# 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-almosteveryone-who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25 (https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almosteveryone-who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25)
- https://www.youtube.com/watch?v=UwbuW7oK8rk (https://www.youtube.com/watch?v=UwbuW7oK8rk)
- https://www.youtube.com/watch?v=qxXRKVompl8 (https://www.youtube.com/watch? v=qxXRKVompl8)

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

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

## 2. Machine Learning Problem Formulation

#### 2.1. Data

#### 2.1.1. Data Overview

- Source: <a href="https://www.kaggle.com/c/msk-redefining-cancer-treatment/data">https://www.kaggle.com/c/msk-redefining-cancer-treatment/data</a>
   (<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 class ified into => Multi class classification problem

#### 2.2.2. Performance Metric

Source: <a href="https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation">https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation</a>)

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

#### Metric(s):

- · Multi class log-loss
- Confusion matrix

### 2.2.3. Machine Learing Objectives and Constraints

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

#### Constraints:

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

## 2.3. Train, CV and Test Datasets

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

## 3. Exploratory Data Analysis

```
In [1]: from google.colab import drive
drive.mount('/content/drive')
```

Drive already mounted at /content/drive; to attempt to forcibly remount, call d rive.mount("/content/drive", force\_remount=True).

```
In [2]:
        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
```

/usr/local/lib/python3.6/dist-packages/sklearn/utils/deprecation.py:144: Future Warning: The sklearn.metrics.classification module is deprecated in version 0. 22 and will be removed in version 0.24. The corresponding classes / functions s hould instead be imported from sklearn.metrics. Anything that cannot be imported from sklearn.metrics is now part of the private API.

warnings.warn(message, FutureWarning)

/usr/local/lib/python3.6/dist-packages/sklearn/externals/six.py:31: FutureWarni ng: The module is deprecated in version 0.21 and will be removed in version 0.2 3 since we've dropped support for Python 2.7. Please rely on the official versi on of six (https://pypi.org/project/six/).

"(https://pypi.org/project/six/).", FutureWarning)

/usr/local/lib/python3.6/dist-packages/sklearn/utils/deprecation.py:144: Future Warning: The sklearn.neighbors.base module is deprecated in version 0.22 and w ill be removed in version 0.24. The corresponding classes / functions should in stead be imported from sklearn.neighbors. Anything that cannot be imported from sklearn.neighbors is now part of the private API.

warnings.warn(message, FutureWarning)

## 3.1. Reading Data

#### 3.1.1. Reading Gene and Variation Data

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

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

Fields are

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

#### 3.1.2. Reading Text Data

```
In [4]: # note the seprator in this file
         data_text =pd.read_csv("/content/drive/My Drive/Colab Notebooks/training_text",se
         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[4]:
             ID
                                                   TEXT
          0
             0
                 Cyclin-dependent kinases (CDKs) regulate a var...
             1
                   Abstract Background Non-small cell lung canc...
                   Abstract Background Non-small cell lung canc...
          2
             3 Recent evidence has demonstrated that acquired...
```

#### 3.1.3. Preprocessing of text

Oncogenic mutations in the monomeric Casitas B...

```
import nltk
In [5]:
        nltk.download('stopwords')
        [nltk_data] Downloading package stopwords to /root/nltk_data...
        [nltk data]
                      Package stopwords is already up-to-date!
Out[5]: True
        # loading stop words from nltk library
In [0]:
        stop words = set(stopwords.words('english'))
        def nlp_preprocessing(total_text, index, column):
            if type(total_text) is not int:
                string = ""
                # replace every special char with space
                total_text = re.sub('[^a-zA-Z0-9\n]', ' ', total_text)
                # replace multiple spaces with single space
                total_text = re.sub('\s+',' ', total_text)
                # converting all the chars into lower-case.
                total_text = total_text.lower()
                for word in total_text.split():
                # if the word is a not a stop word then retain that word from the data
                    if not word in stop words:
                         string += word + " "
                data text[column][index] = string
```

```
In [7]: #text processing stage.
          start_time = time.clock()
          for index, row in data text.iterrows():
               if type(row['TEXT']) is str:
                   nlp_preprocessing(row['TEXT'], index, 'TEXT')
               else:
                   print("there is no text description for id:",index)
          print('Time took for preprocessing the text :',time.clock() - start time, "second
          there is no text description for id: 1109
          there is no text description for id: 1277
          there is no text description for id: 1407
          there is no text description for id: 1639
          there is no text description for id: 2755
          Time took for preprocessing the text: 26.29429499999998 seconds
          #merging both gene variations and text data based on ID
 In [8]:
          result = pd.merge(data, data text,on='ID', how='left')
          result.head()
 Out[8]:
              ID
                                  Variation Class
                    Gene
                                                                                     TEXT
           0
                 FAM58A
                         Truncating Mutations
                                               1
                                                    cyclin dependent kinases cdks regulate variety...
                     CBL
                                     W802*
                                                   abstract background non small cell lung cancer...
              1
                                               2
              2
                     CBL
                                    Q249E
                                                   abstract background non small cell lung cancer...
                                               2
                     CBL
                                    N454D
                                               3 recent evidence demonstrated acquired uniparen...
              3
                     CBL
                                     L399V
                                                  oncogenic mutations monomeric casitas b lineag...
 In [9]:
          result[result.isnull().any(axis=1)]
 Out[9]:
                   ID
                        Gene
                                       Variation Class TEXT
           1109
                1109
                       FANCA
                                        S1088F
                                                        NaN
           1277 1277
                      ARID5B
                              Truncating Mutations
                                                        NaN
           1407 1407
                                         K508M
                                                        NaN
                       FGFR3
           1639
                1639
                         FLT1
                                     Amplification
                                                        NaN
           2755 2755
                        BRAF
                                         G596C
                                                        NaN
          result.loc[result['TEXT'].isnull(), 'TEXT'] = result['Gene'] +' '+result['Variation
 In [0]:
In [11]: result[result['ID']==1109]
Out[11]:
                        Gene Variation Class
                                                     TEXT
           1109 1109 FANCA
                               S1088F
                                           1 FANCA S1088F
```

### 3.1.4. Test, Train and Cross Validation Split

ס. ו.ד.ו. סףוונווווץ שמנמ ווונט נומווו, וכטו מווע טוטסט צמוועמנוטוו (טד.בט. וט*ן* 

