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 (https://www.youtube.com/watch?v=UwbuW7oK8rk)
- 3. https://www.youtube.com/watch?v=qxXRKVompl8)

1.3. Real-world/Business objectives and constraints.

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

2. Machine Learning Problem Formulation

2.1. Data

2.1.1. Data Overview

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

2.1.2. Example Data Point

training_variants

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

• • •

training_text

ID,Text

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

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

2.2.1. Type of Machine Learning Problem

There are nine different classes a genetic mutation can be classified into => Multi class classification problem

2.2.2. Performance Metric

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

Metric(s):

- Multi class log-loss
- · Confusion matrix

2.2.3. Machine Learing Objectives and Constraints

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

Constraints:

* Interpretability * Class probabilities are needed. * Penalize the errors in class probabilities => Metric is Logloss. * No Latency constraints.

2.3. Train, CV and Test Datasets

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

3. Exploratory Data Analysis

In [1]:

```
import pandas as pd
import matplotlib.pyplot as plt
import re
import time
import warnings
import numpy as np
from nltk.corpus import stopwords
from sklearn.decomposition import TruncatedSVD
from sklearn.preprocessing import normalize
from sklearn.feature extraction.text import CountVectorizer
from sklearn.manifold import TSNE
import seaborn as sns
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics.classification import accuracy_score, log_loss
from sklearn.feature extraction.text import TfidfVectorizer
from sklearn.linear_model import SGDClassifier
from imblearn.over_sampling import SMOTE
from collections import Counter
from scipy.sparse import hstack
from sklearn.multiclass import OneVsRestClassifier
from sklearn.svm import SVC
from 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
Using TensorFlow backend.
```

```
/home/shanud6711/.local/lib/python3.5/site-packages/tensorflow/python/framew
ork/dtypes.py:516: FutureWarning: Passing (type, 1) or '1type' as a synonym
of type is deprecated; in a future version of numpy, it will be understood a
s (type, (1,)) / '(1,)type'.
  _np_qint8 = np.dtype([("qint8", np.int8, 1)])
/home/shanud6711/.local/lib/python3.5/site-packages/tensorflow/python/framew
ork/dtypes.py:517: FutureWarning: Passing (type, 1) or '1type' as a synonym
of type is deprecated; in a future version of numpy, it will be understood a
s (type, (1,)) / '(1,)type'.
  _np_quint8 = np.dtype([("quint8", np.uint8, 1)])
/home/shanud6711/.local/lib/python3.5/site-packages/tensorflow/python/framew
ork/dtypes.py:518: FutureWarning: Passing (type, 1) or '1type' as a synonym
of type is deprecated; in a future version of numpy, it will be understood a
s (type, (1,)) / '(1,)type'.
  _np_qint16 = np.dtype([("qint16", np.int16, 1)])
/home/shanud6711/.local/lib/python3.5/site-packages/tensorflow/python/framew
ork/dtypes.py:519: FutureWarning: Passing (type, 1) or '1type' as a synonym
of type is deprecated; in a future version of numpy, it will be understood a
```

s (type, (1,)) / '(1,)type'.

```
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                                            PersonalizedCancerDiagnosis
    _np_quint16 = np.dtype([("quint16", np.uint16, 1)])
 /home/shanud6711/.local/lib/python3.5/site-packages/tensorflow/python/framew
 ork/dtypes.py:520: FutureWarning: Passing (type, 1) or '1type' as a synonym
 of type is deprecated; in a future version of numpy, it will be understood a
 s (type, (1,)) / '(1,)type'.
    _np_qint32 = np.dtype([("qint32", np.int32, 1)])
  /home/shanud6711/.local/lib/python3.5/site-packages/tensorflow/python/framew
 ork/dtypes.py:525: FutureWarning: Passing (type, 1) or '1type' as a synonym
 of type is deprecated; in a future version of numpy, it will be understood a
 s (type, (1,)) / '(1,)type'.
    np_resource = np.dtype([("resource", np.ubyte, 1)])
 /home/shanud6711/.local/lib/python3.5/site-packages/tensorboard/compat/tenso
 rflow_stub/dtypes.py:541: FutureWarning: Passing (type, 1) or '1type' as a s
 ynonym of type is deprecated; in a future version of numpy, it will be under
 stood as (type, (1,)) / '(1,)type'.
    _np_qint8 = np.dtype([("qint8", np.int8, 1)])
 /home/shanud6711/.local/lib/python3.5/site-packages/tensorboard/compat/tenso
 rflow_stub/dtypes.py:542: FutureWarning: Passing (type, 1) or '1type' as a s
 ynonym of type is deprecated; in a future version of numpy, it will be under
 stood as (type, (1,)) / '(1,)type'.
    _np_quint8 = np.dtype([("quint8", np.uint8, 1)])
 /home/shanud6711/.local/lib/python3.5/site-packages/tensorboard/compat/tenso
 rflow_stub/dtypes.py:543: FutureWarning: Passing (type, 1) or '1type' as a s
 ynonym of type is deprecated; in a future version of numpy, it will be under
 stood as (type, (1,)) / '(1,)type'.
    _np_qint16 = np.dtype([("qint16", np.int16, 1)])
 /home/shanud6711/.local/lib/python3.5/site-packages/tensorboard/compat/tenso
 rflow_stub/dtypes.py:544: FutureWarning: Passing (type, 1) or '1type' as a s
 ynonym of type is deprecated; in a future version of numpy, it will be under
 stood as (type, (1,)) / '(1,)type'.
    _np_quint16 = np.dtype([("quint16", np.uint16, 1)])
 /home/shanud6711/.local/lib/python3.5/site-packages/tensorboard/compat/tenso
 rflow_stub/dtypes.py:545: FutureWarning: Passing (type, 1) or '1type' as a s
 ynonym of type is deprecated; in a future version of numpy, it will be under
 stood as (type, (1,)) / '(1,)type'.
    _np_qint32 = np.dtype([("qint32", np.int32, 1)])
```

/home/shanud6711/.local/lib/python3.5/site-packages/tensorboard/compat/tenso rflow_stub/dtypes.py:550: FutureWarning: Passing (type, 1) or '1type' as a s ynonym of type is deprecated; in a future version of numpy, it will be under stood as (type, (1,)) / '(1,)type'.

np_resource = np.dtype([("resource", np.ubyte, 1)])

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

In [2]:

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

Number of data points : 3321 Number of features : 4

Features : ['ID' 'Gene' 'Variation' 'Class']

Out[2]:

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

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

Fields are

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

3.1.2. Reading Text Data

In [3]:

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

Number of data points : 3321
Number of features : 2
Features : ['ID' 'TEXT']
Out[3]:

ID TEXT

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

3.1.3. Preprocessing of text

In [4]:

```
import nltk
```

In [5]:

```
nltk.download('stopwords')
[nltk_data] Downloading package stopwords to
[nltk_data] /home/shanud6711/nltk_data...
```

Package stopwords is already up-to-date!

Out[5]:

[nltk_data]

True

In [6]:

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

In [7]:

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

there is no text description for id: 1109
there is no text description for id: 1277
there is no text description for id: 1407
there is no text description for id: 1639
there is no text description for id: 2755
Time took for preprocessing the text : 35.79307 seconds

In [8]:
```

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

Out[8]:

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

In [9]:

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

Out[9]:

		ID	Gene	Variation	Class	TEXT
-	1109	1109	FANCA	S1088F	1	NaN
1	1277	1277	ARID5B	Truncating Mutations	1	NaN
1	1407	1407	FGFR3	K508M	6	NaN
1	1639	1639	FLT1	Amplification	6	NaN
2	2755	2755	BRAF	G596C	7	NaN

In [10]:

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

In [11]:

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

Out[11]:

	ID	Gene	variation	Class	IEXI
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 [12]:

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

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

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

In [13]:

