    A =(((C.T)/(C.sum(axis=1))).T)
    #divid each element of the confusion matrix with the sum of element
s 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 correspo
nds to rows in two diamensional array
    # 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 element
s in that row
    # C = [[1, 2],
    #     [3, 4]]
    # C.sum(axis = 0)  axis=0 corresonds to columns and axis=1 correspo
nds to rows in two diamensional array
    # 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=la
bels, yticklabels=labels)
    plt.xlabel('Predicted Class')
```

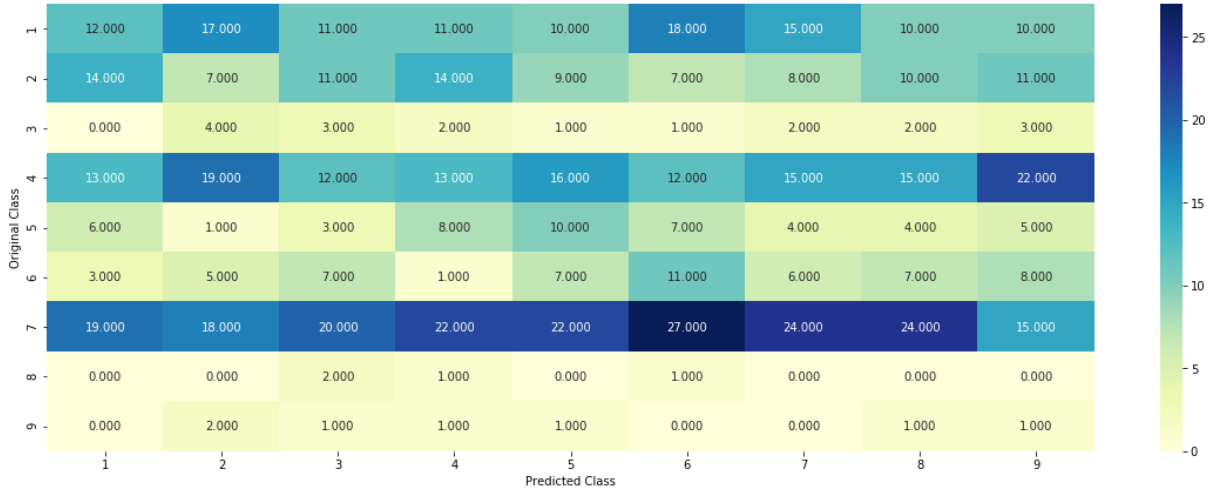
```
    plt.ylabel('Original Class')
    plt.show()

    print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=la
bels, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()

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

In [14]:

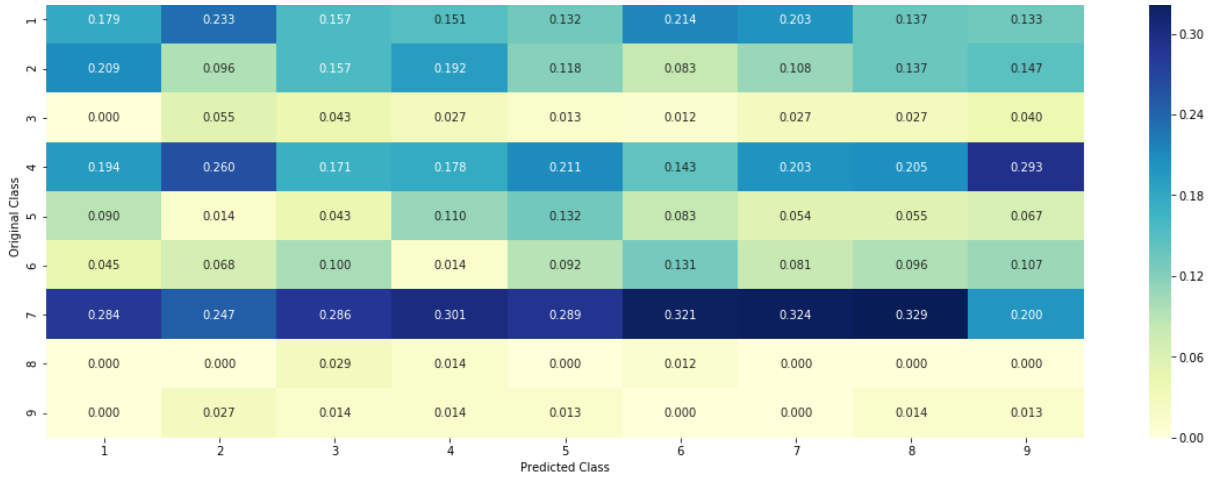
```
# we need to generate 9 numbers and the sum of numbers should be 1
# one solution is to genarate 9 numbers and divide each of the numbers
 by their sum
# ref: https://stackoverflow.com/a/18662466/4084039
test_data_len = test_df.shape[0]
cv_data_len = cv_df.shape[0]

# 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, eps=1e-15))


# Test-Set error.
#we create a output array that has exactly same as the test data
test_predicted_y = np.zeros((test_data_len,9))
```

```
for i in range(test_data_len):
    rand_probs = np.random.rand(1,9)
    test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Test Data using Random Model",log_loss(y_test,test_p
redicted_y, eps=1e-15))

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

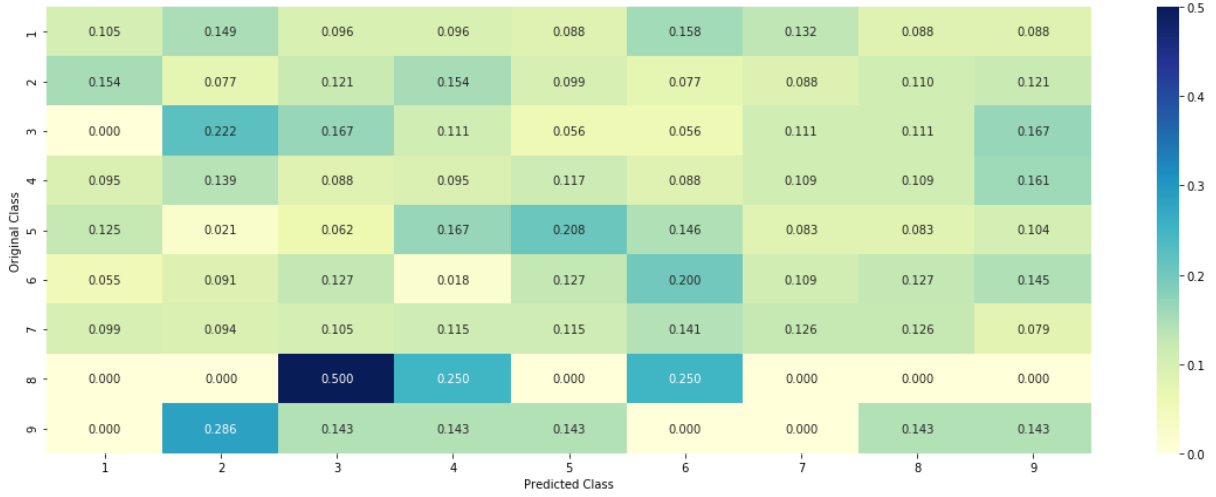
```
Log loss on Cross Validation Data using Random Model 2.4988338497153006
Log loss on Test Data using Random Model 2.4832428022542268
-------------------- Confusion matrix --------------------
```




```
-------------------- 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 feat
ure in train data dataframe
# build a vector (1*9) , the first element = (number of times it occure
d in class1 + 10*alpha / number of time it occurred in total data+90*al
pha)
# gv_dict is like a look up table, for every gene it store a (1*9) repr
esentation 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_f
ea'
# 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 arr
ay for each gene/variation
    gv_dict = dict()

    # denominator will contain the number of time that particular featu
re occured in whole data
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation b
elongs to perticular class
        # vec is 9 diamensional vector
        vec = []
        for k in range(1,10):
            # print(train_df.loc[(train_df['Class']==1) & (train_df['Ge
ne']=='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[f
eature]==i)]

            # cls_cnt.shape[0](numerator) will contain the number of ti
```

```
me that particular feature occured in whole data
            vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90
*alpha))

        # we are adding the gene/variation to the dict as key and vec a
s 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, 0.068181
818181818177, 0.13636363636363635, 0.25, 0.19318181818181818, 0.0378787
8787878788, 0.03787878787878788, 0.03787878787878788],
    #      'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224
489795918366, 0.27040816326530615, 0.061224489795918366, 0.066326530612
244902, 0.051020408163265307, 0.051020408163265307, 0.05612244897959183
7],
    #      'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625,
 0.06818181818181818177, 0.06818181818181818177, 0.0625, 0.3465909090909091
2, 0.0625, 0.056818181818181816],
    #      'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.06060
6060606060608, 0.078787878787878782, 0.1393939393939394, 0.345454545454
54546, 0.060606060606060608, 0.060606060606060608, 0.0606060606060606060
8],
    #      'PTEN': [0.069182389937106917, 0.062893081761006289, 0.06918
2389937106917, 0.46540880503144655, 0.075471698113207544, 0.06289308176
1006289, 0.069182389937106917, 0.062893081761006289, 0.0628930817610062
89],
    #      'KIT': [0.066225165562913912, 0.25165562913907286, 0.0728476
82119205295, 0.072847682119205295, 0.066225165562913912, 0.066225165562
913912, 0.27152317880794702, 0.066225165562913912, 0.06622516556291391
2],
    #      'BRAF': [0.066666666666666666, 0.17999999999999999, 0.073333
333333333334, 0.073333333333333334, 0.093333333333333338, 0.080000000000
0000002, 0.29999999999999999, 0.066666666666666666, 0.06666666666666666
6],
    #      ...
```

```
    #     }
    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 e
ach feature value in the data
    gv_fea = []
    # for every feature values in the given data frame we will check if
 it is there in the train data then we will add the feature to gv_fea
    # 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_fe
a
    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])
```

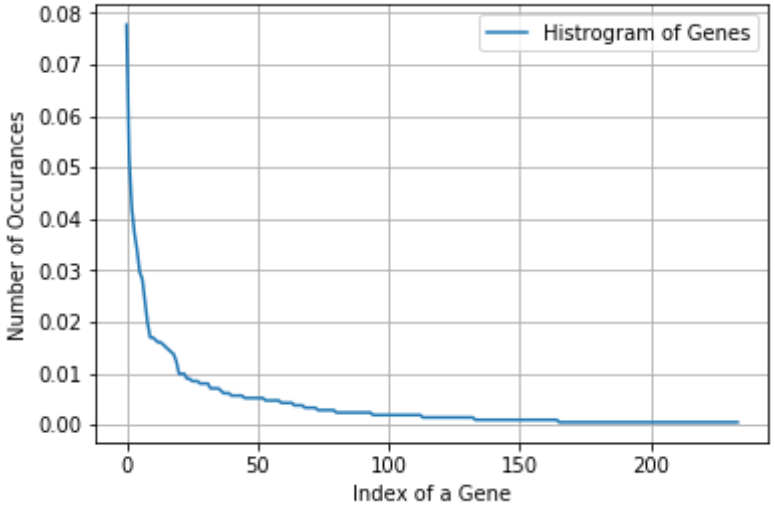
```
# the top 10 genes that occured most
print(unique_genes.head(10))
```

```
Number of Unique Genes : 234
BRCA1     165
TP53      110
EGFR       89
PTEN       79
BRCA2      72
KIT        63
BRAF       60
ALK        51
ERBB2      42
PIK3CA     36
Name: Gene, dtype: int64
```

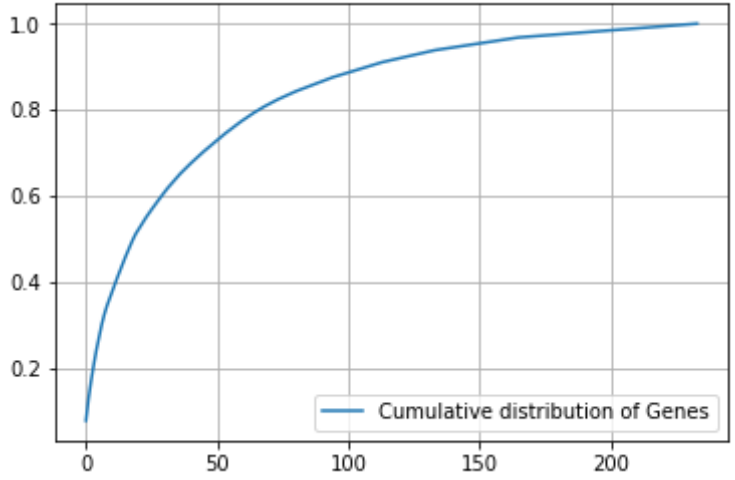
In [17]:
```
print("Ans: There are", unique_genes.shape[0] ,"different categories of
 genes in the train data, and they are distibuted as follows",)
```

```
Ans: There are 234 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/

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, "Gen
e", train_df))
# test gene feature
test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gen
e", 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 res
pone coding method. The shape of gene feature:", train_gene_feature_res
ponseCoding.shape)
```

```
train_gene_feature_responseCoding is converted feature using respone co
ding 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_d
f['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]:
```
2691      BRAF
3080    NOTCH1
2094     CDK12
2375    PTPN11
1109     FANCA
Name: Gene, dtype: object
```

In [24]:
```
print("train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature:", train_gene_feature_onehotCoding.shape)
```

```
train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature: (2124, 233)
```

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

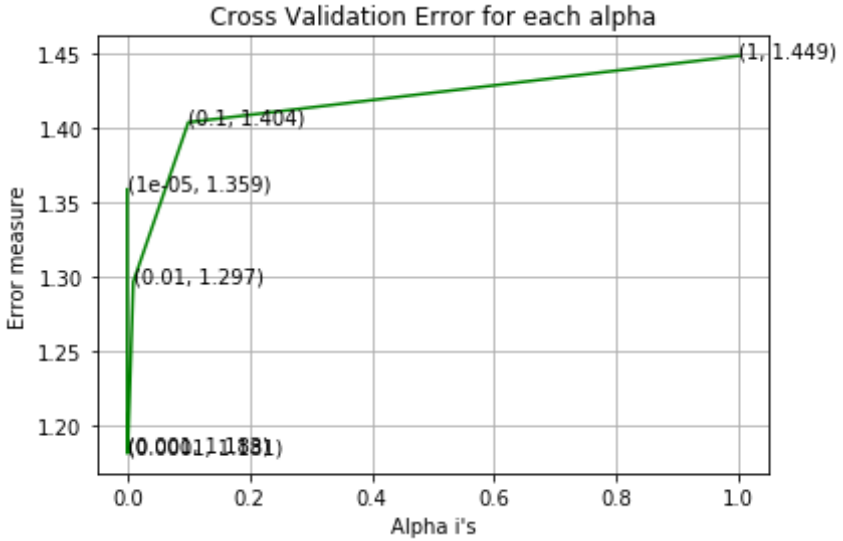
There are many ways to estimate how good a feature is, in predicting y_i. One of the good methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y_i.

In [25]:
```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
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.clas
```

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

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_arra
y[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_train, predict_y, labels=clf.classes_, eps=1e-15
))
predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha =  1e-05 The log loss is: 1.3587917028188434
For values of alpha =  0.0001 The log loss is: 1.181190500485675
For values of alpha =  0.001 The log loss is: 1.182840437898451
For values of alpha =  0.01 The log loss is: 1.2966172760667634
```

```
For values of alpha =  0.1 The log loss is: 1.4039760454796084
For values of alpha =  1 The log loss is: 1.4486913485894128
```




```
For values of best alpha =  0.0001 The train log loss is: 1.05676103760
78556
For values of best alpha =  0.0001 The cross validation log loss is: 1.
181190500485675
For values of best alpha =  0.0001 The test log loss is: 1.200884286258
9408
```

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 [26]:
```
print("Q6. How many data points in Test and CV datasets are covered by
 the ", unique_genes.shape[0], " genes in train dataset?")

