# 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

- 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. <a href="https://www.youtube.com/watch?v=UwbuW7oK8rk">https://www.youtube.com/watch?v=UwbuW7oK8rk</a>
- 3. https://www.youtube.com/watch?v=qxXRKVompI8

# 1.3. Real-world/Business objectives and constraints.

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

# 2. Machine Learning Problem Formulation

# 2.1. Data

#### 2.1.1. Data Overview

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

# 2.1.2. Example Data Point

#### training\_variants

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

...

### training\_text

#### ID.Text

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

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

# 2.2.1. Type of Machine Learning Problem

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

### 2.2.2. Performance Metric

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

Metric(s):

- · Multi class log-loss
- Confusion matrix

# 2.2.3. Machine Learing Objectives and Constraints

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

Constraints:

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

# 2.3. Train, CV and Test Datasets

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

# 3. Exploratory Data Analysis

```
In [0]:
```

```
In [0]:
```

```
import pandas as pd
import matplotlib.pyplot as plt
import re
import time
import warnings
import numpy as np
from nltk.corpus import stopwords
from sklearn.decomposition import TruncatedSVD
from sklearn.preprocessing import normalize
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.manifold import TSNE
import seaborn as sns
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion matrix
from sklearn.metrics.classification import accuracy score, log loss
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.linear_model import SGDClassifier
from imblearn.over_sampling import SMOTE
from collections import Counter
from scipy.sparse import hstack
from sklearn.multiclass import OneVsRestClassifier
from sklearn.svm import SVC
from sklearn.model selection import StratifiedKFold
from collections import Counter, defaultdict
from sklearn.calibration import CalibratedClassifierCV
from sklearn.naive bayes import MultinomialNB
from sklearn.naive_bayes import GaussianNB
from sklearn.model selection import train test split
from sklearn.model_selection import GridSearchCV
import math
from sklearn.metrics import normalized_mutual_info_score
from sklearn.ensemble import RandomForestClassifier
warnings.filterwarnings("ignore")
from mlxtend.classifier import StackingClassifier
from sklearn import model selection
from sklearn.linear model import LogisticRegression
```

# 3.1. Reading Data

# 3.1.1. Reading Gene and Variation Data

```
In [0]:
```

```
!pip install -U -q PyDrive
from pydrive.auth import GoogleAuth
from pydrive.drive import GoogleDrive
from google.colab import auth
from oauth2client.client import GoogleCredentials
# Authenticate and create the PyDrive client.
auth.authenticate_user()
gauth = GoogleAuth()
gauth.credentials = GoogleCredentials.get_application_default()
drive = GoogleDrive(gauth)
```

```
link= 'https://drive.google.com/open?id=1gP70Fh4rhyfhQQ9PPVhekW2e-5I9Vu0t'
In [5]:
fluff, id = link.split('=')
print (id)
1gP70Fh4rhyfhQQ9PPVhekW2e-5I9Vu0t
In [0]:
downloaded = drive.CreateFile({'id':id})
downloaded.GetContentFile('training_variants')
In [0]:
!pip install -U -q PyDrive
from pydrive.auth import GoogleAuth
from pydrive.drive import GoogleDrive
from google.colab import auth
from oauth2client.client import GoogleCredentials
# Authenticate and create the PyDrive client.
auth.authenticate user()
gauth = GoogleAuth()
gauth.credentials = GoogleCredentials.get_application_default()
drive = GoogleDrive(gauth)
In [0]:
link= 'https://drive.google.com/open?id=1ttR9xZC5lct5CocLP7Ft01pt7E0-qJkf'
In [9]:
fluff, id = link.split('=')
print (id)
1ttR9xZC5lct5CocLP7FtO1pt7E0-qJkf
In [0]:
downloaded = drive.CreateFile({'id':id})
downloaded.GetContentFile('training_text')
In [11]:
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[11]:
  ID
     Gene
             Variation
                              Class
0 0
     FAM58A Truncating Mutations
                              1
1 1
     CBL
             W802*
                              2
2 2
                              2
     CBL
             Q249E
```

**3** 3

**CBL** 

**CBL** 

N454D

L399V

3

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 [12]:
```

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

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

#### Out[12]:

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

# 3.1.3. Preprocessing of text

```
In [13]:
```

```
import nltk
nltk.download('stopwords')
[nltk data] Downloading package stopwords to /root/nltk data...
[nltk_data]
            Package stopwords is already up-to-date!
Out[13]:
True
In [0]:
# 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 [15]:

```
#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")
```

Time took for preprocessing the text : 272.647463 seconds

#### In [16]:

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

# Out[16]:

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

#### In [17]:

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

## Out[17]:

ID Gene Variation Class	TEXT
-------------------------	------

## In [0]:

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

#### In [19]:

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

# Out[19]:

	ID	Gene	Variation	Class	TEXT
1109	1109	FANCA	S1088F	1	null

# 3.1.4. Test, Train and Cross Validation Split

# 3.1.4.1. Splitting data into train, test and cross validation (64:20:16)

```
y_true = result['Class'].values
result.Gene = result.Gene.str.replace('\s+', '_')
result.Variation = result.Variation.str.replace('\s+', '_')
# split the data into test and train by maintaining same distribution of output varaible 'y_true'[
stratify=y_true]
X_train, test_df, y_train, y_test = train_test_split(result, y_true, stratify=y_true, test_size=0.2
)
# split the train data into train and cross validation by maintaining same distribution of
outputvaraible 'y_train' [stratify=y_train]
train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train, stratify=y_train, test_size=0.2
)
```

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

```
In [21]:
```

```
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
```

#### 3.1.4.2. Distribution of y\_i's in Train, Test and Cross Validation datasets

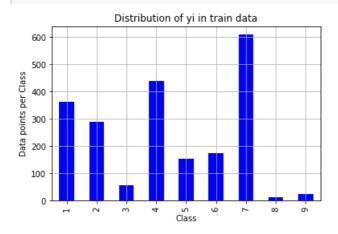
Number of data points in cross validation data: 532

#### In [22]:

```
# it returns a dict, keys as class labels and values as the number of data points in that class
train class distribution = train df['Class'].value counts().sortlevel()
test_class_distribution = test_df['Class'].value_counts().sortlevel()
cv class distribution = cv df['Class'].value counts().sortlevel()
my colors = 'rgbkymc'
train class distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in train data')
plt.grid()
plt.show()
{\tt\#\ ref:\ argsort\ https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html}
# -(train class distribution.values): the minus sign will give us in decreasing order
sorted yi = np.argsort(-train class distribution.values)
for i in sorted yi:
    print('Number of data points in class', i+1, ':', train class distribution.values[i], '(', np.ro
und((train class distribution.values[i]/train df.shape[0]*100), 3), '%)')
print('-'*80)
my colors = 'rgbkymc'
test class distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in test data')
plt.grid()
plt.show()
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train class distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-test_class_distribution.values)
for i in sorted yi:
    print('Number of data points in class', i+1, ':', test class distribution.values[i], '(', np.rou
nd((test_class_distribution.values[i]/test_df.shape[0]*100), 3), '%)')
print('-'*80)
my colors = 'rgbkymc'
cv_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in cross validation data')
nlt.arid()
```

```
plt.show()

# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',cv_class_distribution.values[i], '(', np.round
((cv_class_distribution.values[i]/cv_df.shape[0]*100), 3), '%)')
```



```
Number of data points in class 7: 609 (28.672 %)

Number of data points in class 4: 439 (20.669 %)

Number of data points in class 1: 363 (17.09 %)

Number of data points in class 2: 289 (13.606 %)

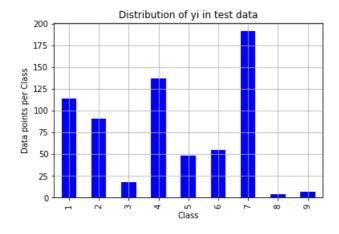
Number of data points in class 6: 176 (8.286 %)

Number of data points in class 5: 155 (7.298 %)

Number of data points in class 3: 57 (2.684 %)

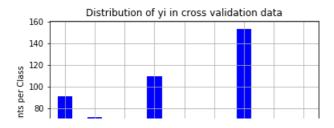
Number of data points in class 9: 24 (1.13 %)

Number of data points in class 8: 12 (0.565 %)
```



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

-----



```
60 40 40 40 Class
```

```
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.

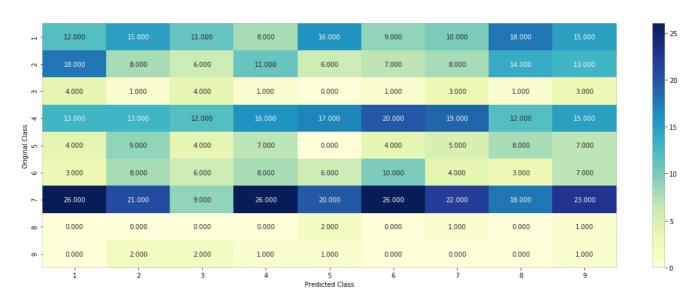
```
# This function plots the confusion matrices given y_i, y_i_hat.
def plot confusion matrix(test y, predict y):
   C = confusion_matrix(test_y, predict_y)
   \# C = 9,9 matrix, each cell (i,j) represents number of points of class i are predicted class j
   A = (((C.T) / (C.sum(axis=1))).T)
   #divid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

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

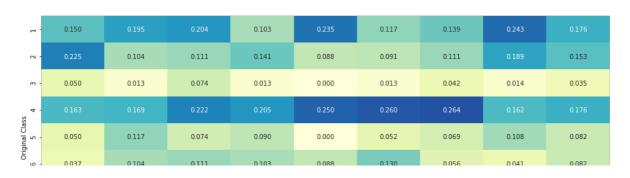
#### In [24]:

```
# we need to generate 9 numbers and the sum of numbers should be 1
# one solution is to genarate 9 numbers and divide each of the numbers by their sum
# ref: https://stackoverflow.com/a/18662466/4084039
test data len = test df.shape[0]
cv data len = cv df.shape[0]
# we create a output array that has exactly same size as the CV data
cv_predicted_y = np.zeros((cv_data_len,9))
for i in range(cv_data_len):
   rand probs = np.random.rand(1,9)
    cv_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Cross Validation Data using Random Model",log loss(y cv,cv predicted y, eps=1e-
15))
# Test-Set error.
#we create a output array that has exactly same as the test data
test predicted y = np.zeros((test data len,9))
for i in range(test data len):
   rand probs = np.random.rand(1,9)
    test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Test Data using Random Model",log_loss(y_test,test_predicted_y, eps=1e-15))
predicted_y =np.argmax(test_predicted_y, axis=1)
plot_confusion_matrix(y_test, predicted_y+1)
```

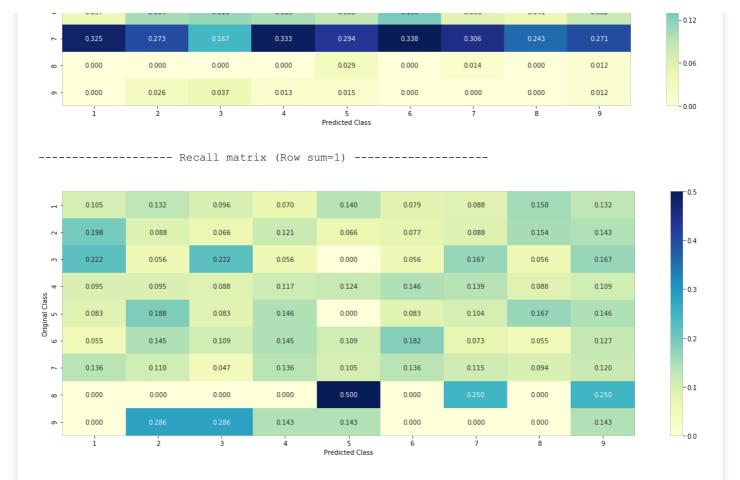
Log loss on Cross Validation Data using Random Model 2.521919391680851 Log loss on Test Data using Random Model 2.4576412291665304 ------- Confusion matrix ------