```
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])
```

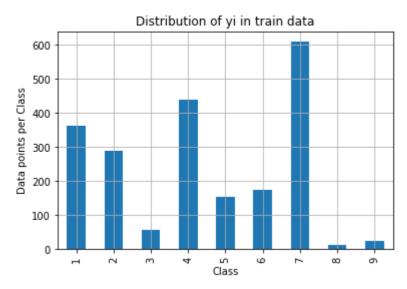
Number of data points in train data: 2124 Number of data points in test data: 665

Number of data points in cross validation data: 532

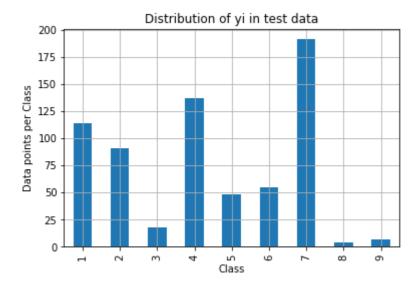
3.1.4.2. Distribution of y_i's in Train, Test and Cross Validation datasets

In [14]:

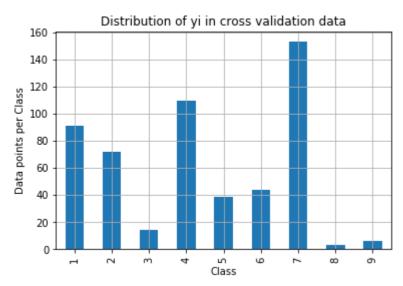
```
# it returns a dict, keys as class labels and values as the number of data points in that d
train_class_distribution = train_df['Class'].value_counts().sort_index()
test_class_distribution = test_df['Class'].value_counts().sort_index()
cv class distribution = cv df['Class'].value counts().sort index()
my colors = 'rgbkymc'
train_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in train data')
plt.grid()
plt.show()
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted yi = np.argsort(-train class distribution.values)
for i in sorted yi:
    print('Number of data points in class', i+1, ':',train_class_distribution.values[i], '(
print('-'*80)
my colors = 'rgbkymc'
test class distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in test data')
plt.grid()
plt.show()
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-test_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',test_class_distribution.values[i], '(')
print('-'*80)
my colors = 'rgbkymc'
cv_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in cross validation data')
plt.grid()
plt.show()
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train class distribution.values): the minus sign will give us in decreasing order
sorted yi = np.argsort(-train class distribution.values)
for i in sorted yi:
    print('Number of data points in class', i+1, ':',cv_class_distribution.values[i], '(',
```



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



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



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

3.2 Prediction using a 'Random' Model

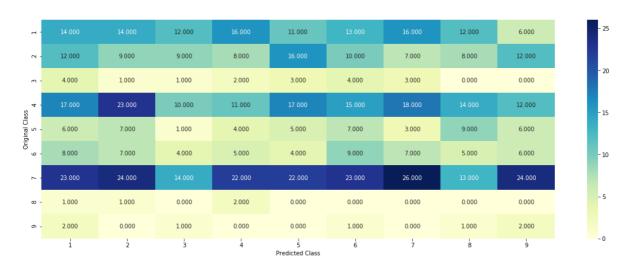
In a 'Random' Model, we generate the NINE class probabilites randomly such that they sum to 1.

In [15]:

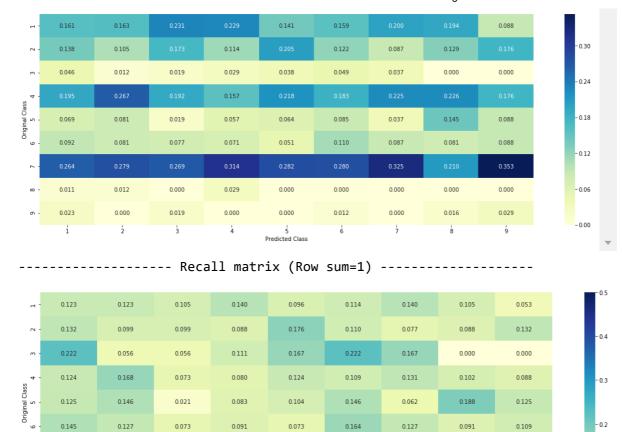
```
# This function plots the confusion matrices given y i, y i hat.
def plot_confusion_matrix(test_y, predict_y):
    C = confusion_matrix(test_y, predict_y)
    # C = 9,9 matrix, each cell (i,j) represents number of points of class i are predicted
    A = (((C.T)/(C.sum(axis=1))).T)
    #divid each element of the confusion matrix with the sum of elements in that column
    \# C = [[1, 2],
         [3, 41]
    # C.T = [[1, 3],
             [2, 4]]
    # C.sum(axis = 1) axis=0 corresonds to columns and axis=1 corresponds to rows in two d
    \# C.sum(axix = 1) = [[3, 7]]
    \# ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
                                [2/3, 4/711]
    \# ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]
                                [3/7, 4/7]]
    # sum of row elements = 1
    B = (C/C.sum(axis=0))
    #divid each element of the confusion matrix with the sum of elements in that row
    \# C = [[1, 2],
         [3, 4]]
    # C.sum(axis = 0) axis=0 corresonds to columns and axis=1 corresponds to rows in two d
    \# C.sum(axix = 0) = [[4, 6]]
    \# (C/C.sum(axis=0)) = [[1/4, 2/6],
                           [3/4, 4/6]]
    labels = [1,2,3,4,5,6,7,8,9]
    # representing A in heatmap format
    print("-"*20, "Confusion matrix", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=la
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()
    print("-"*20, "Precision matrix (Column Sum=1)", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=la
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()
    # representing B in heatmap format
    print("-"*20, "Recall matrix (Row sum=1)", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(A, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=la
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()
```

In [16]:

```
# we need to generate 9 numbers and the sum of numbers should be 1
# one solution is to genarate 9 numbers and divide each of the numbers by their sum
# ref: https://stackoverflow.com/a/18662466/4084039
test_data_len = test_df.shape[0]
cv_data_len = cv_df.shape[0]
# we create a output array that has exactly same size as the CV data
cv_predicted_y = np.zeros((cv_data_len,9))
for i in range(cv_data_len):
    rand probs = np.random.rand(1,9)
    cv_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Cross Validation Data using Random Model",log_loss(y_cv,cv_predicted_y,
# Test-Set error.
#we create a output array that has exactly same as the test data
test_predicted_y = np.zeros((test_data_len,9))
for i in range(test_data_len):
    rand_probs = np.random.rand(1,9)
    test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Test Data using Random Model",log_loss(y_test,test_predicted_y, eps=1e-1
predicted_y =np.argmax(test_predicted_y, axis=1)
plot_confusion_matrix(y_test, predicted_y+1)
```



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



0.115

0.000

0.000

5 Predicted Class 0.120

0.000

0.143

0.136

0.000

0.000

0.068

0.000

0.143

0.126

0.000

0.1

- 0.0

3.3 Univariate Analysis

0.126

0.000

0.073

0.000

0.143

0.115

0.000

0.120

In [17]:

```
# code for response coding with Laplace smoothing.
# alpha: used for laplace smoothing
# feature: ['gene', 'variation']
# df: ['train_df', 'test_df', 'cv_df']
# algorithm
# Consider all unique values and the number of occurances of given feature in train data da
# build a vector (1*9) , the first element = (number of times it occured in class1 + 10*alp
# gv_dict is like a look up table, for every gene it store a (1*9) representation of it
# for a value of feature in df:
# if it is in train data:
# we add the vector that was stored in 'gv_dict' look up table to 'qv fea'
# if it is not there is train:
# we add [1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9] to 'gv_fea'
# return 'gv_fea'
# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
    # value_count: it contains a dict like
    # print(train_df['Gene'].value_counts())
    # output:
             {BRCA1
                         174
              TP53
                         106
    #
    #
              EGFR
                          86
             BRCA2
                          75
    #
              PTEN
    #
                          69
    #
                          61
             KTT
    #
              BRAF
                          60
              ERBB2
                          47
    #
    #
              PDGFRA
                          46
              ...}
    # print(train_df['Variation'].value_counts())
    # output:
    # {
    # Truncating Mutations
                                                63
                                                43
    # Deletion
    # Amplification
                                                43
                                                22
    # Fusions
    # Overexpression
                                                 3
    # E17K
                                                 3
                                                 3
    # 061L
                                                 2
    # S222D
    # P130S
                                                 2
    # ...
    # }
    value count = train df[feature].value counts()
    # qv dict : Gene Variation Dict, which contains the probability array for each gene/var
    gv_dict = dict()
    # denominator will contain the number of time that particular feature occured in whole
    for i, denominator in value count.items():
        # vec will contain (p(yi==1/Gi)) probability of gene/variation belongs to perticular
        # vec is 9 diamensional vector
        vec = []
        for k in range(1,10):
            # print(train_df.loc[(train_df['Class']==1) & (train_df['Gene']=='BRCA1')])
                                             Variation Class
```

ID

Gene

```
# 2470 2470 BRCA1
                                               S1715C
            # 2486 2486 BRCA1
                                               S1841R
                                                           1
            # 2614 2614 BRCA1
                                                           1
                                                  M1R
            # 2432 2432 BRCA1
                                               L1657P
                                                           1
            # 2567 2567 BRCA1
                                               T1685A
                                                           1
            # 2583 2583 BRCA1
                                                           1
                                               E1660G
            # 2634 2634 BRCA1
                                                           1
                                               W1718L
            # cls_cnt.shape[0] will return the number of rows
            cls_cnt = train_df.loc[(train_df['Class']==k) & (train_df[feature]==i)]
            # cls_cnt.shape[0](numerator) will contain the number of time that particular f
            vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
        # we are adding the gene/variation to the dict as key and vec as value
        gv dict[i]=vec
    return gv_dict
# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
    # print(qv dict)
          {'BRCA1': [0.20075757575757575, 0.03787878787878788, 0.068181818181818177, 0.1363
    #
           'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 0.2704
           'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.0681818181818177
    #
           'BRCA2': [0.1333333333333333, 0.0606060606060608, 0.060606060606060608, 0.078
    #
    #
           'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 0.465
           'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.07284
    #
           'BRAF': [0.0666666666666666666, 0.17999999999999, 0.073333333333333334, 0.0733
    gv_dict = get_gv_fea_dict(alpha, feature, df)
    # value_count is similar in get_gv_fea_dict
    value_count = train_df[feature].value_counts()
    # gv_fea: Gene_variation feature, it will contain the feature for each feature value in
    gv_fea = []
    # for every feature values in the given data frame we will check if it is there in the
    # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to gv_fea
    for index, row in df.iterrows():
        if row[feature] in dict(value count).keys():
            gv_fea.append(gv_dict[row[feature]])
            gv_fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
#
              gv_fea.append([-1,-1,-1,-1,-1,-1,-1,-1])
    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 [18]:

```
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: 228
BRCA1
          168
TP53
          101
           94
EGFR
           82
BRCA2
           80
PTEN
KIT
           63
           55
BRAF
ALK
           44
           39
PIK3CA
           35
PDGFRA
Name: Gene, dtype: int64
```

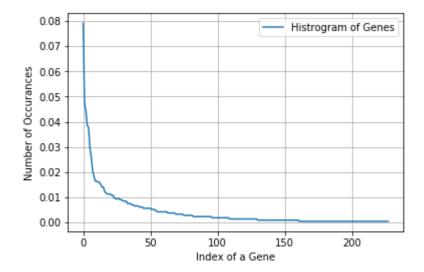
In [19]:

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

Ans: There are 228 different categories of genes in the train data, and they are distibuted as follows

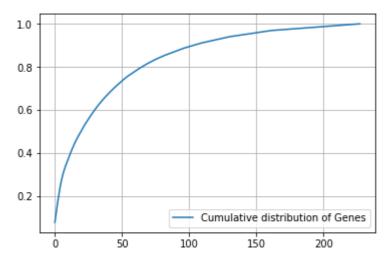
In [20]:

```
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 [21]:

```
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 [22]:

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

```
In [23]:
```

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

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

In [24]:

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

In [25]:

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

Out[25]:

568    SMAD3
1464    FGFR2
407    TP53
```

2794 BRCA2 Name: Gene, dtype: object

FLT3

In [26]:

1652

```
gene_vectorizer.get_feature_names()
Out[26]:
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
 'akt3',
 'alk',
 'apc',
 'ar',
 'araf',
 'arid1b',
 'arid2',
 'atm',
 'atr',
 'atrx',
 'aurka',
 'aurkb',
 'axl'.
```

In [27]:

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

train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature: (2124, 228)

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

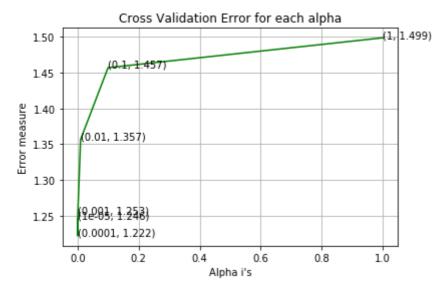
There are many ways to estimate how good a feature is, in predicting y_i. One of the good methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y_i.

In [28]:

```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklea
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Desce
              Predict class labels for samples in X.
# predict(X)
#-----
# video link:
cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
    clf.fit(train_gene_feature_onehotCoding, y_train)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_gene_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, labels=
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
clf.fit(train gene feature onehotCoding, y train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_gene_feature_onehotCoding, y_train)
predict_y = sig_clf.predict_proba(train_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y
predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:"
predict_y = sig_clf.predict_proba(test_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_
For values of alpha = 1e-05 The log loss is: 1.2456271966894141
For values of alpha = 0.0001 The log loss is: 1.2220223754893744
For values of alpha = 0.001 The log loss is: 1.2531249246853366
```

For values of alpha = 0.01 The log loss is: 1.356509885364869

For values of alpha = 0.1 The log loss is: 1.4567985889396995 For values of alpha = 1 The log loss is: 1.498546347144676



For values of best alpha = 0.0001 The train log loss is: 0.979604956147648

For values of best alpha = 0.0001 The cross validation log loss is: 1.22202

23754893744

For values of best alpha = 0.0001 The test log loss is: 1.196223635012313

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 [29]:

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

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

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

print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_coverage/t print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(cv_coverage)
```

Q6. How many data points in Test and CV datasets are covered by the 228 ge nes in train dataset?