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

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

print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_coverage/test_df.shape[0])*100)
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_coverage/cv_df.shape[0])*100)
```

```
Q6. How many data points in Test and CV datasets are covered by the  234  genes in train dataset?
Ans
1. In test data 643 out of 665 : 96.69172932330827
2. In cross validation data 517 out of  532 : 97.18045112781954
```

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 [27]:
```
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))
```

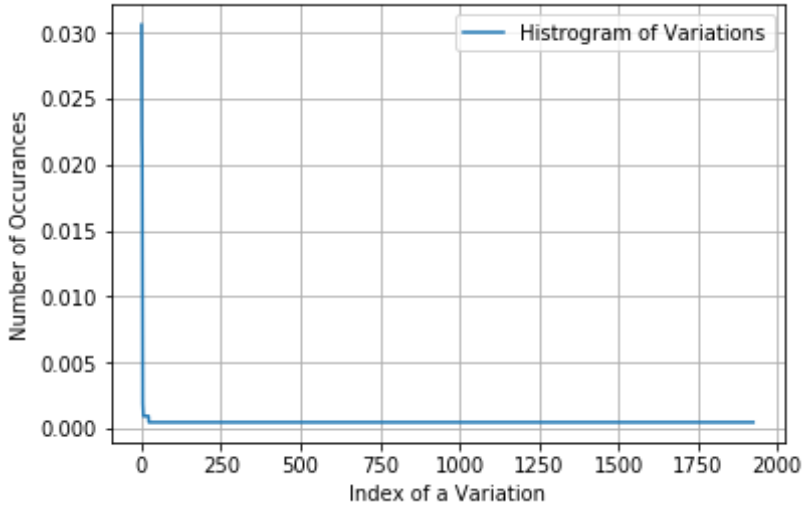
```
Number of Unique Variations : 1925
Truncating_Mutations         65
Amplification                47
Deletion                     44
Fusions                      25
Overexpression                4
G12V                          3
G12D                          2
G35R                          2
Promoter_Hypermethylation     2
```

```
Q61R                            2
Name: Variation, dtype: int64
```

In [28]:
```
print("Ans: There are", unique_variations.shape[0] ,"different categori
es of variations in the train data, and they are distibuted as follows"
,)
```

```
Ans: There are 1925 different categories of variations in the train dat
a, and they are distibuted as follows
```

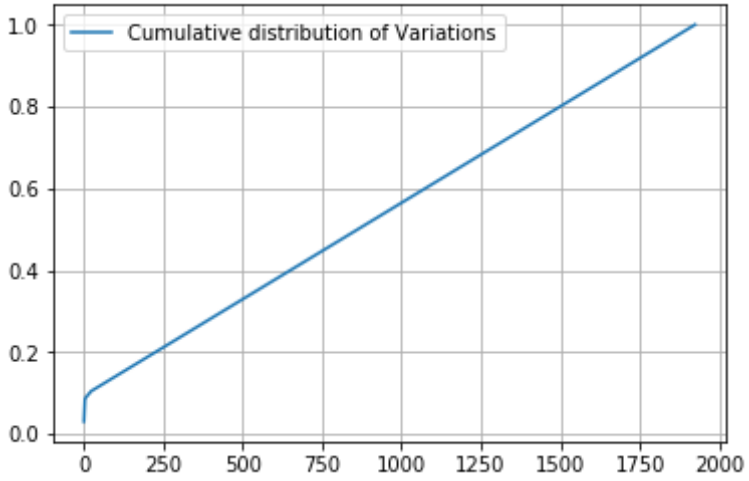
In [29]:
```
s = sum(unique_variations.values);
h = unique_variations.values/s;
plt.plot(h, label="Histrogram of Variations")
plt.xlabel('Index of a Variation')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



In [30]:
```
c = np.cumsum(h)
print(c)
plt.plot(c,label='Cumulative distribution of Variations')
```

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

```
[0.03060264 0.0527307  0.07344633 ... 0.99905838 0.99952919 1.        ]
```



Q9. How to featurize this Variation feature ?

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

1. One hot Encoding
2. Response coding

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

In [31]:
```
# alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha,
 "Variation", train_df))
```

```
# test gene feature
test_variation_feature_responseCoding = np.array(get_gv_feature(alpha,
"Variation", test_df))
# cross validation gene feature
cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "V
ariation", cv_df))
```

In [32]:
```
print("train_variation_feature_responseCoding is a converted feature us
ing the response coding method. The shape of Variation feature:", train
_variation_feature_responseCoding.shape)
```

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

In [33]:
```
# one-hot encoding of variation feature.
variation_vectorizer = TfidfVectorizer()
train_variation_feature_onehotCoding = variation_vectorizer.fit_transfo
rm(train_df['Variation'])
test_variation_feature_onehotCoding = variation_vectorizer.transform(te
st_df['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_d
f['Variation'])
```

In [34]:
```
print("train_variation_feature_onehotEncoded is converted feature using
 the onne-hot encoding method. The shape of Variation feature:", train_
variation_feature_onehotCoding.shape)
```

```
train_variation_feature_onehotEncoded is converted feature using the on
ne-hot encoding method. The shape of Variation feature: (2124, 1954)
```

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

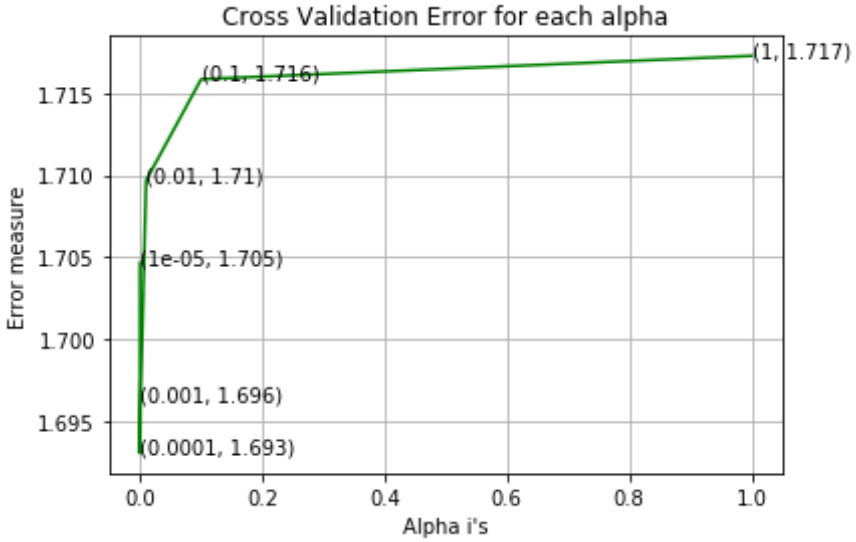
Let's build a model just like the earlier!

In [35]:
```
alpha = [10 ** x for x in range(-5, 1)]

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

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_arra
y[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_train, predict_y, labels=clf.classes_, eps=1e-15
))
predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
```

```
print('For values of best alpha = ', alpha[best_alpha], "The cross vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha =  1e-05 The log loss is: 1.7046446293709139
For values of alpha =  0.0001 The log loss is: 1.6930481720347585
For values of alpha =  0.001 The log loss is: 1.696217703260624
For values of alpha =  0.01 The log loss is: 1.7096684684554209
For values of alpha =  0.1 The log loss is: 1.7158347825611844
For values of alpha =  1 The log loss is: 1.7172572666506558
```




```
For values of best alpha =  0.0001 The train log loss is: 0.83200869942
24568
For values of best alpha =  0.0001 The cross validation log loss is: 1.
6930481720347585
For values of best alpha =  0.0001 The test log loss is: 1.726922594770
1154
```

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 [36]:
```
print("Q12. How many data points are covered by total ", unique_variati
ons.shape[0], " genes in test and cross validation data sets?")
test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Vari
ation'])))].shape[0]
cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'
])))].shape[0]
print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0],
":",(test_coverage/test_df.shape[0])*100)
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[
0],":" ,(cv_coverage/cv_df.shape[0])*100)
```

```
Q12. How many data points are covered by total  1925  genes in test and
cross validation data sets?
Ans
1. In test data 55 out of 665 : 8.270676691729323
2. In cross validation data 62 out of  532 : 11.654135338345863
```

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 [37]:
```
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 [38]:
```
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 )/(t
otal_dict.get(word,0)+90)))
            text_feature_responseCoding[row_index][i] = math.exp(sum_pr
ob/len(row['TEXT'].split()))
            row_index += 1
    return text_feature_responseCoding
```

In [39]:
```
# building a CountVectorizer with all the words that occured minimum 3
 times in train data
text_vectorizer = TfidfVectorizer(min_df=3,max_features=1000)
train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_d
f['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and
 returns (1*number of features) vector
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 num
ber of times it occured
text_fea_dict = dict(zip(list(train_text_features),train_text_fea_count
s))


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

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

In [40]:
```
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 [41]:
```
#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 [42]:
```
# https://stackoverflow.com/a/16202486
# we convert each row values such that they sum to 1
train_text_feature_responseCoding = (train_text_feature_responseCoding.
T/train_text_feature_responseCoding.sum(axis=1)).T
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/
test_text_feature_responseCoding.sum(axis=1)).T
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_t
ext_feature_responseCoding.sum(axis=1)).T
```

In [43]:
```
# don't forget to normalize every feature
train_text_feature_onehotCoding = normalize(train_text_feature_onehotCo
```

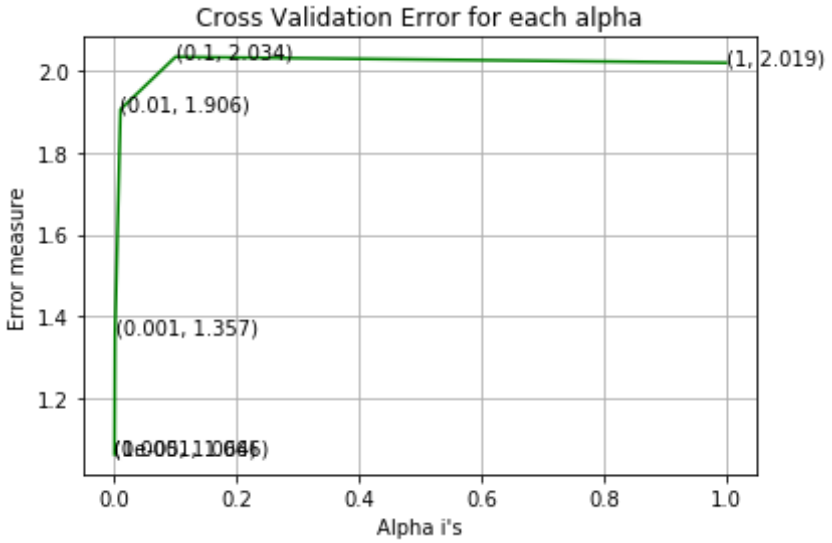
```
ding, axis=0)

# we use the same vectorizer that was trained on train data
test_text_feature_onehotCoding = text_vectorizer.transform(test_df['TEX
T'])
# don't forget to normalize every feature
test_text_feature_onehotCoding = normalize(test_text_feature_onehotCodi
ng, 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 [44]:
```
#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 [45]:
```
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.clas
ses_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv
, predict_y, labels=clf.classes_, eps=1e-15))

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_arra
```

```
y[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_train, predict_y, labels=clf.classes_, eps=1e-15
))
predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha =  1e-05 The log loss is: 1.063514208057455
For values of alpha =  0.0001 The log loss is: 1.0664353574977676
For values of alpha =  0.001 The log loss is: 1.3572360580365894
For values of alpha =  0.01 The log loss is: 1.9056641963110768
For values of alpha =  0.1 The log loss is: 2.034014992120592
For values of alpha =  1 The log loss is: 2.019440492698908
```




```
For values of best alpha =  1e-05 The train log loss is: 0.801885043506
0898
For values of best alpha =  1e-05 The cross validation log loss is: 1.0
63514208057455
For values of best alpha =  1e-05 The test log loss is: 1.1226306342984
214
```

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

Ans. Yes, it seems like!

In [46]:
```
def get_intersec_text(df):
    df_text_vec = TfidfVectorizer(min_df=3,max_features=1000)
    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_coun
ts))
    len1 = len(set(df_text_features))
```

```
    len2 = len(set(train_text_features) & set(df_text_features))
    return len1,len2
```

In [47]:
```
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 appe
ared in train data")
```

```
3.536 % of word of test data appeared in train data
3.857 % of word of Cross Validation appeared in train data
```

4. Machine Learning Models

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

#Misc. functionns for ML models


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

    # for calculating log_loss we willl provide the array of probabilit
ies belongs to each class
    print("Log loss :",log_loss(test_y, sig_clf.predict_proba(test_x)))
    # calculating the number of data points that are misclassified
    print("Number of mis-classified points :", np.count_nonzero((pred_y
- test_y))/test_y.shape[0])
    plot_confusion_matrix(test_y, pred_y)
```

In [49]:
```
def report_log_loss(train_x, train_y, test_x, test_y,  clf):
    clf.fit(train_x, train_y)
```

```
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x, train_y)
    sig_clf_probs = sig_clf.predict_proba(test_x)
    return log_loss(test_y, sig_clf_probs, eps=1e-15)
```

In [50]:

```
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,max_features=1000)

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

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

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

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

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

Stacking the three types of features

In [51]:
```
train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,t
rain_variation_feature_onehotCoding))
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,tes
t_variation_feature_onehotCoding))
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_vari
ation_feature_onehotCoding))

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

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

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


train_gene_var_responseCoding = np.hstack((train_gene_feature_responseC
oding,train_variation_feature_responseCoding))
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCod
ing,test_variation_feature_responseCoding))
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,
cv_variation_feature_responseCoding))

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, trai
n_text_feature_responseCoding))
```

```
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_t
ext_feature_responseCoding))
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_fe
ature_responseCoding))
```

In [52]:
```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ",
train_x_onehotCoding.shape)
print("(number of data points * number of features) in test data = ", t
est_x_onehotCoding.shape)
print("(number of data points * number of features) in cross validation
 data =", cv_x_onehotCoding.shape)
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 31
87)
(number of data points * number of features) in test data =  (665, 318
7)
(number of data points * number of features) in cross validation data =
(532, 3187)
```

In [53]:
```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ",
train_x_responseCoding.shape)
print("(number of data points * number of features) in test data = ", t
est_x_responseCoding.shape)
print("(number of data points * number of features) in cross validation
 data =", cv_x_responseCoding.shape)
```

```
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 2
7)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data =
(532, 27)
```

4.1. Base Line Model

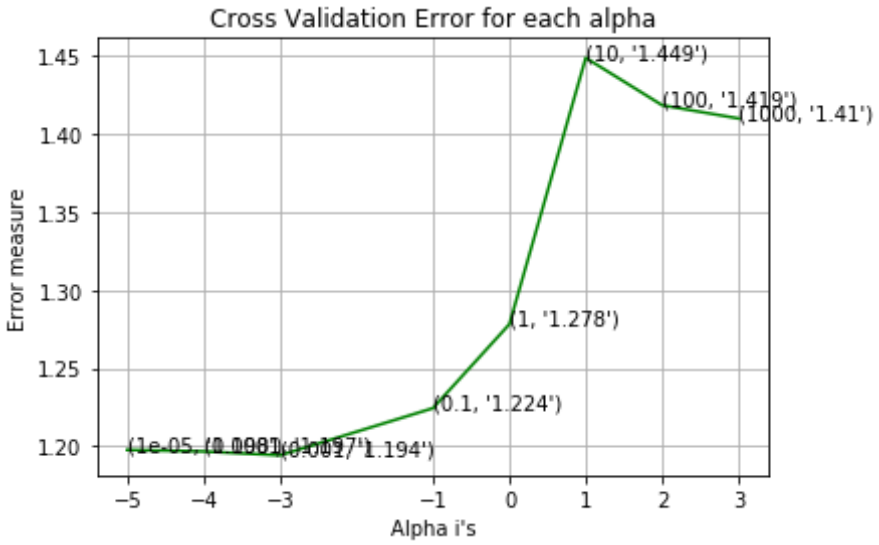
4.1.1. Naive Bayes

4.1.1.1. Hyper parameter tuning

In [54]:
```
alpha = [0.00001, 0.0001, 0.001, 0.1, 1, 10, 100,1000]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = MultinomialNB(alpha=i)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.
classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log
-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

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_a
rray[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_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 vali
dation 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 l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-05
Log Loss : 1.1975151607667922
for alpha = 0.0001
Log Loss : 1.1965545649873415
for alpha = 0.001
Log Loss : 1.1940538974331243
for alpha = 0.1
Log Loss : 1.2242655314019777
for alpha = 1
Log Loss : 1.27809398346991
for alpha = 10
Log Loss : 1.4489865413682526
for alpha = 100
Log Loss : 1.418572373823781
for alpha = 1000
Log Loss : 1.4100828623770916
```




```
For values of best alpha =  0.001 The train log loss is: 0.533641047319
9265
For values of best alpha =  0.001 The cross validation log loss is: 1.1
940538974331243
For values of best alpha =  0.001 The test log loss is: 1.1979282550254
062
```

