Personalized cancer diagnosis

1. Business Problem

1.1. Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training_variants.zip and training_text.zip from Kaggle.

Context:

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

Problem statement :

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

1.2. Source/Useful Links

Some articles and reference blogs about the problem statement

1. https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almost-everyone-who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25

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

1.3. Real-world/Business objectives and constraints.

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

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 [24]:
```
import pandas as pd
import matplotlib.pyplot as plt
import re
import time
import warnings
import numpy as np
from nltk.corpus import stopwords
from sklearn.decomposition import TruncatedSVD
from sklearn.preprocessing import normalize
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.manifold import TSNE
import seaborn as sns
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics.classification import accuracy_score, log_loss
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.linear_model import SGDClassifier
```

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

from mlxtend.classifier import StackingClassifier

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/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/training_text",sep="\|\|",engine="pyth
on",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 : 211.52816454299833 seconds
```

In [13]:
```
#merging both gene_variations and text data based on ID
result = pd.merge(data, data_text,on='ID', how='left')
result.head()
```

Out[13]:

	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 [14]:
```
result[result.isnull().any(axis=1)]
```

Out[14]:

	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

	ID	Gene	Variation	Class	TEXT
2755	2755	BRAF	G596C	7	NaN

In [15]:
```
result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result
['Variation']
```

In [16]:
```
result[result['ID']==1109]
```

Out[16]:

	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 [17]:
```
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 o
f output varaible 'y_true' [stratify=y_true]
X_train, test_df, y_train, y_test = train_test_split(result, y_true, st
ratify=y_true, test_size=0.2)
# split the train data into train and cross validation by maintaining s
ame 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 [18]:
```
print('Number of data points in train data:', train_df.shape[0])
```

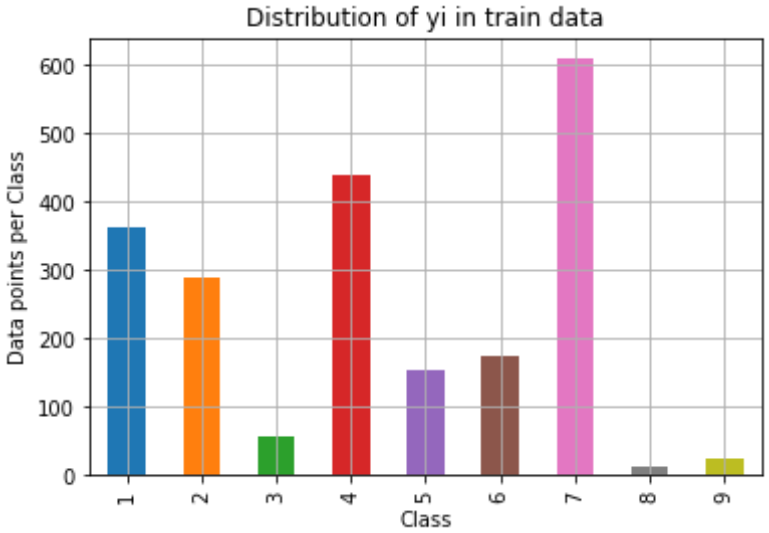
```
print('Number of data points in test data:', test_df.shape[0])
print('Number of data points in cross validation data:', cv_df.shape[0
])
```

```
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
```

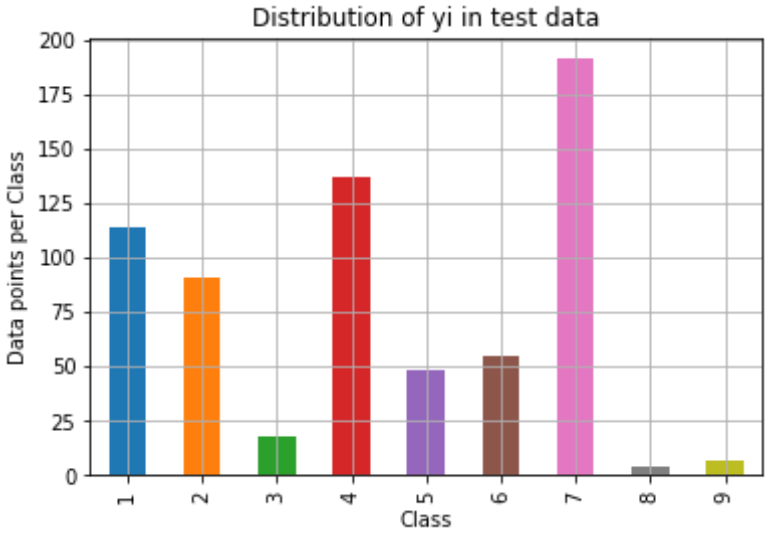
3.1.4.2. Distribution of y_i's in Train, Test and Cross Validation datasets

In [21]:
```
# 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')
```

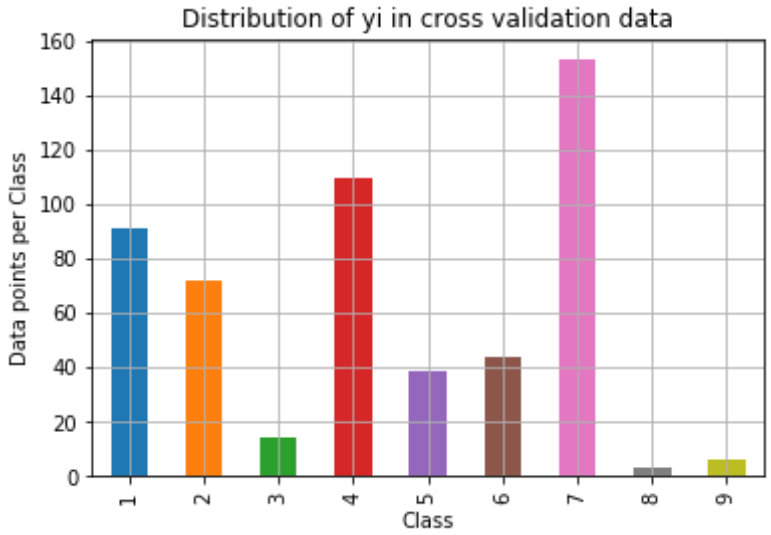
```
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in test data')
plt.grid()
plt.show()

# 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()

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 [25]:
```
# 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
```

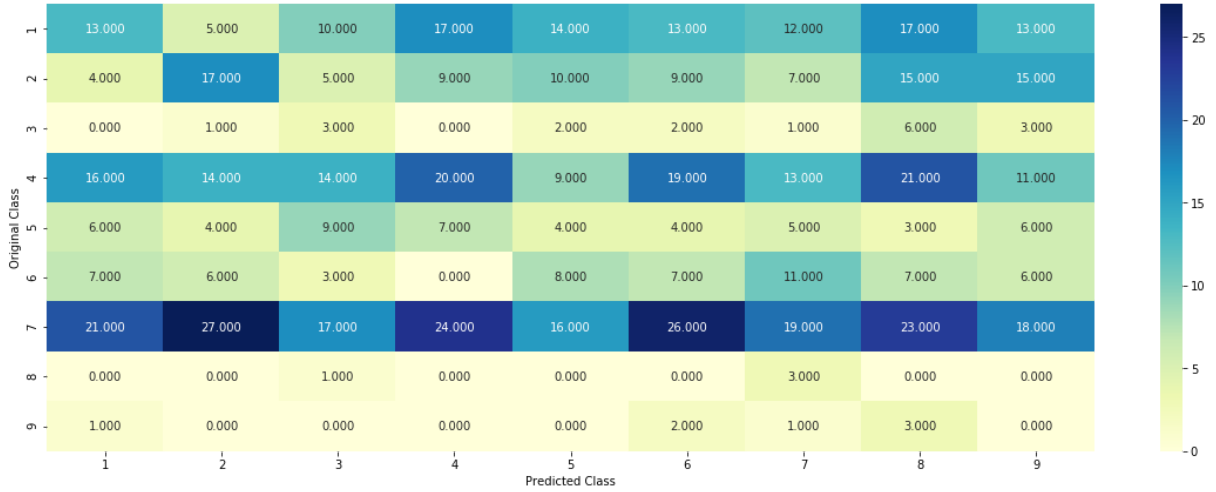
```
ass i are predicted class j

    A =(((C.T)/(C.sum(axis=1))).T)


    B =(C/C.sum(axis=0))


    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 [26]:

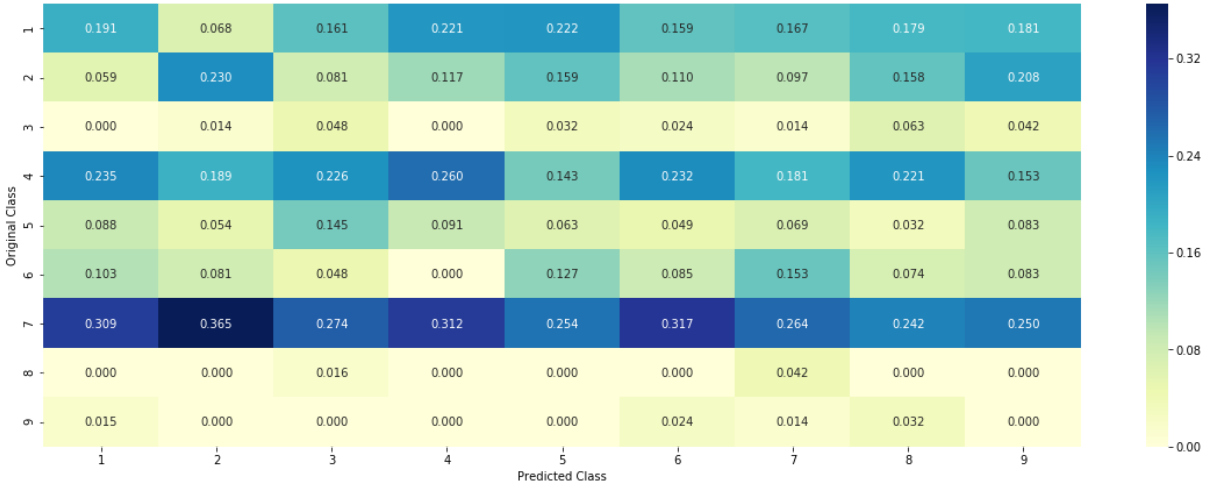
```
test_data_len = test_df.shape[0]
cv_data_len = cv_df.shape[0]

# 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)
```

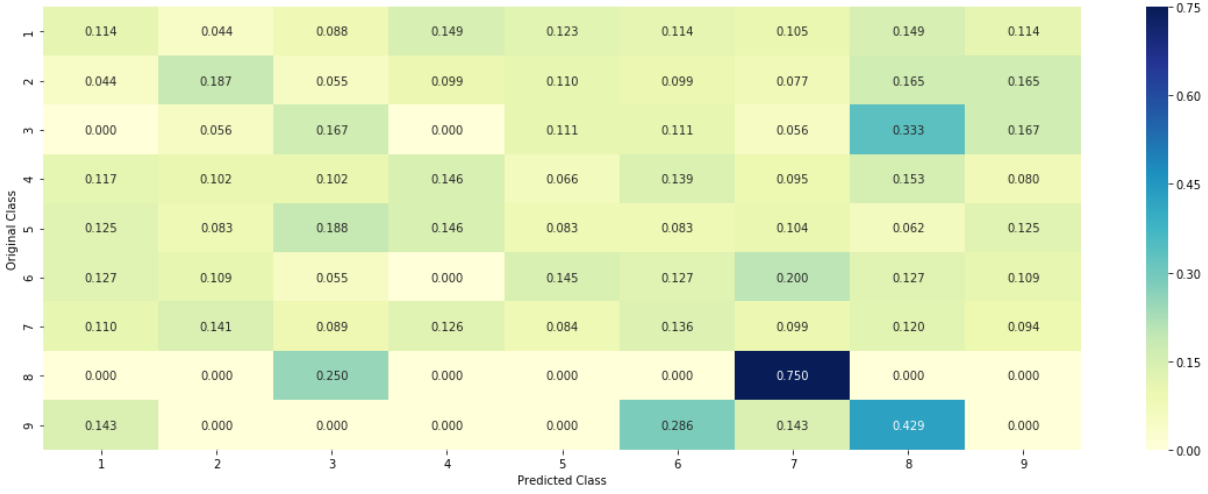
```
Log loss on Cross Validation Data using Random Model 2.536598785706848
Log loss on Test Data using Random Model 2.501572555849742
-------------------- Confusion matrix --------------------
```



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




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



3.3 Univariate Analysis

In [27]:
```
# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):

    value_count = train_df[feature].value_counts()

    # gv_dict : 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):

            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):

    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 index, row in df.iterrows():
        if row[feature] in dict(value_count).keys():
            gv_fea.append(gv_dict[row[feature]])
        else:
            gv_fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
    return gv_fea
```

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 [28]:
```
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))
```