Ans

- 1. In test data 642 out of 665 : 96.54135338345866
- 2. In cross validation data 509 out of 532 : 95.67669172932331

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 [30]:

```
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: 1936 Truncating Mutations Deletion 51 **Amplification** 39 **Fusions** 20 Q61L 3 **Overexpression** 3 T73I 2 2 R841K EWSR1-ETV1_Fusion 2 Q61R Name: Variation, dtype: int64

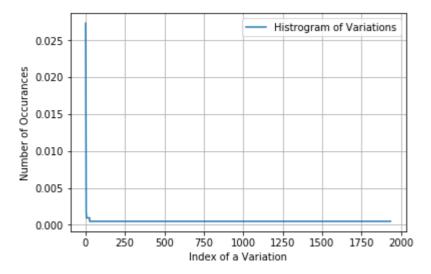
In [31]:

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

Ans: There are 1936 different categories of variations in the train data, an d they are distibuted as follows

In [32]:

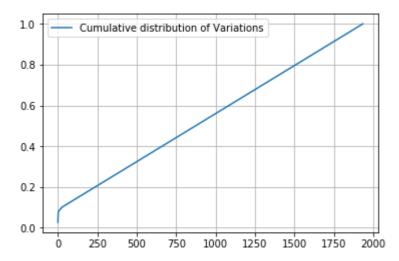
```
s = sum(unique_variations.values);
h = unique_variations.values/s;
plt.plot(h, label="Histrogram of Variations")
plt.xlabel('Index of a Variation')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



In [33]:

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

[0.02730697 0.05131827 0.06967985 ... 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 [34]:

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

In [35]:

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

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

In [36]:

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

In [37]:

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

train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method. The shape of Variation feature: (2124, 1972)

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

Let's build a model just like the earlier!

In [38]:

```
alpha = [10 ** x for x in range(-5, 1)]
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skled
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Desce
# predict(X)
              Predict class labels for samples in X.
#-----
# video link:
cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
    clf.fit(train_variation_feature_onehotCoding, y_train)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_variation_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, labels=
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
clf.fit(train_variation_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train variation feature onehotCoding, y train)
predict_y = sig_clf.predict_proba(train_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y
predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:"
predict y = sig clf.predict proba(test variation feature onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_
```

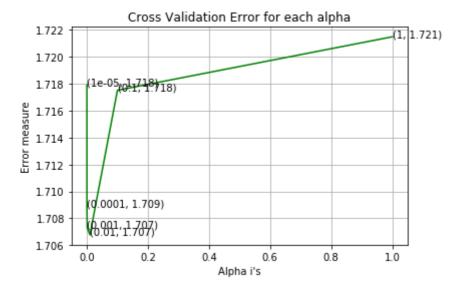
```
For values of alpha = 1e-05 The log loss is: 1.7178995794879857
For values of alpha = 0.0001 The log loss is: 1.7088565257522494
```

```
For values of alpha = 0.001 The log loss is: 1.707293888553472

For values of alpha = 0.01 The log loss is: 1.7067671033699205

For values of alpha = 0.1 The log loss is: 1.7175163628299621

For values of alpha = 1 The log loss is: 1.7214919736628163
```



```
For values of best alpha = 0.01 The train log loss is: 1.4280332974169734

For values of best alpha = 0.01 The cross validation log loss is: 1.7067671
033699205

For values of best alpha = 0.01 The test log loss is: 1.6937332184885605
```

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 [39]:

```
print("Q12. How many data points are covered by total ", unique_variations.shape[0], " gene
test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_coverage/t
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(cv_coverage/t)
```

Q12. How many data points are covered by total 1936 genes in test and cros s validation data sets?

Ans

- 1. In test data 71 out of 665 : 10.676691729323307
- 2. In cross validation data 57 out of 532 : 10.714285714285714

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 [40]:

In [41]:

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

In [42]:

```
# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer = TfidfVectorizer(min_df=10,max_features=1000)
train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()

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

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

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

Total number of unique words in train data: 1000

In [43]:

```
dict list = []
# dict_list =[] contains 9 dictoinaries each corresponds to a class
for i in range(1,10):
    cls text = train_df[train_df['Class']==i]
    # build a word dict based on the words in that class
    dict_list.append(extract_dictionary_paddle(cls_text))
    # append it to dict_list
# dict_list[i] is build on i'th class text data
# total dict is buid on whole training text data
total_dict = extract_dictionary_paddle(train_df)
confuse_array = []
for i in train_text_features:
    ratios = []
    max val = -1
    for j in range(0,9):
        ratios.append((dict_list[j][i]+10 )/(total_dict[i]+90))
    confuse_array.append(ratios)
confuse_array = np.array(confuse_array)
```

In [44]:

```
#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 [45]:

```
# https://stackoverflow.com/a/16202486
# we convert each row values such that they sum to 1
train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train_text_feature
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_re
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_response
```

In [46]:

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

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

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

In [47]:

```
#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 [48]:

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

63573224: 1, 6.995574265725332: 1, 38.346939368013906: 1, 39.8512283099524 8: 1, 40.2304771143921: 1, 41.160059436431276: 1, 42.94197355886691: 1, 7. 68827555535155: 1, 44.70165950878922: 1, 45.30696641378176: 1, 46.78762189 676073: 1, 47.81112414010709: 1, 27.62544157494064: 1, 8.80986532288027: 1, 10.195161198666451: 1, 51.188666695284454: 1, 17.195434608029487: 1, 9. 131157423077568: 1, 56.56876107527138: 1, 57.5866766986556: 1, 59.30791995 335007: 1, 10.101672307669627: 1, 63.31080707223666: 1, 64.53516323191826: 1, 9.967345632780207: 1, 11.946384260600714: 1, 68.2742994035185: 1, 69.76 390959425093: 1, 70.56577707934976: 1, 8.057117570355384: 1, 15.9472396275 85725: 1, 12.419868725550492: 1, 75.91318627430823: 1, 13.82056436084741: 1, 11.723408104072913: 1, 81.63401788955598: 1, 83.8351178062782: 1, 14.04 5842325114856: 1, 12.966845793584433: 1, 90.96819968915806: 1, 15.62124826 2094392: 1, 20.02724037487328: 1, 16.87913339896523: 1, 9.347462471409726: 1, 18.016978078126467: 1, 7.612533731567131: 1, 8.372251250227386: 1, 17.4 3885769992849: 1, 7.552574407413243: 1, 105.84936125682741: 1, 29.75797509 4965804: 1, 18.489247746277876: 1, 12.615044441166784: 1, 112.596534529018 6: 1, 19.482914987565206: 1, 8.133908981588688: 1, 20.673000687756872: 1, 21.489085679059166: 1, 21.58306866837075: 1, 130.40654630009806: 1, 8.8531 00244944835: 1, 10.065690468213301: 1, 22.37425621009435: 1, 135.920818253

In [49]:

```
# Train a Logistic regression+Calibration model using text features whicha re on-hot encode
alpha = [10 ** x for x in range(-5, 1)]
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skled
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Desce
\# predict(X) Predict class labels for samples in X.
# video link:
#-----
cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
    clf.fit(train_text_feature_onehotCoding, y_train)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_text_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, labels=
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
clf.fit(train_text_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_onehotCoding, y_train)
predict_y = sig_clf.predict_proba(train_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y
predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:"
predict y = sig clf.predict proba(test text feature onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_
```

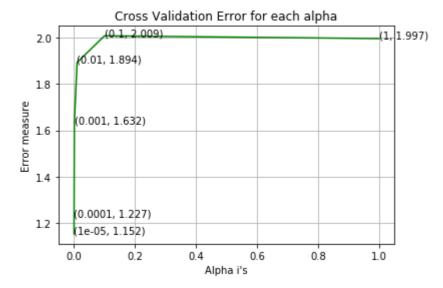
For values of alpha = 1e-05 The log loss is: 1.1518024669520401 For values of alpha = 0.0001 The log loss is: 1.2270787596796686

```
For values of alpha = 0.001 The log loss is: 1.6319913255112053

For values of alpha = 0.01 The log loss is: 1.8938478417263278

For values of alpha = 0.1 The log loss is: 2.0091810720221455

For values of alpha = 1 The log loss is: 1.9971050574484712
```



```
For values of best alpha = 1e-05 The train log loss is: 0.7062087090008116
For values of best alpha = 1e-05 The cross validation log loss is: 1.151802
4669520401
For values of best alpha = 1e-05 The test log loss is: 1.157071624391242
```

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

Ans. Yes, it seems like!

In [52]:

```
def get_intersec_text(df):
    df_text_vec = TfidfVectorizer(max_features=1000)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

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

In [53]:

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

95.4 % of word of test data appeared in train data 94.3 % of word of Cross Validation appeared in train data

4. Machine Learning Models

In [54]:

```
#Data preparation for ML models.

#Misc. functionns for ML models

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

# for calculating log_loss we will provide the array of probabilities belongs to each
    print("Log loss:",log_loss(test_y, sig_clf.predict_proba(test_x)))
    # calculating the number of data points that are misclassified
    print("Number of mis-classified points:", np.count_nonzero((pred_y- test_y))/test_y.sh
    plot_confusion_matrix(test_y, pred_y)
```

In [55]:

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

In [56]:

```
# this function will be used just for naive bayes
# for the given indices, we will print the name of the features
# and we will check whether the feature present in the test point text or not
def get_impfeature_names(indices, text, gene, var, no_features):
    gene_count_vec = TfidfVectorizer()
    var_count_vec = TfidfVectorizer()
    text_count_vec = TfidfVectorizer(min_df=10, max_features= 1000)
    gene_vec = gene_count_vec.fit(train_df['Gene'])
    var vec = var count vec.fit(train df['Variation'])
    text_vec = text_count_vec.fit(train_df['TEXT'])
    fea1_len = len(gene_vec.get_feature_names())
    fea2_len = len(var_count_vec.get_feature_names())
    word present = 0
    for i,v in enumerate(indices):
        if (v < fea1_len):</pre>
            word = gene_vec.get_feature_names()[v]
            yes_no = True if word == gene else False
            if yes_no:
                word_present += 1
                print(i, "Gene feature [{}] present in test data point [{}]".format(word,ye
        elif (v < fea1_len+fea2_len):</pre>
            word = var_vec.get_feature_names()[v-(fea1_len)]
            yes_no = True if word == var else False
            if yes_no:
                word_present += 1
                print(i, "variation feature [{}] present in test data point [{}]".format(wo

        else:
            word = text_vec.get_feature_names()[v-(fea1_len+fea2_len)]
            yes_no = True if word in text.split() else False
            if yes_no:
                word present += 1
                print(i, "Text feature [{}] present in test data point [{}]".format(word,ye
    print("Out of the top ",no_features," features ", word_present, "are present in query p
```

Stacking the three types of features

In [57]:

```
# merging gene, variance and text features
# building train, test and cross validation data sets
\# a = [[1, 2],
      [3, 4]]
#
#b = [[4, 5],
      [6, 7]]
# hstack(a, b) = [[1, 2, 4, 5],
                 [ 3, 4, 6, 7]]
train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,train_variation_featu
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehot
train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text_feature_onehotCoding
train_y = np.array(list(train_df['Class']))
test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_feature_onehotCoding)).
test_y = np.array(list(test_df['Class']))
cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text_feature_onehotCoding)).tocsr(
cv_y = np.array(list(cv_df['Class']))
train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,train_variatid
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_f
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature
train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_responseCoding)
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_response
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding
```

In [58]:

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

One hot encoding features :
   (number of data points * number of features) in train data = (2124, 3200)
   (number of data points * number of features) in test data = (665, 3200)
   (number of data points * number of features) in cross validation data = (53
2, 3200)
```

In [59]:

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

4.1. Base Line Model

4.1.1. Naive Bayes

4.1.1.1. Hyper parameter tuning

In [60]:

```
# find more about Multinomial Naive base function here http://scikit-learn.org/stable/modul
# default paramters
# sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_prior=None)
# some of methods of MultinomialNB()
# fit(X, y[, sample_weight]) Fit Naive Bayes classifier according to X, y
\# predict(X) Perform classification on an array of test vectors X.
# predict_log_proba(X) Return log-probability estimates for the test vector X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive
# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])
Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict_proba(X) Posterior probabilities of classification
# ------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive
# -----
alpha = [0.00001, 0.0001, 0.001, 0.1, 1, 10, 100,1000]
cv_log_error_array = []
for i in alpha:
   print("for alpha =", i)
   clf = MultinomialNB(alpha=i)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15)
    # to avoid rounding error while multiplying probabilites we use log-probability estimat
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(np.log10(alpha), cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv_log_error_array[i]))
plt.grid()
plt.xticks(np.log10(alpha))
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = MultinomialNB(alpha=alpha[best alpha])
clf.fit(train_x_onehotCoding, train_y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
```

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

for alpha = 1e-05

Log Loss: 1.2645488930508384

for alpha = 0.0001

Log Loss: 1.264292740788423

for alpha = 0.001

Log Loss: 1.2650585223720952

for alpha = 0.1

Log Loss: 1.3056714137681062

for alpha = 1

Log Loss: 1.3520832079915182

for alpha = 10

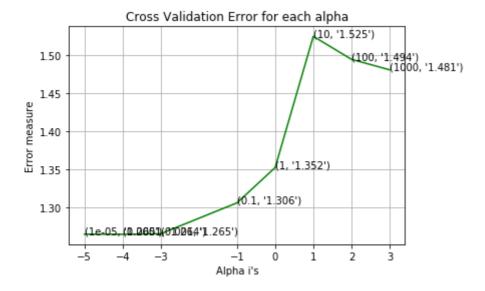
Log Loss: 1.524623462754661

for alpha = 100

Log Loss: 1.4943555708221936

for alpha = 1000

Log Loss: 1.4805602945213652



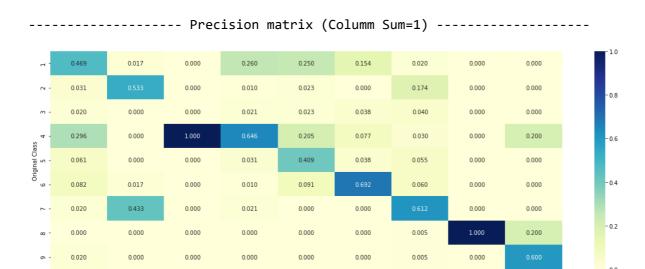
For values of best alpha = 0.0001 The train log loss is: 0.4954882009441721 For values of best alpha = 0.0001 The cross validation log loss is: 1.26429 2740788423 For values of best alpha = 0.0001 The test log loss is: 1.2378410438559158

4.1.1.2. Testing the model with best hyper paramters

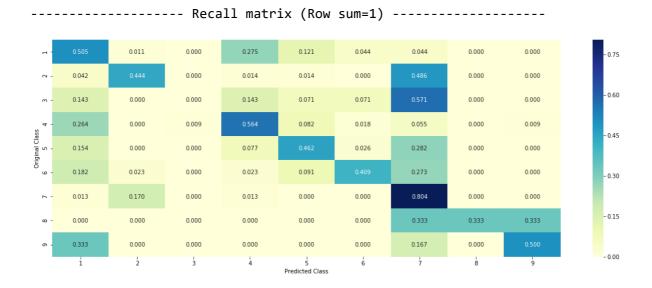
In [61]:

```
# find more about Multinomial Naive base function here http://scikit-learn.org/stable/modul
#
# default paramters
# sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_prior=None)
# some of methods of MultinomialNB()
\# fit(X, y[, sample_weight]) Fit Naive Bayes classifier according to X, y
              Perform classification on an array of test vectors X.
# predict(X)
# predict_log_proba(X) Return log-probability estimates for the test vector X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive
# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])
Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict_proba(X) Posterior probabilities of classification
clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
# to avoid rounding error while multiplying probabilites we use log-probability estimates
print("Log Loss :",log_loss(cv_y, sig_clf_probs))
print("Number of missclassified point :", np.count_nonzero((sig_clf.predict(cv_x_onehotCodi
plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray()))
```



Predicted Class



4.1.1.3. Feature Importance, Correctly classified point

```
In [66]:
```

```
test point index = 1
no_feature = 1000
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[
print("Actual Class :", test_y[test_point_index])
indices=np.argsort(abs(-clf.coef_))[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].ilc
Predicted Class: 4
Predicted Class Probabilities: [[0.0585 0.0482 0.2353 0.2954 0.0336 0.035
0.2876 0.0038 0.0025]]
Actual Class: 5
485 Text feature [1000] present in test data point [True]
540 Text feature [106] present in test data point [True]
698 Text feature [13] present in test data point [True]
804 Text feature [10] present in test data point [True]
835 Text feature [000] present in test data point [True]
849 Text feature [12] present in test data point [True]
969 Text feature [11] present in test data point [True]
Out of the top 1000 features 7 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

```
In [67]:
```

```
test_point_index = 5
no feature = 1000
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].ilo
Predicted Class: 4
Predicted Class Probabilities: [[0.0514 0.0415 0.0107 0.7467 0.0297 0.0307
0.0838 0.0032 0.0023]]
Actual Class: 4
371 Text feature [111] present in test data point [True]
588 Text feature [00001] present in test data point [True]
804 Text feature [10] present in test data point [True]
849 Text feature [12] present in test data point [True]
969 Text feature [11] present in test data point [True]
Out of the top 1000 features 5 are present in query point
```

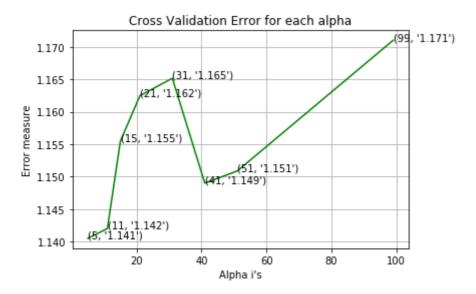
4.2. K Nearest Neighbour Classification

4.2.1. Hyper parameter tuning

In [68]:

```
# find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/genera
# default parameter
# KNeighborsClassifier(n_neighbors=5, weights='uniform', algorithm='auto', leaf_size=30, p=
# metric='minkowski', metric_params=None, n_jobs=1, **kwargs)
# methods of
# fit(X, y): Fit the model using X as training data and y as target values
# predict(X):Predict the class labels for the provided data
\# predict proba(X):Return probability estimates for the test data X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/k-ned
# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# -----
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])
Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict_proba(X) Posterior probabilities of classification
#-----
# video link:
#-----
alpha = [5, 11, 15, 21, 31, 41, 51, 99]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = KNeighborsClassifier(n_neighbors=i)
    clf.fit(train_x_responseCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_responseCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
   cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15)
    # to avoid rounding error while multiplying probabilites we use log-probability estimat
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train_x_responseCoding, train_y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)
```

for alpha = 5Log Loss: 1.1405173382165168 for alpha = 11Log Loss: 1.1420228632847649 for alpha = 15Log Loss: 1.1554667928927245 for alpha = 21Log Loss: 1.1624568547448222 for alpha = 31Log Loss: 1.1651466337190677 for alpha = 41Log Loss: 1.149010029002536 for alpha = 51Log Loss: 1.1508787763855548 for alpha = 99Log Loss: 1.1709911264796269



For values of best alpha = 5 The train log loss is: 0.49191662742442116

For values of best alpha = 5 The cross validation log loss is: 1.1405173382

165168

For values of best alpha = 5 The test log loss is: 1.1284356445815504

4.2.2. Testing the model with best hyper paramters

In [69]:

Log loss : 1.1405173382165168

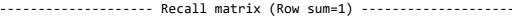
Number of mis-classified points: 0.37406015037593987