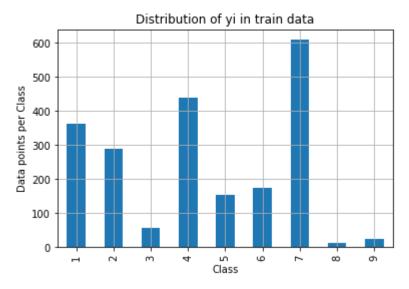
We split the data into train, test and cross validation data sets, preserving the ratio of class distribution in the original data set

```
In [13]: print('Number of data points in train data:', train_df.shape[0])
    print('Number of data points in test data:', test_df.shape[0])
    print('Number of data points in cross validation data:', cv_df.shape[0])

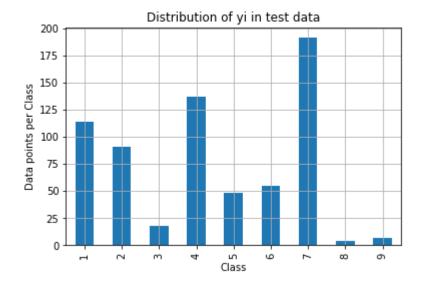
Number of data points in train data: 2124
    Number of data points in test data: 665
    Number of data points in cross validation data: 532
```

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

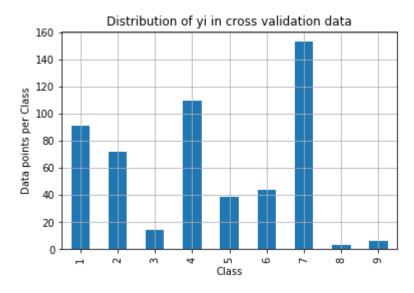
```
In [14]: # it returns a dict, keys as class labels and values as the number of data points
         train_class_distribution = train_df['Class'].value_counts().sort_index()
         test class distribution = test df['Class'].value counts().sort index()
         cv class distribution = cv df['Class'].value counts().sort index()
         my colors = 'rgbkymc'
         train class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in train data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsor
         # -(train class distribution.values): the minus sign will give us in decreasing
         sorted_yi = np.argsort(-train_class_distribution.values)
         for i in sorted vi:
             print('Number of data points in class', i+1, ':', train class distribution.val
         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.argsor
         # -(train class distribution.values): the minus sign will give us in decreasing of
         sorted_yi = np.argsort(-test_class_distribution.values)
         for i in sorted vi:
             print('Number of data points in class', i+1, ':',test_class_distribution.val
         print('-'*80)
         my colors = 'rgbkymc'
         cv class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in cross validation data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsor
         # -(train class distribution.values): the minus sign will give us in decreasing
         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.value
```



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



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



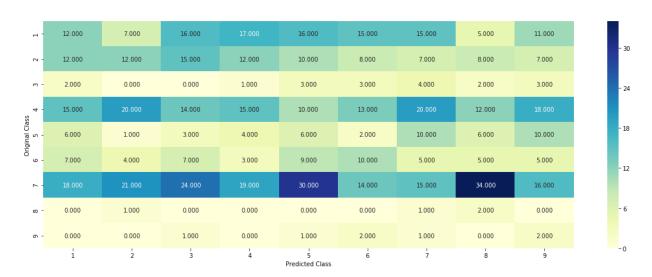
```
Number of data points in class 7 : 153 ( 28.759 %) Number of data points in class 4 : 110 ( 20.677 %) Number of data points in class 1 : 91 ( 17.105 %) Number of data points in class 2 : 72 ( 13.534 %) Number of data points in class 6 : 44 ( 8.271 %) Number of data points in class 5 : 39 ( 7.331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

## 3.2 Prediction using a 'Random' Model

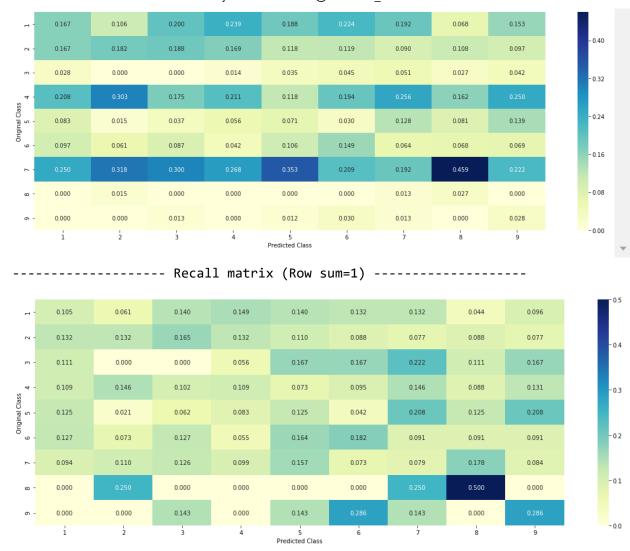
In a 'Random' Model, we generate the NINE class probabilites randomly such that they sum to 1.

```
In [0]: # 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
            A = (((C.T)/(C.sum(axis=1))).T)
            #divid each element of the confusion matrix with the sum of elements in that
            \# C = [[1, 2],
                  [3, 4]]
             \# C.T = [[1, 3],
                     [2, 4]]
            # C.sum(axis = 1) axis=0 corresponds to columns and axis=1 corresponds to rol
            # 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
            \# C = [[1, 2],
                  [3, 4]]
            # C.sum(axis = 0) axis=0 corresonds to columns and axis=1 corresponds to rol
            # 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, ytic
             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, ytic
             plt.xlabel('Predicted Class')
             plt.ylabel('Original Class')
            plt.show()
            # representing B in heatmap format
             print("-"*20, "Recall matrix (Row sum=1)", "-"*20)
             plt.figure(figsize=(20,7))
            sns.heatmap(A, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, ytic
             plt.xlabel('Predicted Class')
            plt.ylabel('Original Class')
             plt.show()
```

```
In [192]: # 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
          # 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_pre-
          # 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_)
          predicted y =np.argmax(test predicted y, axis=1)
          plot_confusion_matrix(y_test, predicted_y+1)
```



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



## 3.3 Univariate Analysis