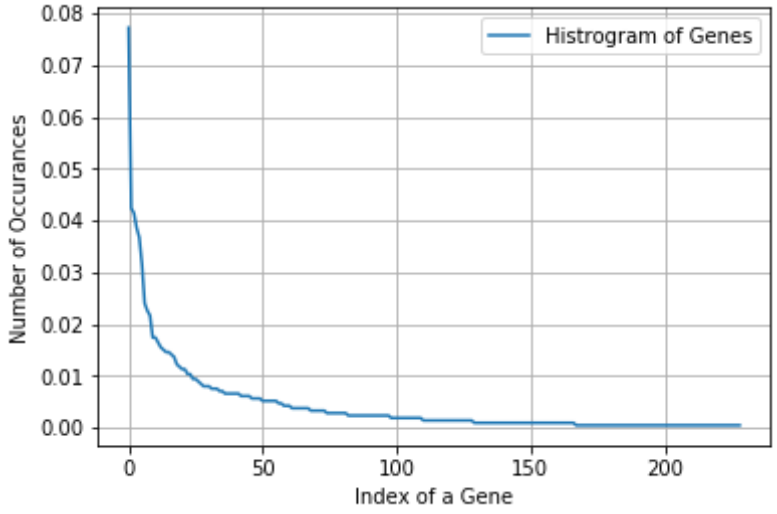
```
Number of Unique Genes : 229
BRCA1     164
TP53       90
EGFR       88
PTEN       82
BRCA2      78
KIT        67
BRAF       51
ALK        48
ERBB2      46
```

```
PIK3CA     37
Name: Gene, dtype: int64
```

In [29]:
```
print("Ans: There are", unique_genes.shape[0] ,"different categories of
 genes in the train data, and they are distibuted as follows",)
```

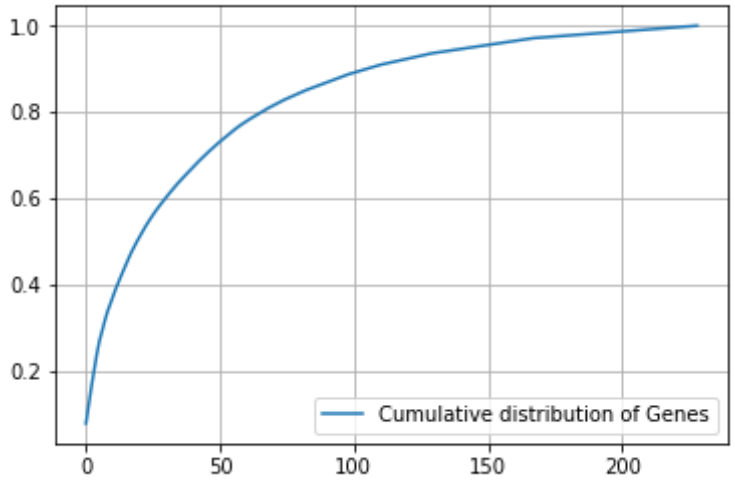
```
Ans: There are 229 different categories of genes in the train data, and
they are distibuted as follows
```

In [30]:
```
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 [31]:
```
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 [32]:
```
#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 [33]:
```
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 [34]:
```
# one-hot encoding of Gene feature.
gene_vectorizer = CountVectorizer()
train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_d
f['Gene'])
test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gen
e'])
cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
```

In [35]:
```
train_df['Gene'].head()
```

Out[35]:
```
2988       KIT
1718    KNSTRN
2076      TET2
751      ERBB2
462       TP53
Name: Gene, dtype: object
```

In [36]:
```
gene_vectorizer.get_feature_names()
```

Out[36]:
```
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
```

```
                'akt3',
                'alk',
                'apc',
                'ar',
                'araf',
                'arid1a',
                'arid2',
                'arid5b',
                'asxl1',
                'atm',
                'atr',
                'atrx',
                'aurka',
                'axl',
                'b2m',
                'bap1',
                'bcl10',
                'bcl2l11',
                'bcor',
                'braf',
                'brca1',
                'brca2',
                'brd4',
                'brip1',
                'btk',
                'card11',
                'carm1',
                'casp8',
                'cbl',
                'ccnd1',
                'ccnd2',
                'ccnd3',
                'ccne1',
                'cdh1',
                'cdk12',
                'cdk4',
                'cdk6',
                'cdk8',
                'cdkn1a',
```

```
                'cdkn1b',
                'cdkn2a',
                'cdkn2b',
                'cdkn2c',
                'cebpa',
                'chek2',
                'cic',
                'crebbp',
                'ctcf',
                'ctnnb1',
                'ddr2',
                'dicer1',
                'dnmt3a',
                'dnmt3b',
                'dusp4',
                'egfr',
                'elf3',
                'ep300',
                'epas1',
                'epcam',
                'erbb2',
                'erbb3',
                'erbb4',
                'ercc2',
                'ercc3',
                'ercc4',
                'erg',
                'esr1',
                'etv1',
                'etv6',
                'ewsr1',
                'ezh2',
                'fanca',
                'fancc',
                'fat1',
                'fbxw7',
                'fgf19',
                'fgf3',
                'fgfr1',
```

```
                'fgfr2',
                'fgfr3',
                'fgfr4',
                'flt3',
                'foxa1',
                'foxl2',
                'foxo1',
                'foxp1',
                'gata3',
                'gna11',
                'gnaq',
                'gnas',
                'h3f3a',
                'hist1h1c',
                'hla',
                'hnf1a',
                'hras',
                'idh1',
                'idh2',
                'igf1r',
                'ikzf1',
                'jak1',
                'jak2',
                'jun',
                'kdm5a',
                'kdm5c',
                'kdm6a',
                'kdr',
                'keap1',
                'kit',
                'kmt2a',
                'kmt2b',
                'kmt2c',
                'kmt2d',
                'knstrn',
                'kras',
                'lats1',
                'map2k1',
                'map2k2',
```

```
                'map2k4',
                'map3k1',
                'mapk1',
                'mdm4',
                'med12',
                'mef2b',
                'met',
                'mga',
                'mlh1',
                'mpl',
                'msh2',
                'msh6',
                'mtor',
                'myc',
                'mycn',
                'myd88',
                'myod1',
                'ncor1',
                'nf1',
                'nf2',
                'nfe2l2',
                'nfkbia',
                'nkx2',
                'notch1',
                'npm1',
                'nras',
                'nsd1',
                'ntrk1',
                'ntrk3',
                'nup93',
                'pax8',
                'pbrm1',
                'pdgfra',
                'pdgfrb',
                'pik3ca',
                'pik3cb',
                'pik3cd',
                'pik3r1',
                'pik3r2',
```

```
                'pik3r3',
                'pim1',
                'pms1',
                'pms2',
                'pole',
                'ppp2r1a',
                'ppp6c',
                'prdm1',
                'ptch1',
                'pten',
                'ptpn11',
                'ptprd',
                'ptprt',
                'rac1',
                'rad21',
                'rad50',
                'rad51b',
                'rad51c',
                'rad54l',
                'raf1',
                'rasa1',
                'rb1',
                'rbm10',
                'ret',
                'rheb',
                'rhoa',
                'rit1',
                'rnf43',
                'ros1',
                'rras2',
                'runx1',
                'rxra',
                'rybp',
                'sdhb',
                'sdhc',
                'setd2',
                'sf3b1',
                'shq1',
                'smad2',
```

```
'smad3',
'smad4',
'smarca4',
'smarcb1',
'smo',
'sos1',
'sox9',
'spop',
'src',
'stag2',
'stat3',
'stk11',
'tcf7l2',
'tert',
'tet1',
'tet2',
'tgfbr1',
'tgfbr2',
'tmprss2',
'tp53',
'tp53bp1',
'tsc1',
'tsc2',
'u2af1',
'vhl',
'whsc1',
'xpo1',
'xrcc2',
'yap1']
```

In [37]:
```
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, 229)
```

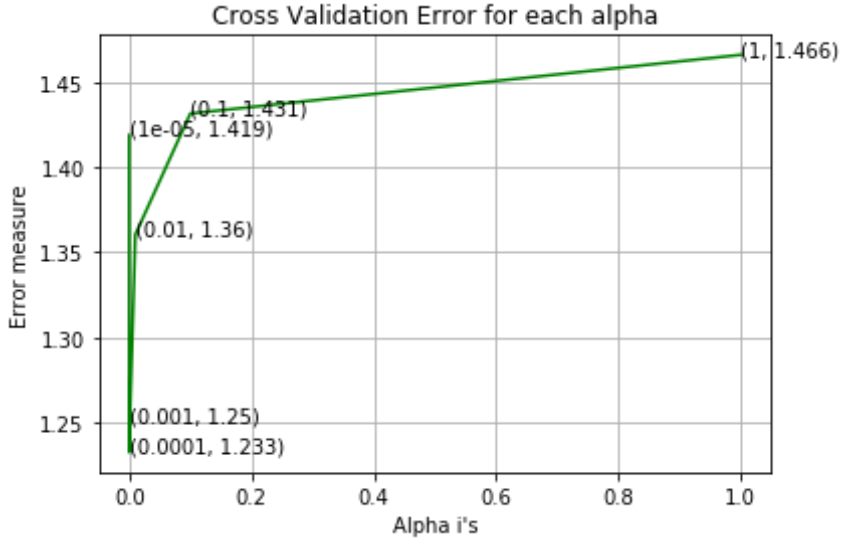
Q4. How good is this gene feature in predicting y_i?

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 [38]:
```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifie
r.


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: 1.418841767162939
For values of alpha =  0.0001 The log loss is: 1.2325868001617826
For values of alpha =  0.001 The log loss is: 1.2503129272158073
For values of alpha =  0.01 The log loss is: 1.360379976757511
For values of alpha =  0.1 The log loss is: 1.4314392521126913
For values of alpha =  1 The log loss is: 1.4659143358159061
```




```
For values of best alpha =  0.0001 The train log loss is: 1.04256043001
19806
```

```
For values of best alpha =  0.0001 The cross validation log loss is: 1.
2325868001617826
For values of best alpha =  0.0001 The test log loss is: 1.200905436534
172
```

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 [39]:
```
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'])))].shap
e[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  22
9  genes in train dataset?
Ans
1. In test data 643 out of 665 : 96.69172932330827
2. In cross validation data 514 out of  532 : 96.61654135338345
```

3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it ?

Ans. Variation is a categorical variable

Q8. How many categories are there?

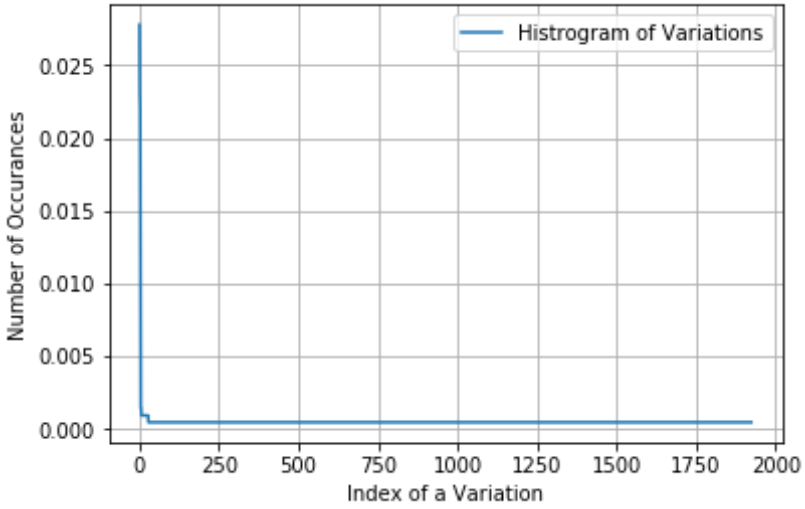
In [40]:
```
unique_variations = train_df['Variation'].value_counts()
print('Number of Unique Variations :', unique_variations.shape[0])
# the top 10 variations that occured most
print(unique_variations.head(10))
```

```
Number of Unique Variations : 1924
Truncating_Mutations         59
Deletion                     49
Amplification                47
Fusions                      23
E17K                          3
Overexpression                3
Q22K                          2
Promoter_Hypermethylation     2
G13D                          2
T73I                          2
Name: Variation, dtype: int64
```

In [41]:
```
print("Ans: There are", unique_variations.shape[0] ,"different categori
es of variations in the train data, and they are distibuted as follows"
,)
```

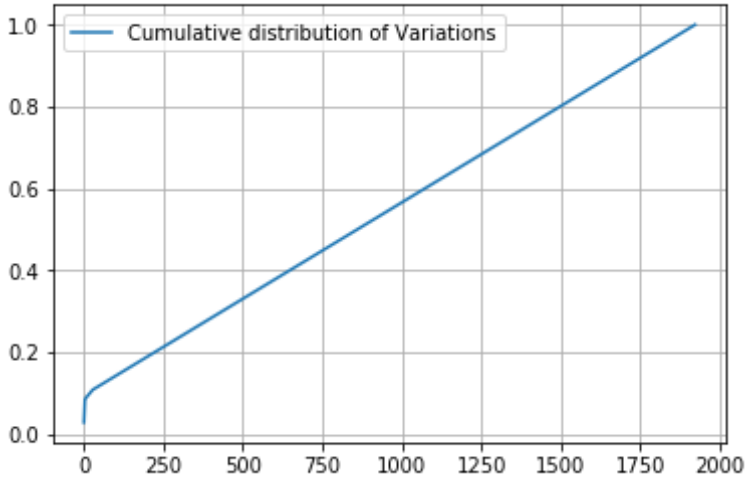
```
Ans: There are 1924 different categories of variations in the train dat
a, and they are distibuted as follows
```