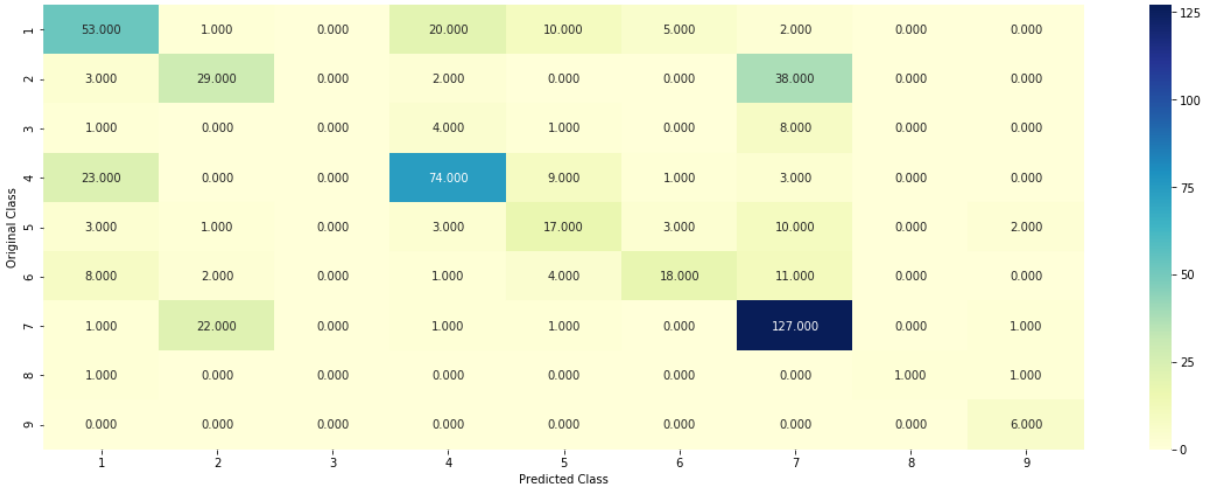
4.1.1.2. Testing the model with best hyper paramters

In [55]:

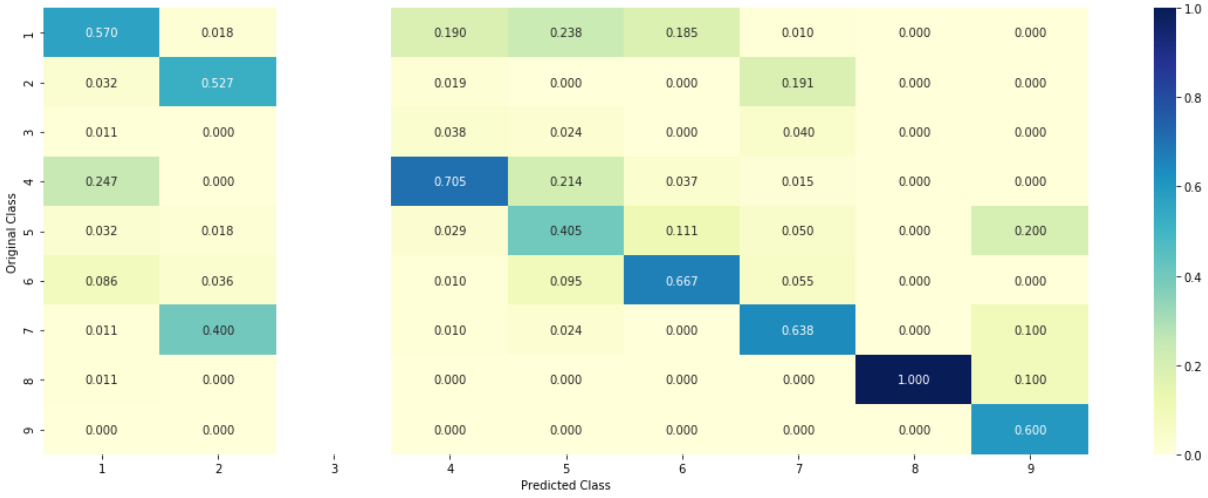
```
clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
# to avoid rounding error while multiplying probabilites we use log-pro
bability estimates
print("Log Loss :",log_loss(cv_y, sig_clf_probs))
print("Number of missclassified point :", np.count_nonzero((sig_clf.pre
dict(cv_x_onehotCoding)- cv_y))/cv_y.shape[0])
```

```
plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray
()))
```

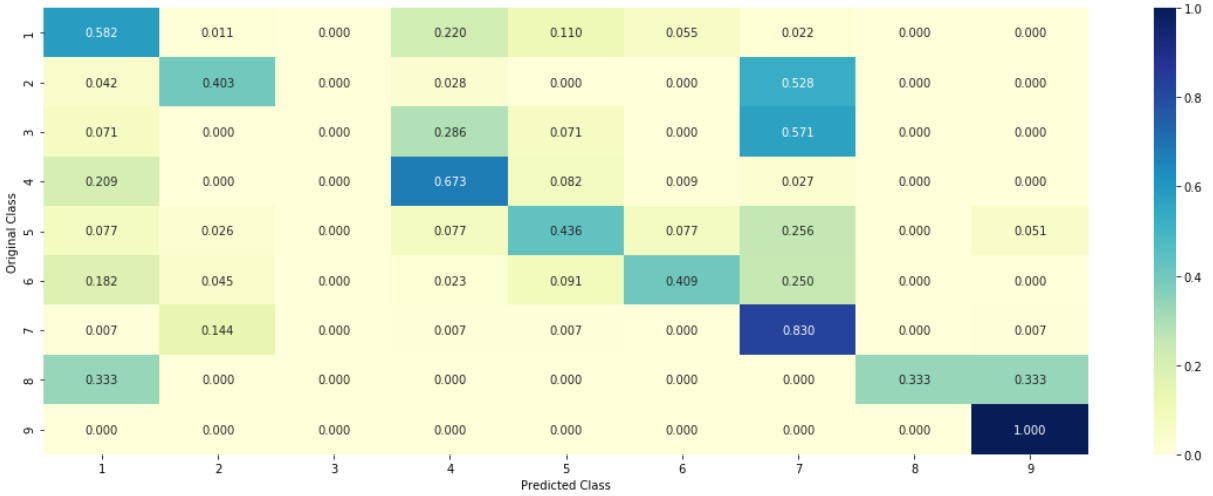
```
Log Loss : 1.1940538974331243
Number of missclassified point : 0.3890977443609023
-------------------- Confusion matrix --------------------
```




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



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



4.1.1.3. Feature Importance, Correctly classified point

In [56]:

```
test_point_index = 1
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.0624 0.042  0.0116 0.7295 0.0306 0.0
316 0.0871 0.0028 0.0023]]
Actual Class : 4
--------------------------------------------------

10 Text feature [activity] present in test data point [True]
```

```
10 Text feature [activity] present in test data point [True]
12 Text feature [protein] present in test data point [True]
13 Text feature [proteins] present in test data point [True]
14 Text feature [experiments] present in test data point [True]
15 Text feature [whereas] present in test data point [True]
17 Text feature [shown] present in test data point [True]
18 Text feature [missense] present in test data point [True]
19 Text feature [results] present in test data point [True]
20 Text feature [function] present in test data point [True]
24 Text feature [described] present in test data point [True]
25 Text feature [also] present in test data point [True]
26 Text feature [suppressor] present in test data point [True]
27 Text feature [acid] present in test data point [True]
28 Text feature [amino] present in test data point [True]
29 Text feature [determined] present in test data point [True]
30 Text feature [type] present in test data point [True]
31 Text feature [whether] present in test data point [True]
32 Text feature [important] present in test data point [True]
33 Text feature [two] present in test data point [True]
34 Text feature [wild] present in test data point [True]
35 Text feature [mutations] present in test data point [True]
37 Text feature [functional] present in test data point [True]
38 Text feature [reduced] present in test data point [True]
39 Text feature [may] present in test data point [True]
40 Text feature [purified] present in test data point [True]
41 Text feature [previously] present in test data point [True]
42 Text feature [ability] present in test data point [True]
43 Text feature [containing] present in test data point [True]
44 Text feature [three] present in test data point [True]
45 Text feature [therefore] present in test data point [True]
46 Text feature [either] present in test data point [True]
48 Text feature [indicated] present in test data point [True]
49 Text feature [determine] present in test data point [True]
50 Text feature [bind] present in test data point [True]
51 Text feature [vitro] present in test data point [True]
52 Text feature [although] present in test data point [True]
54 Text feature [discussion] present in test data point [True]
56 Text feature [tagged] present in test data point [True]
57 Text feature [similar] present in test data point [True]

58 Text feature [levels] present in test data point [True]
```

```
59 Text feature [30] present in test data point [True]
60 Text feature [indicate] present in test data point [True]
61 Text feature [suggesting] present in test data point [True]
62 Text feature [buffer] present in test data point [True]
63 Text feature [thus] present in test data point [True]
64 Text feature [one] present in test data point [True]
65 Text feature [introduction] present in test data point [True]
66 Text feature [associated] present in test data point [True]
67 Text feature [mutation] present in test data point [True]
68 Text feature [however] present in test data point [True]
69 Text feature [found] present in test data point [True]
70 Text feature [transfection] present in test data point [True]
71 Text feature [loss] present in test data point [True]
72 Text feature [several] present in test data point [True]
73 Text feature [transfected] present in test data point [True]
74 Text feature [figure] present in test data point [True]
75 Text feature [expressed] present in test data point [True]
76 Text feature [could] present in test data point [True]
77 Text feature [10] present in test data point [True]
78 Text feature [show] present in test data point [True]
79 Text feature [suggest] present in test data point [True]
80 Text feature [mutants] present in test data point [True]
81 Text feature [effect] present in test data point [True]
82 Text feature [effects] present in test data point [True]
84 Text feature [analysis] present in test data point [True]
85 Text feature [sds] present in test data point [True]
86 Text feature [addition] present in test data point [True]
87 Text feature [suggested] present in test data point [True]
88 Text feature [cells] present in test data point [True]
89 Text feature [terminal] present in test data point [True]
90 Text feature [reported] present in test data point [True]
91 Text feature [assay] present in test data point [True]
92 Text feature [using] present in test data point [True]
93 Text feature [within] present in test data point [True]
94 Text feature [fact] present in test data point [True]
96 Text feature [mm] present in test data point [True]
97 Text feature [lower] present in test data point [True]
98 Text feature [result] present in test data point [True]

99 Text feature [site] present in test data point [True]
```

```
Out of the top  100  features  79 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

In [57]:
```
test_point_index = 100
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0588 0.0423 0.0116 0.0642 0.0305 0.0
313 0.7561 0.0028 0.0023]]
Actual Class : 7
--------------------------------------------------
14 Text feature [activation] present in test data point [True]
17 Text feature [activated] present in test data point [True]
18 Text feature [kinase] present in test data point [True]
19 Text feature [downstream] present in test data point [True]
20 Text feature [cells] present in test data point [True]
23 Text feature [expressing] present in test data point [True]
24 Text feature [independent] present in test data point [True]
25 Text feature [signaling] present in test data point [True]
26 Text feature [inhibitor] present in test data point [True]
27 Text feature [growth] present in test data point [True]
28 Text feature [presence] present in test data point [True]
29 Text feature [factor] present in test data point [True]
30 Text feature [also] present in test data point [True]
31 Text feature [10] present in test data point [True]
32 Text feature [shown] present in test data point [True]
33 Text feature [contrast] present in test data point [True]
```

```
34 Text feature [treated] present in test data point [True]
35 Text feature [treatment] present in test data point [True]
36 Text feature [however] present in test data point [True]
37 Text feature [well] present in test data point [True]
38 Text feature [activating] present in test data point [True]
39 Text feature [mutations] present in test data point [True]
40 Text feature [constitutive] present in test data point [True]
41 Text feature [compared] present in test data point [True]
42 Text feature [similar] present in test data point [True]
43 Text feature [previously] present in test data point [True]
44 Text feature [found] present in test data point [True]
46 Text feature [addition] present in test data point [True]
47 Text feature [higher] present in test data point [True]
48 Text feature [recently] present in test data point [True]
49 Text feature [cell] present in test data point [True]
50 Text feature [showed] present in test data point [True]
51 Text feature [potential] present in test data point [True]
52 Text feature [may] present in test data point [True]
53 Text feature [without] present in test data point [True]
54 Text feature [mechanism] present in test data point [True]
55 Text feature [oncogenic] present in test data point [True]
56 Text feature [phosphorylation] present in test data point [True]
57 Text feature [inhibitors] present in test data point [True]
58 Text feature [increased] present in test data point [True]
59 Text feature [reported] present in test data point [True]
60 Text feature [inhibition] present in test data point [True]
61 Text feature [activate] present in test data point [True]
62 Text feature [although] present in test data point [True]
63 Text feature [enhanced] present in test data point [True]
64 Text feature [pathways] present in test data point [True]
69 Text feature [described] present in test data point [True]
70 Text feature [suggest] present in test data point [True]
71 Text feature [observed] present in test data point [True]
72 Text feature [results] present in test data point [True]
73 Text feature [constitutively] present in test data point [True]
74 Text feature [tyrosine] present in test data point [True]
75 Text feature [20] present in test data point [True]
76 Text feature [total] present in test data point [True]
77 Text feature [increase] present in test data point [True]
```

```
78 Text feature [survival] present in test data point [True]
79 Text feature [fig] present in test data point [True]
80 Text feature [studies] present in test data point [True]
81 Text feature [different] present in test data point [True]
82 Text feature [interestingly] present in test data point [True]
83 Text feature [proliferation] present in test data point [True]
84 Text feature [consistent] present in test data point [True]
85 Text feature [examined] present in test data point [True]
86 Text feature [therapeutic] present in test data point [True]
87 Text feature [pathway] present in test data point [True]
88 Text feature [receptor] present in test data point [True]
89 Text feature [two] present in test data point [True]
90 Text feature [3a] present in test data point [True]
91 Text feature [various] present in test data point [True]
92 Text feature [mutation] present in test data point [True]
93 Text feature [3b] present in test data point [True]
94 Text feature [active] present in test data point [True]
95 Text feature [12] present in test data point [True]
96 Text feature [followed] present in test data point [True]
97 Text feature [identified] present in test data point [True]
98 Text feature [absence] present in test data point [True]
99 Text feature [figure] present in test data point [True]
Out of the top  100  features  77 are present in query point
```

4.2. K Nearest Neighbour Classification

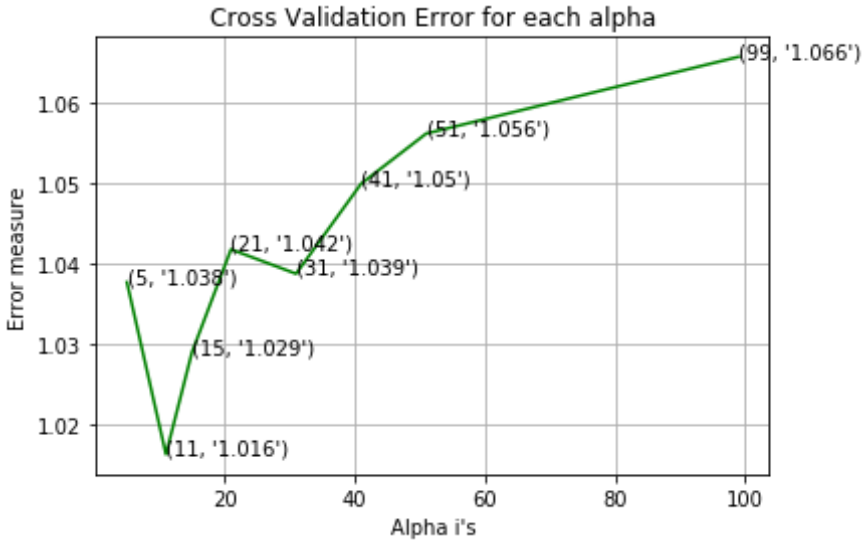
4.2.1. Hyper parameter tuning

In [58]:
```
alpha = [5, 11, 15, 21, 31, 41, 51, 99]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = KNeighborsClassifier(n_neighbors=i)
    clf.fit(train_x_responseCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_responseCoding, train_y)
```

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

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


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

predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log
 loss is:",log_loss(y_train, predict_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 vali
dation 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 l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 5
Log Loss : 1.0376422790667827
for alpha = 11
```

```
Log Loss : 1.0162484996033 78
for alpha = 15
Log Loss : 1.0289321197352617
for alpha = 21
Log Loss : 1.041727010713954
for alpha = 31
Log Loss : 1.0386955543313292
for alpha = 41
Log Loss : 1.049885464454094
for alpha = 51
Log Loss : 1.056119102717704
for alpha = 99
Log Loss : 1.0656619650640908
```



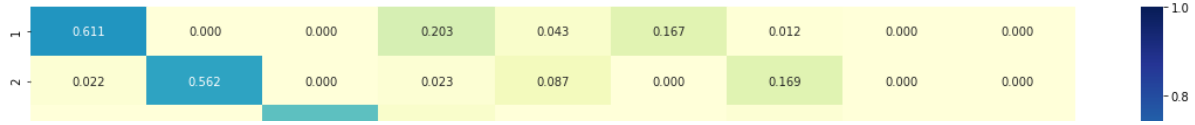

```
For values of best alpha =  11 The train log loss is: 0.656751056063116
9
For values of best alpha =  11 The cross validation log loss is: 1.0162
48499603378
For values of best alpha =  11 The test log loss is: 1.044273939609876
```