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



- 0.30 - 0.24 - 0.18



# 3.3 Univariate Analysis

```
# code for response coding with Laplace smoothing.
# alpha : used for laplace smoothing
# feature: ['gene', 'variation']
# df: ['train_df', 'test_df', 'cv_df']
# algorithm
# Consider all unique values and the number of occurances of given feature in train data dataframe
\# build a vector (1*9) , the first element = (number of times it occured in class1 + 10*alpha / nu
mber of time it occurred in total data+90*alpha)
# gv dict is like a look up table, for every gene it store a (1*9) representation of it
# for a value of feature in df:
# if it is in train data:
 we add the vector that was stored in 'gv dict' look up table to 'gv fea'
# if it is not there is train:
# we add [1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9] to 'gv fea'
# return 'qv fea'
# get gv fea dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
    # value count: it contains a dict like
    # print(train df['Gene'].value counts())
    # output:
              {BRCA1
                          174
              TP53
                          106
              EGFR
                           86
              BRCA2
                           75
              PTEN
                           69
              KIT
                           61
              BRAF
              ERBB2
                           47
              PDGFRA
                           46
     print(train_df['Variation'].value_counts())
     output:
      Truncating Mutations
```

```
# Deletion
                                         43
   # Amplification
                                         43
   # Fusions
   # Overexpression
                                          3
   # E17K
                                          .3
                                          3
   # 0611
   # 52220
                                          2
   # P130S
   # ...
   # }
   value count = train df[feature].value counts()
   # qv dict : Gene Variation Dict, which contains the probability array for each gene/variation
   gv_dict = dict()
   # denominator will contain the number of time that particular feature occured in whole data
   for i, denominator in value count.items():
      # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticular class
      # vec is 9 diamensional vector
      vec = []
      for k in range (1,10):
          # print(train df.loc[(train df['Class']==1) & (train df['Gene']=='BRCA1')])
                  TD Gene
                                      Variation Class
          # 2470 2470 BRCA1
                                        S1715C
          # 2486 2486 BRCA1
                                         S1841R
          # 2614 2614 BRCA1
# 2432 2432 BRCA1
                                           M1R
                                         L1657P
          # 2567 2567 BRCA1
                                         T1685A
          # 2583 2583 BRCA1
                                         E1660G
          # 2634 2634 BRCA1
                                         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 feature (
ccured in whole data
          vec.append((cls cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
       # we are adding the gene/variation to the dict as key and vec as value
      gv dict[i]=vec
   return gv dict
# Get Gene variation feature
def get gv feature(alpha, feature, df):
   # print(gv dict)
        {'BRCA1': [0.20075757575757575, 0.037878787878788, 0.06818181818181817,
0.13636363636363635,\ 0.25,\ 0.1931818181818181818,\ 0.03787878787878788,\ 0.03787878787878788,
0.03787878787878787881,
         'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366,
163265307, 0.056122448979591837],
         'EGFR': [0.05681818181818181816, 0.215909090909091, 0.0625, 0.068181818181818177,
0.06818181818181818177,\ 0.0625,\ 0.346590909090912,\ 0.0625,\ 0.05681818181818181816],
         'BRCA2': [0.13333333333333333, 0.0606060606060608, 0.0606060606060608,
0.07878787878787878782,\ 0.1393939393939394,\ 0.345454545454546,\ 0.060606060606060608,
0.06060606060606060608, 0.06060606060606081,
   # 'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917,
761006289, 0.062893081761006289],
         'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295,
0.072847682119205295,\ 0.066225165562913912,\ 0.066225165562913912,\ 0.27152317880794702,
0.066225165562913912, 0.066225165562913912],
         'BRAF': [0.066666666666666666, 0.17999999999999, 0.07333333333333334,
#
       }
   gv dict = get gv fea dict(alpha, feature, df)
   # value count is similar in get gv fea dict
   value count = train df[feature].value counts()
   # gv fea: Gene variation feature, it will contain the feature for each feature value in the da
ta
   gv fea = []
   # for every feature values in the given data frame we will check if it is there in the train
data then we will add the feature to gv fea
```

```
II HOU WE WIII QUU [1/J,1/J,1/J,1/J,1/J,1/J,1/J,1/J,1/J,1/J] CO gv_1ea
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 [26]:
```

```
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: 239
        169
BRCA1
TP53
         107
EGFR
          89
          81
PTEN
BRCA2
           76
           70
KTT
           58
BRAF
ALK
          46
          39
PDGFRA
          39
ERBB2
Name: Gene, dtype: int64
```

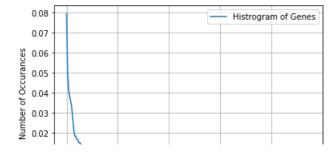
# In [27]:

```
\verb|print("Ans: There are", unique\_genes.shape[0]|, "different categories of genes in the train data, an area of the train data," and the train data of the train data of the train data, and the train data of the train data of the train data of the train data. There are ", unique\_genes.shape[0]|, "different categories of genes in the train data," and the train data of th
  d they are distibuted as follows",)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I
```

Ans: There are 239 different categories of genes in the train data, and they are distibuted as fol lows

## In [28]:

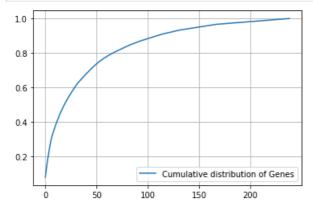
```
s = sum(unique_genes.values);
h = unique_genes.values/s;
plt.plot(h, label="Histrogram of Genes")
plt.xlabel('Index of a Gene')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



```
0.01
0.00
0 50 100 150 200
Index of a Gene
```

#### In [29]:

```
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 [0]:

```
#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 [31]:

```
print("train_gene_feature_responseCoding is converted feature using respone coding method. The sha
pe of gene feature:", train_gene_feature_responseCoding.shape)
```

train\_gene\_feature\_responseCoding is converted feature using respone coding method. The shape of g ene feature: (2124, 9)

# **Using Tfidf Vectorizer**

```
# 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 [33]:
train_df['Gene'].head()
Out[33]:
       ERBB4
793
1572
          ALK
905
       PDGFRA
1762
         IDH1
2194
         PTEN
Name: Gene, dtype: object
In [34]:
gene_vectorizer.get_feature_names()
Out[34]:
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
 'akt3',
 'alk',
 'apc',
 'ar',
 'araf',
 'arid1b',
 'arid2',
 'arid5b',
 'asxl2',
 'atm',
 'atr',
 'aurkb',
 'axin1',
 'axl',
 'b2m',
 'bap1',
 'bard1',
 'bcl10',
 'bc12',
 'bcl2111',
 'bcor',
 'braf',
 'brca1',
 'brca2',
 'brd4',
 'brip1',
 'btk',
 'card11',
 'carm1',
 'casp8',
 'cbl',
 'ccnd1',
 'ccnd3',
 'ccne1',
 'cdh1',
 'cdk12',
 'cdk4',
 'cdk6',
 'cdk8',
 'cdkn1a',
 'cdkn1b',
 'cdkn2a',
 'cdkn2b',
 'cdkn2c',
 'cebpa',
 'chek2',
 'cic',
 'crebbp',
```

```
'ctcf',
'ctla4',
'ctnnb1',
'ddr2',
'dicer1',
'dnmt3a',
'dnmt3b',
'dusp4',
'egfr',
'elf3',
'ep300',
'epas1',
'epcam',
'erbb2',
'erbb3',
'erbb4',
'ercc2',
'ercc3',
'ercc4',
'erg',
'errfil',
'esr1',
'etv1',
'etv6',
'ewsr1',
'ezh2',
'fanca',
'fat1',
'fbxw7',
'fgf19',
'fgf3',
'fgfr1',
'fgfr2',
'fgfr3',
'fgfr4',
'flt3',
'foxa1',
'fox12',
'foxo1',
'foxp1',
'gata3',
'gli1',
'gnaq',
'gnas',
'h3f3a',
'hla',
'hnfla',
'hras',
'idh1',
'idh2',
'igf1r',
'ikbke',
'ikzf1',
'il7r',
'inpp4b',
'jak1',
'jak2',
'jun',
'kdm5c',
'kdm6a',
'kdr',
'keap1',
'kit',
'klf4',
'kmt2a',
'kmt2c',
'kmt2d',
'kras',
'lats1',
'lats2',
'map2k1',
'map2k2',
'map2k4',
'map3k1',
'mapk1',
'mdm2',
'mdm4',
```

```
'med12',
'mef2b',
'met',
'mga',
'mlh1',
'mpl',
'msh2',
'msh6',
'mtor',
'myc',
'myd88',
'ncor1',
'nf1',
'nf2',
'nfe212',
'nfkbia',
'nkx2',
'notch1',
'notch2',
'npm1',
'nras',
'nsd1',
'ntrk1',
'ntrk2',
'ntrk3',
'nup93',
'pak1',
'pax8',
'pbrm1',
'pdgfra',
'pdgfrb',
'pik3ca',
'pik3cb',
'pik3cd',
'pik3r1',
'pik3r2',
'pim1',
'pms1',
'pms2',
'pole',
'ppmld',
'ppp2r1a',
'ppp6c',
'prdm1',
'pten',
'ptpn11',
'ptprd',
'ptprt',
'rab35',
'rac1',
'rad21',
'rad50',
'rad51b',
'rad51c',
'rad51d',
'rad541',
'raf1',
'rara',
'rasal',
'rb1',
'rbm10',
'ret',
'rheb',
'rhoa',
'rictor',
'rit1',
'rnf43',
'ros1',
'rras2',
'runx1',
'rxra',
'rybp',
'sdhb',
'sdhc',
'setd2',
'sf3b1',
'shoc2'.
```

```
'shq1',
 'smad2',
 'smad3'.
 'smad4',
 'smarca4'
 'smarcb1',
 'sos1'.
 'sox9',
 'spop',
 'src',
 'srsf2',
 'stat3',
 'stk11',
 'tert',
 'tet1',
 'tet2',
 'tgfbr1',
 'tgfbr2',
 'tmprss2',
 'tp53',
 'tp53bp1',
 'tsc1',
 'tsc2',
 'u2af1',
 'vegfa',
 'vhl',
 'whsc1',
 'xpol',
 'xrcc2',
 'yap1']
In [35]:
print ("train gene feature onehotCoding is converted feature using one-hot encoding method. The sha
pe of gene feature:", train gene feature onehotCoding.shape)
```

# **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.

train gene feature onehotCoding is converted feature using one-hot encoding method. The shape of g

## In [36]:

ene feature: (2124, 238)

```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0
=0.0, power t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link:
cv log error array=[]
for i in alpha:
   clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
    clf.fit(train_gene_feature_onehotCoding, y_train)
   sig clf = CalibratedClassifierCV(clf method="sigmoid")
```

```
SIY CII - CAIIDIACEUCIASSIIIEICV (CII, MECHOU- SIYMOIU
    sig clf.fit(train_gene_feature_onehotCoding, y_train)
    predict y = sig clf.predict proba(cv gene feature onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
   print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, labels=clf.clas
ses , eps=1e-15))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error 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 train,
predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log lo
ss(y cv, predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(test gene feature onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.2082456766821463

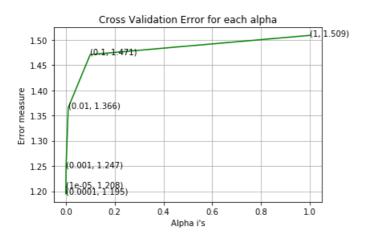
For values of alpha = 0.0001 The log loss is: 1.1946670411978328

For values of alpha = 0.001 The log loss is: 1.2472342198772528

For values of alpha = 0.01 The log loss is: 1.3655907759998371

For values of alpha = 0.1 The log loss is: 1.4707121497035074

For values of alpha = 1 The log loss is: 1.5087073831885303
```



```
For values of best alpha = 0.0001 The train log loss is: 1.0127147944076107 For values of best alpha = 0.0001 The cross validation log loss is: 1.1946670411978328 For values of best alpha = 0.0001 The test log loss is: 1.14452987307423
```

# 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 [37]:
```