In [42]:
```
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 [43]:
```
c = np.cumsum(h)
print(c)
plt.plot(c,label='Cumulative distribution of Variations')
plt.grid()
plt.legend()
plt.show()
```

```
[0.02777778 0.05084746 0.07297552 ... 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 [44]:
```
# 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 [45]:
```
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 [46]:
```
# one-hot encoding of variation feature.
variation_vectorizer = CountVectorizer()
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 [47]:
```
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, 1960)
```

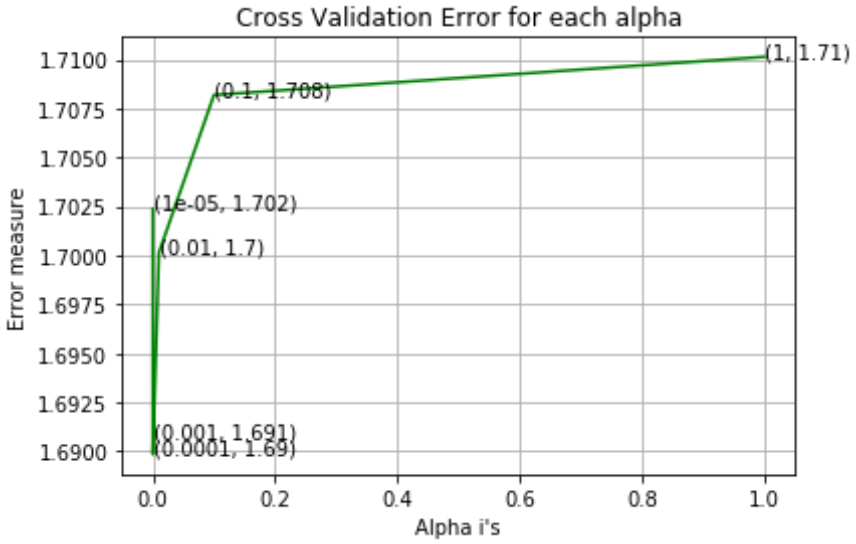
Q10. How good is this Variation feature in predicting y_i?

Let's build a model just like the earlier!

In [48]:
```
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: 1.7023621747765858
For values of alpha =  0.0001 The log loss is: 1.689842322110077
For values of alpha =  0.001 The log loss is: 1.6907130717518253
For values of alpha =  0.01 The log loss is: 1.7001345396142153
For values of alpha =  0.1 The log loss is: 1.7081826775989355
For values of alpha =  1 The log loss is: 1.710131025593559
```




```
For values of best alpha =  0.0001 The train log loss is: 0.8255455900343496
For values of best alpha =  0.0001 The cross validation log loss is: 1.689842322110077
For values of best alpha =  0.0001 The test log loss is: 1.7362385768757977
```

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 [49]:
```
print("Q12. How many data points are covered by total ", unique_variations.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  1924  genes in test and
cross validation data sets?
Ans
1. In test data 64 out of 665 : 9.624060150375941
2. In cross validation data 56 out of  532 : 10.526315789473683
```

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 [50]:
```
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 [51]:
```
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 [52]:

```
# building a CountVectorizer with all the words that occured minimum 3
 times in train data
text_vectorizer = CountVectorizer(min_df=3)
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 : 54850
```

In [53]:

```
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 [54]:
```
#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 [55]:
```
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 [56]:
```
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'])

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'])

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

In [57]:
```
#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 [58]:
```
# Number of words for a given frequency.
print(Counter(sorted_text_occur))
```

```
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```
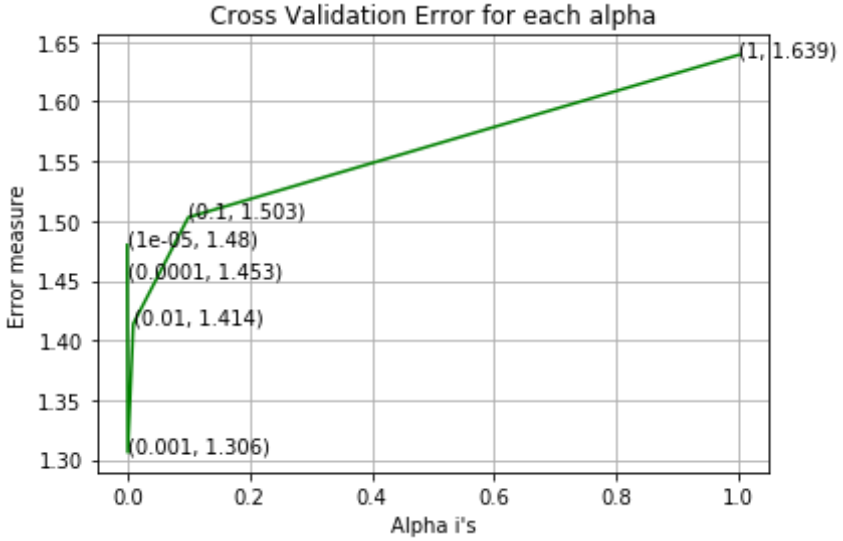

In [59]:

```
# Train a Logistic regression+Calibration model using text features whi
cha re on-hot encoded
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_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: 1.4798785760828574
For values of alpha =  0.0001 The log loss is: 1.4534937808292785
For values of alpha =  0.001 The log loss is: 1.3062465612808916
For values of alpha =  0.01 The log loss is: 1.4138930975129917
For values of alpha =  0.1 The log loss is: 1.5031084843525189
For values of alpha =  1 The log loss is: 1.6391636597237738
```




```
For values of best alpha =  0.001 The train log loss is: 0.761413345736
5512
```

```
For values of best alpha =  0.001 The cross validation log loss is: 1.3
062465612808916
For values of best alpha =  0.001 The test log loss is: 1.1902669954542
044
```

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

Ans. Yes, it seems like!

In [60]:
```
def get_intersec_text(df):
    df_text_vec = CountVectorizer(min_df=3)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

    df_text_fea_counts = df_text_fea.sum(axis=0).A1
    df_text_fea_dict = dict(zip(list(df_text_features),df_text_fea_coun
ts))
    len1 = len(set(df_text_features))
    len2 = len(set(train_text_features) & set(df_text_features))
    return len1,len2
```

In [61]:
```
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")
```

```
97.125 % of word of test data appeared in train data
98.056 % of word of Cross Validation appeared in train data
```

4. Machine Learning Models

In [62]:
```
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 [63]:
```
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 [64]:
```
def get_impfeature_names(indices, text, gene, var, no_features):
    gene_count_vec = CountVectorizer()
    var_count_vec = CountVectorizer()
    text_count_vec = CountVectorizer(min_df=3)

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

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

    word_present = 0
    for i,v in enumerate(indices):
        if (v < fea1_len):
            word = gene_vec.get_feature_names()[v]
            yes_no = True if word == gene else False
```

```
            if yes_no:
                word_present += 1
                print(i, "Gene feature [{}] present in test data point
 [{}]".format(word,yes_no))
        elif (v < fea1_len+fea2_len):
            word = var_vec.get_feature_names()[v-(fea1_len)]
            yes_no = True if word == var else False
            if yes_no:
                word_present += 1
                print(i, "variation feature [{}] present in test data 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 [65]:
```
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 [66]:
```
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, 57
039)
(number of data points * number of features) in test data =  (665, 5703
9)
(number of data points * number of features) in cross validation data =
(532, 57039)
```

In [67]:
```
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

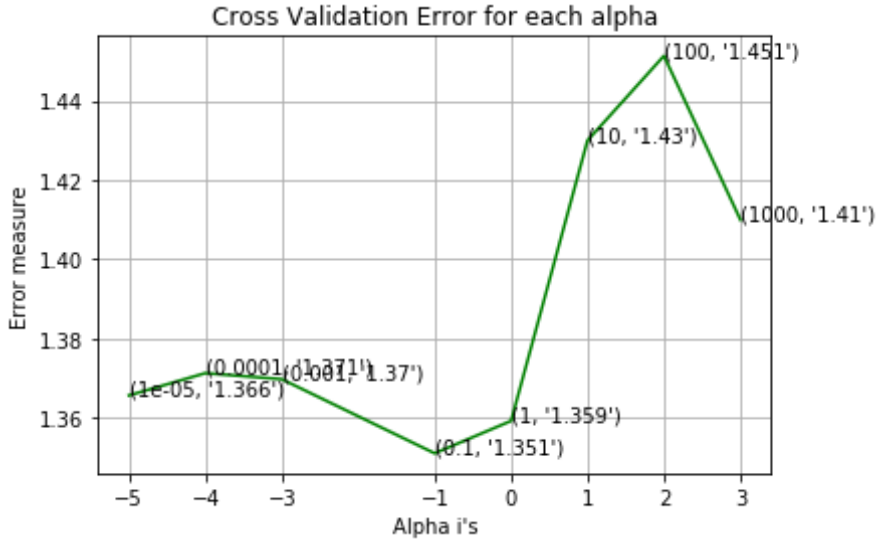
4.1.1.1. Hyper parameter tuning

In [68]:
```
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 : 1.3655537837941127
for alpha = 0.0001
Log Loss : 1.3711793514758466
for alpha = 0.001
Log Loss : 1.3696542195047903
for alpha = 0.1
Log Loss : 1.3509235125982695
```

```
for alpha = 1
Log Loss : 1.3591155403248767
for alpha = 10
Log Loss : 1.4299766791532638
for alpha = 100
Log Loss : 1.451360452876549
for alpha = 1000
Log Loss : 1.4099515277732073
```




```
For values of best alpha =  0.1 The train log loss is: 0.90331184795191
52
For values of best alpha =  0.1 The cross validation log loss is: 1.350
9235125982695
For values of best alpha =  0.1 The test log loss is: 1.278489772465971
4
```

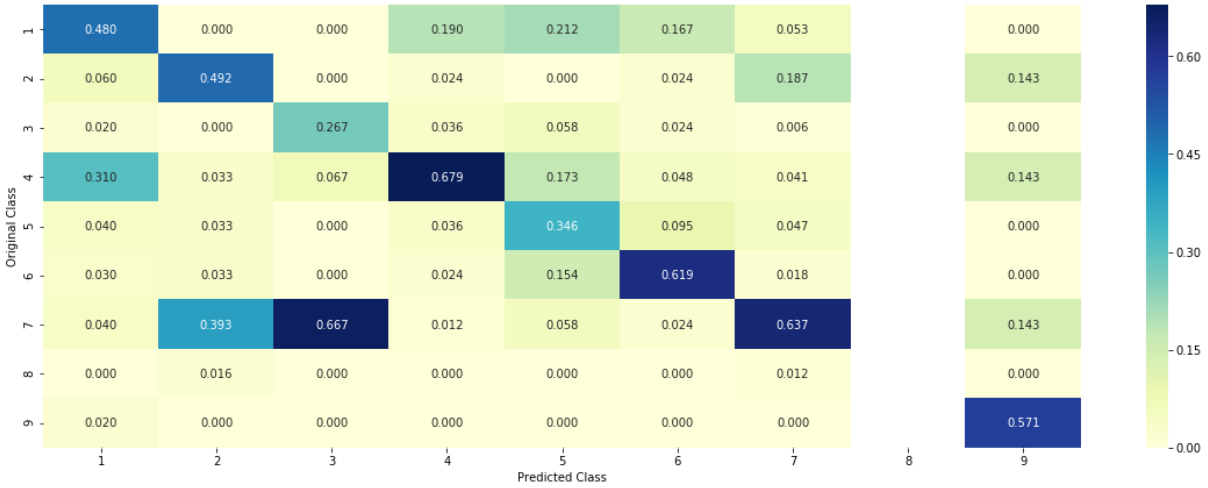
4.1.1.2. Testing the model with best hyper paramters