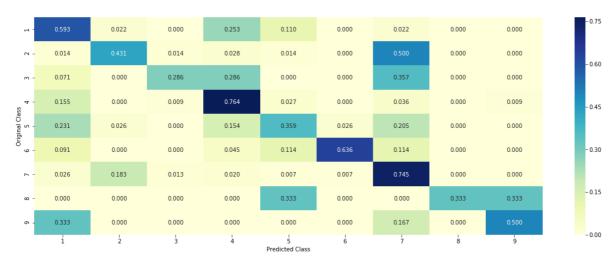
----- Confusion matrix -----



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







4.2.3. Sample Query point -1

```
In [70]:
```

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

test_point_index = 1
predicted_cls = sig_clf.predict(test_x_responseCoding[0].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Actual Class :", test_y[test_point_index])
neighbors = clf.kneighbors(test_x_responseCoding[test_point_index].reshape(1, -1), alpha[be
print("The ",alpha[best_alpha]," nearest neighbours of the test points belongs to classes",
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))

Predicted Class : 7
Actual Class : 5
The 5 nearest neighbours of the test points belongs to classes [4 3 3 7 7]
Fequency of nearest points : Counter({3: 2, 7: 2, 4: 1})
```

4.2.4. Sample Query Point-2

In [71]:

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

test_point_index = 100

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

Predicted Class : 4
Actual Class : 4
the k value for knn is 5 and the nearest neighbours of the test points belon
```

4.3. Logistic Regression

Fequency of nearest points : Counter({4: 5})

4.3.1. With Class balancing

4.3.1.1. Hyper paramter tuning

gs to classes [4 4 4 4 4]

In [72]:

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skled
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Desce
\# predict(X) Predict class labels for samples in X.
#-----
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geome
#-----
# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])
Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict_proba(X) Posterior probabilities of classification
#-----
# video Link:
#-----
alpha = [10 ** x for x in range(-6, 3)]
cv_log_error_array = []
for i in alpha:
   print("for alpha =", i)
   clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='12', loss='log', random
   clf.fit(train_x_onehotCoding, train_y)
   sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
   sig_clf.fit(train_x_onehotCoding, train_y)
   sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
   cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15)
   # to avoid rounding error while multiplying probabilites we use log-probability estimat
   print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
   ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='1
clf.fit(train x onehotCoding, train y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
```

for alpha = 1e-06

Log Loss: 1.1869058291379453

for alpha = 1e-05

Log Loss: 1.128063752361977

for alpha = 0.0001

Log Loss: 1.0921944639064523

for alpha = 0.001

Log Loss: 1.1156273446083163

for alpha = 0.01

Log Loss: 1.2289151207011373

for alpha = 0.1

Log Loss: 1.667026424334042

for alpha = 1

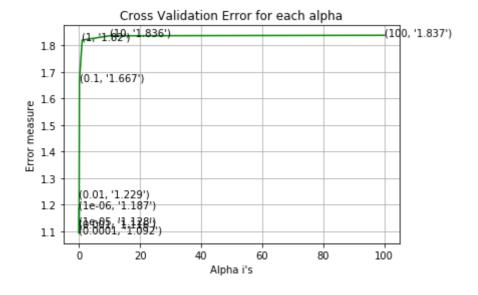
Log Loss: 1.8195702204105595

for alpha = 10

Log Loss: 1.835603157666193

for alpha = 100

Log Loss: 1.8374397384222378



```
For values of best alpha = 0.0001 The train log loss is: 0.4236568818652322 6

For values of best alpha = 0.0001 The cross validation log loss is: 1.09219 44639064523

For values of best alpha = 0.0001 The test log loss is: 1.0726642836359683
```

4.3.1.2. Testing the model with best hyper paramters

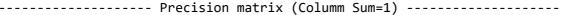
In [73]:

Log loss: 1.0921944639064523

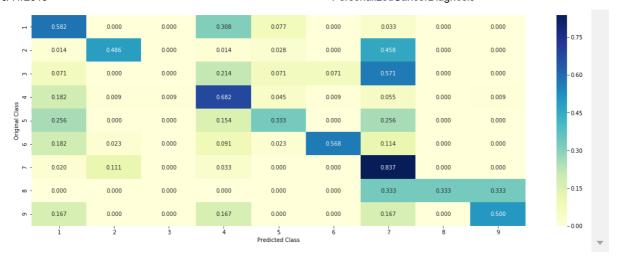
Number of mis-classified points : 0.37406015037593987

----- Confusion matrix -----









4.3.1.3. Feature Importance

In [74]:

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

4.3.1.3.1. Correctly Classified point

```
In [77]:
```

```
# from tabulate import tabulate
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='1
clf.fit(train_x_onehotCoding,train_y)
test point index = 1
no feature = 1000
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].ild
Predicted Class: 7
Predicted Class Probabilities: [[2.800e-03 3.700e-03 1.345e-01 1.004e-01 1.6
00e-03 1.200e-03 7.533e-01
  2.400e-03 1.000e-0411
Actual Class: 5
9 Text feature [106] present in test data point [True]
227 Text feature [000] present in test data point [True]
960 Text feature [11] present in test data point [True]
Out of the top 1000 features 3 are present in query point
4.3.1.3.2. Incorrectly Classified point
In [79]:
```

```
test_point_index = 5
no_feature = 1000
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(abs(-clf.coef_))[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].ilc
Predicted Class: 4
Predicted Class Probabilities: [[6.990e-02 9.700e-03 3.000e-04 8.517e-01 3.4
00e-03 2.400e-03 5.990e-02
  2.700e-03 1.000e-04]]
Actual Class: 4
Out of the top 1000 features 0 are present in query point
```

4.3.2. Without Class balancing

4.3.2.1. Hyper paramter tuning

In [80]:

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skled
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Desce
\# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geome
# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])
Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
              Predict the target of new samples.
# predict(X)
# predict_proba(X) Posterior probabilities of classification
#-----
# video Link:
#-----
alpha = [10 ** x for x in range(-6, 1)]
cv_log_error_array = []
for i in alpha:
   print("for alpha =", i)
    clf = SGDClassifier(alpha=i, penalty='12', 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='12', 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)
```

for alpha = 1e-06

Log Loss: 1.1821489656626742

for alpha = 1e-05

Log Loss: 1.1553738089573742

for alpha = 0.0001

Log Loss: 1.1167227445781467

for alpha = 0.001

Log Loss: 1.2006949984989448

for alpha = 0.01

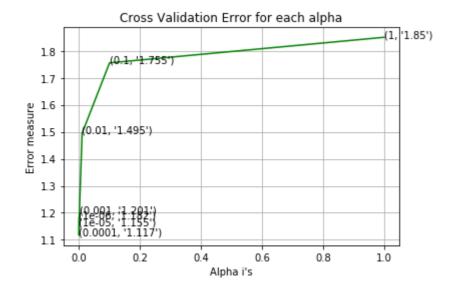
Log Loss: 1.4946019942452347

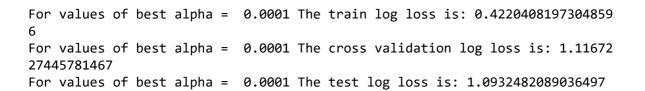
for alpha = 0.1

Log Loss: 1.755365008475997

for alpha = 1

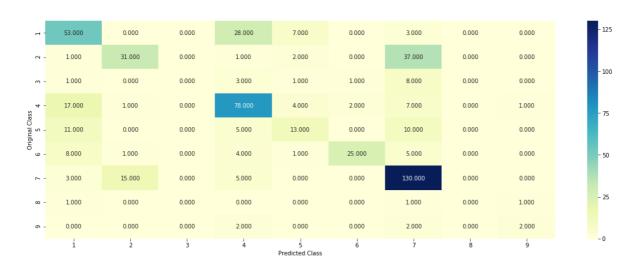
Log Loss: 1.8499972601594277

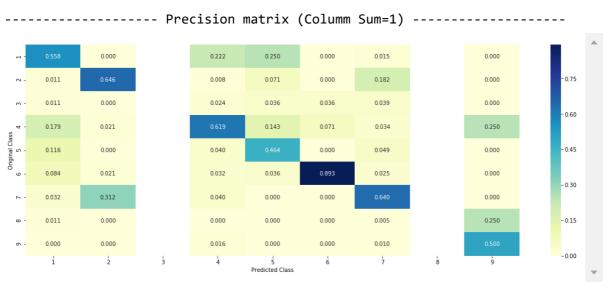


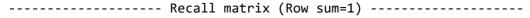


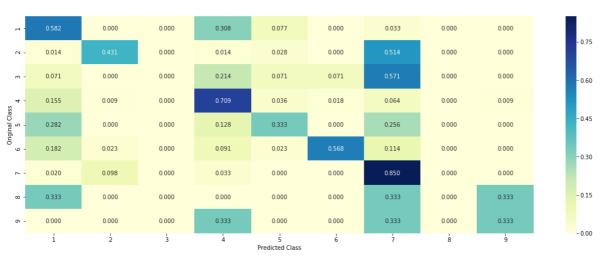
4.3.2.2. Testing model with best hyper parameters

In [81]:









4.3.2.3. Feature Importance, Correctly Classified point

```
In [82]:
```

```
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
no feature = 1000
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].ilc
Predicted Class: 7
Predicted Class Probabilities: [[0.002 0.0044 0.061 0.136 0.0015 0.0012
0.7925 0.0014 0.
                    11
Actual Class: 5
10 Text feature [106] present in test data point [True]
545 Text feature [000] present in test data point [True]
876 Text feature [11] present in test data point [True]
Out of the top 1000 features 3 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

```
In [83]:
```

4.4. Linear Support Vector Machines

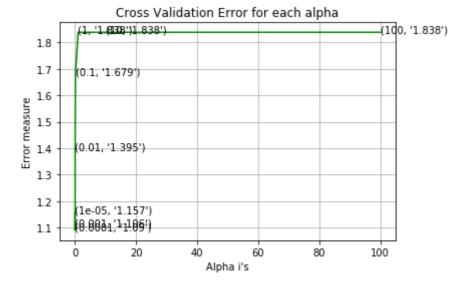
4.4.1. Hyper paramter tuning

In [84]:

```
# read more about support vector machines with linear kernals here http://scikit-learn.org/
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=F
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_shape='o
# Some of methods of SVM()
# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
             Perform classification on samples in X.
# predict(X)
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathe
# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict_proba(X) Posterior probabilities of classification
# video link:
alpha = [10 ** x for x in range(-5, 3)]
cv_log_error_array = []
for i in alpha:
    print("for C =", i)
     clf = SVC(C=i,kernel='linear',probability=True, class_weight='balanced')
    clf = SGDClassifier( class_weight='balanced', alpha=i, penalty='12', loss='hinge', rand
    clf.fit(train x onehotCoding, train y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15)
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
# clf = SVC(C=i,kernel='linear',probability=True, class_weight='balanced')
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='t
clf.fit(train x onehotCoding, train y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
```

for C = 1e-05
Log Loss: 1.1568393252790268
for C = 0.0001
Log Loss: 1.0900081708812448
for C = 0.001
Log Loss: 1.1055507228041028
for C = 0.01
Log Loss: 1.3951858218624766
for C = 0.1
Log Loss: 1.679078309672878
for C = 1
Log Loss: 1.8379624831068808
for C = 10
Log Loss: 1.837960560075746

for C = 100 Log Loss : 1.8379631667980254



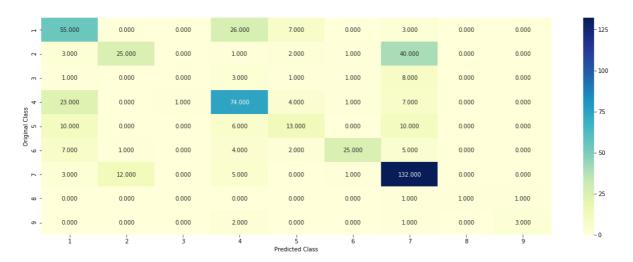
For values of best alpha = 0.0001 The train log loss is: 0.3827356993102211 7

For values of best alpha = 0.0001 The cross validation log loss is: 1.09000 81708812448

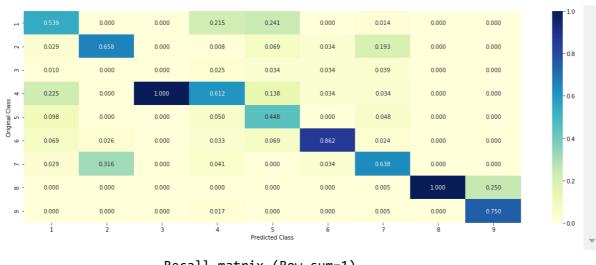
For values of best alpha = 0.0001 The test log loss is: 1.0833162416562274

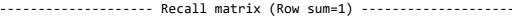
4.4.2. Testing model with best hyper parameters

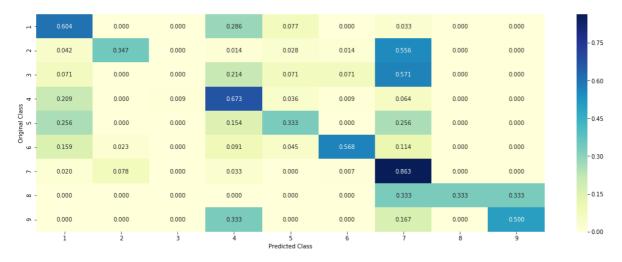
In [85]:



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







4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

```
In [86]:
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='hinge', random_state=42)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
# test_point_index = 100
no_feature = 1000
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].ilc
Predicted Class: 7
Predicted Class Probabilities: [[4.400e-03 9.900e-03 1.361e-01 3.162e-01 1.5
30e-02 2.000e-03 5.136e-01
  2.300e-03 3.000e-0411
Actual Class: 5
991 Text feature [10] present in test data point [True]
Out of the top 1000 features 1 are present in query point
```

4.3.3.2. For Incorrectly classified point

```
In [89]:
```

```
test_point_index = 2
no_feature = 1000
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[print("Actual Class :", test_y[test_point_index])
indices = np.argsort(abs(-clf.coef_))[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].ilc

Predicted Class : 1
Predicted Class Probabilities: [[0.4535 0.0472 0.0189 0.2011 0.0481 0.1413 0.0776 0.0066 0.0057]]
Actual Class : 1
Out of the top 1000 features 0 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

In [90]:

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# class_weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
             Perform classification on samples in X.
# predict_proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/rando
# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict_proba(X) Posterior probabilities of classification
# video link:
alpha = [100,200,500,1000,2000]
max_depth = [5, 10]
cv_log_error_array = []
for i in alpha:
    for j in max depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gini', max_depth=j, random_
        clf.fit(train x onehotCoding, train y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_onehotCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))
'''fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[int(i/2)],max_depth[int(i%2)],str(txt)), (features[i],cv_log_error_a
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
```

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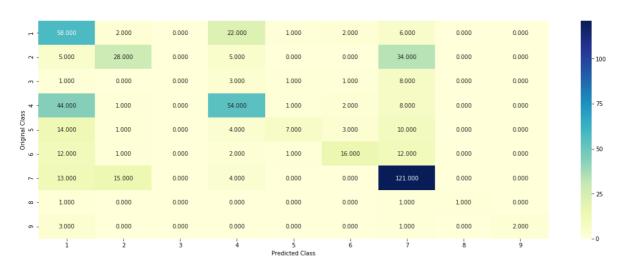
```
1.1.1
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_d
clf.fit(train x onehotCoding, train y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The train log loss is:"
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross validation ld
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss is:",
for n_estimators = 100 and max depth =
Log Loss: 1.2387295883403715
for n estimators = 100 and max depth =
Log Loss: 1.238879272721402
for n_estimators = 200 and max depth = 5
Log Loss: 1.228620465327945
for n_estimators = 200 and max depth = 10
Log Loss: 1.2367300710933677
for n_estimators = 500 and max depth =
Log Loss: 1.2111928242701786
for n_estimators = 500 and max depth = 10
Log Loss: 1.2313581284844777
for n_estimators = 1000 and max depth = 5
Log Loss: 1.207530094090447
for n_estimators = 1000 and max depth = 10
Log Loss: 1.2317271139030703
for n_estimators = 2000 and max depth = 5
Log Loss: 1.2067642466250919
for n_estimators = 2000 and max depth = 10
Log Loss: 1.234487300852763
For values of best estimator = 2000 The train log loss is: 0.82908591048833
For values of best estimator =
                               2000 The cross validation log loss is: 1.206
```

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

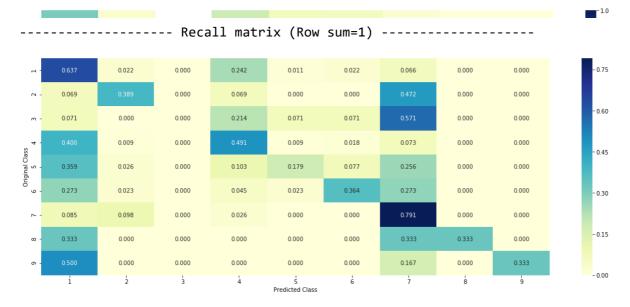
For values of best estimator = 2000 The test log loss is: 1.238737680695162

In [91]:

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# class_weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])
                             Fit the SVM model according to the given training data.
               Perform classification on samples in X.
# predict_proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/rando
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_d
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf
```

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



4.5.3. Feature Importance

4.5.3.1. Correctly Classified point

```
In [92]:
```

```
# test point index = 10
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_d
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
test_point_index = 1
no feature = 1000
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature importances )
print("-"*50)
get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],test_df[
Predicted Class: 7
Predicted Class Probabilities: [[0.0364 0.1216 0.2351 0.0531 0.038 0.0376
0.4687 0.0089 0.0006]]
Actual Class: 5
236 Text feature [000] present in test data point [True]
341 Text feature [106] present in test data point [True]
576 Text feature [05] present in test data point [True]
751 Text feature [1000] present in test data point [True]
778 Text feature [13] present in test data point [True]
872 Text feature [10] present in test data point [True]
928 Text feature [12] present in test data point [True]
985 Text feature [104] present in test data point [True]
Out of the top 1000 features 8 are present in query point
```