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

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

```
print('Ans\n1. In test data',test coverage, 'out of',test df.shape[0], ":",(test coverage/test df.
shape[0])*100)
print('2. In cross validation data',cv coverage, 'out of ',cv df.shape[0],":", (cv coverage/cv df.s
hape[0])*100)
Q6. How many data points in Test and CV datasets are covered by the 239 genes in train dataset?
```

- 1. In test data 646 out of 665 : 97.14285714285714
- 2. In cross validation data 518 out of 532: 97.36842105263158

# 3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it?

Ans. Variation is a categorical variable

**Q8.** How many categories are there?

#### In [38]:

```
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))
```

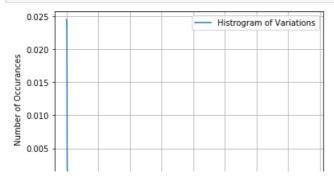
```
Number of Unique Variations: 1927
Deletion
                          50
Amplification
{\tt Truncating\_Mutations}
                          48
Fusions
                          26
                           4
Overexpression
                           4
G12V
E17K
T31M
G13D
T167A
Name: Variation, dtype: int64
```

### In [39]:

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

Ans: There are 1927 different categories of variations in the train data, and they are distibuted as follows

```
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()
```

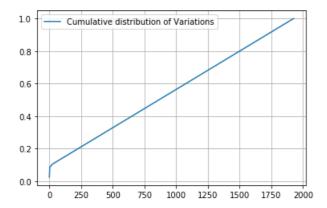


```
0.000 0 250 500 750 1000 1250 1500 1750 2000 Index of a Variation
```

#### In [41]:

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

```
[0.02448211 0.0480226 0.07062147 ... 0.99905838 0.99952919 1.
```



### Q9. How to featurize this Variation feature?

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

- 1. One hot Encoding
- 2. Response coding

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

# In [0]:

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

## In [43]:

```
print("train_variation_feature_responseCoding is a converted feature using the response coding met
hod. The shape of Variation feature:", train_variation_feature_responseCoding.shape)
```

train\_variation\_feature\_responseCoding is a converted feature using the response coding method. The shape of Variation feature: (2124, 9)

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

```
In [45]:
```

```
print("train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding meth
od. The shape of Variation feature:", train_variation_feature_onehotCoding.shape)
```

train\_variation\_feature\_onehotEncoded is converted feature using the onne-hot encoding method. The shape of Variation feature: (2124, 1959)

# **Q10.** How good is this Variation feature in predicting y\_i?

Let's build a model just like the earlier!

```
In [46]:
```

```
alpha = [10 ** x for x in range(-5, 1)]
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear\ model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11_ratio=0.15, fit_intercept=True, max_i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link:
cv_log_error_array=[]
for i in alpha:
   clf = SGDClassifier(alpha=i, penalty='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=clf.clas
ses_, eps=1e-15))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_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 train,
predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict y, labels=clf.classes , eps=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.7208392835367856

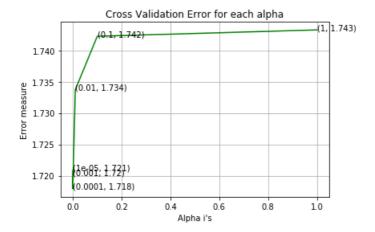
For values of alpha = 0.0001 The log loss is: 1.7179003292506485

For values of alpha = 0.001 The log loss is: 1.720099074143756

For values of alpha = 0.01 The log loss is: 1.7337372678227214

For values of alpha = 0.1 The log loss is: 1.7422574442994867

For values of alpha = 1 The log loss is: 1.7432743435419358
```



```
For values of best alpha = 0.0001 The train log loss is: 0.7629995506005386
For values of best alpha = 0.0001 The cross validation log loss is: 1.7179003292506485
For values of best alpha = 0.0001 The test log loss is: 1.6932538439916989
```

## 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 [47]:

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

Q12. How many data points are covered by total 1927 genes in test and cross validation data sets?

Ans

- 1. In test data 70 out of 665 : 10.526315789473683
- 2. In cross validation data 54 out of 532 : 10.150375939849624

# 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?

```
# cls_text is a data frame
# for every row in data fram consider the 'TEXT'
# split the words by space
# make a dict with those words
# increment its count whenever we see that word

def extract_dictionary_paddle(cls_text):
    dictionary = defaultdict(int)
    for index, row in cls_text.iterrows():
```

```
for word in row['TEXT'].split():
          dictionary[word] +=1
return dictionary
```

#### In [0]:

#### In [50]:

```
# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer = TfidfVectorizer(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).Al will sum every row and returns (1*number of features) vector
train_text_fea_counts = train_text_feature_onehotCoding.sum(axis=0).Al

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

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

Total number of unique words in train data: 1000

#### In [0]:

```
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)
```

```
#response coding of text features
train_text_feature_responseCoding = get_text_responsecoding(train_df)
test_text_feature_responseCoding = get_text_responsecoding(test_df)
cv_text_feature_responseCoding = get_text_responsecoding(cv_df)
```

#### In [0]:

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

#### In [0]:

```
# 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 [0]:

```
#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 [56]:

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

```
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4
```

#### In [57]:

```
# 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=clf.clas
ses , eps=1e-15))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error 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_train,
predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(cv text feature onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict_y, labels=clf.classes_, eps=1e-15))
For values of alpha = 1e-05 The log loss is: 1.1069459696999946
For values of alpha =
                      0.0001 The log loss is: 1.1420375200398865
For values of alpha = 0.001 The log loss is: 1.4630570563310146
```

```
For values of alpha = 1e-05 The log loss is: 1.1069459696999946

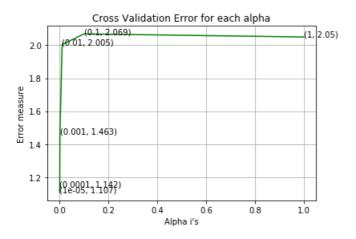
For values of alpha = 0.0001 The log loss is: 1.142037520039886

For values of alpha = 0.001 The log loss is: 1.4630570563310146

For values of alpha = 0.01 The log loss is: 2.0045317035313643

For values of alpha = 0.1 The log loss is: 2.0692483788387004

For values of alpha = 1 The log loss is: 2.0502500290445003
```



```
For values of best alpha = 1e-05 The train log loss is: 0.7305906615711405
For values of best alpha = 1e-05 The cross validation log loss is: 1.1069459696999946
For values of best alpha = 1e-05 The test log loss is: 1.0953012633364543
```

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

Ans. Yes, it seems like!

```
In [0]:
```

```
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).Al
    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 [59]:

```
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")

94.5 % of word of test data appeared in train data
94.4 % of word of Cross Validation appeared in train data
```

#### In [60]:

```
print()
from prettytable import PrettyTable
ptable = PrettyTable()
ptable.field_names=["feature","Train","CV","Test"]
ptable.add_row(["Gene ","1.00","1.14","1.19"])
ptable.add_row(["Variation","0.7","1.7","1.7"])
ptable.add_row(["Text","0.82","1.09","1.124"])
print(ptable)
print()
```

+		+.		+-		٠+٠		-+
İ	feature	İ	Train	İ	CV	İ	Test	İ
İ	Gene Variation Text	i I	1.00 0.7	 	1.14 1.7	 	1.19 1.7	1
+		+-		+-		+-		+

# 4. Machine Learning Models

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

```
In [0]:

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=le-15)
```

```
In [0]:
```

```
# this function will be used just for naive bayes
# for the given indices, we will print the name of the features
# and we will check whether the feature present in the test point text or not
def get impfeature names (indices, text, gene, var, no features):
   gene_count_vec = CountVectorizer()
   var count vec = CountVectorizer()
    text count vec = CountVectorizer(min df=3)
    gene vec = gene count vec.fit(train df['Gene'])
    var vec = var count vec.fit(train df['Variation'])
    text vec = text count vec.fit(train df['TEXT'])
    feal_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 < feal 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,yes no))
        elif (v < feal 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(word,yes_r
0))
        else:
            word = text vec.get feature names()[v-(fea1 len+fea2 len)]
            yes no = True if word in text.split() else False
            if yes no:
                word_present += 1
                print(i, "Text feature [{}] present in test data point [{}]".format(word,yes no))
    print ("Out of the top ", no features," features ", word present, "are present in query point")
4
```

# Stacking the three types of features

```
r()
train y = np.array(list(train df['Class']))
test x onehotCoding = hstack((test gene var onehotCoding, test text feature onehotCoding)).tocsr()
test y = np.array(list(test df['Class']))
cv x onehotCoding = hstack((cv gene var onehotCoding, cv text feature onehotCoding)).tocsr()
cv y = np.array(list(cv df['Class']))
train gene var responseCoding =
np.hstack((train_gene_feature_responseCoding,train_variation_feature responseCoding))
test gene var responseCoding
np.hstack((test_gene_feature_responseCoding,test_variation_feature_responseCoding))
cv gene var responseCoding =
np.hstack((cv gene feature responseCoding,cv variation feature responseCoding))
train x responseCoding = np.hstack((train_gene_var_responseCoding,
train text feature responseCoding))
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_responseCoding)
cv x responseCoding = np.hstack((cv gene var responseCoding, cv text feature responseCoding))
In [65]:
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCoding.shape)
print("(number of data points * number of features) in test data = ", test x onehotCoding.shape)
print("(number of data points * number of features) in cross validation data =", cv x onehotCoding
.shape)
One hot encoding features :
(number of data points * number of features) in train data = (2124, 3197)
(number of data points * number of features) in test data = (665, 3197)
(number of data points * number of features) in cross validation data = (532, 3197)
In [66]:
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train x responseCoding.shap
print("(number of data points * number of features) in test data = ", test x responseCoding.shape)
print("(number of data points * number of features) in cross validation data = ",
cv x responseCoding.shape)
Response encoding features :
(number of data points * number of features) in train data = (2124, 27)
```

4.1. Base Line Model

(number of data points \* number of features) in test data = (665, 27)

(number of data points \* number of features) in cross validation data = (532, 27)

## 4.1.1. Naive Bayes

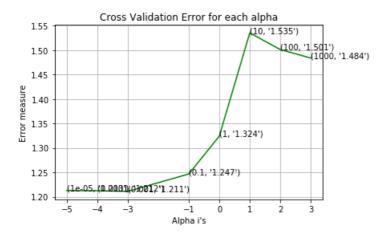
## 4.1.1.1. Hyper parameter tuning

In [67]:

```
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-
algorithm-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
\# fit(X, y[, sample weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-
algorithm-1/
cv log error array = []
for i in alpha:
    print("for alpha =", i)
    clf = MultinomialNB(alpha=i)
    clf.fit(train x onehotCoding, train y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(np.log10(alpha), cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[i], str(txt)), (np.log10(alpha[i]), cv log error 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 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 lo
ss(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, p
redict_y, labels=clf.classes_, eps=1e-15))
for alpha = 1e-05
Log Loss: 1.2125755929750142
for alpha = 0.0001
Log Loss: 1.2123004902465662
for alpha = 0.001
Log Loss: 1.210844748306353
for alpha = 0.1
Log Loss: 1.2465642825244505
for alpha = 1
Log Loss: 1.3239035850077896
for alpha = 10
```

Log Loss: 1.5354989466517543

```
for alpha = 100
Log Loss : 1.5012957920531036
for alpha = 1000
Log Loss : 1.4839734630756507
```