In [69]:
```
clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
```

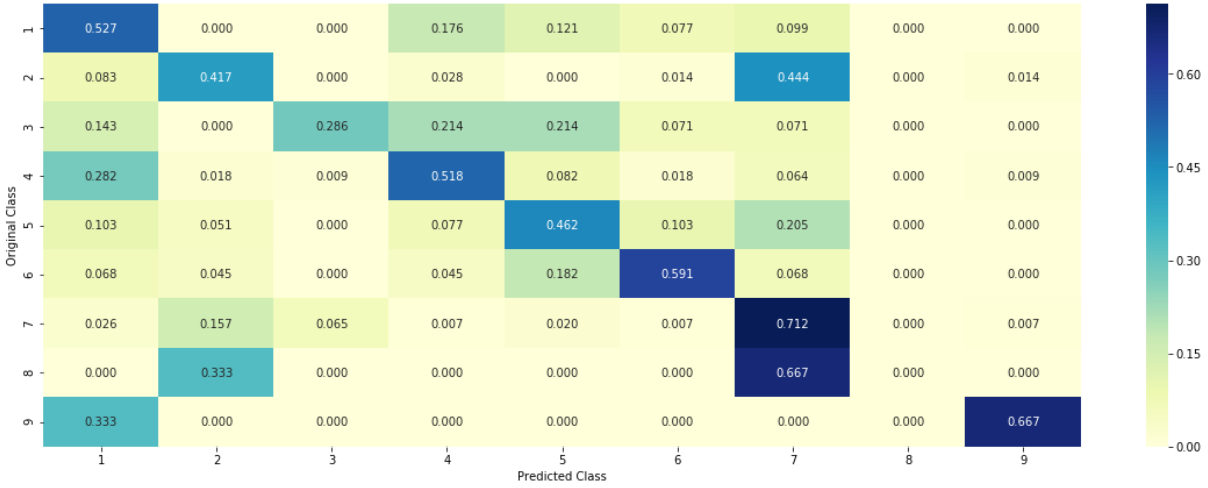
```
sig_clf.fit(train_x_onehotCoding, train_y)
sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
# to avoid rounding error while multiplying probabilites we use log-pro
bability estimates
print("Log Loss :",log_loss(cv_y, sig_clf_probs))
print("Number of missclassified point :", np.count_nonzero((sig_clf.pre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

```
Log Loss : 1.3509235125982695
Number of missclassified point : 0.44360902255639095
-------------------- Confusion matrix --------------------
```


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



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



4.1.1.3. Feature Importance, Correctly classified point

In [70]:
```
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 : 7
Predicted Class Probabilities: [[0.0911 0.1284 0.0141 0.1119 0.0334 0.0
365 0.5764 0.0057 0.0025]]
Actual Class : 7
--------------------------------------------------
16 Text feature [presence] present in test data point [True]
17 Text feature [kinase] present in test data point [True]
18 Text feature [well] present in test data point [True]
19 Text feature [activating] present in test data point [True]
20 Text feature [downstream] present in test data point [True]
21 Text feature [cell] present in test data point [True]
22 Text feature [inhibitor] present in test data point [True]
23 Text feature [cells] present in test data point [True]
24 Text feature [independent] present in test data point [True]
25 Text feature [contrast] present in test data point [True]
26 Text feature [recently] present in test data point [True]
29 Text feature [shown] present in test data point [True]
30 Text feature [potential] present in test data point [True]
31 Text feature [also] present in test data point [True]
32 Text feature [obtained] present in test data point [True]
33 Text feature [growth] present in test data point [True]
34 Text feature [activation] present in test data point [True]
35 Text feature [suggest] present in test data point [True]
36 Text feature [showed] present in test data point [True]
37 Text feature [however] present in test data point [True]
38 Text feature [expressing] present in test data point [True]
39 Text feature [addition] present in test data point [True]
40 Text feature [found] present in test data point [True]
41 Text feature [10] present in test data point [True]
42 Text feature [previously] present in test data point [True]
```

```
42 Text feature [previously] present in test data point [True]
43 Text feature [factor] present in test data point [True]
44 Text feature [compared] present in test data point [True]
45 Text feature [treated] present in test data point [True]
46 Text feature [inhibition] present in test data point [True]
47 Text feature [higher] present in test data point [True]
48 Text feature [observed] present in test data point [True]
49 Text feature [described] present in test data point [True]
50 Text feature [may] present in test data point [True]
51 Text feature [similar] present in test data point [True]
52 Text feature [total] present in test data point [True]
53 Text feature [furthermore] present in test data point [True]
54 Text feature [studies] present in test data point [True]
55 Text feature [using] present in test data point [True]
56 Text feature [without] present in test data point [True]
57 Text feature [concentrations] present in test data point [True]
58 Text feature [1a] present in test data point [True]
59 Text feature [various] present in test data point [True]
60 Text feature [including] present in test data point [True]
61 Text feature [mutations] present in test data point [True]
62 Text feature [respectively] present in test data point [True]
63 Text feature [12] present in test data point [True]
64 Text feature [followed] present in test data point [True]
65 Text feature [enhanced] present in test data point [True]
66 Text feature [although] present in test data point [True]
67 Text feature [interestingly] present in test data point [True]
68 Text feature [phosphorylation] present in test data point [True]
70 Text feature [new] present in test data point [True]
71 Text feature [inhibited] present in test data point [True]
72 Text feature [constitutively] present in test data point [True]
75 Text feature [1b] present in test data point [True]
76 Text feature [reported] present in test data point [True]
77 Text feature [confirmed] present in test data point [True]
78 Text feature [inhibitors] present in test data point [True]
79 Text feature [proliferation] present in test data point [True]
80 Text feature [report] present in test data point [True]
81 Text feature [either] present in test data point [True]
82 Text feature [molecular] present in test data point [True]
83 Text feature [15] present in test data point [True]

84 Text feature [thus] present in test data point [True]
```

```
85 Text feature [recent] present in test data point [True]
86 Text feature [3b] present in test data point [True]
87 Text feature [fig] present in test data point [True]
88 Text feature [results] present in test data point [True]
89 Text feature [occur] present in test data point [True]
90 Text feature [small] present in test data point [True]
91 Text feature [3a] present in test data point [True]
92 Text feature [approximately] present in test data point [True]
93 Text feature [hours] present in test data point [True]
94 Text feature [consistent] present in test data point [True]
95 Text feature [figure] present in test data point [True]
97 Text feature [suggests] present in test data point [True]
98 Text feature [absence] present in test data point [True]
99 Text feature [measured] present in test data point [True]
Out of the top  100  features  78 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

In [71]:
```
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: [[0.0876 0.0895 0.0136 0.1069 0.0322 0.0
356 0.6267 0.0055 0.0024]]
Actual Class : 7
--------------------------------------------------
17 Text feature [kinase] present in test data point [True]
18 Text feature [well] present in test data point [True]
```

```
19 Text feature [activating] present in test data point [True]
20 Text feature [downstream] present in test data point [True]
21 Text feature [cell] present in test data point [True]
23 Text feature [cells] present in test data point [True]
24 Text feature [independent] present in test data point [True]
25 Text feature [contrast] present in test data point [True]
26 Text feature [recently] present in test data point [True]
29 Text feature [shown] present in test data point [True]
30 Text feature [potential] present in test data point [True]
31 Text feature [also] present in test data point [True]
33 Text feature [growth] present in test data point [True]
34 Text feature [activation] present in test data point [True]
35 Text feature [suggest] present in test data point [True]
36 Text feature [showed] present in test data point [True]
37 Text feature [however] present in test data point [True]
39 Text feature [addition] present in test data point [True]
40 Text feature [found] present in test data point [True]
41 Text feature [10] present in test data point [True]
42 Text feature [previously] present in test data point [True]
44 Text feature [compared] present in test data point [True]
46 Text feature [inhibition] present in test data point [True]
47 Text feature [higher] present in test data point [True]
48 Text feature [observed] present in test data point [True]
50 Text feature [may] present in test data point [True]
51 Text feature [similar] present in test data point [True]
54 Text feature [studies] present in test data point [True]
55 Text feature [using] present in test data point [True]
56 Text feature [without] present in test data point [True]
58 Text feature [1a] present in test data point [True]
60 Text feature [including] present in test data point [True]
61 Text feature [mutations] present in test data point [True]
62 Text feature [respectively] present in test data point [True]
63 Text feature [12] present in test data point [True]
64 Text feature [followed] present in test data point [True]
65 Text feature [enhanced] present in test data point [True]
66 Text feature [although] present in test data point [True]
68 Text feature [phosphorylation] present in test data point [True]
69 Text feature [activated] present in test data point [True]
70 Text feature [new] present in test data point [True]
```

```
71 Text feature [inhibited] present in test data point [True]
72 Text feature [constitutively] present in test data point [True]
75 Text feature [1b] present in test data point [True]
78 Text feature [inhibitors] present in test data point [True]
79 Text feature [proliferation] present in test data point [True]
81 Text feature [either] present in test data point [True]
82 Text feature [molecular] present in test data point [True]
83 Text feature [15] present in test data point [True]
85 Text feature [recent] present in test data point [True]
86 Text feature [3b] present in test data point [True]
87 Text feature [fig] present in test data point [True]
88 Text feature [results] present in test data point [True]
89 Text feature [occur] present in test data point [True]
90 Text feature [small] present in test data point [True]
91 Text feature [3a] present in test data point [True]
94 Text feature [consistent] present in test data point [True]
95 Text feature [figure] present in test data point [True]
97 Text feature [suggests] present in test data point [True]
98 Text feature [absence] present in test data point [True]
Out of the top  100  features  60 are present in query point
```

4.2. K Nearest Neighbour Classification

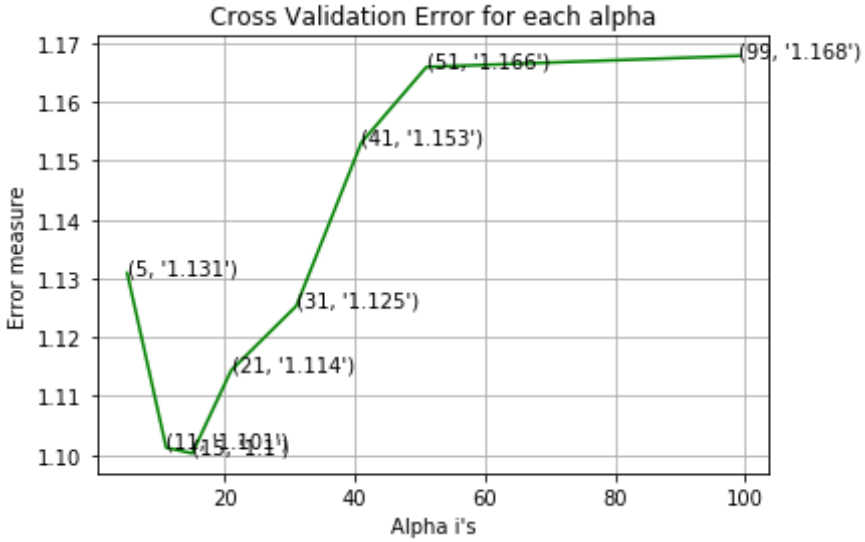
4.2.1. Hyper parameter tuning

In [101]:
```
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 : 1.1309170126692265
for alpha = 11
Log Loss : 1.1012397762291362
for alpha = 15
Log Loss : 1.1002748803755749
for alpha = 21
```

```
Log Loss : 1.1144110925957647
for alpha = 31
Log Loss : 1.1253206995500455
for alpha = 41
Log Loss : 1.1530939773909168
for alpha = 51
Log Loss : 1.1659585643007098
for alpha = 99
Log Loss : 1.1678505034822115
```

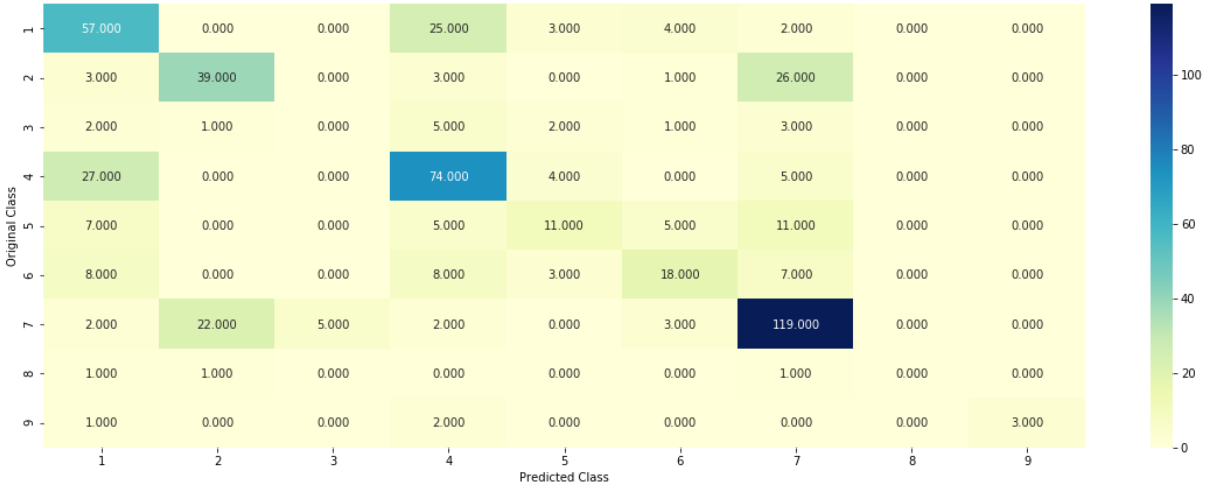



```
For values of best alpha =  15 The train log loss is: 0.705689287122519
3
For values of best alpha =  15 The cross validation log loss is: 1.1002
748803755749
For values of best alpha =  15 The test log loss is: 1.0911901980302394
```