```
In [0]: # 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 tre
        # build a vector (1*9) , the first element = (number of times it occured in class
        # gv_dict is like a look up table, for every gene it store a (1*9) representation
        # 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 'qv fea'
        # return 'gv_fea'
        # -----
        # get_gv_fea_dict: Get Gene varaition Feature Dict
        def get_gv_fea_dict(alpha, feature, df):
            # value count: it contains a dict like
            # print(train_df['Gene'].value_counts())
            # output:
            #
                     {BRCA1
                                  174
                      TP53
                                  106
            #
                      EGFR
                                  86
                                  75
            #
                      BRCA2
            #
                      PTEN
                                  69
            #
                      KIT
                                  61
            #
                      BRAF
                                  60
                      ERBB2
                                  47
            #
                      PDGFRA
                                  46
                      ...}
            # print(train_df['Variation'].value_counts())
            # output:
            # {
            # Truncating Mutations
                                                        63
            # Deletion
                                                        43
            # Amplification
                                                        43
            # Fusions
                                                        22
            # Overexpression
                                                         3
            # E17K
                                                         3
            # 061L
                                                         3
            # S222D
                                                         2
            # P130S
                                                         2
            # ...
            # }
            value_count = train_df[feature].value_counts()
            # gv dict : Gene Variation Dict, which contains the probability array for each
            gv_dict = dict()
            # denominator will contain the number of time that particular feature occured
            for i, denominator in value count.items():
                # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to
                # vec is 9 diamensional vector
                vec = []
```

```
for k in range(1,10):
            # print(train_df.loc[(train_df['Class']==1) & (train_df['Gene']=='BR(
                      ΙD
                           Gene
                                            Variation Class
                    2470 BRCA1
                                               S1715C
            # 2470
                                                           1
            # 2486 2486 BRCA1
                                               S1841R
                                                           1
            # 2614 2614 BRCA1
                                                           1
                                                  M1R
            # 2432 2432 BRCA1
                                               L1657P
                                                           1
            # 2567 2567 BRCA1
                                               T1685A
                                                           1
            # 2583 2583 BRCA1
                                               E1660G
                                                           1
            # 2634 2634 BRCA1
                                               W1718L
                                                           1
            # cls cnt.shape[0] will return the number of rows
            cls cnt = train df.loc[(train df['Class']==k) & (train df[feature]==
            # cls cnt.shape[0](numerator) will contain the number of time that pe
            vec.append((cls cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
        # we are adding the gene/variation to the dict as key and vec as value
        gv dict[i]=vec
    return gv_dict
# Get Gene variation feature
def get gv feature(alpha, feature, df):
    # print(qv dict)
    #
          {'BRCA1': [0.20075757575757575, 0.0378787878787878, 0.06818181818181818
    #
           'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918]
    #
           'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.06818181
           'BRCA2': [0.13333333333333333, 0.0606060606060608, 0.06060606060606
           'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106
           'KIT': [0.066225165562913912, 0.25165562913907286, 0.0728476821192052
           'BRAF': [0.0666666666666666666, 0.179999999999999, 0.0733333333333333
    #
    #
   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()
    # qv fea: Gene variation feature, it will contain the feature for each feature
    gv fea = []
   # for every feature values in the given data frame we will check if it is the
    # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to qv fea
    for index, row in df.iterrows():
        if row[feature] in dict(value count).keys():
            gv fea.append(gv dict[row[feature]])
        else:
            gv fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
              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?

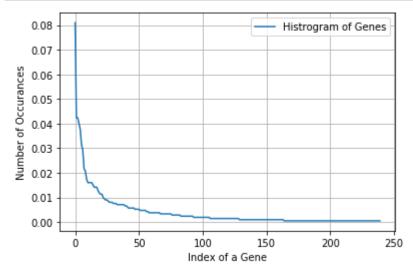
Ans. Gene is a categorical variable

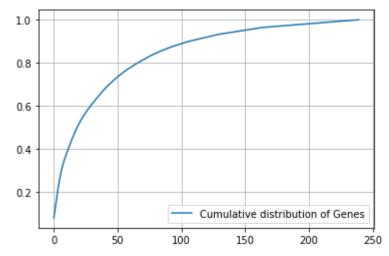
**Q2.** How many categories are there and How they are distributed?

```
In [194]:
          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: 240
          BRCA1
                     172
          TP53
                      90
                      90
          EGFR
          PTEN
                      85
          BRCA2
                      80
          BRAF
                      67
          KIT
                      62
          ALK
                      46
          ERBB2
                      44
          PDGFRA
                      37
          Name: Gene, dtype: int64
In [195]: print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in
```

Ans: There are 240 different categories of genes in the train data, and they are distibuted as follows

```
In [196]: 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()
```





#### 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 codina

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
          # test gene feature
          test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", test_d
          # cross validation gene feature
          cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", cv_df))
In [199]: print("train gene feature responseCoding is converted feature using respone codi
          train gene feature responseCoding is converted feature using respone coding met
          hod. The shape of gene feature: (2124, 9)
  In [0]: # tfidf encoding of Gene feature.
          from sklearn.feature extraction.text import TfidfVectorizer
          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 [201]: train df['Gene'].head()
Out[201]: 2823
                   BRCA2
          3284
                     RET
          1493
                   FGFR2
          838
                    ABL1
          3094
                  NOTCH1
          Name: Gene, dtype: object
```

```
In [202]:
           gene_vectorizer.get_feature_names()
Out[202]: ['abl1',
             'acvr1',
             'ago2',
             'akt1',
             'akt2',
             'akt3',
             'alk',
             'apc',
             'ar',
             'araf'
             'arid1b',
             'arid2',
             'arid5b',
             'asxl1',
             'asx12',
             'atm',
             'atr',
             'atrx',
             'aurka',
In [203]:
           print("train_gene_feature_onehotCoding is converted feature using one-hot encoding)
```

train\_gene\_feature\_onehotCoding is converted feature using one-hot encoding met hod. The shape of gene feature: (2124, 240)

## **Q4.** How good is this gene feature in predicting y\_i?

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

```
In [204]: alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
          # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gene
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_int@
          # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rat
          # 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 Grad
          \# 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")
              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
              print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict
          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_st
          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:"
          predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
          predict_y = sig_clf.predict_proba(test_gene_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",
```

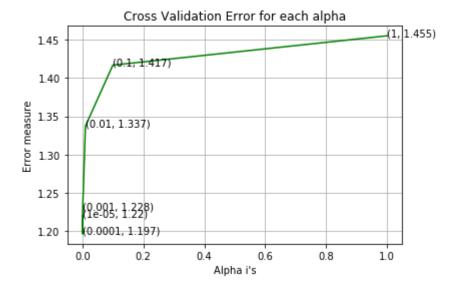
For values of alpha = 1e-05 The log loss is: 1.2196862811575042 For values of alpha = 0.0001 The log loss is: 1.196641798358647