4.5.3.2. Inorrectly Classified point

```
In [93]:
```

```
test_point_index = 100
no feature = 1000
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[
print("Actuall Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],test_df[
Predicted Class: 4
Predicted Class Probabilities: [[0.0794 0.0134 0.0254 0.7915 0.0342 0.0287
0.022 0.004 0.0014]]
Actuall Class: 4
84 Text feature [121] present in test data point [True]
228 Text feature [123] present in test data point [True]
277 Text feature [001] present in test data point [True]
446 Text feature [101] present in test data point [True]
478 Text feature [131] present in test data point [True]
778 Text feature [13] present in test data point [True]
872 Text feature [10] present in test data point [True]
893 Text feature [12er] present in test data point [True]
928 Text feature [12] present in test data point [True]
930 Text feature [130] present in test data point [True]
Out of the top 1000 features 10 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

In [94]:

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# class_weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
             Perform classification on samples in X.
# predict_proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/rando
# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/gen
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict_proba(X) Posterior probabilities of classification
# video link:
alpha = [10,50,100,200,500,1000]
max_depth = [2,3,5,10]
cv_log_error_array = []
for i in alpha:
    for j in max depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gini', max_depth=j, random_
        clf.fit(train x responseCoding, train y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_responseCoding, train_y)
        sig clf probs = sig clf.predict proba(cv x responseCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))
. . .
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[int(i/4)],max_depth[int(i%4)],str(txt)), (features[i],cv_log_error_a
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
```

```
best_alpha = np.argmin(cv_log_error_array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gini', max_c
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

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

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```

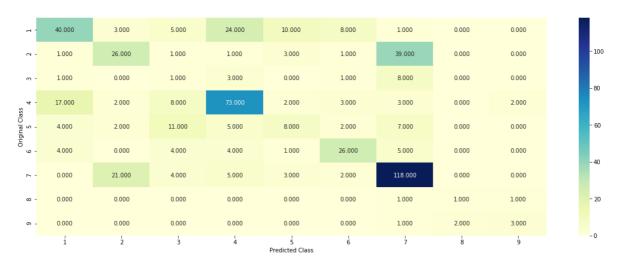
```
for n_estimators = 10 and max depth =
Log Loss: 2.1522298782791687
for n_estimators = 10 and max depth =
Log Loss: 1.6629714433057987
for n_{estimators} = 10 and max depth = 5
Log Loss: 1.2764342386858378
for n_estimators = 10 and max depth =
Log Loss: 1.8627397748657817
for n_estimators = 50 and max depth =
Log Loss: 1.8534498619311652
for n_estimators = 50 and max depth =
Log Loss: 1.5307805678276212
for n estimators = 50 and max depth =
Log Loss: 1.340513725229151
for n_estimators = 50 and max depth = 10
Log Loss: 1.5912748157940886
for n_estimators = 100 and max depth =
Log Loss: 1.7024012567536162
for n_estimators = 100 and max depth =
Log Loss: 1.5635867357857671
for n_estimators = 100 and max depth =
Log Loss: 1.3124310523189844
for n_estimators = 100 and max depth =
                                       10
Log Loss: 1.645438470378069
for n estimators = 200 and max depth =
Log Loss: 1.7587621133438942
for n estimators = 200 and max depth =
Log Loss: 1.5652944217622458
for n_estimators = 200 and max depth =
Log Loss: 1.3405700890055632
for n estimators = 200 and max depth =
                                       10
Log Loss: 1.7329582884802837
for n estimators = 500 and max depth =
Log Loss: 1.728038188321821
for n estimators = 500 and max depth =
Log Loss: 1.5633450562610423
for n estimators = 500 and max depth =
Log Loss: 1.3344305608756897
for n_estimators = 500 and max depth =
Log Loss: 1.7407100664571737
for n_{estimators} = 1000 and max depth = 2
Log Loss: 1.7193219915218592
for n estimators = 1000 and max depth = 3
Log Loss: 1.5582022978461991
```

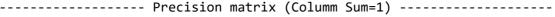
```
for n_estimators = 1000 and max depth = 5
Log Loss : 1.3452157617472396
for n_estimators = 1000 and max depth = 10
Log Loss : 1.705093741458095
For values of best alpha = 10 The train log loss is: 0.08639419728312807
For values of best alpha = 10 The cross validation log loss is: 1.2764342
386858378
For values of best alpha = 10 The test log loss is: 1.2817314579077703
```

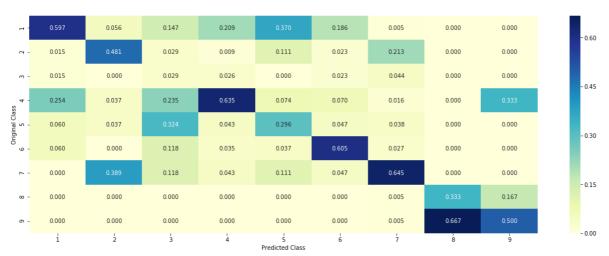
4.5.4. Testing model with best hyper parameters (Response Coding)

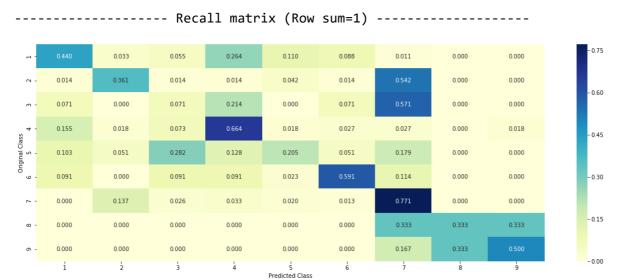
In [95]:

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# class_weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight])
                             Fit the SVM model according to the given training data.
               Perform classification on samples in X.
# predict_proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).
 video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/rando
clf = RandomForestClassifier(max_depth=max_depth[int(best_alpha%4)], n_estimators=alpha[int
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_responseCoding,cv_y,
```









4.5.5. Feature Importance

4.5.5.1. Correctly Classified point

```
In [96]:
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gini', max_d
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)
test_point_index = 1
no_feature = 1000
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_responseCodir
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:
        print("Text is important feature")
Predicted Class: 4
Predicted Class Probabilities: [[0.0062 0.0337 0.057 0.4894 0.0851 0.0184
0.2864 0.0184 0.0055]]
Actual Class : 5
Variation is important feature
Variation is important feature
```

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

4.5.5.2. Incorrectly Classified point

```
In [97]:
```

test point index = 100

```
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_responseCodir
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:
        print("Text is important feature")
Predicted Class: 4
Predicted Class Probabilities: [[0.0531 0.0099 0.2298 0.6646 0.0043 0.008
0.0018 0.019 0.0097]]
Actual Class: 4
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Text is important feature
Variation is important feature
Variation is important feature
Text is important feature
Variation is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
```

4.7 Stack the models

4.7.1 testing with hyper parameter tuning

In [98]:

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skled
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Desce
\# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geome
# read more about support vector machines with linear kernals here http://scikit-learn.org/
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=F
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_shape='o
# Some of methods of SVM()
# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
\# predict(X) Perform classification on samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathe
# read more about support vector machines with linear kernals here http://scikit-learn.org/
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=Non
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, ve
# class weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
\# predict(X) Perform classification on samples in X.
# predict_proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/rando
clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class_weight='balanced', random
clf1.fit(train x onehotCoding, train y)
sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
clf2 = SGDClassifier(alpha=1, penalty='12', loss='hinge', class_weight='balanced', random_s
clf2.fit(train x onehotCoding, train y)
sig_clf2 = CalibratedClassifierCV(clf2, method="sigmoid")
```

```
clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train x onehotCoding, train y)
sig clf3 = CalibratedClassifierCV(clf3, method="sigmoid")
sig_clf1.fit(train_x_onehotCoding, train_y)
print("Logistic Regression : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf1.predict_proba(cv_y))
sig clf2.fit(train x onehotCoding, train y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf2.predict_proba(
sig_clf3.fit(train_x_onehotCoding, train_y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba(cv_x_onehot())
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=1
    sclf.fit(train_x_onehotCoding, train_y)
    print("Stacking Classifer: for the value of alpha: %f Log Loss: %0.3f" % (i, log_loss(
    log error =log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    if best_alpha > log_error:
        best_alpha = log_error
```

4.7.2 testing the model with the best hyper parameters

In [99]:

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

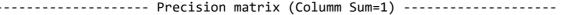
log_error = log_loss(train_y, sclf.predict_proba(train_x_onehotCoding))
print("Log loss (train) on the stacking classifier :",log_error)

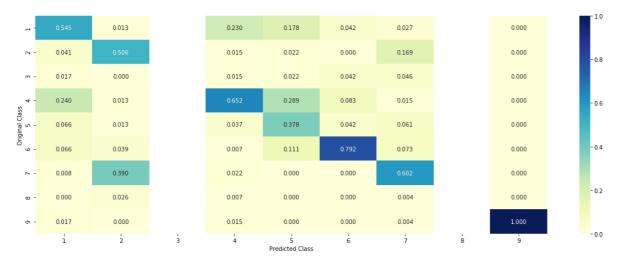
log_error = log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
print("Log loss (CV) on the stacking classifier :",log_error)

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

print("Number of missclassified point :", np.count_nonzero((sclf.predict(test_x_onehotCoding))
print("Number of missclassified point :", np.count_nonzero((sclf.predict(test_x_onehotCoding)))
```







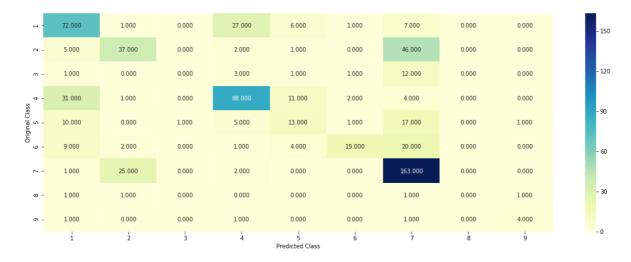
------ Recall matrix (Row sum=1)

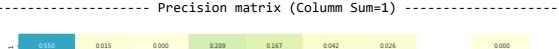


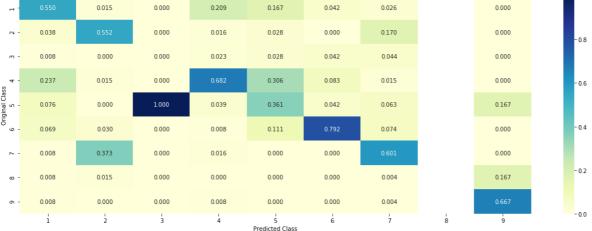
4.7.3 Maximum Voting classifier

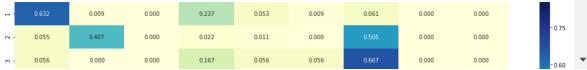
In [100]:

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









5. Assignments

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

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

In [102]:

```
train variation=train df['Variation'].values
test_variation=test_df['Variation'].values
cv_variation=cv_df['Variation'].values
train_gene=train_df['Gene'].values
test_gene=test_df['Gene'].values
cv_gene=cv_df['Gene'].values
train_text=train_df['TEXT'].values
test text=test df['TEXT'].values
cv_text=cv_df['TEXT'].values
from sklearn.feature_extraction.text import CountVectorizer
encode=CountVectorizer(ngram_range=(1, 2))
train_variation=encode.fit_transform(train_variation)
test_variation=encode.transform(test_variation)
cv_variation=encode.transform(cv_variation)
train_gene=encode.fit_transform(train_gene)
test_gene=encode.transform(test_gene)
cv_gene=encode.transform(cv_gene)
train_variation=normalize(train_variation,axis=0)
test_variation=normalize(test_variation,axis=0)
cv_variation=normalize(cv_variation,axis=0)
train_gene=normalize(train_gene,axis=0)
test_gene=normalize(test_gene,axis=0)
cv_gene=normalize(cv_gene,axis=0)
print("Shape of Gene Feature :",train_gene.shape)
print("Shape of Variation Feature :",train_variation.shape)
encode=CountVectorizer(min df=10,ngram range=(1,2))
train_text=encode.fit_transform(train_text)
test text=encode.transform(test text)
cv_text=encode.transform(cv_text)
train_text=normalize(train_text,axis=0)
test text=normalize(test text,axis=0)
cv_text=normalize(cv_text,axis=0)
print("Shape of TEXT Feature :",train_text.shape)
```

```
Shape of Gene Feature : (2124, 228)
Shape of Variation Feature : (2124, 2072)
Shape of TEXT Feature : (2124, 238840)
```

In [104]:

```
from scipy.sparse import hstack

train_data = hstack([train_variation,train_gene,train_text]).tocsr()
cv_data = hstack([cv_variation,cv_gene,cv_text]).tocsr()
test_data = hstack([test_variation,test_gene,test_text]).tocsr()
```