4.2.2. Testing the model with best hyper paramters

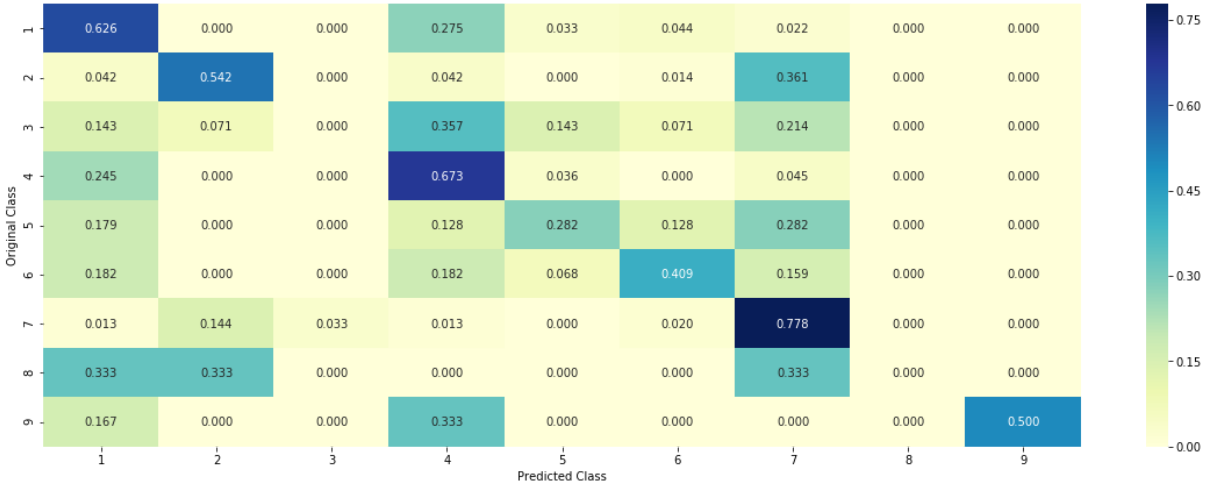
In [102]:
```
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y, cv_x
_responseCoding, cv_y, clf)
```

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




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


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



4.2.3.Sample Query point -1

In [103]:
```
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 : 6
Actual Class : 7
The  15  nearest neighbours of the test points belongs to classes [7 7
7 6 6 7 6 7 6 7 7 7 7 7 6]
Fequency of nearest points : Counter({7: 10, 6: 5})
```

4.2.4. Sample Query Point-2

In [104]:
```
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 15 and the nearest neighbours of the test points
belongs to classes [2 7 5 7 7 2 7 7 7 2 7 7 7 7 7]
Fequency of nearest points : Counter({7: 11, 2: 3, 5: 1})
```

4.3. Logistic Regression

4.3.1. With Class balancing

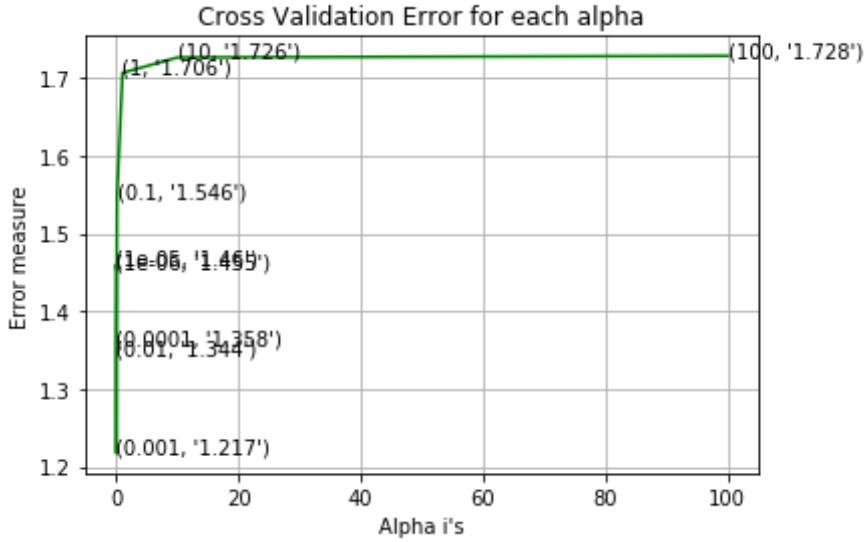
4.3.1.1. Hyper paramter tuning

In [76]:
```
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 : 1.4554353198842396
for alpha = 1e-05
Log Loss : 1.4602144866667575
for alpha = 0.0001
Log Loss : 1.358469527280309
for alpha = 0.001
Log Loss : 1.217324457704446
for alpha = 0.01
Log Loss : 1.3437838209291793
for alpha = 0.1
Log Loss : 1.5457557924182381
for alpha = 1
Log Loss : 1.706360520395438
for alpha = 10
Log Loss : 1.7261917214695601
for alpha = 100
Log Loss : 1.7282505302427342
```

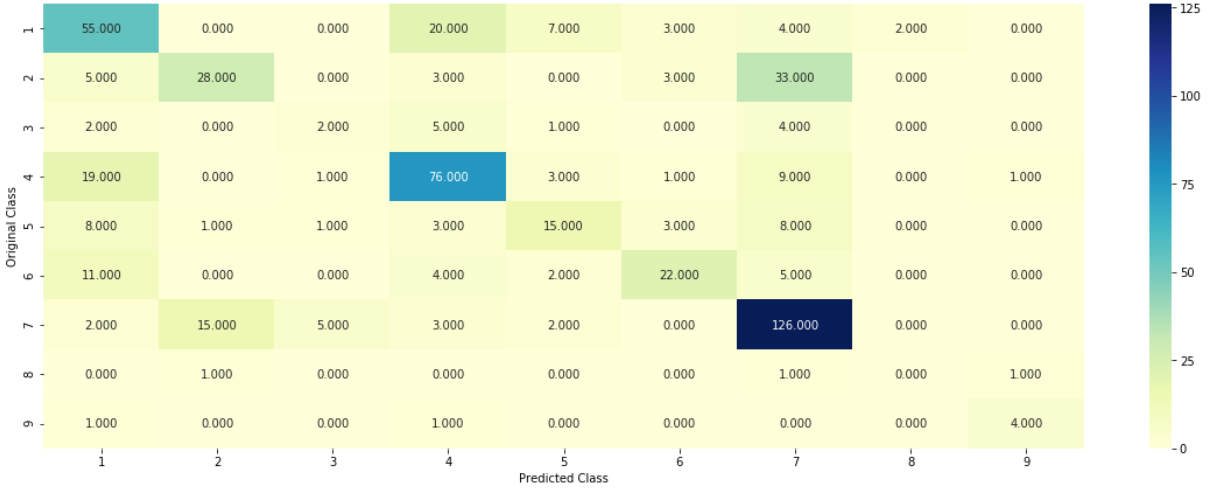


```
For values of best alpha =  0.001 The train log loss is: 0.615317709702
9675
For values of best alpha =  0.001 The cross validation log loss is: 1.2
17324457704446
For values of best alpha =  0.001 The test log loss is: 1.1047257743181
136
```

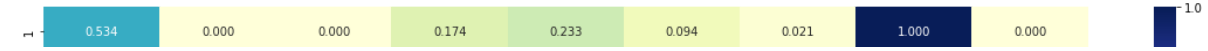
4.3.1.2. Testing the model with best hyper paramters

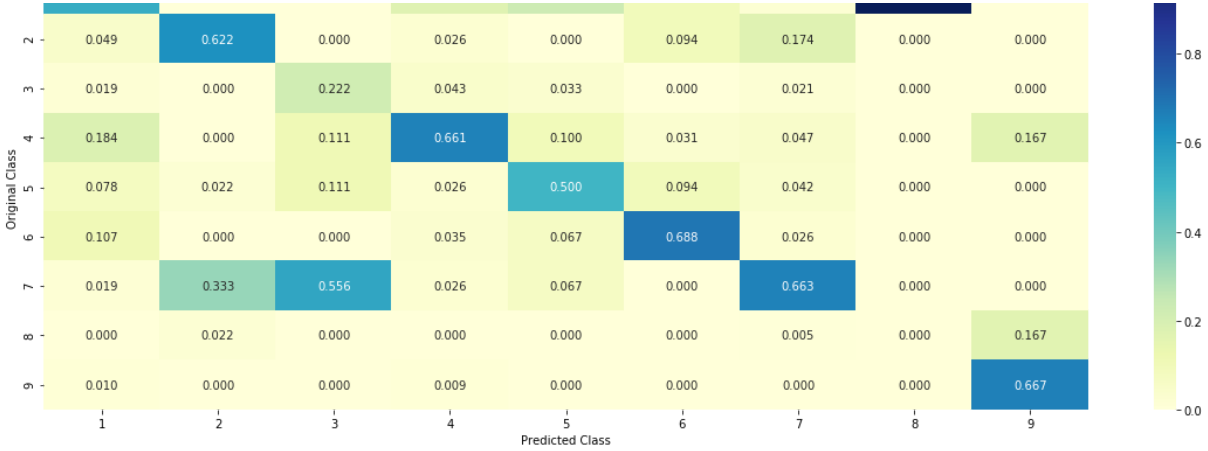
In [77]:
```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], p
enalty='l2', loss='log', random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_o
nehotCoding, cv_y, clf)
```

```
Log loss : 1.217324457704446
Number of mis-classified points : 0.38345864661654133
-------------------- Confusion matrix --------------------
```




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





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

4.3.1.3. Feature Importance

In [78]:
```
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 [79]:
```
# 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 : 7
Predicted Class Probabilities: [[0.0045 0.1905 0.0012 0.0012 0.0047 0.0
014 0.7872 0.0076 0.0017]]
Actual Class : 7
--------------------------------------------------
23 Text feature [constitutively] present in test data point [True]
39 Text feature [flt1] present in test data point [True]
79 Text feature [oncogene] present in test data point [True]
80 Text feature [oncogenes] present in test data point [True]
84 Text feature [cysteine] present in test data point [True]
89 Text feature [inhibited] present in test data point [True]
137 Text feature [technology] present in test data point [True]
160 Text feature [dramatic] present in test data point [True]
162 Text feature [gaiix] present in test data point [True]
166 Text feature [ligand] present in test data point [True]
177 Text feature [downstream] present in test data point [True]
181 Text feature [concentrations] present in test data point [True]
182 Text feature [thyroid] present in test data point [True]
187 Text feature [expressing] present in test data point [True]
217 Text feature [activating] present in test data point [True]
241 Text feature [cdnas] present in test data point [True]
250 Text feature [manageable] present in test data point [True]
265 Text feature [axilla] present in test data point [True]
302 Text feature [inhibitor] present in test data point [True]
311 Text feature [cot] present in test data point [True]
313 Text feature [viability] present in test data point [True]
334 Text feature [activation] present in test data point [True]
352 Text feature [forced] present in test data point [True]
368 Text feature [subcutaneous] present in test data point [True]
371 Text feature [melanocyte] present in test data point [True]
376 Text feature [erk1] present in test data point [True]
388 Text feature [hours] present in test data point [True]
446 Text feature [procure] present in test data point [True]
448 Text feature [doses] present in test data point [True]
480 Text feature [mapk] present in test data point [True]
Out of the top  500  features  30 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

In [80]:
```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[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: [[0.0482 0.2032 0.0108 0.0446 0.071  0.0
164 0.5932 0.0078 0.0046]]
Actual Class : 7
--------------------------------------------------
23 Text feature [constitutively] present in test data point [True]
29 Text feature [constitutive] present in test data point [True]
47 Text feature [activated] present in test data point [True]
79 Text feature [oncogene] present in test data point [True]
89 Text feature [inhibited] present in test data point [True]
93 Text feature [transforming] present in test data point [True]
108 Text feature [transform] present in test data point [True]
148 Text feature [receptors] present in test data point [True]
177 Text feature [downstream] present in test data point [True]
210 Text feature [isozyme] present in test data point [True]
217 Text feature [activating] present in test data point [True]
232 Text feature [exchange] present in test data point [True]
326 Text feature [murine] present in test data point [True]
333 Text feature [agar] present in test data point [True]
334 Text feature [activation] present in test data point [True]
Out of the top  500  features  15 are present in query point
```