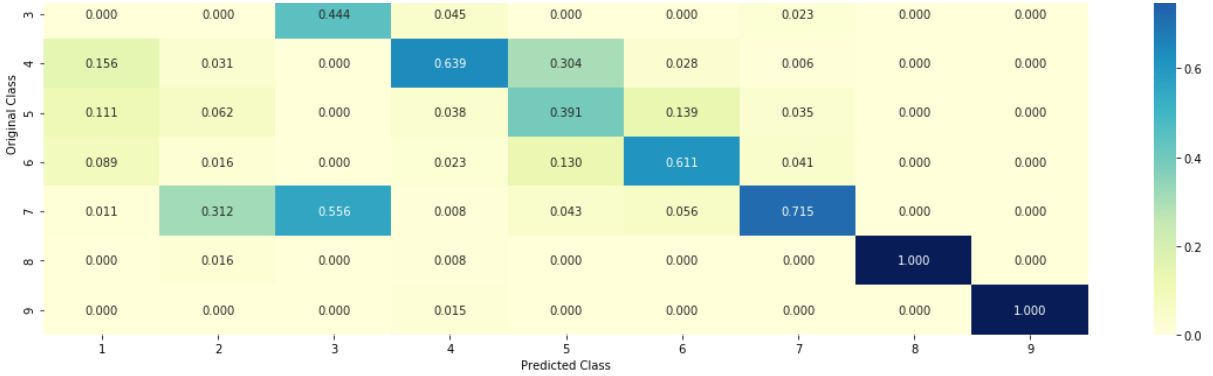
4.2.2. Testing the model with best hyper paramters

In [59]:
```
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y, cv_x
_responseCoding, cv_y, clf)
```

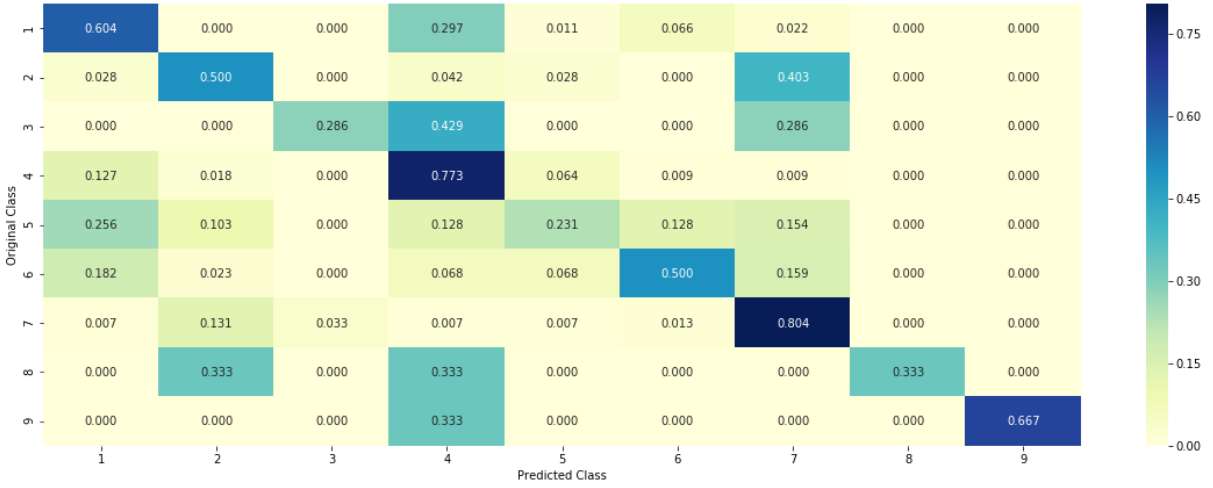
```
Log loss : 1.016248499603378
Number of mis-classified points : 0.36278195488721804
-------------------- Confusion matrix --------------------
```


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






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



4.2.3.Sample Query point -1

In [60]:
```
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].resh
ape(1, -1), alpha[best_alpha])
print("The ",alpha[best_alpha]," nearest neighbours of the test points
 belongs to classes",train_y[neighbors[1][0]])
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

```
Predicted Class : 1
Actual Class : 4
The  11  nearest neighbours of the test points belongs to classes [4 1
4 4 4 1 4 4 4 4 6]
Fequency of nearest points : Counter({4: 8, 1: 2, 6: 1})
```

4.2.4. Sample Query Point-2

In [61]:
```
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].resh
ape(1, -1), alpha[best_alpha])
print("the k value for knn is",alpha[best_alpha],"and the nearest neigh
bours of the test points belongs to classes",train_y[neighbors[1][0]])
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

```
Predicted Class : 7
Actual Class : 7
the k value for knn is 11 and the nearest neighbours of the test points
belongs to classes [7 7 7 2 7 7 7 7 7 7 2]
Fequency of nearest points : Counter({7: 9, 2: 2})
```

4.3. Logistic Regression

4.3.1. With Class balancing

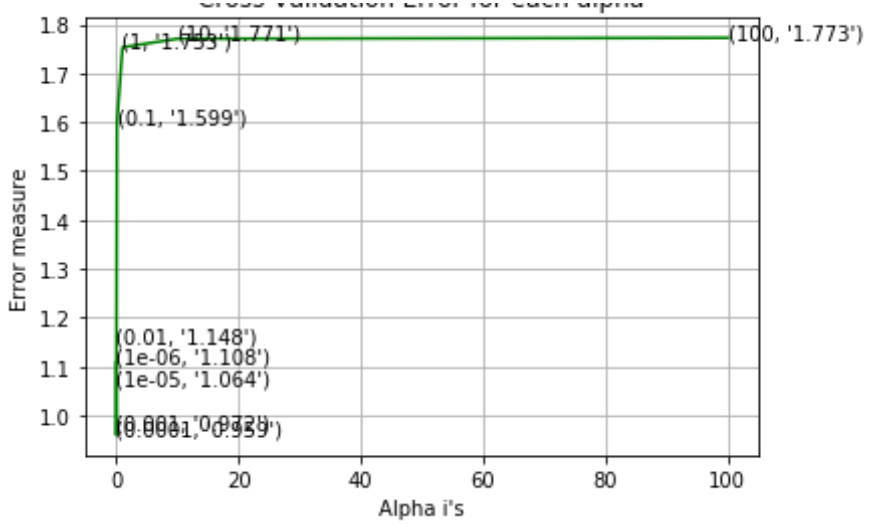
4.3.1.1. Hyper paramter tuning

In [62]:
```
alpha = [10 ** x for x in range(-6, 3)]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2',
 loss='log', random_state=42)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.
classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log
-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

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


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], p
```

```
enalty='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_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 vali
dation 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 l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.108379867362291
for alpha = 1e-05
Log Loss : 1.0636232826483523
for alpha = 0.0001
Log Loss : 0.9592272390857216
for alpha = 0.001
Log Loss : 0.9717007813828615
for alpha = 0.01
Log Loss : 1.1477122779931386
for alpha = 0.1
Log Loss : 1.5993481596684025
for alpha = 1
Log Loss : 1.7532191183130108
for alpha = 10
Log Loss : 1.7707088947584813
for alpha = 100
Log Loss : 1.7725675127835385
```

Cross Validation Error for each alpha

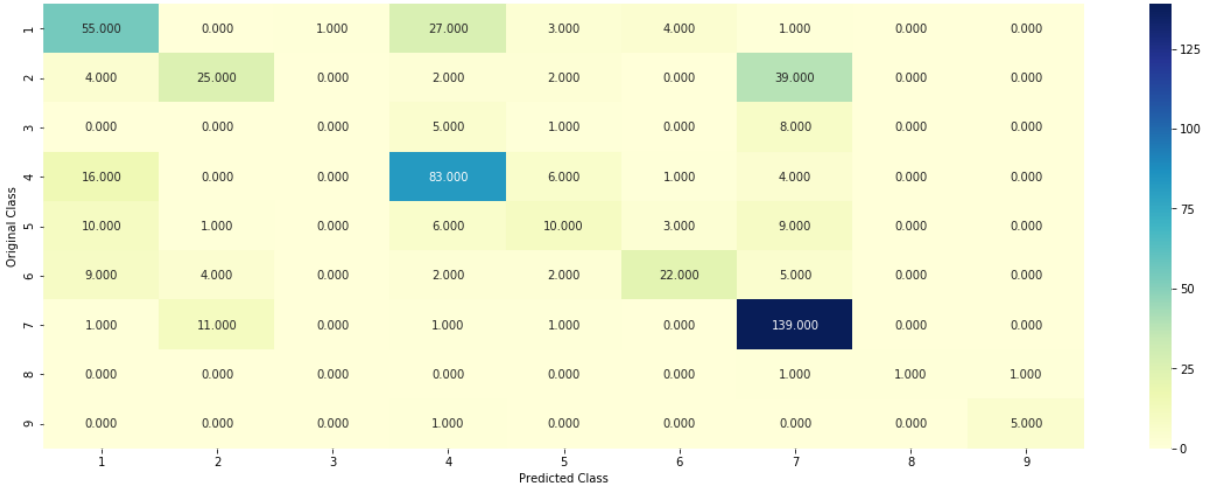



```
For values of best alpha =  0.0001 The train log loss is: 0.45969599094
32371
For values of best alpha =  0.0001 The cross validation log loss is: 0.
9592272390857216
For values of best alpha =  0.0001 The test log loss is: 0.981812207166
8812
```

4.3.1.2. Testing the model with best hyper paramters

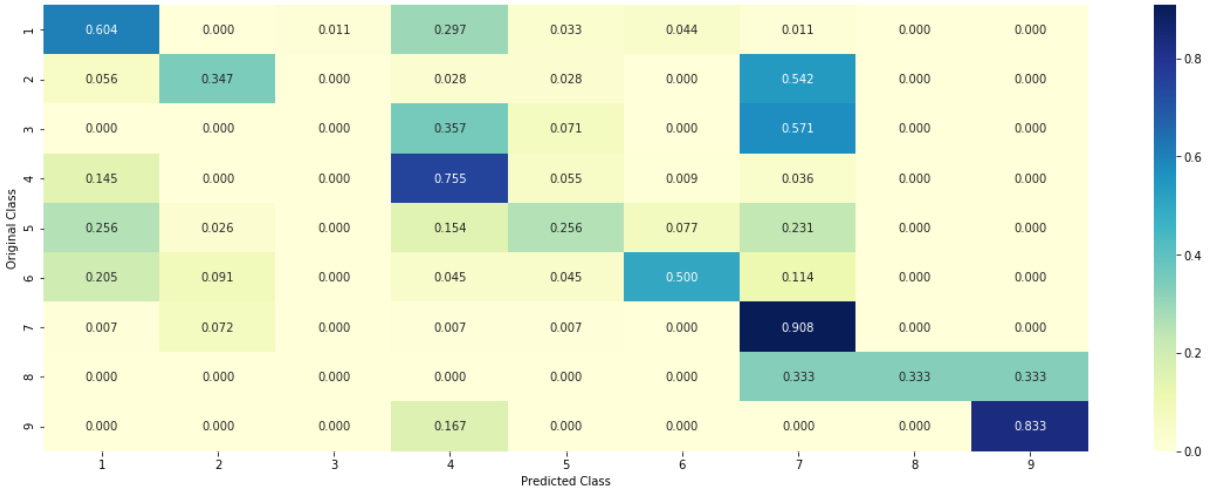
In [63]:
```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], p
enalty='l2', loss='log', random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_o
nehotCoding, cv_y, clf)
```

```
Log loss : 0.9592272390857216
Number of mis-classified points : 0.3609022556390977
-------------------- Confusion matrix --------------------
```



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

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



4.3.1.3. Feature Importance

In [64]:
```
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 que
```

```
ry point")
    print("-"*50)
    print("The features that are most importent of the ",predicted_cls[
0]," class:")
    print (tabulate(tabulte_list, headers=["Index",'Feature name', 'Pre
sent or Not']))
```

4.3.1.3.1. Correctly Classified point

In [65]:
```
# from tabulate import tabulate
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], p
enalty='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[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.0469 0.0068 0.0035 0.91   0.0056 0.0
106 0.0137 0.0015 0.0015]]
Actual Class : 4
--------------------------------------------------
10 Text feature [suppressor] present in test data point [True]
66 Text feature [inactivation] present in test data point [True]
82 Text feature [missense] present in test data point [True]
106 Text feature [families] present in test data point [True]
107 Text feature [mice] present in test data point [True]
124 Text feature [unable] present in test data point [True]
127 Text feature [tagged] present in test data point [True]
```

```
160 Text feature [mm] present in test data point [True]
164 Text feature [transfected] present in test data point [True]
166 Text feature [lanes] present in test data point [True]
169 Text feature [null] present in test data point [True]
172 Text feature [tumorigenesis] present in test data point [True]
175 Text feature [specifically] present in test data point [True]
177 Text feature [germline] present in test data point [True]
203 Text feature [caused] present in test data point [True]
212 Text feature [high] present in test data point [True]
221 Text feature [show] present in test data point [True]
243 Text feature [iii] present in test data point [True]
249 Text feature [displayed] present in test data point [True]
261 Text feature [functionally] present in test data point [True]
267 Text feature [protein] present in test data point [True]
271 Text feature [family] present in test data point [True]
272 Text feature [regions] present in test data point [True]
277 Text feature [suggesting] present in test data point [True]
278 Text feature [ca] present in test data point [True]
282 Text feature [phenotype] present in test data point [True]
284 Text feature [nature] present in test data point [True]
288 Text feature [relatively] present in test data point [True]
289 Text feature [lane] present in test data point [True]
290 Text feature [isolated] present in test data point [True]
292 Text feature [low] present in test data point [True]
296 Text feature [purified] present in test data point [True]
299 Text feature [cycle] present in test data point [True]
303 Text feature [kinases] present in test data point [True]
304 Text feature [bind] present in test data point [True]
306 Text feature [age] present in test data point [True]
327 Text feature [western] present in test data point [True]
332 Text feature [characterized] present in test data point [True]
335 Text feature [functional] present in test data point [True]
337 Text feature [reduced] present in test data point [True]
350 Text feature [washed] present in test data point [True]
352 Text feature [bound] present in test data point [True]
353 Text feature [due] present in test data point [True]
361 Text feature [cannot] present in test data point [True]
365 Text feature [representative] present in test data point [True]
376 Text feature [stability] present in test data point [True]
```

```
398 Text feature [dominant] present in test data point [True]
405 Text feature [investigated] present in test data point [True]
411 Text feature [p16ink4a] present in test data point [True]
412 Text feature [lack] present in test data point [True]
413 Text feature [stably] present in test data point [True]
415 Text feature [defective] present in test data point [True]
416 Text feature [indicate] present in test data point [True]
420 Text feature [comparison] present in test data point [True]
424 Text feature [transfection] present in test data point [True]
425 Text feature [suggested] present in test data point [True]
434 Text feature [nucleus] present in test data point [True]
441 Text feature [resulting] present in test data point [True]
443 Text feature [elevated] present in test data point [True]
444 Text feature [fact] present in test data point [True]
445 Text feature [min] present in test data point [True]
452 Text feature [mutants] present in test data point [True]
455 Text feature [proteins] present in test data point [True]
457 Text feature [determine] present in test data point [True]
463 Text feature [dna] present in test data point [True]
468 Text feature [anti] present in test data point [True]
470 Text feature [despite] present in test data point [True]
473 Text feature [negative] present in test data point [True]
476 Text feature [often] present in test data point [True]
479 Text feature [26] present in test data point [True]
488 Text feature [buffer] present in test data point [True]
489 Text feature [sds] present in test data point [True]
490 Text feature [locus] present in test data point [True]
491 Text feature [described] present in test data point [True]
492 Text feature [induced] present in test data point [True]
494 Text feature [membrane] present in test data point [True]
496 Text feature [lines] present in test data point [True]
497 Text feature [similarly] present in test data point [True]
498 Text feature [blue] present in test data point [True]
Out of the top  500  features  79 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

In [66]:
```
test_point_index = 101
```