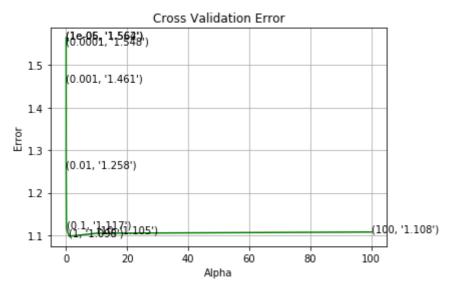
In [105]:

```
cv_scores=[]
alpha=[10 ** x for x in range(-6, 3)]
for c in alpha:
    print("for alpha =", c)
    lr = LogisticRegression(random_state=0, C=c,class_weight='balanced',n_jobs=-1)
    clf=CalibratedClassifierCV(base_estimator=lr,method='sigmoid')
    clf.fit(train_data,y_train)
    cv_op=clf.predict_proba(cv_data)
    print(c,log_loss(y_cv, cv_op))
    cv_scores.append(log_loss(y_cv, cv_op))
```

```
for alpha = 1e-06
1e-06 1.5636068914840113
for alpha = 1e-05
1e-05 1.5620365747365672
for alpha = 0.0001
0.0001 1.5484754853220843
for alpha = 0.001
0.001 1.4613507829096732
for alpha = 0.01
0.01 1.258194173975514
for alpha = 0.1
0.1 1.1165329729714053
for alpha = 1
1 1.0979281098542863
for alpha = 10
10 1.104837372780513
for alpha = 100
100 1.1077883511048137
```

In [106]:

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



In [107]:

```
lr = LogisticRegression(random_state=0, C=10,class_weight='balanced',n_jobs=-1)
clf=CalibratedClassifierCV(base_estimator=lr,method='sigmoid')
clf.fit(train_data,y_train)
test_op=clf.predict_proba(test_data)
print("Log Loss value for the test data is(10) ",log_loss(y_test, test_op))
```

Log Loss value for the test data is(10) 1.1184160359473547

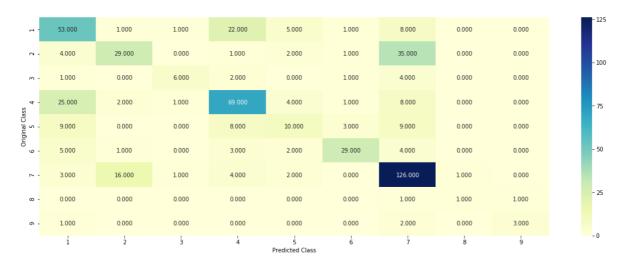
In [108]:

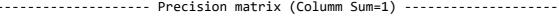
```
lr = LogisticRegression(random_state=0, C=10,class_weight='balanced',n_jobs=-1)
clf=CalibratedClassifierCV(base_estimator=lr,method='sigmoid')
predict_and_plot_confusion_matrix(train_data, y_train, cv_data,y_cv, clf)
```

Log loss : 1.101943266430425

Number of mis-classified points : 0.38721804511278196

----- Confusion matrix -----







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



In [109]:

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

x_train, x_test, y_train, y_test = train_test_split(result, y_true, stratify=y_true, test_s
x_train, x_cv, y_train, y_cv = train_test_split(x_train, y_train, stratify=y_train, test_si
```

In [110]:

```
def get_gv_fea_dict(alpha, feature, df):
    value_count = x_train[feature].value_counts()
    gv_dict = dict()
    for i, denominator in value count.items():
        vec = []
        for k in range(1,10):
            cls_cnt = x_train.loc[(x_train['Class']==k) & (x_train[feature]==i)]
            vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
        gv dict[i]=vec
    return gv_dict
# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
    gv_dict = get_gv_fea_dict(alpha, feature, df)
    value count = x train[feature].value counts()
    gv_fea = []
    for index, row in df.iterrows():
        if row[feature] in dict(value_count).keys():
            gv_fea.append(gv_dict[row[feature]])
        else:
            gv_fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
    return gv_fea
```

In [111]:

```
alpha = 1

# train gene feature
train_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", x_train))

# test gene feature
test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", x_test))

# cross validation gene feature
cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", x_cv))
```

In [112]:

```
gene_vectorizer = TfidfVectorizer()
train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(x_train['Gene'])
test_gene_feature_onehotCoding = gene_vectorizer.transform(x_test['Gene'])
cv_gene_feature_onehotCoding = gene_vectorizer.transform(x_cv['Gene'])
```

In [113]:

```
alpha = 1

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

# test gene feature
test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", x_test)

# cross validation gene feature
cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", x_cv))
```

In [114]:

```
variation_vectorizer = TfidfVectorizer()
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(x_train['Variation_test_variation_feature_onehotCoding = variation_vectorizer.transform(x_test['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(x_cv['Variation'])
```

In [115]:

```
def extract_dictionary_paddle(cls_text):
    dictionary = defaultdict(int)
    for index, row in cls_text.iterrows():
        for word in row['TEXT'].split():
            dictionary[word] +=1
    return dictionary
import math
#https://stackoverflow.com/a/1602964
def get_text_responsecoding(df):
    text_feature_responseCoding = np.zeros((df.shape[0],9))
    for i in range(0,9):
        row_index = 0
        for index, row in df.iterrows():
            sum prob = 0
            for word in row['TEXT'].split():
                sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(total_dict.get(word,0)
            text feature responseCoding[row index][i] = math.exp(sum prob/len(row['TEXT'].s
            row index += 1
    return text_feature_responseCoding
```

In [116]:

```
text_vectorizer = TfidfVectorizer()
train_text_feature_onehotCoding = text_vectorizer.fit_transform(x_train['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 train_text_fea_counts = train_text_feature_onehotCoding.sum(axis=0).A1

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

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

Total number of unique words in train data : 125760

In [117]:

```
dict list = []
# dict_list =[] contains 9 dictoinaries each corresponds to a class
for i in range(1,10):
    cls_text = x_train[x_train['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(x_train)
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 [118]:

```
train_text_feature_responseCoding = get_text_responsecoding(x_train)
test_text_feature_responseCoding = get_text_responsecoding(x_test)
cv_text_feature_responseCoding = get_text_responsecoding(x_cv)

# https://stackoverflow.com/a/16202486
# we convert each row values such that they sum to 1
train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train_text_feature_test_text_feature_responseCoding.T/test_text_feature_recv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.T/cv_text_feature_re
```

In [119]:

```
test_text_feature_onehotCoding = text_vectorizer.transform(x_test['TEXT'])
cv_text_feature_onehotCoding = text_vectorizer.transform(x_cv['TEXT'])
```

In [120]:

```
gene_variation = []

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

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

In [121]:

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

train_text = tfidfVectorizer.transform(x_train['TEXT'])
test_text = tfidfVectorizer.transform(x_test['TEXT'])
cv_text = tfidfVectorizer.transform(x_cv['TEXT'])
```

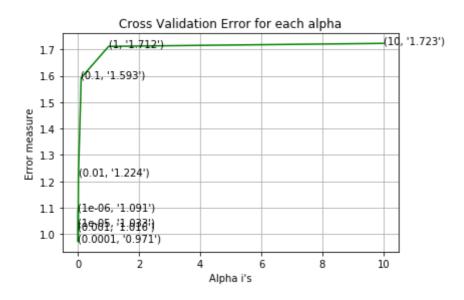
In [122]:

```
train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,train_variation_featu
test_gene_var onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehot
# Adding the train text feature
train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text))
train_x_onehotCoding = hstack((train_x_onehotCoding, train_text_feature_onehotCoding)).tocs
train_y = np.array(list(x_train['Class']))
# Adding the test_text feature
test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text))
test_x_onehotCoding = hstack((test_x_onehotCoding, test_text_feature_onehotCoding)).tocsr()
test_y = np.array(list(x_test['Class']))
# Adding the cv_text feature
cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text))
cv x onehotCoding = hstack((cv x onehotCoding, cv text feature onehotCoding)).tocsr()
cv_y = np.array(list(x_cv['Class']))
train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,train_variation)
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_f
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature
train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_responseCoding)
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_response
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding
```

In [123]:

```
alpha = [10 ** x for x in range(-6, 2)]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='12', loss='log', random
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15)
    # to avoid rounding error while multiplying probabilites we use log-probability estimat
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
```

```
for alpha = 1e-06
Log Loss: 1.0908479300023448
for alpha = 1e-05
Log Loss: 1.0333214082484075
for alpha = 0.0001
Log Loss: 0.9712781607057535
for alpha = 0.001
Log Loss: 1.0164025208637213
for alpha = 0.01
Log Loss: 1.2242152526556815
for alpha = 0.1
Log Loss: 1.5925006826787442
for alpha = 1
Log Loss: 1.7115396224665458
for alpha = 10
Log Loss: 1.7229451280110866
```



In [124]:

```
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='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 alpha = ',
      alpha[best_alpha],
      "The train log loss is:",
      log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ',
      alpha[best alpha],
      "The cross validation log loss is:",
      log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ',
      alpha[best_alpha], "The test log loss is:",
      log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of best alpha = 0.0001 The train log loss is: 0.4407184947063184 6

For values of best alpha = 0.0001 The cross validation log loss is: 0.97754 81772330057

For values of best alpha = 0.0001 The test log loss is: 1.019468769549301
```

In [125]:

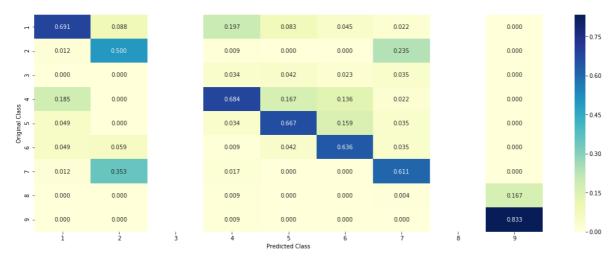
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='1
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, c

Log loss: 0.9728824249099982

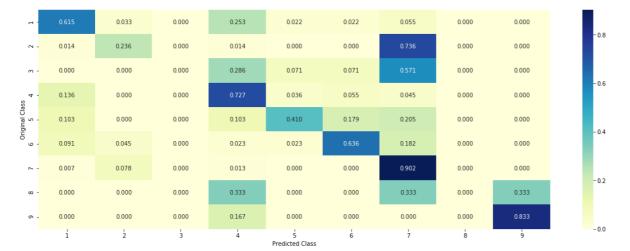
Number of mis-classified points: 0.3609022556390977

----- Confusion matrix ------





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



In [126]:

```
from prettytable import PrettyTable
x=PrettyTable()
x.field_names=["model","train_log_loss","cv_log_loss","test_log_loss"]
x.add_row(["Logistic regression with CountVectorizer Features, including both unigrams and
x.add_row(["feature Engg.","0.42","0.97","0.97"])
print(x)
 train_log_loss | cv_log_loss | test_log_loss |
  -----+
| Logistic regression with CountVectorizer Features, including both unigrams
and bigrams
             1.11
                       1.01 | 1.04
                                 feature Engg.
      0.42
                   0.97
                                 0.97
In [ ]:
In [ ]:
```