4.3.2. Without Class balancing

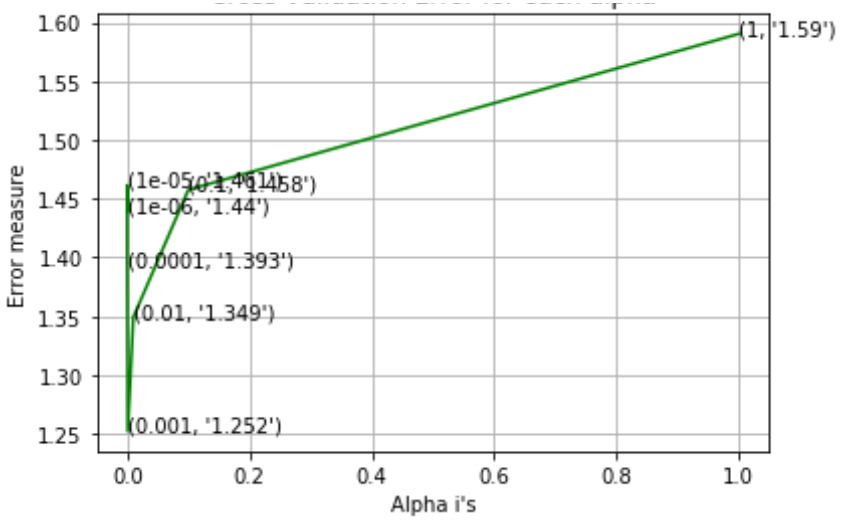
4.3.2.1. Hyper paramter tuning

In [81]:
```
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 : 1.4395190222240433
for alpha = 1e-05
Log Loss : 1.4613951945118617
for alpha = 0.0001
Log Loss : 1.392640595913179
for alpha = 0.001
Log Loss : 1.2521811628755943
for alpha = 0.01
Log Loss : 1.349151219922669
for alpha = 0.1
Log Loss : 1.457591708320943
for alpha = 1
Log Loss : 1.5902258764770603
```

Cross Validation Error for each alpha




```
For values of best alpha =  0.001 The train log loss is: 0.625742267741
2771
For values of best alpha =  0.001 The cross validation log loss is: 1.2
521811628755943
For values of best alpha =  0.001 The test log loss is: 1.1306020069615
057
```

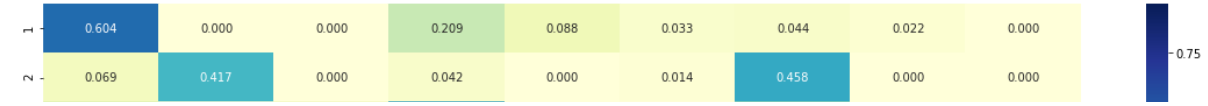
4.3.2.2. Testing model with best hyper parameters

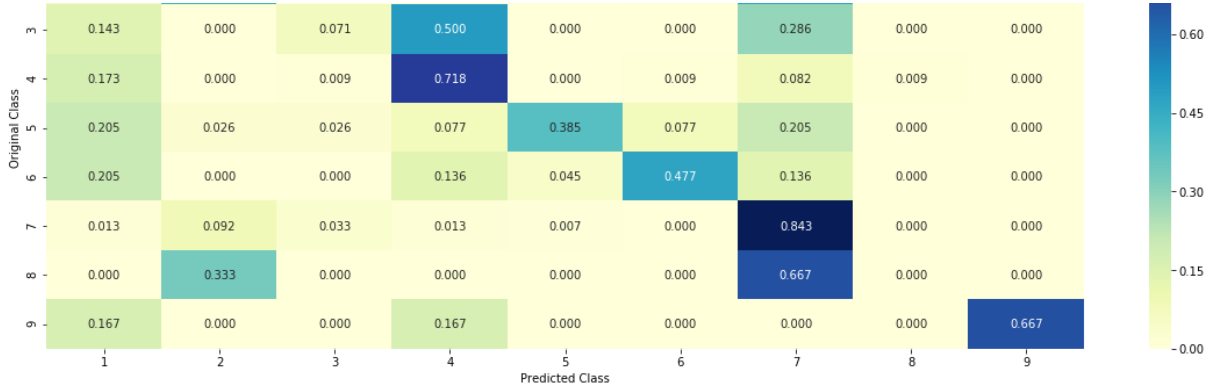
In [82]:
```
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log',
random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_o
nehotCoding, cv_y, clf)
```

```
Log loss : 1.2521811628755943
Number of mis-classified points : 0.37218045112781956
-------------------- Confusion matrix --------------------
```

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

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





4.3.2.3. Feature Importance, Correctly Classified point

In [83]:
```
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 : 7
Predicted Class Probabilities: [[5.100e-03 1.255e-01 2.000e-04 1.300e-0
3 2.300e-03 1.400e-03 8.556e-01
  8.500e-03 1.000e-04]]
Actual Class : 7
--------------------------------------------------
60 Text feature [constitutively] present in test data point [True]
107 Text feature [flt1] present in test data point [True]
```

```
124 Text feature [cysteine] present in test data point [True]
157 Text feature [oncogenes] present in test data point [True]
158 Text feature [inhibited] present in test data point [True]
195 Text feature [activating] present in test data point [True]
200 Text feature [ligand] present in test data point [True]
203 Text feature [oncogene] present in test data point [True]
204 Text feature [technology] present in test data point [True]
257 Text feature [gaiix] present in test data point [True]
260 Text feature [concentrations] present in test data point [True]
265 Text feature [downstream] present in test data point [True]
314 Text feature [hki] present in test data point [True]
316 Text feature [dramatic] present in test data point [True]
323 Text feature [expressing] present in test data point [True]
371 Text feature [cdnas] present in test data point [True]
380 Text feature [viability] present in test data point [True]
412 Text feature [thyroid] present in test data point [True]
459 Text feature [activation] present in test data point [True]
461 Text feature [manageable] present in test data point [True]
462 Text feature [ser473] present in test data point [True]
468 Text feature [axilla] present in test data point [True]
495 Text feature [extracellular] present in test data point [True]
Out of the top  500  features  23 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

In [84]:
```
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 : 7
Predicted Class Probabilities: [[0.0485 0.1851 0.0052 0.0442 0.0617 0.0
143 0.6317 0.0072 0.0022]]
Actual Class : 7
--------------------------------------------------
60 Text feature [constitutively] present in test data point [True]
89 Text feature [constitutive] present in test data point [True]
116 Text feature [activated] present in test data point [True]
158 Text feature [inhibited] present in test data point [True]
159 Text feature [transforming] present in test data point [True]
193 Text feature [receptors] present in test data point [True]
195 Text feature [activating] present in test data point [True]
203 Text feature [oncogene] present in test data point [True]
226 Text feature [transform] present in test data point [True]
241 Text feature [isozyme] present in test data point [True]
265 Text feature [downstream] present in test data point [True]
377 Text feature [agar] present in test data point [True]
442 Text feature [interatomic] present in test data point [True]
459 Text feature [activation] present in test data point [True]
Out of the top  500  features  14 are present in query point
```

4.4. Linear Support Vector Machines

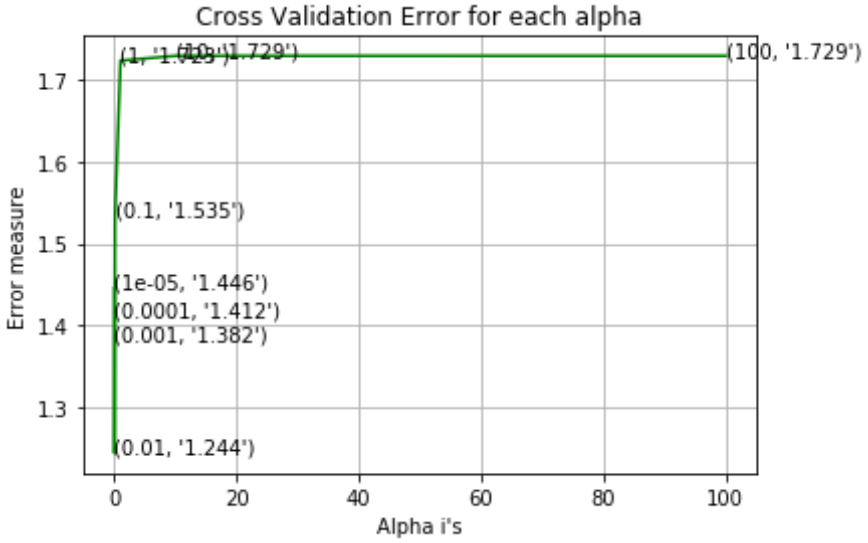
4.4.1. Hyper paramter tuning

In [85]:
```
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 : 1.4456349250609233
for C = 0.0001
```

```
Log Loss : 1.4117883301099556
for C = 0.001
Log Loss : 1.3818342037841624
for C = 0.01
Log Loss : 1.2442964974823838
for C = 0.1
Log Loss : 1.5346828298587332
for C = 1
Log Loss : 1.722800653929441
for C = 10
Log Loss : 1.7286360420759161
for C = 100
Log Loss : 1.7286184454094997
```



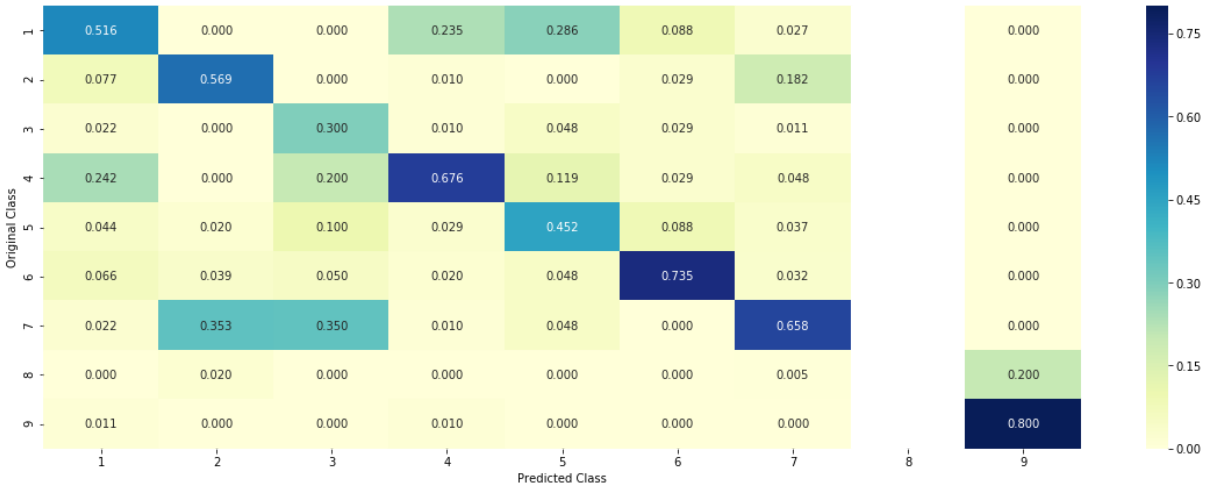

```
For values of best alpha =  0.01 The train log loss is: 0.7628309867716

067
For values of best alpha =  0.01 The cross validation log loss is: 1.24
42964974823838
For values of best alpha =  0.01 The test log loss is: 1.15418919698636
85
```

4.4.2. Testing model with best hyper parameters

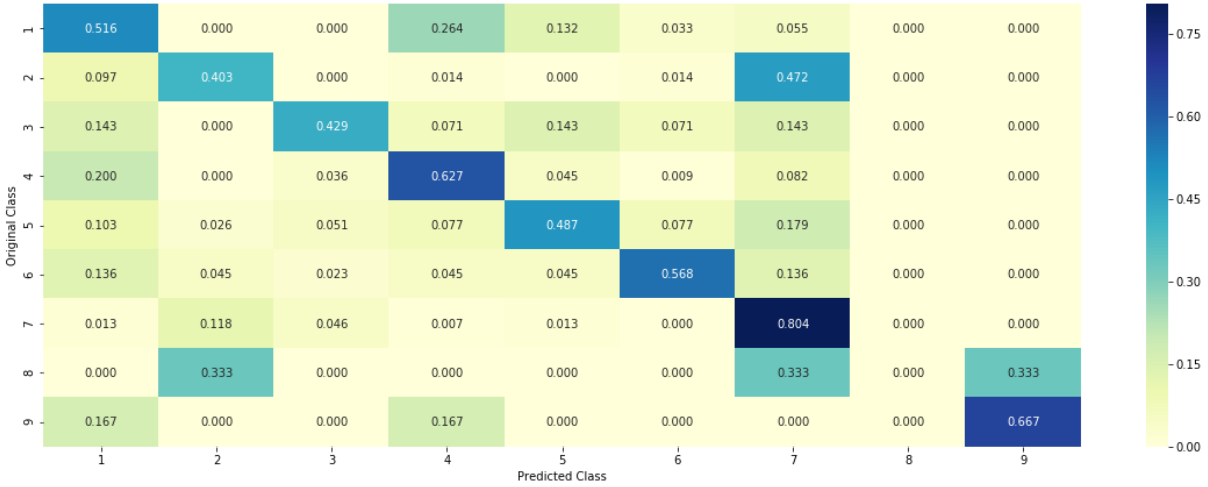
In [86]:
```
# clf = SVC(C=alpha[best_alpha],kernel='linear',probability=True, class_weight='balanced')
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge', random_state=42,class_weight='balanced')
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf)
```