```
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[1.390e-01 1.562e-01 5.700e-03 2.840e-0
2 1.230e-02 1.160e-02 6.442e-01
  2.000e-03 6.000e-04]]
Actual Class : 2
--------------------------------------------------
7 Text feature [activation] present in test data point [True]
8 Text feature [downstream] present in test data point [True]
22 Text feature [activated] present in test data point [True]
31 Text feature [oncogene] present in test data point [True]
32 Text feature [factor] present in test data point [True]
42 Text feature [activate] present in test data point [True]
44 Text feature [lung] present in test data point [True]
47 Text feature [enhanced] present in test data point [True]
50 Text feature [advanced] present in test data point [True]
56 Text feature [transformed] present in test data point [True]
57 Text feature [transforming] present in test data point [True]
59 Text feature [raf] present in test data point [True]
73 Text feature [pathways] present in test data point [True]
85 Text feature [open] present in test data point [True]
90 Text feature [codon] present in test data point [True]
101 Text feature [adenocarcinoma] present in test data point [True]
116 Text feature [epithelial] present in test data point [True]
124 Text feature [positive] present in test data point [True]
128 Text feature [oncogenic] present in test data point [True]
134 Text feature [volume] present in test data point [True]
142 Text feature [days] present in test data point [True]
144 Text feature [tyrosine] present in test data point [True]
```

```
148 Text feature [pi3k] present in test data point [True]
149 Text feature [ras] present in test data point [True]
152 Text feature [bone] present in test data point [True]
157 Text feature [mapk] present in test data point [True]
167 Text feature [14] present in test data point [True]
182 Text feature [cdna] present in test data point [True]
196 Text feature [activating] present in test data point [True]
198 Text feature [survival] present in test data point [True]
206 Text feature [regulated] present in test data point [True]
208 Text feature [signals] present in test data point [True]
212 Text feature [stat3] present in test data point [True]
216 Text feature [expressing] present in test data point [True]
218 Text feature [ligand] present in test data point [True]
228 Text feature [signaling] present in test data point [True]
229 Text feature [leading] present in test data point [True]
234 Text feature [3b] present in test data point [True]
240 Text feature [mechanisms] present in test data point [True]
249 Text feature [constitutively] present in test data point [True]
255 Text feature [phosphorylated] present in test data point [True]
262 Text feature [promote] present in test data point [True]
270 Text feature [presence] present in test data point [True]
282 Text feature [serum] present in test data point [True]
297 Text feature [added] present in test data point [True]
298 Text feature [2a] present in test data point [True]
299 Text feature [fold] present in test data point [True]
313 Text feature [000] present in test data point [True]
321 Text feature [cultured] present in test data point [True]
323 Text feature [contribute] present in test data point [True]
326 Text feature [leukemia] present in test data point [True]
327 Text feature [examined] present in test data point [True]
329 Text feature [size] present in test data point [True]
342 Text feature [kinase] present in test data point [True]
352 Text feature [approximately] present in test data point [True]
360 Text feature [long] present in test data point [True]
366 Text feature [mechanism] present in test data point [True]
372 Text feature [2b] present in test data point [True]
382 Text feature [additional] present in test data point [True]
389 Text feature [without] present in test data point [True]
396 Text feature [differentiation] present in test data point [True]
```

```
401 Text feature [concentrations] present in test data point [True]
402 Text feature [increased] present in test data point [True]
424 Text feature [elevated] present in test data point [True]
425 Text feature [genomic] present in test data point [True]
428 Text feature [inhibitor] present in test data point [True]
438 Text feature [per] present in test data point [True]
440 Text feature [position] present in test data point [True]
453 Text feature [carcinoma] present in test data point [True]
461 Text feature [cancers] present in test data point [True]
465 Text feature [medium] present in test data point [True]
493 Text feature [occur] present in test data point [True]
498 Text feature [4a] present in test data point [True]
Out of the top  500  features  73 are present in query point
```

4.3.2. Without Class balancing

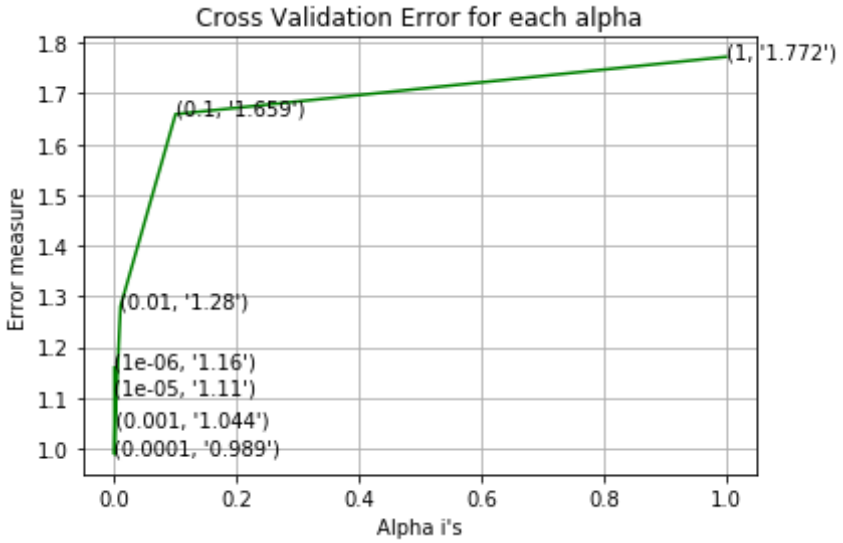
4.3.2.1. Hyper paramter tuning

In [67]:

```
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_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 vali
dation 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 l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.159663444368
for alpha = 1e-05
Log Loss : 1.1097127772102164
for alpha = 0.0001
Log Loss : 0.9885670178607632
for alpha = 0.001
Log Loss : 1.0437443129599728
for alpha = 0.01
Log Loss : 1.2803226548582942
for alpha = 0.1
Log Loss : 1.6590207410042168
for alpha = 1
Log Loss : 1.772123502722826
```

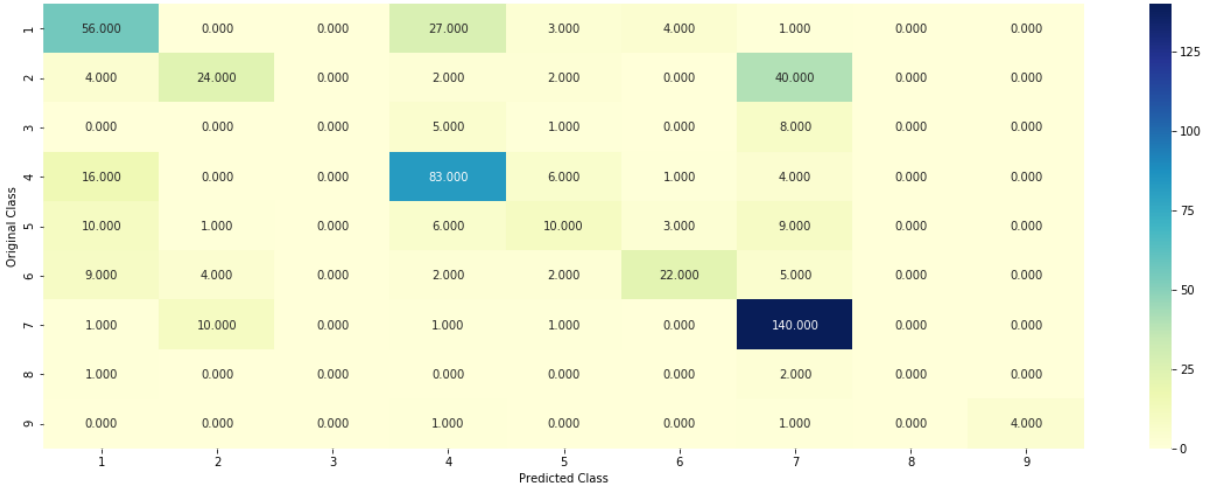



```
For values of best alpha =  0.0001 The train log loss is: 0.45039701510
94821
For values of best alpha =  0.0001 The cross validation log loss is: 0.
9885670178607632
For values of best alpha =  0.0001 The test log loss is: 1.003869542113
4203
```

4.3.2.2. Testing model with best hyper parameters

In [68]:
```
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_o
nehotCoding, cv_y, clf)
```

```
Log loss : 0.9885670178607632
Number of mis-classified points : 0.36278195488721804
-------------------- Confusion matrix --------------------
```



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

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

4.3.2.3. Feature Importance, Correctly Classified point

In [69]:
```
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[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[5.010e-02 7.100e-03 2.600e-03 9.075e-0
1 5.000e-03 1.010e-02 1.600e-02
```

```
  1.000e-03 5.000e-04]]
Actual Class : 4
--------------------------------------------------
22 Text feature [suppressor] present in test data point [True]
73 Text feature [inactivation] present in test data point [True]
93 Text feature [mice] present in test data point [True]
97 Text feature [missense] present in test data point [True]
137 Text feature [families] present in test data point [True]
140 Text feature [unable] present in test data point [True]
159 Text feature [tagged] present in test data point [True]
161 Text feature [specifically] present in test data point [True]
167 Text feature [tumorigenesis] present in test data point [True]
172 Text feature [lanes] present in test data point [True]
179 Text feature [null] present in test data point [True]
183 Text feature [caused] present in test data point [True]
199 Text feature [transfected] present in test data point [True]
200 Text feature [show] present in test data point [True]
201 Text feature [mm] present in test data point [True]
209 Text feature [high] present in test data point [True]
223 Text feature [regions] present in test data point [True]
239 Text feature [germline] present in test data point [True]
246 Text feature [functionally] present in test data point [True]
257 Text feature [displayed] present in test data point [True]
271 Text feature [protein] present in test data point [True]
272 Text feature [family] present in test data point [True]
273 Text feature [characterized] present in test data point [True]
274 Text feature [due] present in test data point [True]
277 Text feature [ca] present in test data point [True]
281 Text feature [suggesting] present in test data point [True]
289 Text feature [cannot] present in test data point [True]
290 Text feature [isolated] present in test data point [True]
291 Text feature [cycle] present in test data point [True]
292 Text feature [iii] present in test data point [True]
294 Text feature [bind] present in test data point [True]
296 Text feature [age] present in test data point [True]
298 Text feature [kinases] present in test data point [True]
300 Text feature [relatively] present in test data point [True]
301 Text feature [bound] present in test data point [True]

303 Text feature [low] present in test data point [True]
```

```
303 Text feature [low] present in test data point [True]
304 Text feature [western] present in test data point [True]
311 Text feature [functional] present in test data point [True]
315 Text feature [phenotype] present in test data point [True]
316 Text feature [lane] present in test data point [True]
331 Text feature [reduced] present in test data point [True]
336 Text feature [washed] present in test data point [True]
337 Text feature [purified] present in test data point [True]
354 Text feature [nature] present in test data point [True]
365 Text feature [representative] present in test data point [True]
387 Text feature [stably] present in test data point [True]
395 Text feature [investigated] present in test data point [True]
401 Text feature [defective] present in test data point [True]
405 Text feature [lack] present in test data point [True]
409 Text feature [often] present in test data point [True]
412 Text feature [mutants] present in test data point [True]
414 Text feature [elevated] present in test data point [True]
417 Text feature [dominant] present in test data point [True]
418 Text feature [indicate] present in test data point [True]
423 Text feature [stability] present in test data point [True]
424 Text feature [transfection] present in test data point [True]
425 Text feature [suggested] present in test data point [True]
430 Text feature [dna] present in test data point [True]
435 Text feature [resulting] present in test data point [True]
436 Text feature [fact] present in test data point [True]
439 Text feature [anti] present in test data point [True]
441 Text feature [comparison] present in test data point [True]
445 Text feature [membrane] present in test data point [True]
447 Text feature [determine] present in test data point [True]
448 Text feature [described] present in test data point [True]
449 Text feature [induced] present in test data point [True]
450 Text feature [nucleus] present in test data point [True]
453 Text feature [26] present in test data point [True]
454 Text feature [despite] present in test data point [True]
462 Text feature [proteins] present in test data point [True]
463 Text feature [observed] present in test data point [True]
466 Text feature [experiments] present in test data point [True]
467 Text feature [negative] present in test data point [True]
469 Text feature [min] present in test data point [True]

470 Text feature [p16ink4a] present in test data point [True]
```

```
470 Text feature [p16ink4a] present in test data point [True]
471 Text feature [similarly] present in test data point [True]
476 Text feature [figure] present in test data point [True]
477 Text feature [according] present in test data point [True]
479 Text feature [blue] present in test data point [True]
481 Text feature [lines] present in test data point [True]
483 Text feature [antibody] present in test data point [True]
485 Text feature [finally] present in test data point [True]
486 Text feature [3b] present in test data point [True]
487 Text feature [mouse] present in test data point [True]
492 Text feature [conserved] present in test data point [True]
493 Text feature [carcinomas] present in test data point [True]
495 Text feature [alone] present in test data point [True]
496 Text feature [buffer] present in test data point [True]
Out of the top  500  features  88 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

In [70]:
```
test_point_index = 101
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[1.459e-01 1.531e-01 5.000e-03 2.570e-0
2 1.110e-02 1.050e-02 6.474e-01
  1.100e-03 1.000e-04]]
Actual Class : 2
--------------------------------------------------
13 Text feature [downstream] present in test data point [True]
20 Text feature [activation] present in test data point [True]
```

```
39 Text feature [activated] present in test data point [True]
41 Text feature [factor] present in test data point [True]
47 Text feature [advanced] present in test data point [True]
48 Text feature [oncogene] present in test data point [True]
58 Text feature [activate] present in test data point [True]
61 Text feature [lung] present in test data point [True]
69 Text feature [raf] present in test data point [True]
97 Text feature [codon] present in test data point [True]
107 Text feature [adenocarcinoma] present in test data point [True]
110 Text feature [enhanced] present in test data point [True]
112 Text feature [transforming] present in test data point [True]
125 Text feature [transformed] present in test data point [True]
129 Text feature [open] present in test data point [True]
149 Text feature [volume] present in test data point [True]
151 Text feature [positive] present in test data point [True]
152 Text feature [epithelial] present in test data point [True]
154 Text feature [ras] present in test data point [True]
167 Text feature [signals] present in test data point [True]
171 Text feature [regulated] present in test data point [True]
175 Text feature [pathways] present in test data point [True]
186 Text feature [pi3k] present in test data point [True]
195 Text feature [bone] present in test data point [True]
226 Text feature [tyrosine] present in test data point [True]
228 Text feature [cdna] present in test data point [True]
229 Text feature [activating] present in test data point [True]
230 Text feature [3b] present in test data point [True]
234 Text feature [14] present in test data point [True]
249 Text feature [oncogenic] present in test data point [True]
253 Text feature [days] present in test data point [True]
255 Text feature [expressing] present in test data point [True]
263 Text feature [mapk] present in test data point [True]
265 Text feature [mechanisms] present in test data point [True]
266 Text feature [phosphorylated] present in test data point [True]
270 Text feature [survival] present in test data point [True]
275 Text feature [fold] present in test data point [True]
280 Text feature [000] present in test data point [True]
287 Text feature [presence] present in test data point [True]
297 Text feature [contribute] present in test data point [True]
308 Text feature [added] present in test data point [True]
```

```
314 Text feature [stat3] present in test data point [True]
316 Text feature [additional] present in test data point [True]
317 Text feature [approximately] present in test data point [True]
318 Text feature [size] present in test data point [True]
319 Text feature [constitutively] present in test data point [True]
320 Text feature [regions] present in test data point [True]
323 Text feature [cultured] present in test data point [True]
329 Text feature [2a] present in test data point [True]
333 Text feature [examined] present in test data point [True]
340 Text feature [serum] present in test data point [True]
341 Text feature [genomic] present in test data point [True]
342 Text feature [without] present in test data point [True]
343 Text feature [ligand] present in test data point [True]
349 Text feature [leading] present in test data point [True]
368 Text feature [signaling] present in test data point [True]
385 Text feature [2b] present in test data point [True]
398 Text feature [kinase] present in test data point [True]
404 Text feature [concentrations] present in test data point [True]
406 Text feature [differentiation] present in test data point [True]
409 Text feature [promote] present in test data point [True]
420 Text feature [increased] present in test data point [True]
424 Text feature [inhibitor] present in test data point [True]
425 Text feature [occur] present in test data point [True]
426 Text feature [cancers] present in test data point [True]
435 Text feature [mechanism] present in test data point [True]
441 Text feature [long] present in test data point [True]
453 Text feature [myc] present in test data point [True]
457 Text feature [effective] present in test data point [True]
462 Text feature [elevated] present in test data point [True]
474 Text feature [carcinoma] present in test data point [True]
486 Text feature [position] present in test data point [True]
490 Text feature [leukemia] present in test data point [True]
494 Text feature [high] present in test data point [True]
498 Text feature [lead] present in test data point [True]
499 Text feature [prior] present in test data point [True]
Out of the top  500  features  76 are present in query point
```