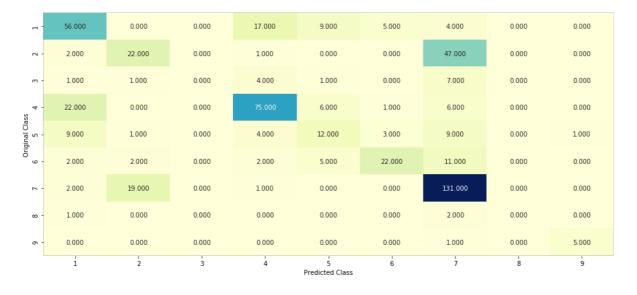


```
For values of best alpha = 0.001 The train log loss is: 0.5434329610130213
For values of best alpha = 0.001 The cross validation log loss is: 1.210844748306353
For values of best alpha = 0.001 The test log loss is: 1.144397692835139
```

### 4.1.1.2. Testing the model with best hyper paramters

#### In [68]:

```
# find more about Multinomial Naive base function here http://scikit-
learn.org/stable/modules/generated/sklearn.naive bayes.MultinomialNB.html
# default paramters
# sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=None)
# some of methods of MultinomialNB()
# fit(X, y[, sample weight]) Fit Naive Bayes classifier according to X, y
# predict(X) Perform classification on an array of test vectors X.
# predict log proba(X) Return log-probability estimates for the test vector X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-
algorithm-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight]) Fit the calibrated model
# get params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
clf = MultinomialNB(alpha=alpha[best alpha])
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
# to avoid rounding error while multiplying probabilites we use log-probability estimates
print("Log Loss :",log loss(cv y, sig clf probs))
print("Number of missclassified point:", np.count_nonzero((sig_clf.predict(cv_x_onehotCoding)- cv
y))/cv y.shape[0])
plot confusion matrix(cv y, sig clf.predict(cv x onehotCoding.toarray()))
```



- 125

- 100

- 75

- 50

- 25

- 0.75

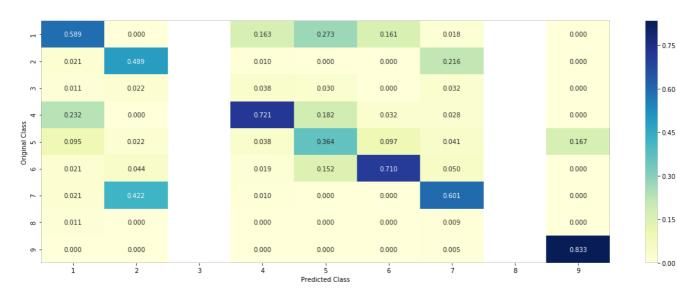
- 0.60

- 0.45

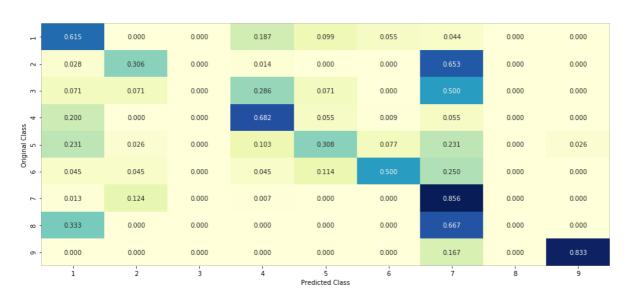
- 0.30

-0.15

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



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



# 4.1.1.3. Feature Importance, Correctly classified point

```
resr_bornr_rndev
no feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test point index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices=np.argsort(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'].iloc[test point index],test df['Variation']
.iloc[test point index], no feature)
Predicted Class: 6
Predicted Class Probabilities: [[0.0862 0.0513 0.0141 0.1126 0.0565 0.5613 0.111 0.0035 0.0035]]
Actual Class : 6
21 Text feature [1093] present in test data point [True]
29 Text feature [13] present in test data point [True]
34 Text feature [000] present in test data point [True]
Out of the top 100 features 3 are present in query point
```

#### 4.1.1.4. Feature Importance, Incorrectly classified point

```
In [70]:
```

```
test_point_index = 100
no feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(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'].iloc[test point index],test df['Variation']
.iloc[test point index], no feature)
Predicted Class: 7
Predicted Class Probabilities: [[0.0649 0.135 0.011 0.0689 0.035 0.0351 0.644 0.0031 0.003 ]]
Actual Class : 2
54 Text feature [100] present in test data point [True]
Out of the top 100 features 1 are present in query point
```

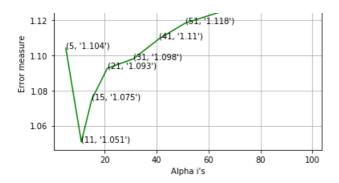
# 4.2. K Nearest Neighbour Classification

# 4.2.1. Hyper parameter tuning

In [71]:

```
| learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
# video link:
alpha = [5, 11, 15, 21, 31, 41, 51, 99]
cv log error array = []
for i in alpha:
   print("for alpha =", i)
    clf = KNeighborsClassifier(n neighbors=i)
    clf.fit(train_x_responseCoding, train_y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig clf.fit(train x responseCoding, train y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)
predict y = sig clf.predict proba(train x responseCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train,
predict y, labels=clf.classes , eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y test, p
redict y, labels=clf.classes , eps=1e-15))
for alpha = 5
Log Loss: 1.1041895517146412
for alpha = 11
Log Loss: 1.050662310152841
for alpha = 15
Log Loss: 1.0749793348560823
for alpha = 21
Log Loss: 1.0927206671680691
for alpha = 31
Log Loss: 1.0980682733516993
for alpha = 41
Log Loss: 1.1096475806100037
for alpha = 51
Log Loss: 1.1184911601659036
for alpha = 99
Log Loss: 1.1411770041583293
```

1.14



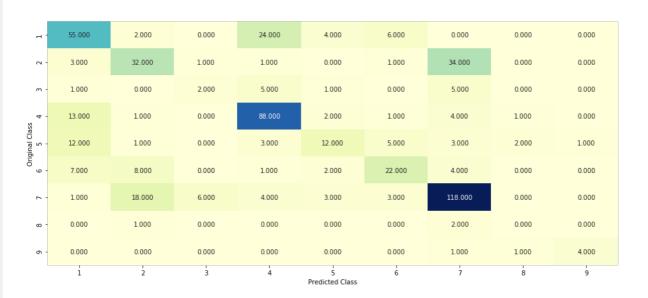
```
For values of best alpha = 11 The train log loss is: 0.640073218674863

For values of best alpha = 11 The cross validation log loss is: 1.050662310152841

For values of best alpha = 11 The test log loss is: 0.9543879907068362
```

#### 4.2.2. Testing the model with best hyper paramters

#### In [72]:



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

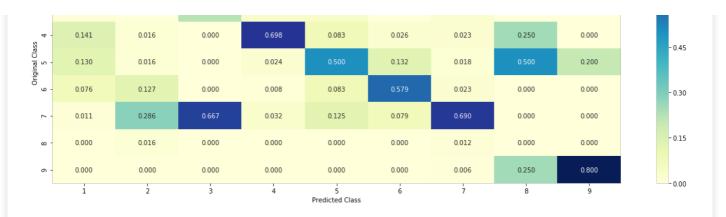
г.	0.598	0.032	0.000	0.190	0.167	0.158	0.000	0.000	0.000
2 -	0.033	0.508	0.111	0.008	0.000	0.026	0.199	0.000	0.000
m -	0.011	0.000	0.222	0.040	0.042	0.000	0.029	0.000	0.000

- 0.75 - 0.60

- 100

- 80

60



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



#### 4.2.3. Sample Query point -1

```
In [73]:
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)
test point index = 1
predicted_cls = sig_clf.predict(test_x_responseCoding[0].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Actual Class :", test_y[test_point_index])
neighbors = clf.kneighbors(test x responseCoding[test point index].reshape(1, -1), alpha[best alpha
print("The ",alpha[best alpha]," nearest neighbours of the test points belongs to classes",train y
[neighbors[1][0]])
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
Predicted Class: 9
Actual Class : 6
The 11 nearest neighbours of the test points belongs to classes [6 6 6 6 6 6 6 6 6 6]
Fequency of nearest points : Counter({6: 11})
```

#### 4.2.4. Sample Query Point-2

```
In [74]:
```

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

```
test_point_index = 100

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

Predicted Class : 7
Actual Class : 2
the k value for knn is 11 and the nearest neighbours of the test points belongs to classes [2 7 7 7 2 2 2 7 7 7]
Fequency of nearest points : Counter({7: 7, 2: 4})
```

### 4.3. Logistic Regression

#### 4.3.1. With Class balancing

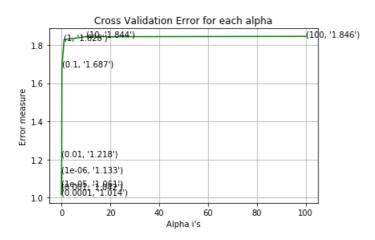
#### 4.3.1.1. Hyper paramter tuning

In [75]:

```
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear\ model.SGDC lassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power_t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# 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 state=42
   clf.fit(train x onehotCoding, train y)
   sig clf = CalibratedClassifierCV(clf, method="sigmoid")
   sig_clf.fit(train_x_onehotCoding, train_y)
   sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
   cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
```

```
# to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.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='log', ran
dom state=42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y train,
predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
ss(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, p
redict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-06Log Loss: 1.1332607894229252 for alpha = 1e-05Log Loss: 1.0610327461109685 for alpha = 0.0001Log Loss: 1.0138413983629366 for alpha = 0.001Log Loss: 1.042474659076955 for alpha = 0.01Log Loss: 1.217843678634886 for alpha = 0.1Log Loss: 1.6868047353360354 for alpha = 1Log Loss: 1.8284832711964811 for alpha = 10Log Loss: 1.843791685699172 for alpha = 100Log Loss: 1.8455839386011739



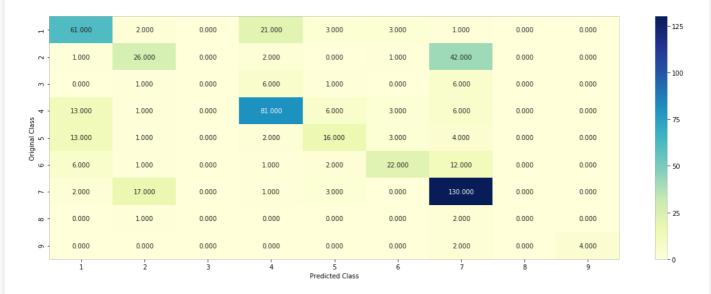
```
For values of best alpha = 0.0001 The train log loss is: 0.45786829431688403
For values of best alpha = 0.0001 The cross validation log loss is: 1.0138413983629366
For values of best alpha = 0.0001 The test log loss is: 0.9218869949078555
```

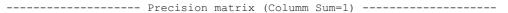
```
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', ran
dom state=42)
predict and plot confusion matrix(train x onehotCoding, train y, cv x onehotCoding, cv y, clf)
```

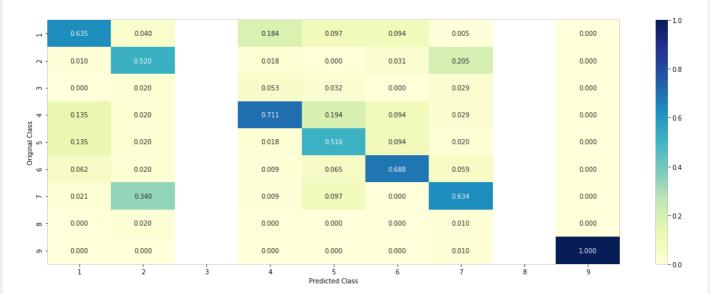
Log loss : 1.0138413983629366

Number of mis-classified points : 0.3609022556390977

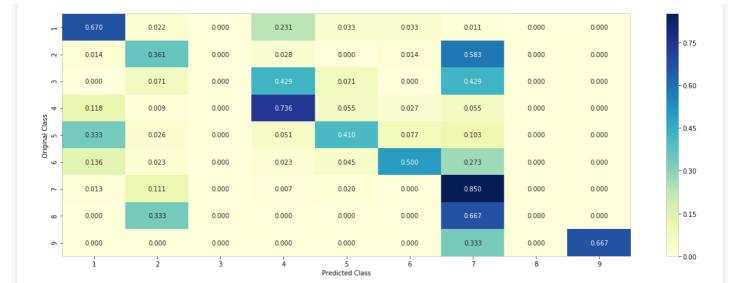
----- Confusion matrix -----







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



#### 4.3.1.3. Feature Importance

In [0]:

```
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 [78]:

```
# from tabulate import tabulate
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', ran
dom state=42)
clf.fit(train x onehotCoding,train y)
test point index = 1
no feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:",
np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(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'].iloc[test_point_index],test_df['Variation']
.iloc[test point index], no feature)
Predicted Class: 6
Predicted Class Probabilities: [[0.0441 0.0049 0.0217 0.1046 0.0389 0.7784 0.0031 0.0031 0.0012]]
Actual Class : 6
349 Text feature [11] present in test data point [True]
```

#### 4.3.1.3.2. Incorrectly Classified point

```
In [79]:
```

```
test point index = 100
no feature = 500
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:",
\verb"np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]), 4)")" \\
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'].iloc[test point index],test df['Variation']
.iloc[test point index], no feature)
Predicted Class: 7
Predicted Class Probabilities: [[0.0183 0.1899 0.0021 0.0212 0.013 0.0014 0.7516 0.0014 0.0012]]
Actual Class : 2
_____
24 Text feature [100] present in test data point [True]
115 Text feature [005228] present in test data point [True]
473 Text feature [05] present in test data point [True]
Out of the top 500 features 3 are present in query point
```

#### 4.3.2. Without Class balancing

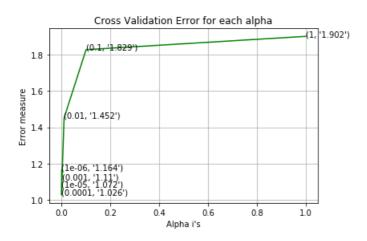
#### 4.3.2.1. Hyper paramter tuning

#### In [80]:

```
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11_ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optimal', eta0
=0.0, power t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# 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 ** v for v in range (-6 1)]
```

```
ατρπα - μτο
              A LOL A LI Lange ( U, I)
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)
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 lo
ss(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, p
redict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.1644814258435812
for alpha = 1e-05
Log Loss : 1.0715194644434234
for alpha = 0.0001
Log Loss : 1.0263873522848197
for alpha = 0.001
Log Loss : 1.1099980263917337
for alpha = 0.01
Log Loss : 1.4521864672252107
for alpha = 0.1
Log Loss : 1.8289766949862687
for alpha = 1
Log Loss : 1.9024470396998319
```



```
For values of best alpha = 0.0001 The train log loss is: 0.4522444261875607
For values of best alpha = 0.0001 The cross validation log loss is: 1.0263873522848197
For values of best alpha = 0.0001 The test log loss is: 0.9455680308302007
```

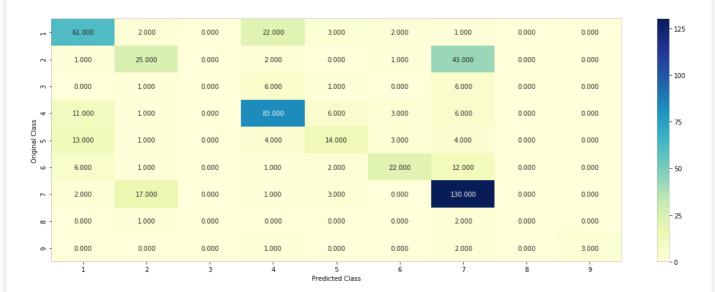
#### 4.3.2.2. Testing model with best hyper parameters

In [81]:

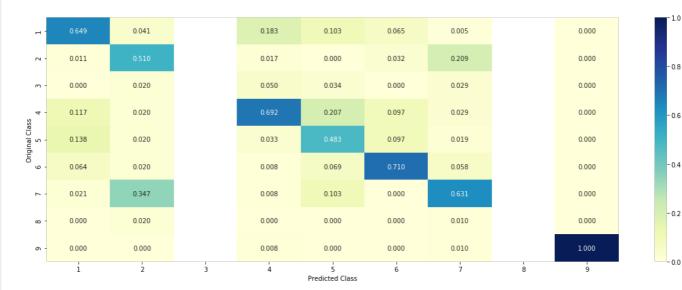
Log loss: 1.0263873522848197

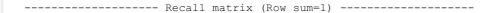
Number of mis-classified points: 0.36466165413533835

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



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







#### 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 = 500
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(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'].iloc[test_point_index],test_df['Variation']
.iloc[test point index], no feature)
Predicted Class : 6
Predicted Class Probabilities: [[3.650e-02 5.600e-03 1.470e-02 9.920e-02 3.840e-02 7.989e-01 4.000
e - 03
 2.300e-03 5.000e-0411
Actual Class : 6
84 Text feature [11] present in test data point [True]
Out of the top 500 features 1 are present in query point
```

#### 4.3.2.4. Feature Importance, Inorrectly Classified point

#### In [83]:

```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(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'].iloc[test_point_index],test_df['Variation']
.iloc[test_point_index], no_feature)
Predicted Class : 7
```

Predicted Class: 7
Predicted Class Probabilities: [[2.060e-02 1.842e-01 1.800e-03 2.420e-02 1.180e-02 1.300e-03 7.532

```
2.300e-03 6.000e-04]]
Actual Class: 2

153 Text feature [005228] present in test data point [True]
375 Text feature [100] present in test data point [True]
Out of the top 500 features 2 are present in query point
```

## 4.4. Linear Support Vector Machines

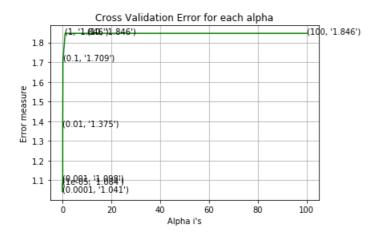
#### 4.4.1. Hyper paramter tuning

```
In [84]:
```

```
# read more about support vector machines with linear kernals here http://scikit-
learn.org/stable/modules/generated/sklearn.svm.SVC.html
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, t
01=0.001.
# cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', ra
ndom_state=None)
# Some of methods of SVM()
# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/mathematical-derivation-copy-8/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# 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', random state
=42.
   clf.fit(train x onehotCoding, train y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig clf.fit(train x onehotCoding, train y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
   print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[i], str(txt)), (alpha[i], cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
```

```
best_alpha = np.argmin(cv_log_error_array)
# clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced')
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='hinge', r
andom state=42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train,
predict y, labels=clf.classes , eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log lo
ss(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, p
redict y, labels=clf.classes , eps=1e-15))
```

```
for C = 1e-05
Log Loss: 1.0843744302025784
for C = 0.0001
Log Loss: 1.040900817608454
for C = 0.001
Log Loss : 1.0984602985534544
for C = 0.01
Log Loss: 1.374999316306491
for C = 0.1
Log Loss: 1.7089660636280517
for C = 1
Log Loss: 1.8461149368397085
for C = 10
Log Loss: 1.8461149449892185
for C = 100
Log Loss: 1.8461149291926422
```



```
For values of best alpha = 0.0001 The train log loss is: 0.40125181651380915
For values of best alpha = 0.0001 The cross validation log loss is: 1.040900817608454
For values of best alpha = 0.0001 The test log loss is: 0.9501105256480938
```

#### 4.4.2. Testing model with best hyper parameters

#### In [85]:

125

100

- 75

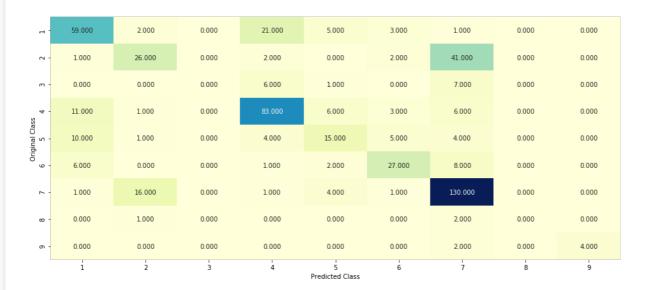
50

- 25

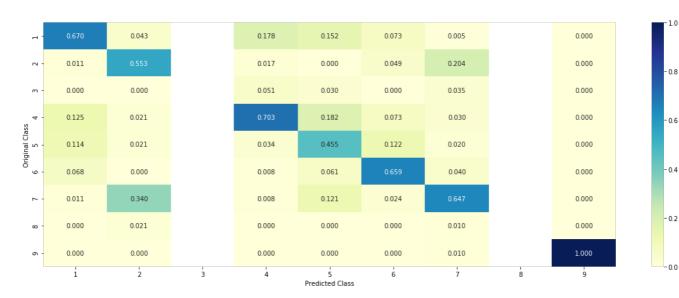
0.75

0.60

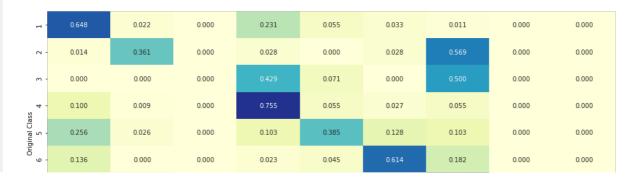
0.45

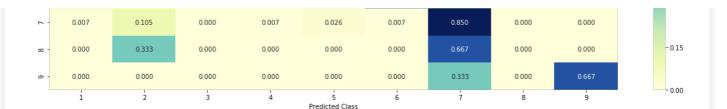


----- Precision matrix (Columm Sum=1) -----



----- Recall matrix (Row 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 = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted cls[0])
print ("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(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'].iloc[test_point_index],test_df['Variation']
.iloc[test point index], no feature)
Predicted Class : 6
Predicted Class Probabilities: [[0.0432 0.0406 0.0175 0.1203 0.013 0.7397 0.021 0.0025 0.0021]]
Actual Class : 6
Out of the top 500 features 0 are present in query point
```

#### 4.3.3.2. For Incorrectly classified point

```
In [87]:
```

```
test_point_index = 100
no feature = 500
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(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'].iloc[test point index],test df['Variation']
.iloc[test_point_index], no_feature)
Predicted Class: 7
Predicted Class Probabilities: [[0.0184 0.235 0.0054 0.0244 0.0439 0.0019 0.6657 0.0015 0.0039]]
Actual Class: 2
                       ______
Out of the top 500 features 0 are present in query point
```

#### 4.5 Random Forest Classifier

#### 4.5.1. Hyper paramter tuning (With One hot Encoding)

```
In [88]:
# ______
```

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_
impurity decrease=0.0,
# min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None,
verbose=0, warm start=False,
# class weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight]) Fit the calibrated model
# get params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
# video link:
alpha = [100, 200, 500, 1000, 2000]
max depth = [5, 10]
cv_log_error_array = []
for i in alpha:
    for j in max depth:
        print("for n_estimators =", i,"and max depth = ", j)
       clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, random state=42
       clf.fit(train_x_onehotCoding, train_y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_onehotCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
        cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
        print("Log Loss :",log loss(cv y, sig clf probs))
'''fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[int(i/2)],max depth[int(i%2)],str(txt)),
(features[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', max depth=max
_depth[int(best_alpha%2)], random_state=42, n_jobs=-1)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The train log loss
ic." log loce/y train predict y labele=clf classes enc=1a-15))
```

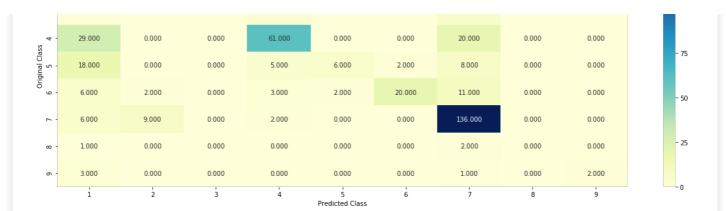
```
is. ,iug_iuss(y_ctain, preutoc_y, tabets-cir.ctasses_, eps-re-iu//
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross validation log loss
is:",log_loss(y_cv, predict_y, labels=clf.classes , eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss
is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
for n estimators = 100 and max depth = 5
Log Loss : 1.249991703830645
for n estimators = 100 and max depth = 10
Log Loss : 1.2634434666158416
for n estimators = 200 and max depth = 5
Log Loss : 1.2286940955122976
for n estimators = 200 and max depth = 10
Log Loss: 1.257575767970522
for n_{estimators} = 500 and max depth = 5
Log Loss : 1.2233633127390762
for n estimators = 500 and max depth = 10
Log Loss: 1.2482453961751725
for n estimators = 1000 and max depth = 5
Log Loss : 1.221825402235456
for n estimators = 1000 and max depth = 10
Log Loss : 1.245599658787943
for n_{estimators} = 2000 and max depth = 5
Log Loss: 1.2179648371934533
for n estimators = 2000 and max depth = 10
Log Loss : 1.2444717603770685
For values of best estimator = 2000 The train log loss is: 0.8684952301597172
For values of best estimator = 2000 The cross validation log loss is: 1.2179648371934533
For values of best estimator = 2000 The test log loss is: 1.1528420612739096
```

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