```
Log loss : 1.2442964974823838
Number of mis-classified points : 0.39473684210526316
-------------------- 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 [87]:
```
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 : 7
Predicted Class Probabilities: [[0.0153 0.1199 0.0029 0.0151 0.0121 0.0
075 0.8104 0.0129 0.0039]]
Actual Class : 7
--------------------------------------------------
28 Text feature [constitutively] present in test data point [True]
29 Text feature [cysteine] present in test data point [True]
49 Text feature [cdnas] present in test data point [True]
76 Text feature [flt1] present in test data point [True]
79 Text feature [concentrations] present in test data point [True]
82 Text feature [gaiix] present in test data point [True]
96 Text feature [technology] present in test data point [True]
101 Text feature [inhibited] present in test data point [True]
104 Text feature [activating] present in test data point [True]
114 Text feature [oncogenes] present in test data point [True]
147 Text feature [expressing] present in test data point [True]
150 Text feature [mapk] present in test data point [True]
151 Text feature [oncogene] present in test data point [True]
169 Text feature [thyroid] present in test data point [True]
171 Text feature [inhibitor] present in test data point [True]
205 Text feature [transduced] present in test data point [True]
211 Text feature [seeded] present in test data point [True]
230 Text feature [ligand] present in test data point [True]
```

```
255 Text feature [activation] present in test data point [True]
279 Text feature [downstream] present in test data point [True]
314 Text feature [doses] present in test data point [True]
351 Text feature [subcutaneous] present in test data point [True]
366 Text feature [atcc] present in test data point [True]
405 Text feature [melanocyte] present in test data point [True]
436 Text feature [hours] present in test data point [True]
445 Text feature [selleck] present in test data point [True]
446 Text feature [dramatic] present in test data point [True]
454 Text feature [chemiluminescence] present in test data point [True]
487 Text feature [viability] present in test data point [True]
489 Text feature [ser473] present in test data point [True]
Out of the top  500  features  30 are present in query point
```

4.3.3.2. For Incorrectly classified point

In [88]:
```
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 : 7
Predicted Class Probabilities: [[0.0786 0.1516 0.0146 0.1064 0.1105 0.0
323 0.4839 0.0128 0.0094]]
Actual Class : 7
--------------------------------------------------
28 Text feature [constitutively] present in test data point [True]
40 Text feature [constitutive] present in test data point [True]
73 Text feature [activated] present in test data point [True]
75 Text feature [transforming] present in test data point [True]
```

```
94 Text feature [receptors] present in test data point [True]
97 Text feature [exchange] present in test data point [True]
101 Text feature [inhibited] present in test data point [True]
104 Text feature [activating] present in test data point [True]
151 Text feature [oncogene] present in test data point [True]
231 Text feature [transform] present in test data point [True]
255 Text feature [activation] present in test data point [True]
279 Text feature [downstream] present in test data point [True]
440 Text feature [doubled] present in test data point [True]
470 Text feature [substituting] present in test data point [True]
Out of the top  500  features  14 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

In [89]:
```
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))
```

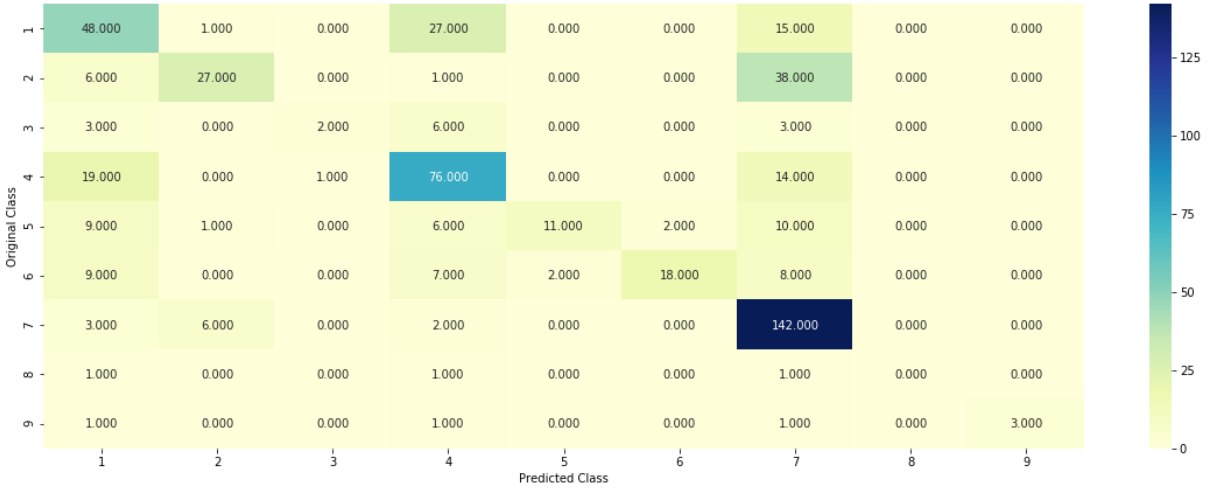
```
for n_estimators = 100 and max depth =  5
Log Loss : 1.2572535683354957
for n_estimators = 100 and max depth =  10
Log Loss : 1.1868414223711878
for n_estimators = 200 and max depth =  5
Log Loss : 1.2378734502517341
for n_estimators = 200 and max depth =  10
Log Loss : 1.1811031780258958
for n_estimators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

```
Log Loss : 1.2368241894319212
for n_estimators = 500 and max depth =  10
Log Loss : 1.176754594516683
for n_estimators = 1000 and max depth =  5
Log Loss : 1.2357829533963691
for n_estimators = 1000 and max depth =  10
Log Loss : 1.174993079576866
for n_estimators = 2000 and max depth =  5
Log Loss : 1.236042392554891
for n_estimators = 2000 and max depth =  10
Log Loss : 1.1759745074379755
For values of best estimator =  1000 The train log loss is: 0.709539673
2082752
For values of best estimator =  1000 The cross validation log loss is:
1.174993079576866
For values of best estimator =  1000 The test log loss is: 1.1630923149
103904
```

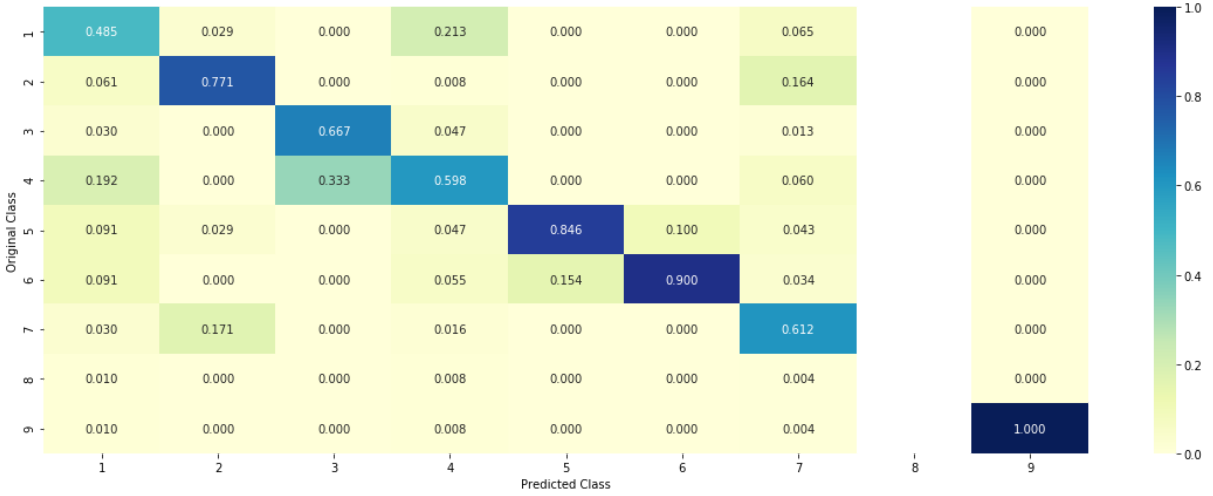
4.5.2. Testing model with best hyper parameters (One Hot Encoding)

In [90]:
```
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 : 1.174993079576866
Number of mis-classified points : 0.38533834586466165
-------------------- Confusion matrix --------------------
```



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



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

4.5.3. Feature Importance

4.5.3.1. Correctly Classified point

In [91]:
```
# 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 : 7
Predicted Class Probabilities: [[0.0454 0.1404 0.0133 0.029  0.036  0.0
294 0.6977 0.005  0.004 ]]
Actual Class : 7
--------------------------------------------------
0 Text feature [inhibitors] present in test data point [True]
1 Text feature [kinase] present in test data point [True]
2 Text feature [activating] present in test data point [True]
3 Text feature [tyrosine] present in test data point [True]
4 Text feature [missense] present in test data point [True]
5 Text feature [inhibitor] present in test data point [True]
7 Text feature [treatment] present in test data point [True]
8 Text feature [oncogenic] present in test data point [True]
9 Text feature [suppressor] present in test data point [True]
10 Text feature [activation] present in test data point [True]
11 Text feature [phosphorylation] present in test data point [True]
12 Text feature [kinases] present in test data point [True]
13 Text feature [nonsense] present in test data point [True]
14 Text feature [akt] present in test data point [True]
15 Text feature [function] present in test data point [True]
17 Text feature [erk] present in test data point [True]
19 Text feature [growth] present in test data point [True]
20 Text feature [variants] present in test data point [True]
22 Text feature [frameshift] present in test data point [True]
24 Text feature [therapeutic] present in test data point [True]
25 Text feature [functional] present in test data point [True]
28 Text feature [signaling] present in test data point [True]
30 Text feature [patients] present in test data point [True]
```

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

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

4.5.3.2. Inorrectly Classified point

In [92]:
```
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("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 : 7
Predicted Class Probabilities: [[0.1337 0.116  0.0224 0.1773 0.0674 0.0
545 0.4156 0.0071 0.0059]]
Actuall Class : 7
--------------------------------------------------
0 Text feature [inhibitors] present in test data point [True]
1 Text feature [kinase] present in test data point [True]
2 Text feature [activating] present in test data point [True]
3 Text feature [tyrosine] present in test data point [True]
6 Text feature [activated] present in test data point [True]
8 Text feature [oncogenic] present in test data point [True]
10 Text feature [activation] present in test data point [True]
11 Text feature [phosphorylation] present in test data point [True]
12 Text feature [kinases] present in test data point [True]
14 Text feature [akt] present in test data point [True]
15 Text feature [function] present in test data point [True]
19 Text feature [growth] present in test data point [True]
21 Text feature [constitutive] present in test data point [True]
```

```
25 Text feature [functional] present in test data point [True]
28 Text feature [signaling] present in test data point [True]
31 Text feature [cells] present in test data point [True]
32 Text feature [constitutively] present in test data point [True]
38 Text feature [activate] present in test data point [True]
39 Text feature [downstream] present in test data point [True]
42 Text feature [protein] present in test data point [True]
43 Text feature [loss] present in test data point [True]
44 Text feature [inhibited] present in test data point [True]
46 Text feature [pten] present in test data point [True]
47 Text feature [transforming] present in test data point [True]
48 Text feature [lines] present in test data point [True]
50 Text feature [proliferation] present in test data point [True]
53 Text feature [neutral] present in test data point [True]
55 Text feature [transform] present in test data point [True]
56 Text feature [stability] present in test data point [True]
58 Text feature [transformation] present in test data point [True]
59 Text feature [inhibition] present in test data point [True]
62 Text feature [sensitivity] present in test data point [True]
64 Text feature [receptor] present in test data point [True]
66 Text feature [assays] present in test data point [True]
69 Text feature [cell] present in test data point [True]
75 Text feature [oncogene] present in test data point [True]
84 Text feature [information] present in test data point [True]
90 Text feature [dna] present in test data point [True]
94 Text feature [binding] present in test data point [True]
Out of the top  100  features  39 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

In [93]:
```
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 : 2.2657048897349608
for n_estimators = 10 and max depth =  3
Log Loss : 1.7459205010556096
for n_estimators = 10 and max depth =  5
Log Loss : 1.4368353925512503
for n_estimators = 10 and max depth =  10
Log Loss : 1.904597809032912
for n_estimators = 50 and max depth =  2
Log Loss : 1.7221951095007484
for n_estimators = 50 and max depth =  3
Log Loss : 1.4984825877845531
for n_estimators = 50 and max depth =  5
Log Loss : 1.4593628982873716
for n_estimators = 50 and max depth =  10
Log Loss : 1.8434939703555409
for n_estimators = 100 and max depth =  2
Log Loss : 1.6182209245331227
for n_estimators = 100 and max depth =  3
Log Loss : 1.5199297988828253
for n_estimators = 100 and max depth =  5
Log Loss : 1.4177501184246677
for n_estimators = 100 and max depth =  10
Log Loss : 1.8227504417195126
for n_estimators = 200 and max depth =  2
Log Loss : 1.6622571648074496
for n_estimators = 200 and max depth =  3
Log Loss : 1.4800771339141767
for n_estimators = 200 and max depth =  5
Log Loss : 1.4412060242341358
for n_estimators = 200 and max depth =  10
Log Loss : 1.7892406351442258
for n_estimators = 500 and max depth =  2
Log Loss : 1.715950314170445
for n_estimators = 500 and max depth =  3
Log Loss : 1.5658682738699774
```