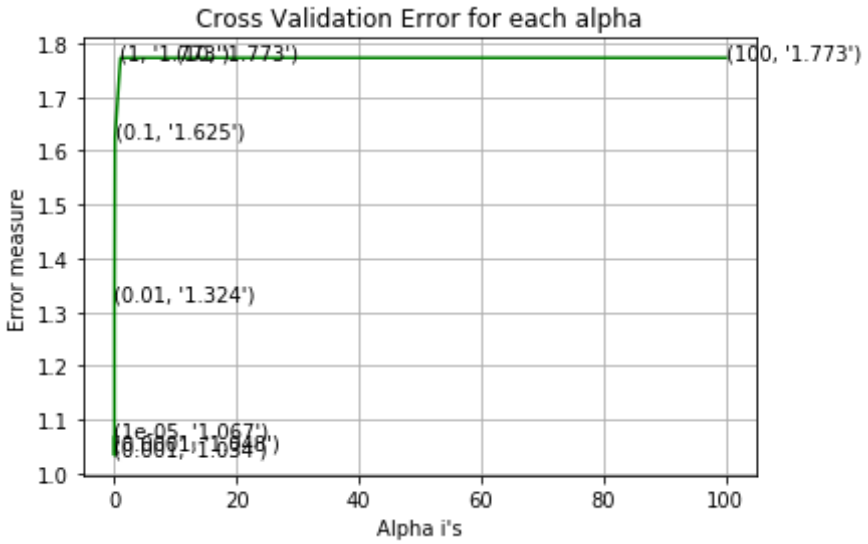
4.4. Linear Support Vector Machines

4.4.1. Hyper paramter tuning

In [71]:
```
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='bal
anced')
    clf = SGDClassifier( class_weight='balanced', alpha=i, penalty='l2'
, loss='hinge', 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 = SVC(C=i,kernel='linear',probability=True, class_weight='balance
d')
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], p
enalty='l2', loss='hinge', 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_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 vali
dation 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 l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for C = 1e-05
Log Loss : 1.0672508450165827
for C = 0.0001
Log Loss : 1.0477046910278855
for C = 0.001
Log Loss : 1.033863744921307
for C = 0.01
Log Loss : 1.3241033994783225
for C = 0.1
Log Loss : 1.6249909916051588
for C = 1
Log Loss : 1.7728091995996178
for C = 10
Log Loss : 1.772809175511976
for C = 100
Log Loss : 1.7728092091521763
```

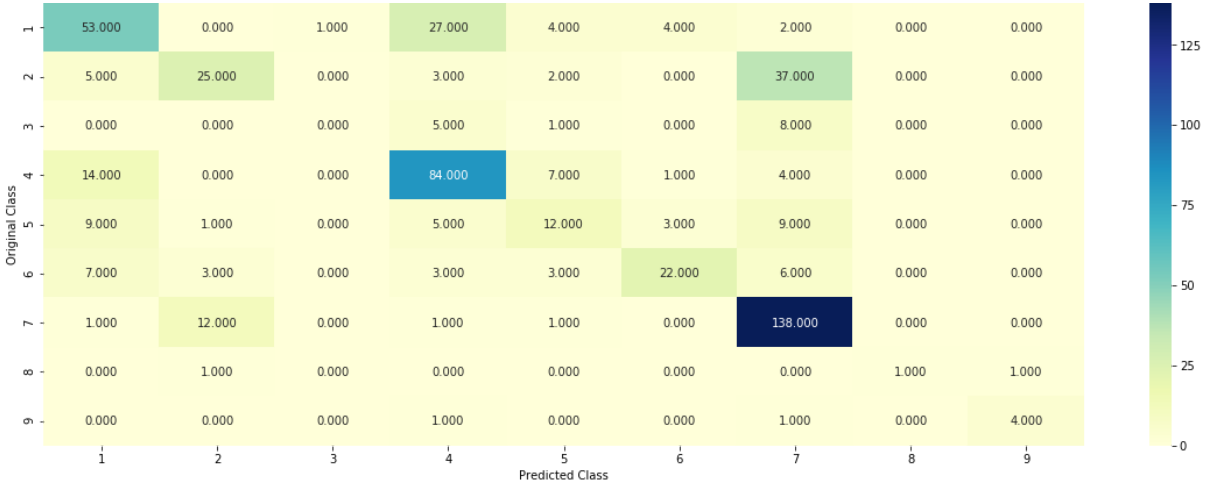



```
For values of best alpha =  0.001 The train log loss is: 0.613998415056
0919
For values of best alpha =  0.001 The cross validation log loss is: 1.0
33863744921307
For values of best alpha =  0.001 The test log loss is: 1.0720934859290
718
```

4.4.2. Testing model with best hyper parameters

In [72]:
```
# clf = SVC(C=alpha[best_alpha],kernel='linear',probability=True, class
_weight='balanced')
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge'
, random_state=42,class_weight='balanced')
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_on
ehotCoding,cv_y, clf)
```

```
Log loss : 1.033863744921307
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 [73]:
```
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge'
, random_state=42)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
# test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.0685 0.025  0.0065 0.8025 0.0107 0.0
144 0.068  0.0013 0.0031]]
Actual Class : 4
--------------------------------------------------
16 Text feature [suppressor] present in test data point [True]
26 Text feature [inactivation] present in test data point [True]
27 Text feature [families] present in test data point [True]
28 Text feature [missense] present in test data point [True]
31 Text feature [unable] present in test data point [True]
33 Text feature [null] present in test data point [True]
35 Text feature [lanes] present in test data point [True]
37 Text feature [suggesting] present in test data point [True]
233 Text feature [germline] present in test data point [True]
235 Text feature [iii] present in test data point [True]
237 Text feature [relatively] present in test data point [True]
238 Text feature [tagged] present in test data point [True]
240 Text feature [transfected] present in test data point [True]
241 Text feature [mice] present in test data point [True]
242 Text feature [show] present in test data point [True]
243 Text feature [family] present in test data point [True]
246 Text feature [comparison] present in test data point [True]
247 Text feature [functionally] present in test data point [True]
249 Text feature [specifically] present in test data point [True]
251 Text feature [age] present in test data point [True]
252 Text feature [stably] present in test data point [True]
253 Text feature [purified] present in test data point [True]
254 Text feature [caused] present in test data point [True]
342 Text feature [high] present in test data point [True]
344 Text feature [mm] present in test data point [True]
345 Text feature [kinases] present in test data point [True]
346 Text feature [nature] present in test data point [True]
347 Text feature [lane] present in test data point [True]
348 Text feature [due] present in test data point [True]
349 Text feature [isolated] present in test data point [True]
355 Text feature [ca] present in test data point [True]
356 Text feature [characterized] present in test data point [True]
359 Text feature [mutants] present in test data point [True]
362 Text feature [displayed] present in test data point [True]
```

```
364 Text feature [regions] present in test data point [True]
365 Text feature [localization] present in test data point [True]
366 Text feature [western] present in test data point [True]
368 Text feature [cycle] present in test data point [True]
369 Text feature [tumorigenesis] present in test data point [True]
370 Text feature [determine] present in test data point [True]
371 Text feature [stability] present in test data point [True]
372 Text feature [reduced] present in test data point [True]
373 Text feature [washed] present in test data point [True]
375 Text feature [plasma] present in test data point [True]
376 Text feature [functional] present in test data point [True]
422 Text feature [university] present in test data point [True]
423 Text feature [phenotype] present in test data point [True]
425 Text feature [lack] present in test data point [True]
426 Text feature [direct] present in test data point [True]
429 Text feature [26] present in test data point [True]
431 Text feature [alone] present in test data point [True]
432 Text feature [primary] present in test data point [True]
434 Text feature [short] present in test data point [True]
435 Text feature [2a] present in test data point [True]
436 Text feature [despite] present in test data point [True]
437 Text feature [elevated] present in test data point [True]
438 Text feature [nucleus] present in test data point [True]
441 Text feature [bound] present in test data point [True]
443 Text feature [fact] present in test data point [True]
444 Text feature [negative] present in test data point [True]
445 Text feature [blue] present in test data point [True]
446 Text feature [loss] present in test data point [True]
449 Text feature [protein] present in test data point [True]
450 Text feature [according] present in test data point [True]
451 Text feature [lines] present in test data point [True]
453 Text feature [dominant] present in test data point [True]
455 Text feature [motif] present in test data point [True]
456 Text feature [induced] present in test data point [True]
457 Text feature [finally] present in test data point [True]
460 Text feature [investigated] present in test data point [True]
461 Text feature [various] present in test data point [True]
462 Text feature [bind] present in test data point [True]
463 Text feature [locus] present in test data point [True]
```

```
466 Text feature [p16ink4a] present in test data point [True]
467 Text feature [low] present in test data point [True]
469 Text feature [figure] present in test data point [True]
470 Text feature [sds] present in test data point [True]
471 Text feature [described] present in test data point [True]
473 Text feature [transfection] present in test data point [True]
475 Text feature [resulting] present in test data point [True]
476 Text feature [co] present in test data point [True]
478 Text feature [suggested] present in test data point [True]
479 Text feature [representative] present in test data point [True]
480 Text feature [percentage] present in test data point [True]
483 Text feature [carried] present in test data point [True]
Out of the top  500  features  85 are present in query point
```

4.3.3.2. For Incorrectly classified point

In [74]:
```
test_point_index = 101
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.1503 0.1159 0.0089 0.0424 0.0108 0.0
2   0.6497 0.001  0.0011]]
Actual Class : 2
--------------------------------------------------
19 Text feature [activation] present in test data point [True]
20 Text feature [downstream] present in test data point [True]
21 Text feature [activated] present in test data point [True]
29 Text feature [activate] present in test data point [True]
```

```
31 Text feature [factor] present in test data point [True]
32 Text feature [raf] present in test data point [True]
38 Text feature [constitutively] present in test data point [True]
39 Text feature [oncogene] present in test data point [True]
42 Text feature [mapk] present in test data point [True]
43 Text feature [enhanced] present in test data point [True]
45 Text feature [codon] present in test data point [True]
46 Text feature [advanced] present in test data point [True]
48 Text feature [expressing] present in test data point [True]
57 Text feature [positive] present in test data point [True]
60 Text feature [open] present in test data point [True]
61 Text feature [promote] present in test data point [True]
62 Text feature [lung] present in test data point [True]
64 Text feature [pi3k] present in test data point [True]
65 Text feature [pathways] present in test data point [True]
66 Text feature [signaling] present in test data point [True]
67 Text feature [transformed] present in test data point [True]
69 Text feature [2a] present in test data point [True]
70 Text feature [transforming] present in test data point [True]
71 Text feature [volume] present in test data point [True]
74 Text feature [ligand] present in test data point [True]
77 Text feature [14] present in test data point [True]
79 Text feature [presence] present in test data point [True]
80 Text feature [activating] present in test data point [True]
226 Text feature [tyrosine] present in test data point [True]
227 Text feature [signals] present in test data point [True]
229 Text feature [phosphorylated] present in test data point [True]
230 Text feature [bone] present in test data point [True]
233 Text feature [days] present in test data point [True]
234 Text feature [cultured] present in test data point [True]
236 Text feature [ras] present in test data point [True]
237 Text feature [adenocarcinoma] present in test data point [True]
238 Text feature [without] present in test data point [True]
239 Text feature [oncogenic] present in test data point [True]
240 Text feature [2b] present in test data point [True]
241 Text feature [stat3] present in test data point [True]
242 Text feature [leading] present in test data point [True]
243 Text feature [cdna] present in test data point [True]
244 Text feature [000] present in test data point [True]
```

```
246 Text feature [mechanism] present in test data point [True]
247 Text feature [approximately] present in test data point [True]
249 Text feature [lead] present in test data point [True]
250 Text feature [regulated] present in test data point [True]
254 Text feature [inhibitor] present in test data point [True]
255 Text feature [additional] present in test data point [True]
256 Text feature [examined] present in test data point [True]
259 Text feature [fold] present in test data point [True]
385 Text feature [inhibition] present in test data point [True]
386 Text feature [effective] present in test data point [True]
387 Text feature [cancers] present in test data point [True]
388 Text feature [mechanisms] present in test data point [True]
397 Text feature [egfr] present in test data point [True]
399 Text feature [75] present in test data point [True]
400 Text feature [survival] present in test data point [True]
402 Text feature [3b] present in test data point [True]
403 Text feature [independent] present in test data point [True]
407 Text feature [increased] present in test data point [True]
408 Text feature [carcinoma] present in test data point [True]
409 Text feature [added] present in test data point [True]
410 Text feature [epithelial] present in test data point [True]
411 Text feature [leukemia] present in test data point [True]
413 Text feature [medium] present in test data point [True]
415 Text feature [elevated] present in test data point [True]
420 Text feature [pathway] present in test data point [True]
425 Text feature [differentiation] present in test data point [True]
427 Text feature [serum] present in test data point [True]
428 Text feature [prior] present in test data point [True]
441 Text feature [long] present in test data point [True]
443 Text feature [versus] present in test data point [True]
445 Text feature [size] present in test data point [True]
448 Text feature [extracellular] present in test data point [True]
449 Text feature [egf] present in test data point [True]
450 Text feature [taken] present in test data point [True]
451 Text feature [met] present in test data point [True]
452 Text feature [fusion] present in test data point [True]
453 Text feature [contribute] present in test data point [True]
454 Text feature [occur] present in test data point [True]
455 Text feature [proliferation] present in test data point [True]
```

```
456 Text feature [concentrations] present in test data point [True]
459 Text feature [leads] present in test data point [True]
460 Text feature [wt] present in test data point [True]
463 Text feature [fig] present in test data point [True]
473 Text feature [cells] present in test data point [True]
Out of the top  500  features  87 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

In [75]:
```
alpha = [100,200,500,1000,2000]
max_depth = [5, 10]
cv_log_error_array = []
for i in alpha:
    for j in max_depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gini',
max_depth=j, random_state=42, n_jobs=-1)
        clf.fit(train_x_onehotCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_onehotCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=
clf.classes_, eps=1e-15))
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))

'''fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ra
vel()
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)), (featur
es[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
```

```
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
'''

best_alpha = np.argmin(cv_log_error_array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], cri
terion='gini', max_depth=max_depth[int(best_alpha%2)], random_state=42,
 n_jobs=-1)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The
 train log loss is:",log_loss(y_train, predict_y, labels=clf.classes_,
eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The
 cross validation log loss is:",log_loss(y_cv, predict_y, labels=clf.cl
asses_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The
 test log loss is:",log_loss(y_test, predict_y, labels=clf.classes_, ep
s=1e-15))
```

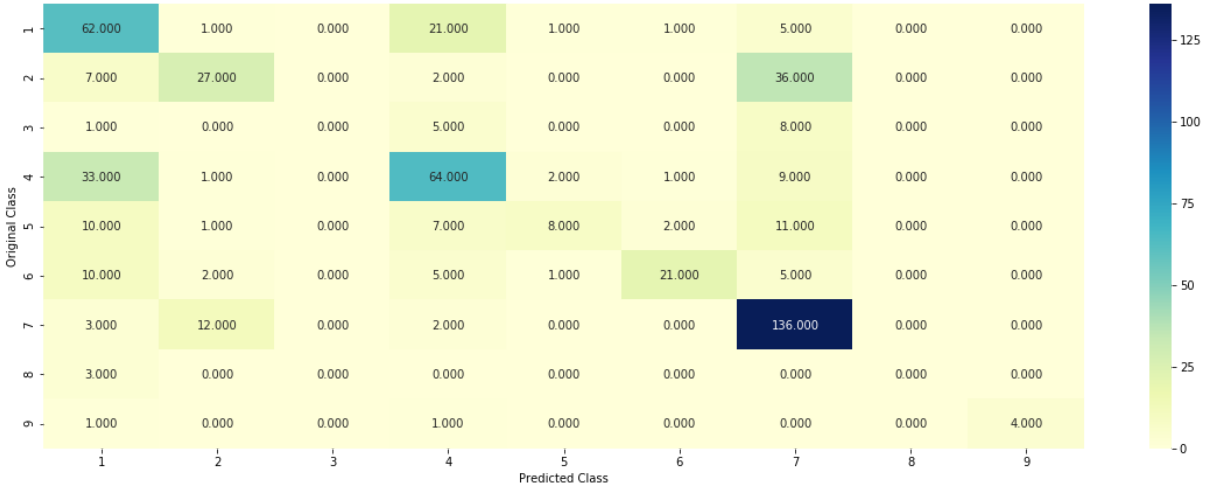
```
for n_estimators = 100 and max depth =  5
Log Loss : 1.1662869706605203
for n_estimators = 100 and max depth =  10
Log Loss : 1.2296173965186212
for n_estimators = 200 and max depth =  5
Log Loss : 1.157020052811411
for n_estimators = 200 and max depth =  10
Log Loss : 1.2252229358729414
for n_estimators = 500 and max depth =  5
Log Loss : 1.14883671793405
for n_estimators = 500 and max depth =  10
Log Loss : 1.2190354457954917
for n_estimators = 1000 and max depth =  5
Log Loss : 1.1465173708083658
```

```
for n_estimators = 1000 and max depth =  10
Log Loss : 1.2148527168802434
for n_estimators = 2000 and max depth =  5
Log Loss : 1.1441176066419199
for n_estimators = 2000 and max depth =  10
Log Loss : 1.2129552465813416
For values of best estimator =  2000 The train log loss is: 0.860645628
2491302
For values of best estimator =  2000 The cross validation log loss is:
1.1441176066419199
For values of best estimator =  2000 The test log loss is: 1.1772003468
316752
```