```
In [89]:
```

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
amples split=2,
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min
impurity decrease=0.0,
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None,
verbose=0, warm start=False,
# class_weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max
_depth[int(best_alpha%2)], random_state=42, n_jobs=-1)
predict and plot confusion matrix(train x onehotCoding, train y,cv x onehotCoding,cv y, clf)
```

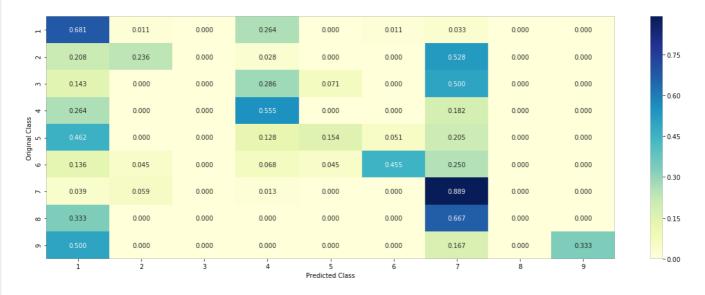
٦ -	62.000	1.000	0.000	24.000	0.000	1.000	3.000	0.000	0.000
- 2	15.000	17.000	0.000	2.000	0.000	0.000	38.000	0.000	0.000
m -	2.000	0.000	0.000	4.000	1.000	0.000	7.000	0.000	0.000



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



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



#### 4.5.3. Feature Importance

#### 4.5.3.1. Correctly Classified point

```
In [90]:
```

```
# test_point_index = 10
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max
_depth[int(best_alpha%2)], random_state=42, n_jobs=-1)
clf.fit(train_x_onehotCoding, train_y)
```

```
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
test point index = 1
no feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print ("Predicted Class Probabilities:",
np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
print("Actual Class :", test y[test point index])
indices = np.argsort(-clf.feature importances )
print("-"*50)
get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point index],test df['Gene'].
iloc[test_point_index],test_df['Variation'].iloc[test_point_index], no_feature)
Predicted Class : 6
Predicted Class Probabilities: [[0.1236 0.0088 0.0136 0.1526 0.0491 0.6265 0.0197 0.0024 0.0036]]
Actual Class : 6
Out of the top 100 features 0 are present in query point
```

#### 4.5.3.2. Inorrectly Classified point

```
In [91]:
```

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

Predicted Class : 7
Predicted Class Probabilities: [[0.0491 0.3776 0.0162 0.0341 0.0468 0.046 0.4194 0.0063 0.0043]]
Actuall Class : 2
Out of the top 100 features 0 are present in query point
```

#### 4.5.3. Hyper paramter tuning (With Response Coding)

#### In [92]:

```
# -----
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
amples split=2,
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min
impurity decrease=0.0,
# min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None,
verbose=0, warm_start=False,
# class weight=None)
# Some of methods of RandomForestClassifier()
\# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
```

```
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
\# fit(X, y[, sample weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
# video link:
alpha = [10,50,100,200,500,1000]
\max depth = [2,3,5,10]
cv log error array = []
for i in alpha:
    for j in max depth:
        print("for n estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, random state=42
, n jobs=-1)
        clf.fit(train_x_responseCoding, train_y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_responseCoding, train_y)
       sig clf probs = sig clf.predict proba(cv x responseCoding)
        cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[int(i/4)],max_depth[int(i%4)],str(txt)),
(features[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='gini', max depth=max
depth[int(best alpha%4)], random state=42, n jobs=-1)
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x responseCoding, train y)
predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The train log loss is:",log_loss(y
train, predict y, labels=clf.classes , eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best alpha/4)], "The cross validation log loss is:"
,log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[int(best alpha/4)], "The test log loss is:",log loss(y
test, predict y, labels=clf.classes , eps=1e-15))
for n estimators = 10 and max depth = 2
Log Loss : 2.1080121490953228
for n estimators = 10 and max depth = 3
Log Loss : 1.7875330928728776
for n estimators = 10 and max depth = 5
Log Loss: 1.6454209542287228
for n estimators = 10 and max depth = 10
Log Loss : 1.7167343424292627
for n estimators = 50 and max depth = 2
Log Loss : 1.6593102816878993
for n estimators = 50 and max depth = 3
Log Loss: 1.4358447509849843
for n_{estimators} = 50 and max depth = 5
Log Loss : 1.3355283052681304
for n estimators = 50 and max depth = 10
Tiod Tioss : 1.653890423888417
```

```
109 1000 · 1.00000012000011
for n estimators = 100 and max depth = 2
Log Loss : 1.55691619818187
for n estimators = 100 and max depth = 3
Log Loss : 1.4899170842820315
for n estimators = 100 and max depth = 5
Log Loss: 1.2904476630206279
for n estimators = 100 and max depth = 10
Log Loss : 1.6144390202839471
for n_{estimators} = 200 and max depth = 2
Log Loss: 1.5916970066602578
for n estimators = 200 and max depth = 3
Log Loss: 1.4802244802840412
for n estimators = 200 and max depth = 5
Log Loss : 1.3442855750037563
for n estimators = 200 and max depth = 10
Log Loss: 1.5759808242107127
for n_{estimators} = 500 and max depth = 2
Log Loss : 1.6408089826467431
for n estimators = 500 and max depth = 3
Log Loss : 1.5226462175717674
for n estimators = 500 and max depth = 5
Log Loss: 1.3440470631973764
for n estimators = 500 and max depth = 10
Log Loss : 1.6195373663093586
for n estimators = 1000 and max depth = 2
Log Loss: 1.6376061369963493
for n estimators = 1000 and max depth = 3
Log Loss : 1.5380426694927507
for n estimators = 1000 and max depth = 5
Log Loss: 1.3554868271063036
for n estimators = 1000 and max depth = 10
Log Loss: 1.6386133055541394
For values of best alpha = 100 The train log loss is: 0.06119518112523
For values of best alpha = 100 The cross validation log loss is: 1.2904476630206279
For values of best alpha = 100 The test log loss is: 1.1845141128617311
```

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

Log loss: 1.2904476630206279

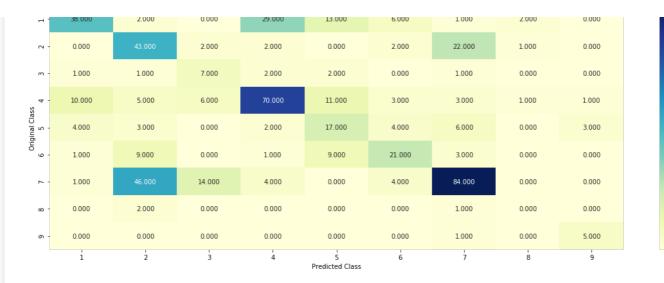
Number of mis-classified points : 0.4642857142857143

2000 2000

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

```
In [93]:
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
amples split=2,
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min
impurity decrease=0.0,
# min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None,
verbose=0, warm_start=False,
# class weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
{\tt clf} = {\tt RandomForestClassifier\,(max\_depth=max\_depth\,[int\,(best\_alpha\$4)\,]\,,}
n estimators=alpha[int(best alpha/4)], criterion='gini', max features='auto',random state=42)
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_responseCoding,cv_y, clf)
```

22.000 2.000 2.000



- 60

- 45

- 30

- 15

0.60

- 0.45

- 0.30

-0.15

- 0.00

0.75

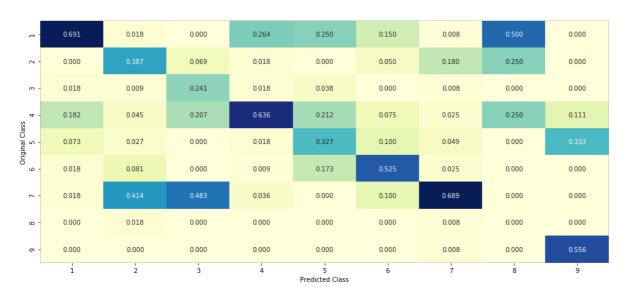
- 0.60

- 0.45

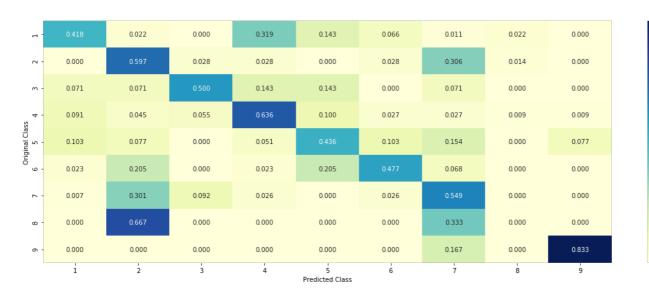
- 0.30

-0.15

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



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



#### 4.5.5. Feature Importance

#### 4.5.5.1. Correctly Classified point

```
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='gini', max depth=max
_depth[int(best_alpha%4)], random_state=42, n_jobs=-1)
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)
test point index = 1
no feature = 27
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_responseCoding[test_point_index].reshape(1,-1)),4))
print("Actual Class :", test y[test point index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
      print("Variation is important feature")
    else:
       print("Text is important feature")
Predicted Class : 6
Predicted Class Probabilities: [[0.0138 0.0046 0.1074 0.0267 0.1574 0.6791 0.0039 0.0036 0.0033]]
Actual Class : 6
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Text is important feature
Gene is important feature
```

#### 4.5.5.2. Incorrectly Classified point

#### In [95]:

```
test_point_index = 100
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_responseCoding[test_point_index].reshape(1,-1)),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:</pre>
```

```
print("Text is important feature")
Predicted Class: 2
Predicted Class Probabilities: [[0.0129 0.7378 0.0286 0.0137 0.0169 0.0288 0.1391 0.0149 0.0073]]
Actual Class : 2
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Text is important feature
Gene is important feature
```

#### 4.7 Stack the models

#### 4.7.1 testing with hyper parameter tuning

```
In [96]:
```

```
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
# read more about support vector machines with linear kernals here http://scikit-
learn.org/stable/modules/generated/sklearn.svm.SVC.html
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, t
01=0.001,
# cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', ra
ndom_state=None)
# Some of methods of SVM()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
```