```
For values of alpha = 0.001 The log loss is: 1.2280511960589267

For values of alpha = 0.01 The log loss is: 1.3372997135932572

For values of alpha = 0.1 The log loss is: 1.416848537161832

For values of alpha = 1 The log loss is: 1.4551437846180135
```



For values of best alpha = 0.0001 The train log loss is: 0.9616445599819275
For values of best alpha = 0.0001 The cross validation log loss is: 1.19664179
8358647
For values of best alpha = 0.0001 The test log loss is: 1.2583283581324405

**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 [205]: print("Q6. How many data points in Test and CV datasets are covered by the ", un:
    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_print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(
```

Q6. How many data points in Test and CV datasets are covered by the 240 genes in train dataset?

Ans

- 1. In test data 647 out of 665 : 97.29323308270676
- 2. In cross validation data 521 out of 532 : 97.93233082706767

### 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?

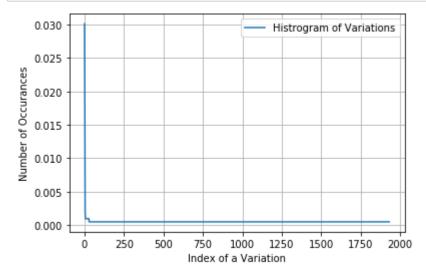
```
In [206]: unique_variations = train_df['Variation'].value_counts()
    print('Number of Unique Variations :', unique_variations.shape[0])
# the top 10 variations that occured most
    print(unique_variations.head(10))
```

Number of Unique Variations: 1932 Truncating\_Mutations Deletion 45 38 Amplification **Fusions** 21 **G12V** 4 T58I 3 Y42C 2 2 M1R 2 Q61R 2 **G67R** Name: Variation, dtype: int64

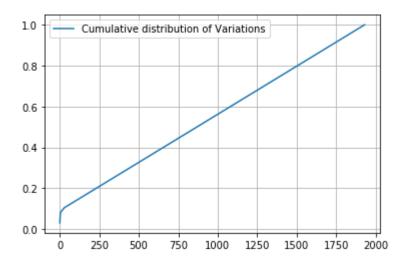
```
In [207]: print("Ans: There are", unique_variations.shape[0] ,"different categories of variations.shape[0] ,"
```

Ans: There are 1932 different categories of variations in the train data, and they are distibuted as follows

```
In [208]: 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()
```



[0.03013183 0.05131827 0.06920904 ... 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")
    # test gene feature
    test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation")
    # cross validation gene feature
    cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation")
```

]

```
In [211]: print("train_variation_feature_responseCoding is a converted feature using the retrain_variation_feature_responseCoding is a converted feature using the response coding method. The shape of Variation feature: (2124, 9)
```

In [0]: # one-hot encoding of variation feature.
 variation\_vectorizer = TfidfVectorizer()
 train\_variation\_feature\_onehotCoding = variation\_vectorizer.fit\_transform(train\_otext\_variation\_feature\_onehotCoding = variation\_vectorizer.transform(test\_df['Variation\_vectorizer.transform(cv\_df

In [213]: print("train\_variation\_feature\_onehotEncoded is converted feature using the onne

train\_variation\_feature\_onehotEncoded is converted feature using the onne-hot e ncoding method. The shape of Variation feature: (2124, 1962)

**Q10.** How good is this Variation feature in predicting y i?

Let's build a model just like the earlier!

```
In [214]: alpha = [10 ** x for x in range(-5, 1)]
          # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gene
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_int@
          # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning ra
          # 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 Grad
          \# 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
              print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict
          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_st
          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:"
          predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best alpha], "The cross validation log
          predict y = sig clf.predict proba(test variation feature onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",
```

```
For values of alpha = 1e-05 The log loss is: 1.7268113070391837

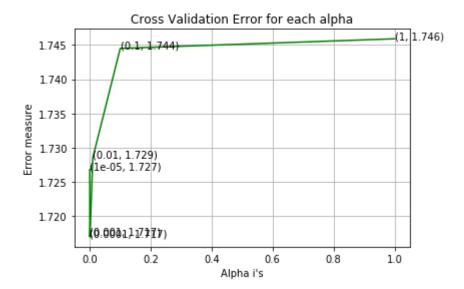
For values of alpha = 0.0001 The log loss is: 1.7169873046873894

For values of alpha = 0.001 The log loss is: 1.7173715562297662

For values of alpha = 0.01 The log loss is: 1.7285280214950953

For values of alpha = 0.1 The log loss is: 1.7444983395011235

For values of alpha = 1 The log loss is: 1.7458978788999457
```



For values of best alpha = 0.0001 The train log loss is: 0.666138849940641

For values of best alpha = 0.0001 The cross validation log loss is: 1.71698730
46873894

For values of best alpha = 0.0001 The test log loss is: 1.7095908167434941

# **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 [215]: print("Q12. How many data points are covered by total ", unique_variations.shape
    test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation']))
    cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'])))].shap print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(
```

Q12. How many data points are covered by total  $\,$  1932  $\,$  genes in test and cross  $\,$  alidation data sets?