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

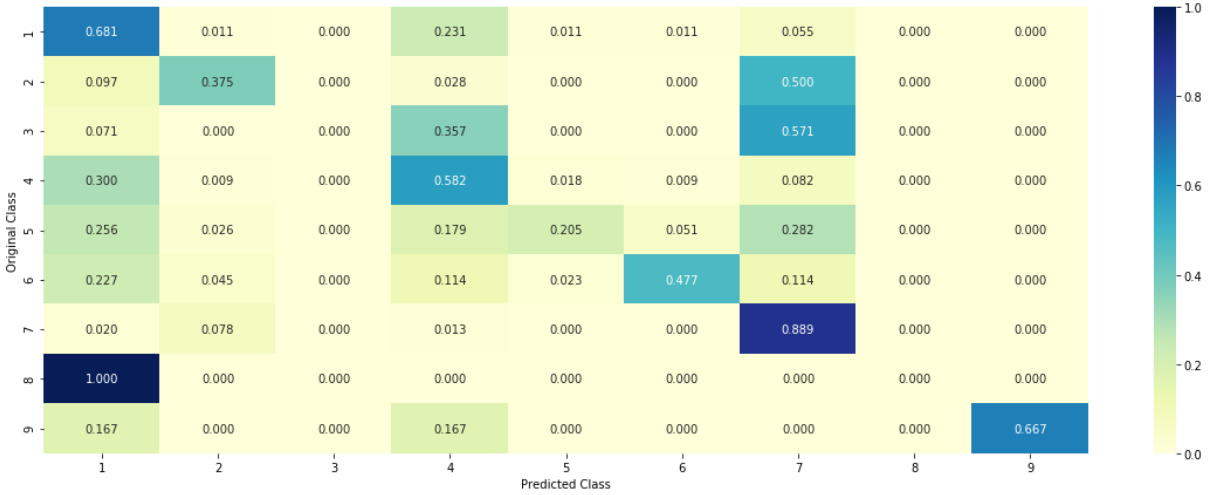
In [76]:
```
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], cri
terion='gini', max_depth=max_depth[int(best_alpha%2)], random_state=42,
 n_jobs=-1)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_on
ehotCoding,cv_y, clf)
```

```
Log loss : 1.1441176066419199
Number of mis-classified points : 0.39473684210526316
-------------------- 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 [77]:
```
# test_point_index = 10
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], cri
terion='gini', max_depth=max_depth[int(best_alpha%2)], random_state=42,
 n_jobs=-1)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

test_point_index = 1
```

```
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
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_po
int_index],test_df['Gene'].iloc[test_point_index],test_df['Variation'].
iloc[test_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.1981 0.0359 0.0153 0.5714 0.042  0.0
399 0.0824 0.0055 0.0095]]
Actual Class : 4
--------------------------------------------------
0 Text feature [kinase] present in test data point [True]
1 Text feature [activating] present in test data point [True]
2 Text feature [inhibitors] present in test data point [True]
3 Text feature [suppressor] present in test data point [True]
4 Text feature [activation] present in test data point [True]
5 Text feature [function] present in test data point [True]
6 Text feature [activated] present in test data point [True]
7 Text feature [phosphorylation] present in test data point [True]
10 Text feature [inhibitor] present in test data point [True]
12 Text feature [loss] present in test data point [True]
14 Text feature [missense] present in test data point [True]
20 Text feature [therapeutic] present in test data point [True]
23 Text feature [protein] present in test data point [True]
25 Text feature [stability] present in test data point [True]
27 Text feature [functional] present in test data point [True]
29 Text feature [growth] present in test data point [True]
31 Text feature [cells] present in test data point [True]
36 Text feature [cell] present in test data point [True]
39 Text feature [treated] present in test data point [True]
43 Text feature [proteins] present in test data point [True]
50 Text feature [defective] present in test data point [True]
52 Text feature [kinases] present in test data point [True]

55 Text feature [expression] present in test data point [True]
```

```
60 Text feature [patients] present in test data point [True]
63 Text feature [inhibition] present in test data point [True]
64 Text feature [proliferation] present in test data point [True]
67 Text feature [inactivation] present in test data point [True]
69 Text feature [phosphorylated] present in test data point [True]
76 Text feature [functions] present in test data point [True]
77 Text feature [potential] present in test data point [True]
78 Text feature [clinical] present in test data point [True]
81 Text feature [expected] present in test data point [True]
85 Text feature [null] present in test data point [True]
87 Text feature [nuclear] present in test data point [True]
92 Text feature [variant] present in test data point [True]
94 Text feature [tagged] present in test data point [True]
Out of the top  100  features  36 are present in query point
```

4.5.3.2. Inorrectly Classified point

In [78]:
```
test_point_index = 101
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
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_po
int_index],test_df['Gene'].iloc[test_point_index],test_df['Variation'].
iloc[test_point_index], no_feature)
```

```
Predicted Class : 1
Predicted Class Probabilities: [[0.4103 0.1778 0.014  0.0521 0.0416 0.0
415 0.2365 0.0159 0.0102]]
Actuall Class : 2
--------------------------------------------------
0 Text feature [kinase] present in test data point [True]
1 Text feature [activating] present in test data point [True]
2 Text feature [inhibitors] present in test data point [True]
```

```
3 Text feature [suppressor] present in test data point [True]
4 Text feature [activation] present in test data point [True]
5 Text feature [function] present in test data point [True]
6 Text feature [activated] present in test data point [True]
7 Text feature [phosphorylation] present in test data point [True]
9 Text feature [tyrosine] present in test data point [True]
10 Text feature [inhibitor] present in test data point [True]
11 Text feature [treatment] present in test data point [True]
12 Text feature [loss] present in test data point [True]
13 Text feature [oncogenic] present in test data point [True]
14 Text feature [missense] present in test data point [True]
16 Text feature [therapy] present in test data point [True]
18 Text feature [downstream] present in test data point [True]
19 Text feature [pathogenic] present in test data point [True]
20 Text feature [therapeutic] present in test data point [True]
21 Text feature [receptor] present in test data point [True]
22 Text feature [deleterious] present in test data point [True]
23 Text feature [protein] present in test data point [True]
26 Text feature [months] present in test data point [True]
27 Text feature [functional] present in test data point [True]
29 Text feature [growth] present in test data point [True]
30 Text feature [activate] present in test data point [True]
31 Text feature [cells] present in test data point [True]
33 Text feature [signaling] present in test data point [True]
36 Text feature [cell] present in test data point [True]
38 Text feature [variants] present in test data point [True]
39 Text feature [treated] present in test data point [True]
41 Text feature [constitutively] present in test data point [True]
42 Text feature [57] present in test data point [True]
43 Text feature [proteins] present in test data point [True]
44 Text feature [trials] present in test data point [True]
48 Text feature [extracellular] present in test data point [True]
49 Text feature [survival] present in test data point [True]
50 Text feature [defective] present in test data point [True]
51 Text feature [transforming] present in test data point [True]
52 Text feature [kinases] present in test data point [True]
53 Text feature [classified] present in test data point [True]
55 Text feature [expression] present in test data point [True]
58 Text feature [resistance] present in test data point [True]
```

```
59 Text feature [drug] present in test data point [True]
60 Text feature [patients] present in test data point [True]
61 Text feature [efficacy] present in test data point [True]
63 Text feature [inhibition] present in test data point [True]
64 Text feature [proliferation] present in test data point [True]
67 Text feature [inactivation] present in test data point [True]
69 Text feature [phosphorylated] present in test data point [True]
70 Text feature [predicted] present in test data point [True]
71 Text feature [sensitivity] present in test data point [True]
72 Text feature [expressing] present in test data point [True]
74 Text feature [mammalian] present in test data point [True]
75 Text feature [response] present in test data point [True]
76 Text feature [functions] present in test data point [True]
77 Text feature [potential] present in test data point [True]
78 Text feature [clinical] present in test data point [True]
79 Text feature [oncogene] present in test data point [True]
80 Text feature [phospho] present in test data point [True]
81 Text feature [expected] present in test data point [True]
82 Text feature [advanced] present in test data point [True]
83 Text feature [mapk] present in test data point [True]
84 Text feature [risk] present in test data point [True]
85 Text feature [null] present in test data point [True]
86 Text feature [ligand] present in test data point [True]
87 Text feature [nuclear] present in test data point [True]
89 Text feature [ras] present in test data point [True]
90 Text feature [dose] present in test data point [True]
92 Text feature [variant] present in test data point [True]
94 Text feature [tagged] present in test data point [True]
98 Text feature [harboring] present in test data point [True]
99 Text feature [responses] present in test data point [True]
Out of the top  100  features  72 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

In [79]:
```
alpha = [10,50,100,200,500,1000]
max_depth = [2,3,5,10]
cv_log_error_array = []
for i in alpha:
```

```
    for j in max_depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gini',
max_depth=j, random_state=42, n_jobs=-1)
        clf.fit(train_x_responseCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_responseCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=
clf.classes_, eps=1e-15))
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))
'''
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ra
vel()
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)), (featur
es[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
'''

best_alpha = np.argmin(cv_log_error_array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], cri
terion='gini', max_depth=max_depth[int(best_alpha%4)], random_state=42,
 n_jobs=-1)
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 tra
in 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[int(best_alpha/4)], "The cro
ss validation log loss is:",log_loss(y_cv, predict_y, labels=clf.classe
s_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The tes
t log loss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e
-15))
```

```
for n_estimators = 10 and max depth =  2
Log Loss : 1.9631974601380937
for n_estimators = 10 and max depth =  3
Log Loss : 1.571900472816233
for n_estimators = 10 and max depth =  5
Log Loss : 1.34315438719086
for n_estimators = 10 and max depth =  10
Log Loss : 2.0639700372551846
for n_estimators = 50 and max depth =  2
Log Loss : 1.5919995200872872
for n_estimators = 50 and max depth =  3
Log Loss : 1.2775554311030006
for n_estimators = 50 and max depth =  5
Log Loss : 1.2530961687853788
for n_estimators = 50 and max depth =  10
Log Loss : 1.8655690389433899
for n_estimators = 100 and max depth =  2
Log Loss : 1.4389948345196057
for n_estimators = 100 and max depth =  3
Log Loss : 1.3317405913079314
for n_estimators = 100 and max depth =  5
Log Loss : 1.2522258662834134
for n_estimators = 100 and max depth =  10
Log Loss : 1.811717183821225
for n_estimators = 200 and max depth =  2
Log Loss : 1.4820198030530838
for n_estimators = 200 and max depth =  3
Log Loss : 1.3615239831619814
for n_estimators = 200 and max depth =  5
Log Loss : 1.265820738140215
for n_estimators = 200 and max depth =  10
Log Loss : 1.8209139584463039
```

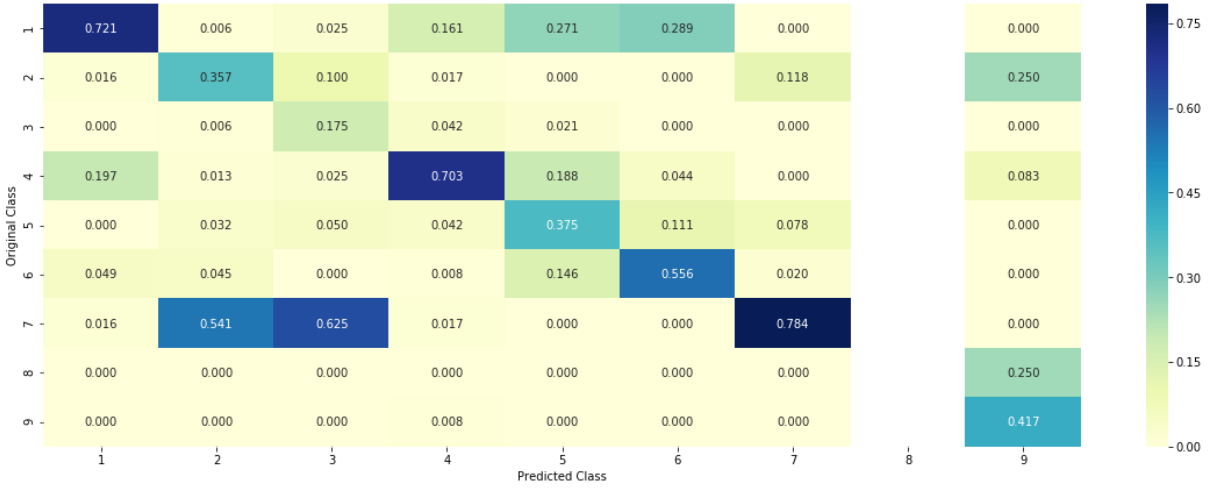
```
for n_estimators = 500 and max depth =  2
Log Loss : 1.5453332867583032
for n_estimators = 500 and max depth =  3
Log Loss : 1.4073920329365985
for n_estimators = 500 and max depth =  5
Log Loss : 1.2726433827825285
for n_estimators = 500 and max depth =  10
Log Loss : 1.830295648507375
for n_estimators = 1000 and max depth =  2
Log Loss : 1.530405054602531
for n_estimators = 1000 and max depth =  3
Log Loss : 1.4148700460644987
for n_estimators = 1000 and max depth =  5
Log Loss : 1.2918426202454447
for n_estimators = 1000 and max depth =  10
Log Loss : 1.7846069319633722
For values of best alpha =  100 The train log loss is: 0.05976203627795
982
For values of best alpha =  100 The cross validation log loss is: 1.252
2258662834136
For values of best alpha =  100 The test log loss is: 1.354323293806235
3
```

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

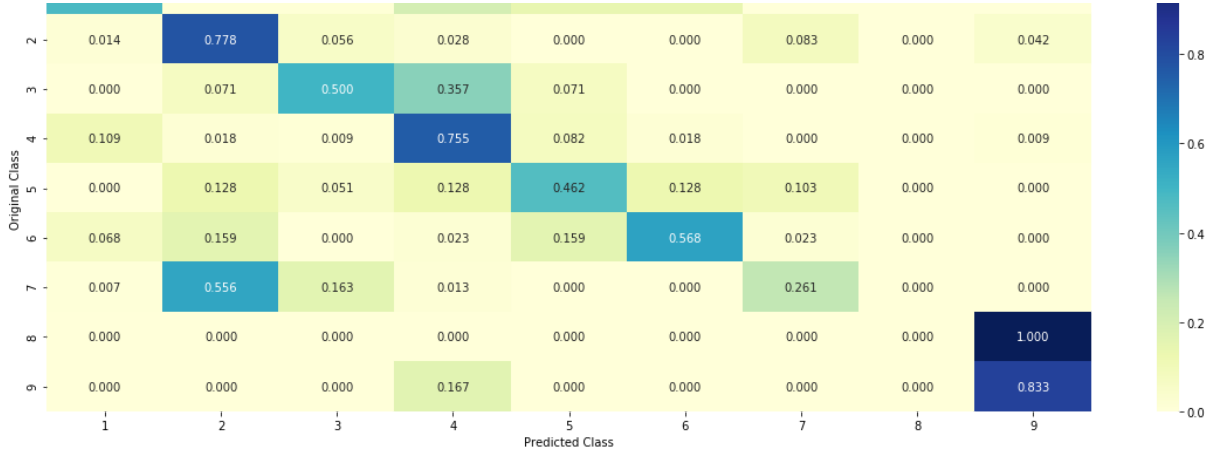
In [80]:
```
clf = RandomForestClassifier(max_depth=max_depth[int(best_alpha%4)], n_
estimators=alpha[int(best_alpha/4)], criterion='gini', max_features='au
to',random_state=42)
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_
responseCoding,cv_y, clf)
```

```
Log loss : 1.2522258662834136
Number of mis-classified points : 0.4774436090225564
-------------------- 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 [81]:

```
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], cri
terion='gini', max_depth=max_depth[int(best_alpha%4)], random_state=42,
 n_jobs=-1)
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)


test_point_index = 1
no_feature = 27
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index]
.reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_responseCoding[test_point_index].reshape(1,-1)),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
```