```
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/mathematical-derivation-copy-8/
# read more about support vector machines with linear kernals here http://scikit-
learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
amples split=2,
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min
impurity decrease=0.0,
# min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None,
verbose=0, warm start=False,
# class_weight=None)
# Some of methods of RandomForestClassifier()
\# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class weight='balanced', random state=0
clf1.fit(train x onehotCoding, train y)
sig clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
clf2 = SGDClassifier(alpha=1, penalty='12', loss='hinge', class weight='balanced', random state=0)
clf2.fit(train x onehotCoding, train y)
sig clf2 = CalibratedClassifierCV(clf2, method="sigmoid")
clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train x onehotCoding, train y)
sig clf3 = CalibratedClassifierCV(clf3, method="sigmoid")
sig clf1.fit(train x onehotCoding, train y)
print("Logistic Regression : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf1.predict_proba(cv_x_onehot
Coding))))
sig clf2.fit(train x onehotCoding, train y)
print("Support vector machines : Log Loss: %0.2f" % (log loss(cv y,
\verb|sig_clf2.predict_proba(cv_x_onehotCoding)|)|
sig clf3.fit(train x onehotCoding, train y)
print("Naive Bayes : Log Loss: %0.2f" % (log loss(cv y, sig clf3.predict proba(cv x onehotCoding)))
print("-"*50)
alpha = [0.0001, 0.001, 0.01, 0.1, 1, 10]
best alpha = 999
for i in alpha:
   lr = LogisticRegression(C=i)
   sclf = StackingClassifier(classifiers=[sig clf1, sig clf2, sig clf3], meta classifier=lr, use p
robas=True)
    sclf.fit(train_x_onehotCoding, train_y)
    print ("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" % (i, log loss(cv y, sc
lf.predict proba(cv x onehotCoding))))
    log error =log loss(cv y, sclf.predict proba(cv x onehotCoding))
    if best alpha > log error:
       best alpha = log error
4
                                                                                                 | | |
Logistic Regression: Log Loss: 1.04
Support vector machines : Log Loss: 1.85
Naive Bayes : Log Loss: 1.21
Stacking Classifer: for the value of alpha: 0.000100 Log Loss: 2.178
Stacking Classifer: for the value of alpha: 0.001000 Log Loss: 2.035
Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.514
```

```
Stacking Classifer: for the value of alpha: 0.100000 Log Loss: 1.181
Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.398
Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.858
```

#### 4.7.2 testing the model with the best hyper parameters

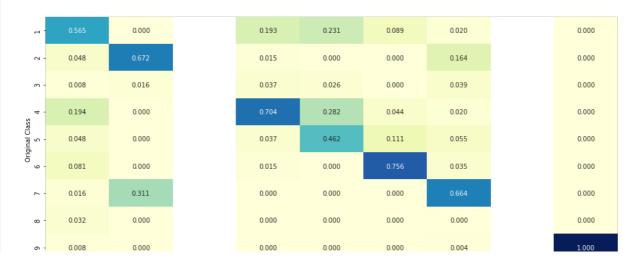
#### In [97]:

```
lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=lr, use_proba
s=True)
sclf.fit(train x onehotCoding, train y)
log_error = log_loss(train_y, sclf.predict_proba(train_x_onehotCoding))
print("Log loss (train) on the stacking classifier :",log error)
log_error = log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
print("Log loss (CV) on the stacking classifier: ",log error)
log_error = log_loss(test_y, sclf.predict_proba(test x onehotCoding))
print("Log loss (test) on the stacking classifier :",log error)
print("Number of missclassified point:", np.count nonzero((sclf.predict(test x onehotCoding)-
test y))/test y.shape[0])
plot_confusion_matrix(test_y=test_y, predict_y=sclf.predict(test_x_onehotCoding))
```

Log loss (train) on the stacking classifier: 0.5538016833228964 Log loss (CV) on the stacking classifier : 1.1809904390953867Log loss (test) on the stacking classifier: 1.1078029125346778 Number of missclassified point : 0.34887218045112783 ----- Confusion matrix ------

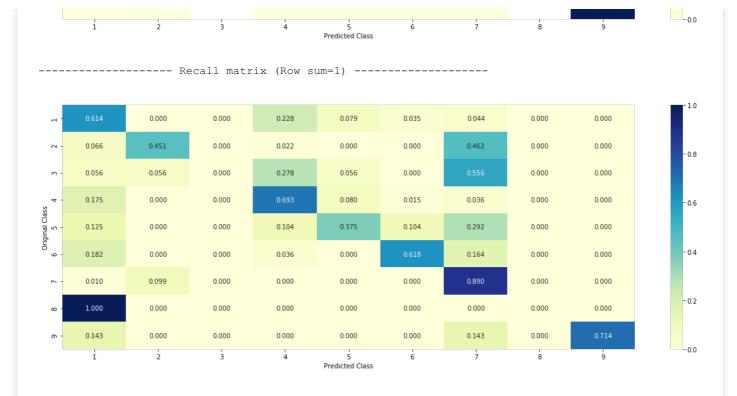


----- Precision matrix (Columm Sum=1) ------



- 0.8 -0.6 -04 - 0.2

60



#### 4.7.3 Maximum Voting classifier

```
In [98]:
```

```
#Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassifier.html
from sklearn.ensemble import VotingClassifier
vclf = VotingClassifier(estimators=[('lr', sig clf1), ('svc', sig clf2), ('rf', sig clf3)], voting=
'soft')
vclf.fit(train x onehotCoding, train y)
print("Log loss (train) on the VotingClassifier :", log_loss(train_y,
vclf.predict_proba(train_x_onehotCoding)))
print("Log loss (CV) on the VotingClassifier :", log loss(cv y,
vclf.predict_proba(cv_x_onehotCoding)))
print("Log loss (test) on the VotingClassifier :", log_loss(test_y,
vclf.predict_proba(test_x_onehotCoding)))
print("Number of missclassified point :", np.count_nonzero((vclf.predict(test_x_onehotCoding)-
test y))/test y.shape[0])
plot confusion matrix(test y=test y, predict y=vclf.predict(test x onehotCoding))
Log loss (train) on the VotingClassifier : 0.8477704570845488
Log loss (CV) on the VotingClassifier: 1.2127729835135057
Log loss (test) on the VotingClassifier: 1.154683840083712
Number of missclassified point : 0.3533834586466165
            ----- Confusion matrix -----
```

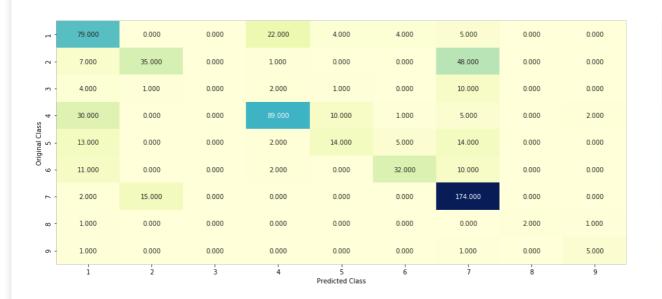
150

- 120

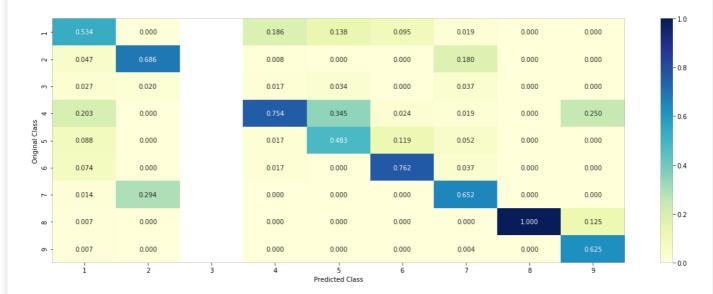
- 90

60

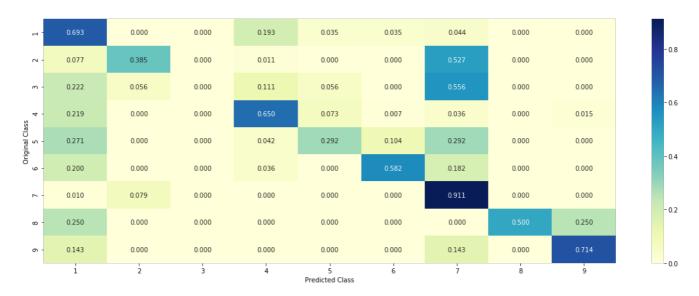
- 30



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



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



# 5. Assignments

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

# Apply Logistic regression with CountVectorizer Features, including both1 unigrams and bigrams

```
In [99]:
```

```
# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer_lr = CountVectorizer(min_df=3,ngram_range=(1,2))
train_text_feature_onehotCoding_lr = text_vectorizer_lr.fit_transform(train_df['TEXT'])
train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding_lr, axis=0)
cv_text_feature_onehotCoding_lr = text_vectorizer_lr.transform(cv_df['TEXT'])
cv_text_feature_onehotCoding = normalize(cv_text_feature_onehotCoding_lr, axis=0)
test_text_feature_onehotCoding_lr = text_vectorizer_lr.transform(test_df['TEXT'])
test_text_feature_onehotCoding = normalize(test_text_feature_onehotCoding_lr, axis=0)
# getting all the feature names (words)
```

```
train text features lr= text vectorizer lr.get feature names()
\# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns (1*number of feature)
res) vector
train text fea counts lr = train text feature onehotCoding lr.sum(axis=0).A1
# zip(list(text_features),text_fea_counts) will zip a word with its number of times it occured
text fea dict lr = dict(zip(list(train text features lr),train text fea counts lr))
print("Total number of unique words in train data :", len(train text features lr))
Total number of unique words in train data: 760779
In [0]:
# one-hot encoding of Gene feature.
gene vectorizer g = CountVectorizer()
train_gene_feature_onehotCoding_g = gene_vectorizer_g.fit_transform(train_df['Gene'])
test gene feature onehotCoding g = gene vectorizer g.transform(test df['Gene'])
cv_gene_feature_onehotCoding_g = gene_vectorizer_g.transform(cv_df['Gene'])
In [101]:
train df['Gene'].head()
Out[101]:
793
       ERBB4
1572
          ALK
905
       PDGFRA
1762
         IDH1
2194
         PTEN
Name: Gene, dtype: object
In [102]:
print("shape of train: ",train gene feature onehotCoding g .shape)
shape of train: (2124, 238)
In [0]:
# one-hot encoding of variation feature.
variation vectorizer g = CountVectorizer()
train_variation_feature_onehotCoding_g = variation_vectorizer_g.fit_transform(train_df['Variation'
test variation feature onehotCoding g = variation vectorizer g.transform(test df['Variation'])
cv_variation_feature_onehotCoding_g = variation_vectorizer_g.transform(cv_df['Variation'])
In [104]:
print("shape of train: ",train variation feature onehotCoding g .shape)
shape of train: (2124, 1959)
In [0]:
train gene var onehotCoding g=hstack((train gene feature onehotCoding g,train variation feature one
hotCoding_g))
test_gene_var_onehotCoding_g
=hstack((test_gene_feature_onehotCoding_g,test_variation_feature_onehotCoding_g))
cv_gene_var_onehotCoding_g
=hstack((cv_gene_feature_onehotCoding_g,cv_variation_feature_onehotCoding_g))
4
In [0]:
train x onehotCoding grams = hstack((train gene var onehotCoding g,
train text feature onehotCoding)).tocsr()
train y = np.array(list(train df['Class']))
test_x_onehotCoding_grams = hstack((test_gene_var_onehotCoding_g, test_text_feature_onehotCoding))
.tocsr()
```

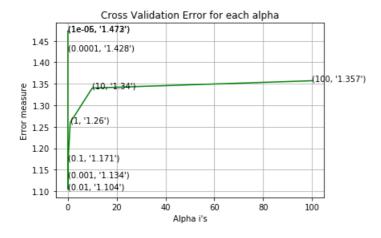
```
test_y = np.array(list(test_df['Class']))
cv_x_onehotCoding_grams = hstack((cv_gene_var_onehotCoding_g, cv_text_feature_onehotCoding)).tocsr
()
cv_y = np.array(list(cv_df['Class']))
```

#### In [107]:

```
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class_weight=None, warm_start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
# find more about CalibratedClassifierCV here at
http://scikitlearn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
# 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 state=42)
 clf.fit(train_x_onehotCoding_grams, train_y)
  sig clf = CalibratedClassifierCV(clf, method="sigmoid")
  sig_clf.fit(train_x_onehotCoding_grams, train_y)
 sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding_grams)
 cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
  # to avoid rounding error while multiplying probabilites we use log-probability estimates
 print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
 ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', ran
dom state=42)
clf.fit(train x onehotCoding grams, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding grams, train y)
predict_y = sig_clf.predict_proba(train_x_onehotCoding_grams)
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_grams)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding_grams)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss(y test, p
redict_y, labels=clf.classes_, eps=1e-15))
for alpha = 1e-06
```