Ans

- 1. In test data 78 out of 665 : 11.729323308270677
- 2. In cross validation data 49 out of 532 : 9.210526315789473

### 3.2.3 Univariate Analysis on Text Feature

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

```
In [218]: # building a CountVectorizer with all the words that occured minimum 3 times in text_vectorizer = CountVectorizer(min_df=3,max_features=1000)
    train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT']
    # getting all the feature names (words)
    train_text_features= text_vectorizer.get_feature_names()

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

# zip(list(text_features),text_fea_counts) will zip a word with its number of tin
    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)
```

- In [0]: #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\_text\_feature\_responseCoding = (test\_text\_feature\_responseCoding.T/test\_text\_cv\_text\_feature\_responseCoding = (cv\_text\_feature\_responseCoding.T/cv\_text\_feature\_responseCoding.
- In [0]: # don't forget to normalize every feature
   train\_text\_feature\_onehotCoding = normalize(train\_text\_feature\_onehotCoding, axi:

  # 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=

  # 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 [224]: # Number of words for a given frequency. print(Counter(sorted text occur))

Counter({3516: 3, 3242: 3, 2947: 3, 2851: 3, 2663: 3, 2646: 3, 9744: 2, 8276: 2, 8169: 2, 8079: 2, 6024: 2, 5997: 2, 5475: 2, 5438: 2, 5321: 2, 5285: 2, 478 5: 2, 4542: 2, 4432: 2, 4361: 2, 4194: 2, 4054: 2, 4023: 2, 3995: 2, 3853: 2, 3 821: 2, 3819: 2, 3718: 2, 3696: 2, 3590: 2, 3540: 2, 3527: 2, 3471: 2, 3442: 2, 3435: 2, 3390: 2, 3372: 2, 3368: 2, 3339: 2, 3277: 2, 3228: 2, 3220: 2, 3104: 2, 2853: 2, 2712: 2, 2708: 2, 2688: 2, 2679: 2, 2664: 2, 2649: 2, 2614: 2, 1562 54: 1, 119335: 1, 79775: 1, 68849: 1, 68432: 1, 68414: 1, 67340: 1, 64430: 1, 6 3845: 1, 56703: 1, 54721: 1, 50009: 1, 49626: 1, 47017: 1, 46396: 1, 44287: 1, 42877: 1, 42723: 1, 42377: 1, 42072: 1, 40889: 1, 40792: 1, 39979: 1, 39166: 1, 38853: 1, 38182: 1, 36492: 1, 36127: 1, 35957: 1, 35597: 1, 35027: 1, 34475: 1, 33849: 1, 33259: 1, 32816: 1, 31506: 1, 30344: 1, 29572: 1, 28174: 1, 26612: 1, 26489: 1, 26463: 1, 26292: 1, 25486: 1, 24859: 1, 24831: 1, 24715: 1, 24555: 1, 24369: 1, 24189: 1, 23988: 1, 23590: 1, 23021: 1, 22483: 1, 22444: 1, 22318: 1, 22182: 1, 21707: 1, 21556: 1, 21055: 1, 21040: 1, 20884: 1, 20616: 1, 20475: 1, 20021: 1, 19721: 1, 19706: 1, 19560: 1, 19510: 1, 19459: 1, 19326: 1, 19065: 1, 18907: 1, 18873: 1, 18662: 1, 18621: 1, 18291: 1, 18263: 1, 18168: 1, 18054: 1, 18022: 1, 17959: 1, 17740: 1, 17715: 1, 17623: 1, 17616: 1, 17538: 1, 17306: 1, 17221: 1, 17205: 1, 17196: 1, 17183: 1, 17163: 1, 17115: 1, 16999: 1, 16630: 1, 16266: 1, 16242: 1, 16228: 1, 16058: 1, 15896: 1, 15863: 1, 15846: 1, 15828: 1, 15751: 1, 15649: 1, 15615: 1, 15418: 1, 15296: 1, 15057: 1, 14985: 1, 14934: 1, 14834: 1, 14736: 1, 14702: 1, 14641: 1, 14602: 1, 14553: 1, 14525: 1, 14288: 1, 14251: 1, 14197: 1, 13948: 1, 13714: 1, 13669: 1, 13498: 1, 13481: 1, 13330: 1, 13326: 1, 13310: 1, 13288: 1, 13179: 1, 13168: 1, 13123: 1, 13110: 1, 13050: 1, 12956: 1, 12921: 1, 12799: 1, 12765: 1, 12715: 1, 12669: 1, 12621: 1, 12620: 1, 12581: 1, 12515: 1, 12466: 1, 12442: 1, 12437: 1, 12425: 1, 12392: 1, 12383: 1, 12381: 1, 12352: 1, 12350: 1, 12332: 1, 12302: 1, 12249: 1, 12136: 1, 12095: 1, 12032: 1, 12016: 1, 12001: 1, 11991: 1, 11972: 1, 11967: 1, 11961: 1, 11942: 1, 11915: 1, 11765: 1, 11762: 1, 11722: 1, 11709: 1, 11644: 1, 11626: 1, 11503: 1, 11473: 1, 11414: 1, 11159: 1, 11145: 1, 11103: 1, 11057: 1, 11033: 1, 11022: 1, 10882: 1, 10875: 1, 10854: 1, 10833: 1, 10827: 1, 10807: 1, 10657: 1, 10622: 1, 10516: 1, 10430: 1, 10428: 1, 10341: 1, 10340: 1, 10251: 1, 10239: 1, 10111: 1, 10080: 1, 10024: 1, 10019: 1, 9992: 1, 9949: 1, 9941: 1, 9910: 1, 9892: 1, 989 1: 1, 9872: 1, 9797: 1, 9795: 1, 9559: 1, 9545: 1, 9518: 1, 9423: 1, 9410: 1, 9 404: 1, 9383: 1, 9354: 1, 9302: 1, 9300: 1, 9193: 1, 9191: 1, 9180: 1, 9158: 1, 9140: 1, 9124: 1, 9075: 1, 9036: 1, 9000: 1, 8991: 1, 8964: 1, 8945: 1, 8914: 1, 8899: 1, 8878: 1, 8854: 1, 8838: 1, 8708: 1, 8688: 1, 8659: 1, 8623: 1, 860 6: 1, 8548: 1, 8525: 1, 8487: 1, 8484: 1, 8444: 1, 8431: 1, 8430: 1, 8425: 1, 8 361: 1, 8338: 1, 8321: 1, 8303: 1, 8299: 1, 8296: 1, 8256: 1, 8240: 1, 8232: 1, 8220: 1, 8178: 1, 8175: 1, 8081: 1, 8057: 1, 8037: 1, 8020: 1, 7989: 1, 7927: 1, 7922: 1, 7905: 1, 7897: 1, 7892: 1, 7877: 1, 7863: 1, 7814: 1, 7810: 1, 780 4: 1, 7789: 1, 7776: 1, 7753: 1, 7744: 1, 7741: 1, 7732: 1, 7726: 1, 7723: 1, 7 667: 1, 7622: 1, 7591: 1, 7561: 1, 7559: 1, 7548: 1, 7527: 1, 7512: 1, 7487: 1, 7418: 1, 7369: 1, 7360: 1, 7358: 1, 7357: 1, 7355: 1, 7299: 1, 7290: 1, 7288: 1, 7277: 1, 7226: 1, 7219: 1, 7215: 1, 7214: 1, 7197: 1, 7165: 1, 7144: 1, 713 6: 1, 7129: 1, 7123: 1, 7117: 1, 7110: 1, 7097: 1, 7079: 1, 7070: 1, 7060: 1, 7 018: 1, 6988: 1, 6969: 1, 6968: 1, 6954: 1, 6941: 1, 6887: 1, 6876: 1, 6851: 1, 6842: 1, 6828: 1, 6826: 1, 6818: 1, 6802: 1, 6798: 1, 6783: 1, 6767: 1, 6756: 1, 6745: 1, 6731: 1, 6729: 1, 6710: 1, 6695: 1, 6693: 1, 6686: 1, 6668: 1, 664 9: 1, 6636: 1, 6635: 1, 6617: 1, 6574: 1, 6565: 1, 6521: 1, 6504: 1, 6500: 1, 6 495: 1, 6447: 1, 6429: 1, 6421: 1, 6419: 1, 6409: 1, 6407: 1, 6402: 1, 6365: 1, 6347: 1, 6326: 1, 6313: 1, 6304: 1, 6302: 1, 6301: 1, 6279: 1, 6258: 1, 6255: 1, 6244: 1, 6241: 1, 6230: 1, 6222: 1, 6218: 1, 6211: 1, 6210: 1, 6204: 1, 619 6: 1, 6179: 1, 6162: 1, 6137: 1, 6100: 1, 6058: 1, 6048: 1, 6042: 1, 6036: 1, 6 034: 1, 6030: 1, 6004: 1, 6002: 1, 5999: 1, 5995: 1, 5993: 1, 5962: 1, 5949: 1,