```
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:
        print("Text is important feature")
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.102  0.0294 0.1132 0.6016 0.023  0.0
441 0.0124 0.0282 0.0461]]
Actual Class : 4
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
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
Gene is important feature
Variation is important feature
Gene is important feature
Text is important feature
Gene is important feature
Variation is important feature
Text is important feature
Variation is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.5.5.2. Incorrectly Classified point

In [82]:
```
test_point_index = 101
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index]
.reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_responseCoding[test_point_index].reshape(1,-1)),4))
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: [[0.0398 0.3042 0.2399 0.0361 0.0391 0.0
748 0.1475 0.0517 0.0668]]
Actual Class : 2
--------------------------------------------------
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
Gene is important feature
Variation is important feature
Gene is important feature
Text is important feature
Gene is important feature
Variation is important feature
Text is important feature
Variation is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.7 Stack the models

4.7.1 testing with hyper parameter tuning

In [83]:
```
clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class_weigh
t='balanced', random_state=0)
clf1.fit(train_x_onehotCoding, train_y)
sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")

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


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

sig_clf1.fit(train_x_onehotCoding, train_y)
print("Logistic Regression :  Log Loss: %0.2f" % (log_loss(cv_y, sig_cl
```

```
f1.predict_proba(cv_x_onehotCoding))))
sig_clf2.fit(train_x_onehotCoding, train_y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig
_clf2.predict_proba(cv_x_onehotCoding))))
sig_clf3.fit(train_x_onehotCoding, train_y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predic
t_proba(cv_x_onehotCoding))))
print("-"*50)
alpha = [0.0001,0.001,0.01,0.1,1,10]
best_alpha = 999
for i in alpha:
    lr = LogisticRegression(C=i)
    sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3
], meta_classifier=lr, use_probas=True)
    sclf.fit(train_x_onehotCoding, train_y)
    print("Stacking Classifer : for the value of alpha: %f Log Loss: %
0.3f" % (i, log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))))
    log_error =log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    if best_alpha > log_error:
        best_alpha = log_error
```

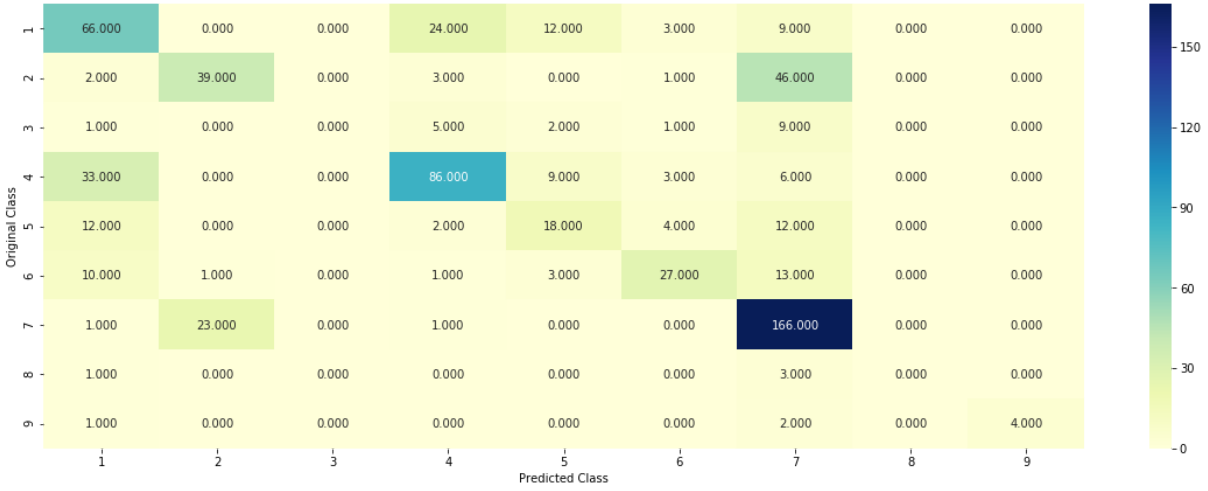
```
Logistic Regression :  Log Loss: 0.98
Support vector machines : Log Loss: 1.77
Naive Bayes : Log Loss: 1.19
--------------------------------------------------
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 2.178
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 2.031
Stacking Classifer : for the value of alpha: 0.010000 Log Loss: 1.493
Stacking Classifer : for the value of alpha: 0.100000 Log Loss: 1.156
Stacking Classifer : for the value of alpha: 1.000000 Log Loss: 1.383
Stacking Classifer : for the value of alpha: 10.000000 Log Loss: 1.853
```

4.7.2 testing the model with the best hyper parameters

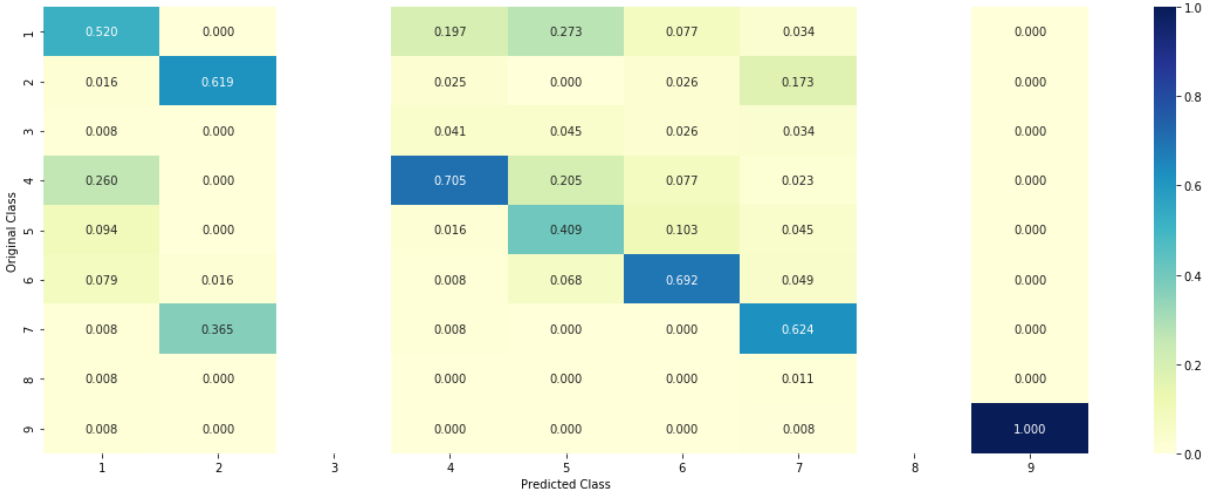
In [84]:
```
lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], m
eta_classifier=lr, use_probas=True)
sclf.fit(train_x_onehotCoding, train_y)
```

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

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

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

print("Number of missclassified point :", np.count_nonzero((sclf.predic
t(test_x_onehotCoding)- test_y))/test_y.shape[0])
plot_confusion_matrix(test_y=test_y, predict_y=sclf.predict(test_x_oneh
otCoding))
```

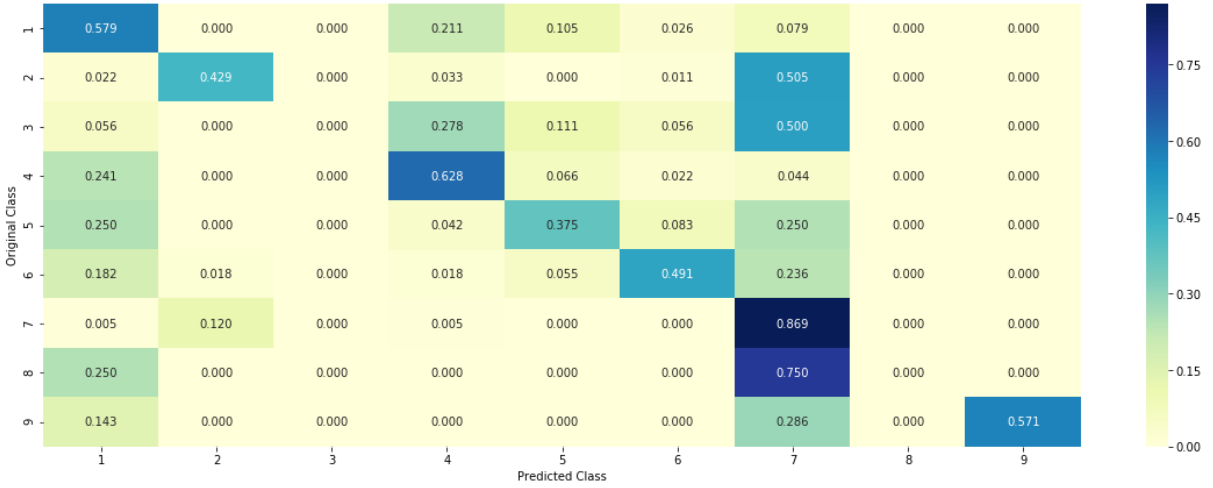
```
Log loss (train) on the stacking classifier : 0.5500466669676215
Log loss (CV) on the stacking classifier : 1.156284809286018
Log loss (test) on the stacking classifier : 1.1736255112748095
Number of missclassified point : 0.3894736842105263
-------------------- Confusion matrix --------------------
```




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



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



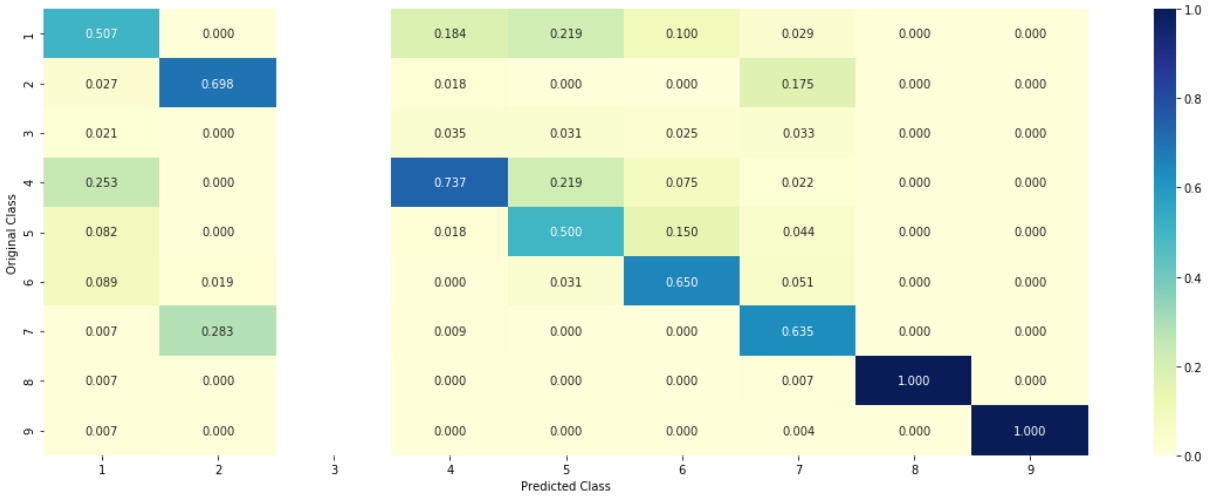
4.7.3 Maximum Voting classifier

In [85]:
```
#Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassifier.html
from sklearn.ensemble import VotingClassifier
```

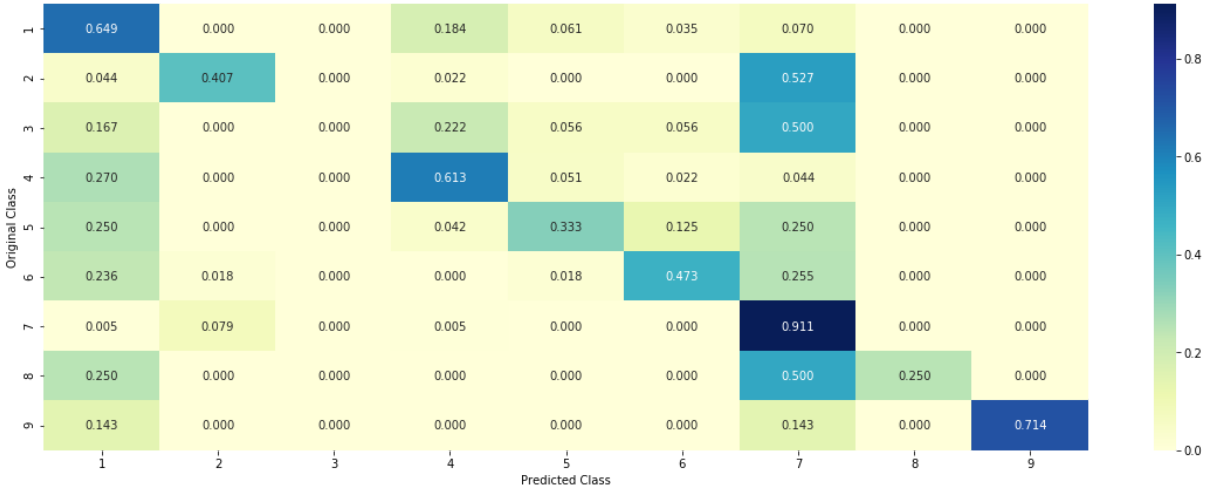
```
vclf = VotingClassifier(estimators=[('lr', sig_clf1), ('svc', sig_clf2
), ('rf', sig_clf3)], voting='soft')
vclf.fit(train_x_onehotCoding, train_y)
print("Log loss (train) on the VotingClassifier :", log_loss(train_y, v
clf.predict_proba(train_x_onehotCoding)))
print("Log loss (CV) on the VotingClassifier :", log_loss(cv_y, vclf.pr
edict_proba(cv_x_onehotCoding)))
print("Log loss (test) on the VotingClassifier :", log_loss(test_y, vcl
f.predict_proba(test_x_onehotCoding)))
print("Number of missclassified point :", np.count_nonzero((vclf.predic
t(test_x_onehotCoding)- test_y))/test_y.shape[0])
plot_confusion_matrix(test_y=test_y, predict_y=vclf.predict(test_x_oneh
otCoding))
```

```
Log loss (train) on the VotingClassifier : 0.8461049942052722
Log loss (CV) on the VotingClassifier : 1.172200763949369
Log loss (test) on the VotingClassifier : 1.1941821012413831
Number of missclassified point : 0.37293233082706767
-------------------- Confusion matrix --------------------
```


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



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



In [87]:
```
from prettytable import PrettyTable

x = PrettyTable()

x.field_names = ["S.No","Model","Train logloss","Cv logloss","Test logl
oss", "Misclassified error"]
```

```
x.add_row(["1","Naive Bayes","0.53","1.19","1.19","0.38"])
x.add_row(["2","KNN","0.65","1.01","1.044","0.36"])
x.add_row(["3","Logistic regression with C.Bal","0.56","1.07","1.08",
"0.336"])
x.add_row(["4","Logistic regression without C.Bal","0.45","0.95","0.98"
,"0.36"])
x.add_row(["5","Linear svm(with one hot encoding)","0.45","0.98","1.00"
,"0.36"])
x.add_row(["6","Random Forest(with one hot encoding)","0.61","1.03","1.
07","0.36"])
x.add_row(["7","Random Forest(with response coding)","0.86","1.14","1.1
77","0.394"])
x.add_row(["8","Stacking classifier","0.55","1.15","1.17","0.389"])
x.add_row(["9","Maximum voting classifier","0.84","1.17","1.19","0.37"
])


print(x)
```

```
+------+---------------------------------------+---------------+--------
----+-------------+---------------------+
| S.No |                Model                  | Train logloss | Cv logl
oss | Test logloss | Misclassified error |
+------+---------------------------------------+---------------+--------
----+-------------+---------------------+
|  1   |             Naive Bayes               |      0.53     |    1.19
    |     1.19     |         0.38        |
|  2   |                 KNN                   |      0.65     |    1.01
    |    1.044     |         0.36        |
|  3   |    Logistic regression with C.Bal     |      0.56     |    1.07
    |     1.08     |        0.336        |
|  4   |  Logistic regression without C.Bal    |      0.45     |    0.95
    |     0.98     |         0.36        |
|  5   |  Linear svm(with one hot encoding)    |      0.45     |    0.98
    |     1.00     |         0.36        |
|  6   | Random Forest(with one hot encoding)  |      0.61     |    1.03
    |     1.07     |         0.36        |
|  7   | Random Forest(with response coding)   |      0.86     |    1.14
    |    1.177     |        0.394        |
```

```
|  8   |         Stacking classifier          |      0.55     |    1.15
    |     1.17     |        0.389        |
|  9   |      Maximum voting classifier       |      0.84     |    1.17
    |     1.19     |         0.37        |
+------+--------------------------------------+---------------+--------
----+-------------+---------------------+
```

Conclusion

Here I replaced everything with Tfidf vectorizer and i top 1000 features and when we observe this Logistic Regression with class balancing has decent logloss values and reasonable Misclassification error compared to all other.. It seems slightly unstable but better than all other ...