```
Log Loss: 1.4717859759937055
for alpha = 1e-05
Log Loss: 1.4731957586237434
for alpha = 0.0001
```

```
Log Loss: 1.4276585834091153
for alpha = 0.001
Log Loss: 1.133614306625563
for alpha = 0.01
Log Loss: 1.104219291122409
for alpha = 0.1
Log Loss: 1.1714893767901464
for alpha = 1
Log Loss: 1.2600880279083857
for alpha = 10
Log Loss: 1.340143444429386
for alpha = 100
Log Loss: 1.3570774829101169
```

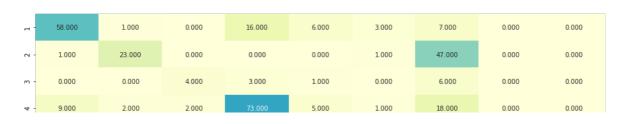


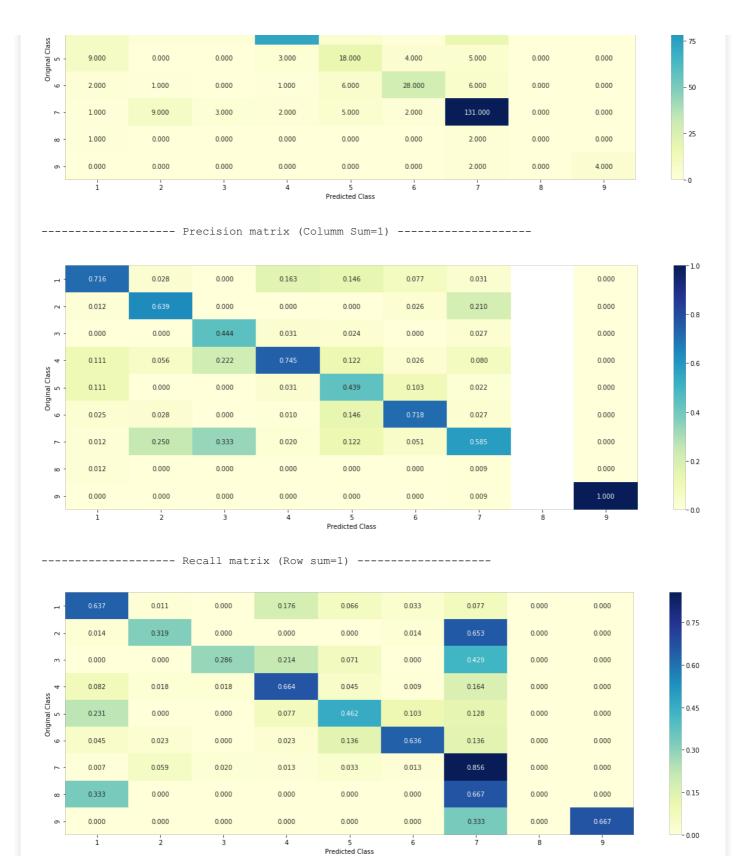
```
For values of best alpha = 0.01 The train log loss is: 0.704499911231661
For values of best alpha = 0.01 The cross validation log loss is: 1.104219291122409
For values of best alpha = 0.01 The test log loss is: 1.1325079445227053
```

## Testing the model with best hyper paramters

```
In [108]:
```

```
# read more about SGDClassifier() at
http://scikitlearn.org/stable/modules/generated/sklearn.linear model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', ran
predict and plot confusion matrix(train x onehotCoding grams, train y, cv x onehotCoding grams, cv
_y, clf)
```





I used balanced parameter because it performs better than unigram and bigram

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

# what if we try to combine both gene and variance

```
In [0]:
gene_variation = []
for gene in result['Gene'].values:
    gene_variation.append(gene)
```

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

In [110]:

gene_variation[0:10]

Out[110]:

['FAM58A', 'CBL', 'CBL', 'CBL', 'CBL', 'CBL', 'CBL', 'CBL', 'CBL']
```

## **Feature Importance**

```
In [0]:
```

```
tfidfVectorizer = TfidfVectorizer(min_df=5,max_features=3000,ngram_range=(1,4))
text2 = tfidfVectorizer.fit_transform(gene_variation)
gene_variation_features = tfidfVectorizer.get_feature_names()
train_text = tfidfVectorizer.transform(train_df['TEXT'])
test_text = tfidfVectorizer.transform(test_df['TEXT'])
cv_text = tfidfVectorizer.transform(cv_df['TEXT'])
```

# **Correctly Classified point**

```
In [124]:
```

for alpha = 0.001

```
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 state=42)
  clf.fit(train_x_onehotCoding, train_y)
  sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
  sig clf.fit(train x onehotCoding, train y)
 sig clf probs = sig clf.predict proba(cv x onehotCoding)
 cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
  # to avoid rounding error while multiplying probabilites we use log-probability estimates
  print("Log Loss:",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
 ax.annotate((alpha[i], str(txt)), (alpha[i], cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', ran
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_lo
ss(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, p
redict_y, labels=clf.classes_, eps=1e-15))
for alpha = 1e-06
Log Loss: 1.1332607894229252
for alpha = 1e-05
Log Loss: 1.0610327461109685
for alpha = 0.0001
Log Loss: 1.0138413983629366
```

Log Loss: 1.042474659076955

for alpha = 0.01

Log Loss : 1.217843678634886

for alpha = 0.1

Log Loss : 1.6868047353360354

for alpha = 1

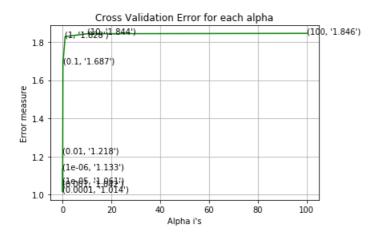
Log Loss: 1.8284832711964811

for alpha = 10

Log Loss: 1.843791685699172

for alpha = 100

Log Loss: 1.8455839386011739



For values of best alpha = 0.0001 The train log loss is: 0.45786829431688403

For values of best alpha = 0.0001 The cross validation log loss is: 1.0138413983629366

For values of best alpha = 0.0001 The test log loss is: 0.9218869949078555

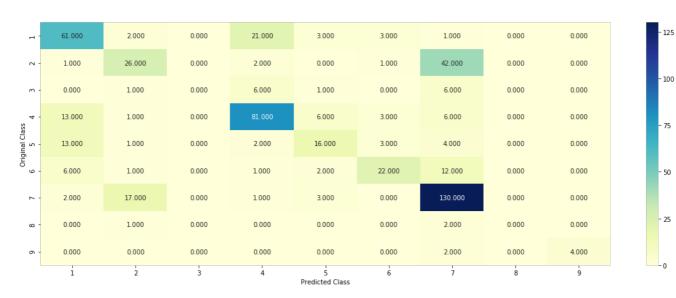
#### In [113]:

clf = SGDClassifier(class\_weight='balanced', alpha=alpha[best\_alpha], penalty='12', loss='log', ran
dom\_state=42)
predict\_and\_plot\_confusion\_matrix(train\_x\_onehotCoding, train\_y, cv\_x\_onehotCoding, cv\_y, clf)

Log loss: 1.0138413983629366

Number of mis-classified points : 0.3609022556390977

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



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

гı -	0.635	0.040	0.184	0.097	0.094	0.005
- 2	0.010		0.018	0.000	0.031	0.205
m -	0.000	0.020	0.053	0.032	0.000	0.029

- 1.0 - 0.8



Predicted Class

# LOgistic regrssion without class imbalancing

```
In [114]:
alpha = [10 ** x for x in range(-6, 3)]
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))
  # to avoid rounding error while multiplying probabilites we use log-probability estimates
 print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
  ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', ran
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)
nrint (!For values of heet alnha = ! alnha[heet alnha] "The cross validation log loss is." log lo
```

```
ss(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, p redict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-06

Log Loss: 1.1644814258435812

for alpha = 1e-05

Log Loss : 1.0715194644434234

for alpha = 0.0001

Log Loss : 1.0263873522848197

for alpha = 0.001

Log Loss: 1.1099980263917337

for alpha = 0.01

Log Loss: 1.4521864672252107

for alpha = 0.1

Log Loss : 1.8289766949862687

for alpha = 1

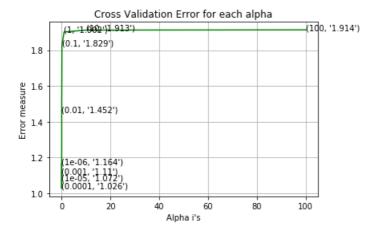
Log Loss: 1.9024470396998319

for alpha = 10

Log Loss: 1.9128041103133233

for alpha = 100

Log Loss: 1.9140498222870896



For values of best alpha = 0.0001 The train log loss is: 0.45786829431688403For values of best alpha = 0.0001 The cross validation log loss is: 1.0138413983629366For values of best alpha = 0.0001 The test log loss is: 0.9218869949078555

#### In [115]:

clf = SGDClassifier( alpha=alpha[best\_alpha], penalty='l2', loss='log', random\_state=42)
predict\_and\_plot\_confusion\_matrix(train\_x\_onehotCoding, train\_y, cv\_x\_onehotCoding, cv\_y, clf)

125

- 100

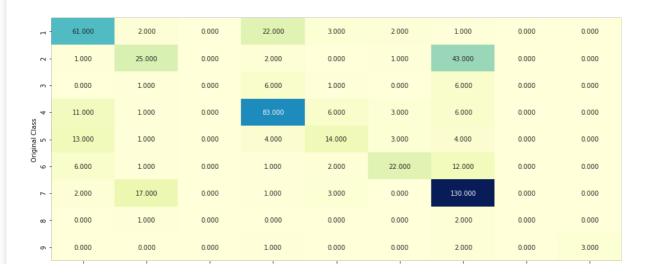
75

- 25

Log loss : 1.0263873522848197

Number of mis-classified points : 0.36466165413533835

----- Confusion matrix



1 2 3 4 5 6 7 8 9
Predicted Class

- 0.8

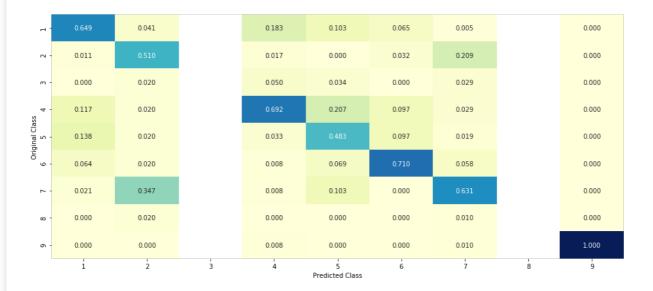
- 0.6

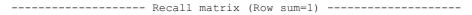
- 0.4

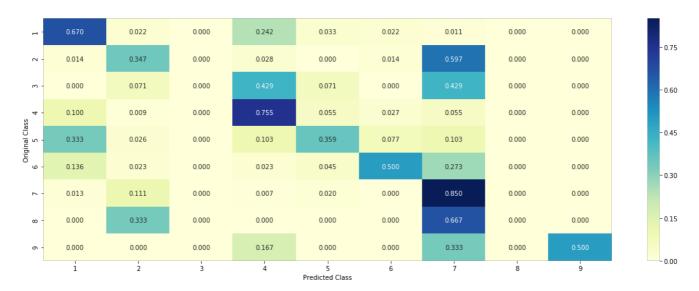
- 0.2

-00

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







#### In [130]:

ptable = PrettyTable()
ptable.field\_names=["Model Name","Train","CV","Test","% Misclassified Points"]
ptable.add\_row(["Logistic Regression With Class balancing","0.45","1.0","0.92","35"])
ptable.add\_row(["Logistic Regression With Class balancing","0.44","1.0","0.92","34"])
print(ptable)

+				% Misclassified Points
Logistic Regression With Class balancing     Logistic Regression With Class balancing	0.45	1.0	0.92	35