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```
In [225]: # Train a Logistic regression+Calibration model using text features whicha re on
          alpha = [10 ** x for x in range(-5, 1)]
          # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gene
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_inte
          # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rat
          # 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 Grad
                       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
              print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict)
          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_st
          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:"
          predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best alpha], "The cross validation log
          predict y = sig clf.predict proba(test text feature onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",
```

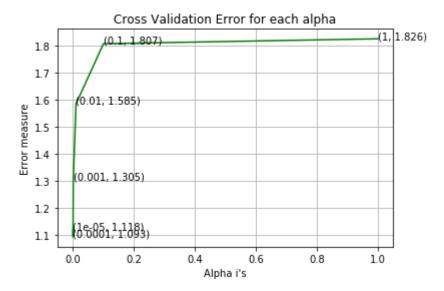
```
For values of alpha = 0.0001 The log loss is: 1.092857045159537

For values of alpha = 0.001 The log loss is: 1.3046340776271625

For values of alpha = 0.01 The log loss is: 1.5850821003235362

For values of alpha = 0.1 The log loss is: 1.807413747288979

For values of alpha = 1 The log loss is: 1.825519846312339
```



For values of best alpha = 0.0001 The train log loss is: 0.9420862854495291
For values of best alpha = 0.0001 The cross validation log loss is: 1.09285704
5159537
For values of best alpha = 0.0001 The test log loss is: 1.2697506177586746

# **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 = CountVectorizer(min_df=3)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

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

```
In [227]: 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 total content.")
```

3.504 % of word of test data appeared in train data 4.028 % of word of Cross Validation appeared in train data

## 4. Machine Learning Models

```
In [0]: #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 below
        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)
        plot_confusion_matrix(test_y, pred_y)
In [0]: def report_log_loss(train_x, train_y, test_x, test_y, clf):
```

```
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=1e-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'])
            fea1_len = len(gene_vec.get_feature_names())
            fea2 len = len(var count vec.get feature names())
            word present = 0
            for i,v in enumerate(indices):
                 if (v < fea1 len):</pre>
                     word = gene_vec.get_feature_names()[v]
                     yes no = True if word == gene else False
                     if yes no:
                         word_present += 1
                         print(i, "Gene feature [{}] present in test data point [{}]".for
                 elif (v < fea1_len+fea2_len):</pre>
                     word = var_vec.get_feature_names()[v-(fea1_len)]
                     yes no = True if word == var else False
                     if yes no:
                         word present += 1
                         print(i, "variation feature [{}] present in test data point [{}]
                 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 [{}]".for
             print("Out of the top ",no_features," features ", word_present, "are present
```

# Stacking the three types of features

```
In [0]: # merging gene, variance and text features
          # building train, test and cross validation data sets
          \# a = [[1, 2],
                 [3, 4]]
          #b = [[4, 5],
                 [6, 7]]
          # hstack(a, b) = [[1, 2, 4, 5],
                            [ 3, 4, 6, 7]]
          train gene var onehotCoding = hstack((train gene feature onehotCoding,train vari
          test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation)
          cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehotCoding)
          train x onehotCoding = hstack((train gene var onehotCoding, train text feature of
          train_y = np.array(list(train_df['Class']))
          test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_feature_onehot
          test_y = np.array(list(test_df['Class']))
          cv x onehotCoding = hstack((cv gene var onehotCoding, cv text feature onehotCoding)
          cv_y = np.array(list(cv_df['Class']))
          train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,tra
          test gene var responseCoding = np.hstack((test gene feature responseCoding,test
          cv gene var responseCoding = np.hstack((cv gene feature responseCoding,cv variat
          train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_fe
          test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature)
          cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding)
          print("One hot encoding features :")
In [232]:
          print("(number of data points * number of features) in train data = ", train_x_o
          print("(number of data points * number of features) in test data = ", test_x_onel
          print("(number of data points * number of features) in cross validation data =",
          One hot encoding features :
          (number of data points * number of features) in train data = (2124, 3202)
          (number of data points * number of features) in test data = (665, 3202)
          (number of data points * number of features) in cross validation data = (532, 3
          202)
In [233]:
          print(" Response encoding features :")
          print("(number of data points * number of features) in train data = ", train_x_r
          print("(number of data points * number of features) in test data = ", test_x_res
          print("(number of data points * number of features) in cross validation data =",
           Response encoding features :
          (number of data points * number of features) in train data = (2124, 27)
          (number of data points * number of features) in test data = (665, 27)
          (number of data points * number of features) in cross validation data = (532, 2
          7)
```

# 4.1. Base Line Model

# 4.1.1. Naive Bayes

4.1.1.1. Hyper parameter tuning