```
for n_estimators = 500 and max depth =  5
Log Loss : 1.4445360301518217
for n_estimators = 500 and max depth =  10
Log Loss : 1.8421097596928397
for n_estimators = 1000 and max depth =  2
Log Loss : 1.6834927870864949
for n_estimators = 1000 and max depth =  3
Log Loss : 1.5631973035931377
for n_estimators = 1000 and max depth =  5
Log Loss : 1.4449980792724129
for n_estimators = 1000 and max depth =  10
Log Loss : 1.85233132619749
For values of best alpha =  100 The train log loss is: 0.06070270944460
8406
For values of best alpha =  100 The cross validation log loss is: 1.417
750118424668
For values of best alpha =  100 The test log loss is: 1.380627899834192
3
```

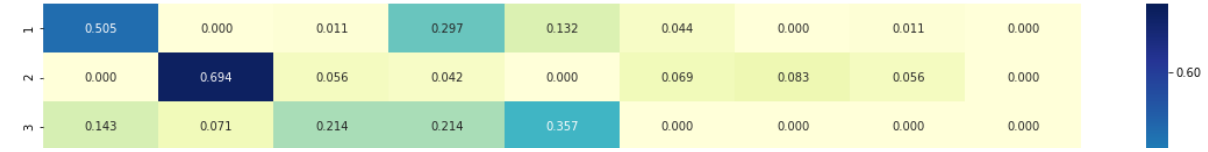
4.5.4. Testing model with best hyper parameters (Response Coding)

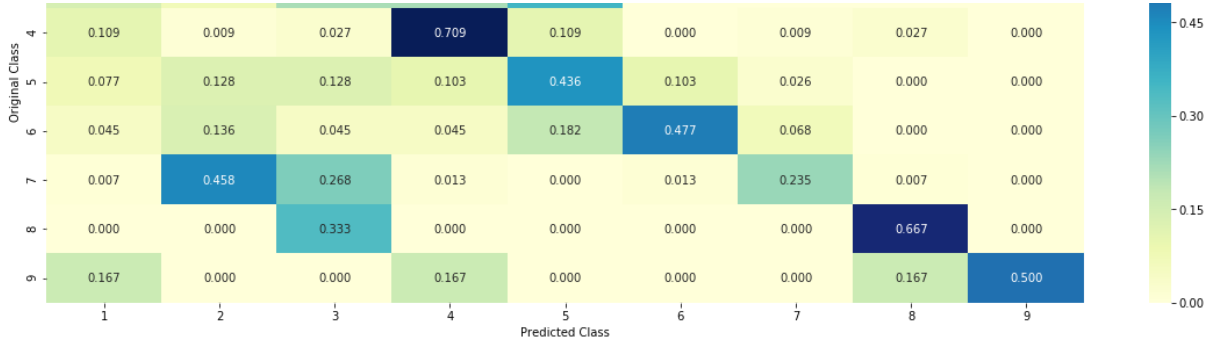
In [94]:
```
clf = RandomForestClassifier(max_depth=max_depth[int(best_alpha%4)], n_
estimators=alpha[int(best_alpha/4)], criterion='gini', max_features='au
to',random_state=42)
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_
responseCoding,cv_y, clf)
```

```
Log loss : 1.4177501184246677
Number of mis-classified points : 0.518796992481203
-------------------- Confusion matrix --------------------
```

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

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





4.5.5. Feature Importance

4.5.5.1. Correctly Classified point

In [95]:
```
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 : 2
Predicted Class Probabilities: [[0.0143 0.5044 0.1471 0.0191 0.0245 0.0
65  0.1724 0.039  0.0142]]
Actual Class : 7
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Text is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.5.5.2. Incorrectly Classified point

In [96]:
```
test_point_index = 100
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index]
.reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_responseCoding[test_point_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 : 7
Predicted Class Probabilities: [[0.0281 0.2006 0.203  0.0857 0.0626 0.0
906 0.2249 0.0676 0.0369]]
Actual Class : 7
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Text is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Variation is important feature
Text is important feature
```

```
Gene is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.7 Stack the models

4.7.1 testing with hyper parameter tuning

In [97]:
```
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
```

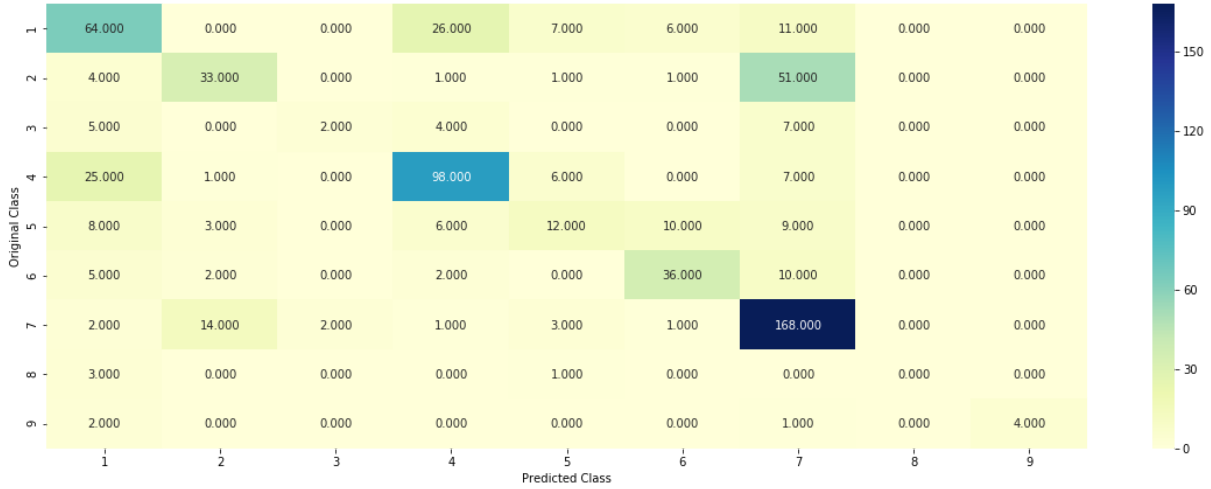
```
Logistic Regression :  Log Loss: 1.24
Support vector machines : Log Loss: 1.72
Naive Bayes : Log Loss: 1.37
--------------------------------------------------
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 2.179
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 2.049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

4.7.2 testing the model with the best hyper parameters

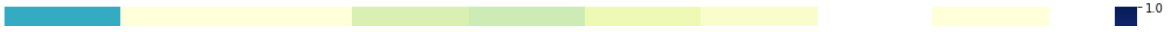
In [98]:
```
lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], m
eta_classifier=lr, use_probas=True)
sclf.fit(train_x_onehotCoding, train_y)

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

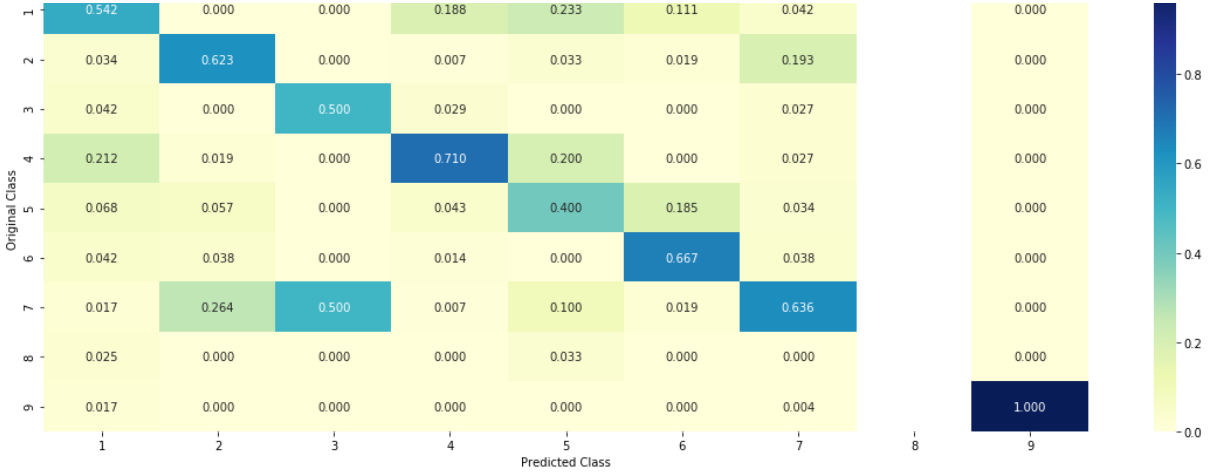
```
log_error = log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
print("Log loss (CV) on the stacking classifier :",log_error)

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

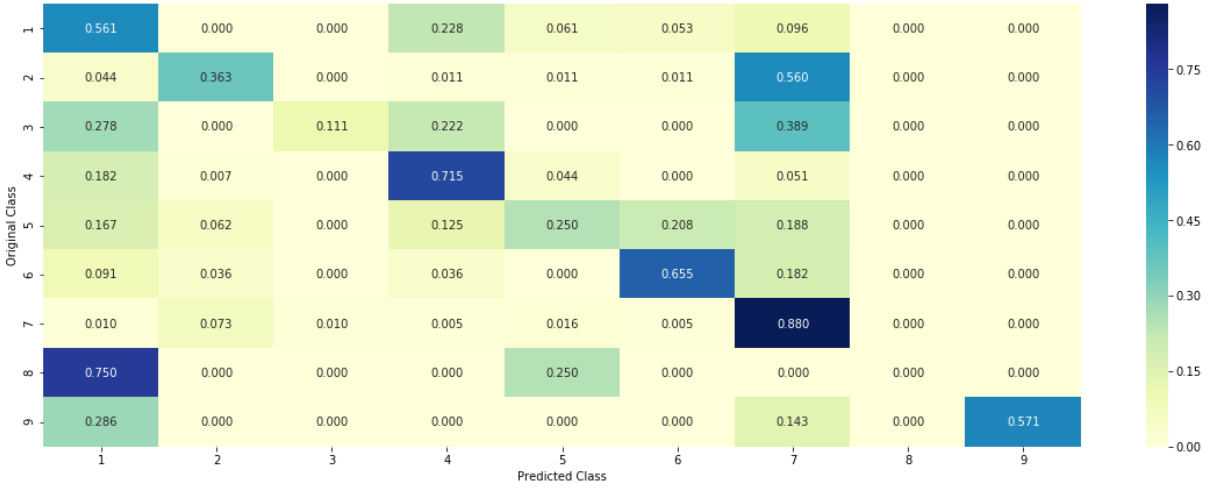



```
-------------------- Precision matrix (Columm Sum=1) ------------------
--
```





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



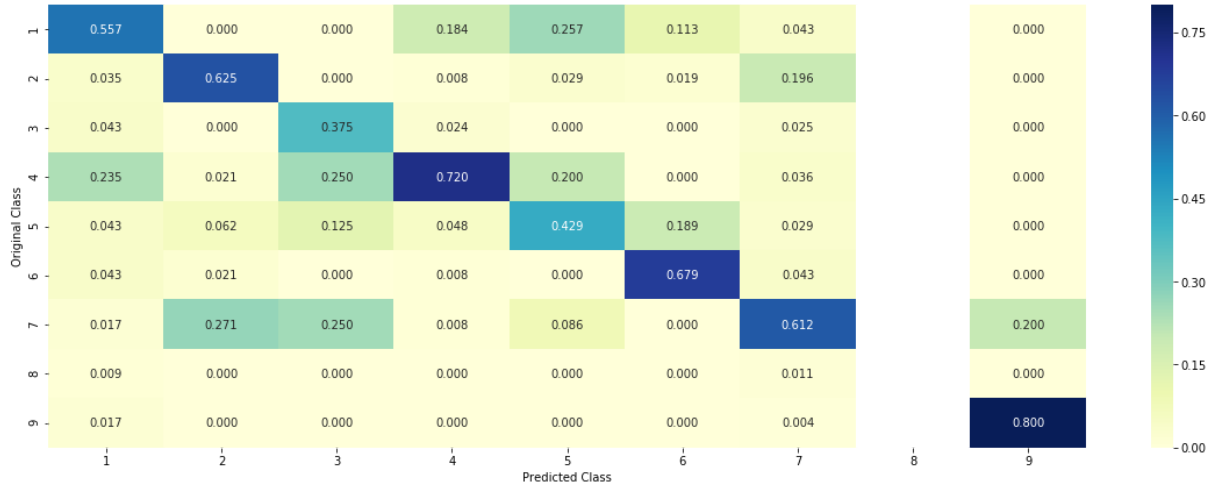
4.7.3 Maximum Voting classifier

In [99]:
```
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 : 0.9407598679043604
Log loss (CV) on the VotingClassifier : 1.2835402100341697
Log loss (test) on the VotingClassifier : 1.223278167176945
Number of missclassified point : 0.3819548872180451
-------------------- Confusion matrix --------------------
```


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



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