```
In [234]: # find more about Multinomial Naive base function here http://scikit-learn.org/s
          # 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/les
          # -----
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
          # 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/les
          alpha = [0.00001, 0.0001, 0.001, 0.1, 1, 10, 100,1000]
          cv log error array = []
          for i in alpha:
              print("for alpha =", i)
              clf = MultinomialNB(alpha=i)
              clf.fit(train_x_onehotCoding, train_y)
              sig clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig clf.fit(train x onehotCoding, train y)
              sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
              cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes ,
              # to avoid rounding error while multiplying probabilites we use log-probabil
              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:"
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",

for alpha = 1e-05
log_loss : 1 2424260280652782
```

Log Loss: 1.2434369280653783

for alpha = 0.0001

Log Loss: 1.242646740693285

for alpha = 0.001

Log Loss: 1.2405020810469456

for alpha = 0.1

Log Loss: 1.259943941894815

for alpha = 1

Log Loss : 1.3727355285780591

for alpha = 10

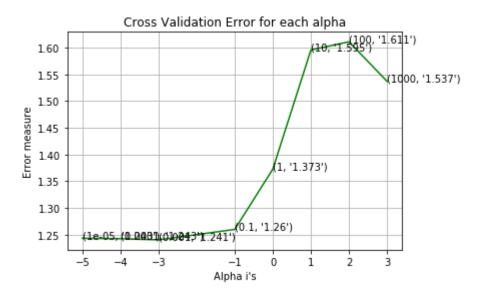
Log Loss: 1.595450541683481

for alpha = 100

Log Loss: 1.6107506046092936

for alpha = 1000

Log Loss: 1.5368193367112561



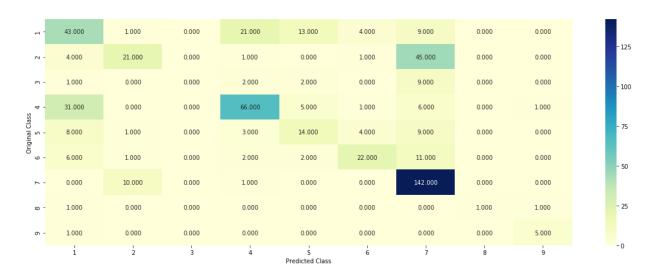
For values of best alpha = 0.001 The train log loss is: 0.4446663236298083

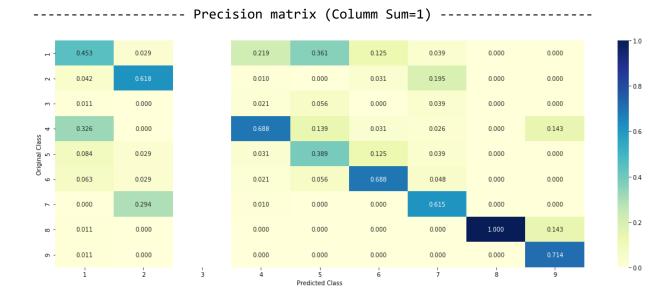
For values of best alpha = 0.001 The cross validation log loss is: 1.240502081
0469456

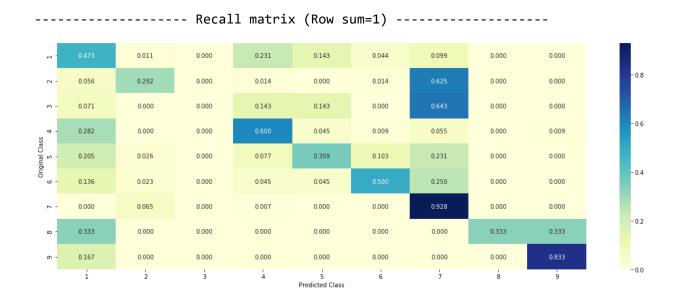
For values of best alpha = 0.001 The test log loss is: 1.2911328494660967

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

```
In [235]: # find more about Multinomial Naive base function here http://scikit-learn.org/s
          # 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/le
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample weight]) Fit the calibrated model
                                 Get parameters for this estimator.
          # get_params([deep])
          \# 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
          print("Log Loss :",log_loss(cv_y, sig_clf_probs))
          print("Number of missclassified point :", np.count_nonzero((sig_clf.predict(cv_x)
          plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray()))
```







#### 4.1.1.3. Feature Importance, Correctly classified point

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

# 4.2. K Nearest Neighbour Classification

# 4.2.1. Hyper parameter tuning

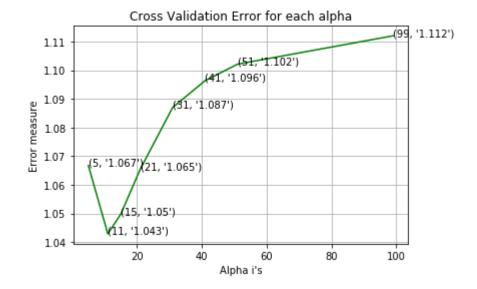
```
In [238]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/mode
          # default parameter
          # KNeighborsClassifier(n neighbors=5, weights='uniform', algorithm='auto', leaf :
          # metric='minkowski', metric params=None, n jobs=1, **kwarqs)
          # methods of
          # fit(X, y): Fit the model using X as training data and y as target values
          # predict(X):Predict the class labels for the provided data
          # predict_proba(X):Return probability estimates for the test data X.
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/le
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
          # 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_,
              # to avoid rounding error while multiplying probabilites we use log-probabil
              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:"
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",.
```

for alpha = 5
Log Loss : 1.0667280502334866
for alpha = 11
Log Loss : 1.042914009281993
for alpha = 15
Log Loss : 1.0497939647357155
for alpha = 21
Log Loss : 1.0654753018649226
for alpha = 31
Log Loss : 1.0869915420692449
for alpha = 41
Log Loss : 1.0963424982920769
for alpha = 51
Log Loss : 1.102095675318619

for alpha = 99 Log Loss : 1.1119909570876292

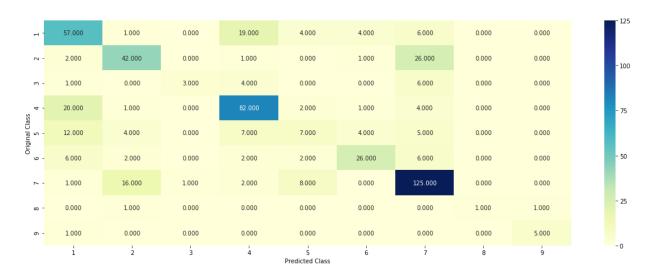


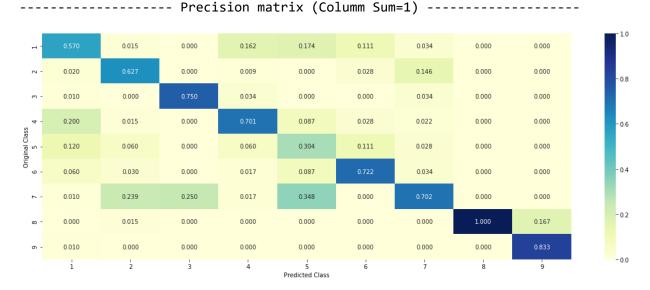
```
For values of best alpha = 11 The train log loss is: 0.5722617567923619
For values of best alpha = 11 The cross validation log loss is: 1.0429140092
81993
For values of best alpha = 11 The test log loss is: 1.167874383009327
```

# 4.2.2. Testing the model with best hyper paramters

Log loss: 1.042914009281993

Number of mis-classified points: 0.3458646616541353
------ Confusion matrix ------





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



### 4.2.3. Sample Query point -1

```
In [240]:
          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
          print("The ",alpha[best_alpha]," nearest neighbours of the test points belongs to
          print("Fequency of nearest points :",Counter(train y[neighbors[1][0]]))
          Predicted Class: 2
          Actual Class : 2
          The 11 nearest neighbours of the test points belongs to classes [2 2 2 2 2 7
          6 7 7 2 2]
          Fequency of nearest points : Counter({2: 7, 7: 3, 6: 1})
```

# 4.2.4. Sample Query Point-2

```
In [241]: 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()
    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)
    print("the k value for knn is",alpha[best_alpha],"and the nearest neighbours of 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 [7 7 7 2 7 7 7 2 7 2 7]
```

# 4.3. Logistic Regression

Fequency of nearest points : Counter({7: 8, 2: 3})

### 4.3.1. With Class balancing

#### 4.3.1.1. Hyper paramter tuning

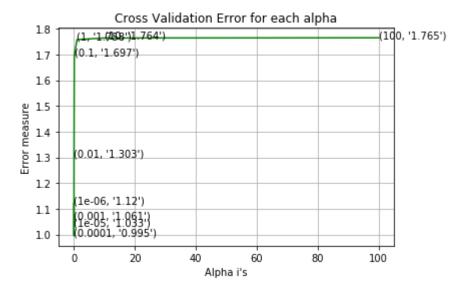
```
In [242]:
          # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gene
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit inte
          # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_ra
          # 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 Grad
          # predict(X) Predict class labels for samples in X.
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
          #-----
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
          # 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
              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_,
              # to avoid rounding error while multiplying probabilites we use log-probabil
              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='l.
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

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

for alpha = 1e-06Log Loss: 1.1196885392067795 for alpha = 1e-05Log Loss: 1.0334671073269235 for alpha = 0.0001Log Loss: 0.9949046441610732 for alpha = 0.001Log Loss: 1.0606835537447814 for alpha = 0.01Log Loss: 1.3026234324919055 for alpha = 0.1Log Loss: 1.6967828939993292 for alpha = 1Log Loss: 1.7579991217024282 for alpha = 10Log Loss: 1.7642823631430968 for alpha = 100

Log Loss: 1.7649934471556046



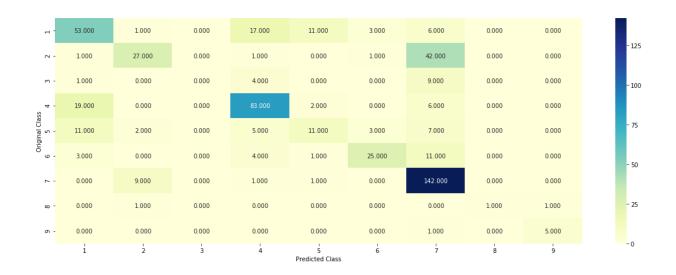
For values of best alpha = 0.0001 The train log loss is: 0.3820179887209377

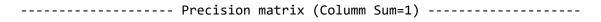
For values of best alpha = 0.0001 The cross validation log loss is: 0.99490464
41610732

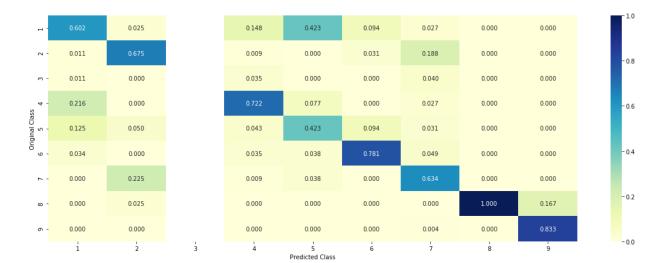
For values of best alpha = 0.0001 The test log loss is: 1.094996784841714

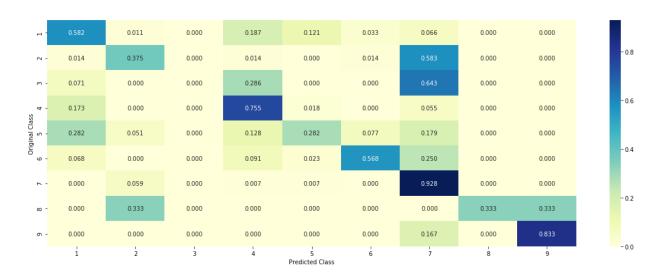
#### 4.3.1.2. Testing the model with best hyper paramters

# 









#### 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
                 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 No
```

#### 4.3.1.3.1. Correctly Classified point

```
In [245]: # from tabulate import tabulate
    clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='lcclf.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_one print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
    print("-"*50)
    get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df[
```

#### 4.3.1.3.2. Incorrectly Classified point

```
In [246]:
          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_one))
          print("Actual Class :", test y[test point index])
          indices = np.argsort(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df[
          Predicted Class: 7
          Predicted Class Probabilities: [[0.0119 0.1657 0.0404 0.0097 0.0606 0.0045 0.70
          14 0.0031 0.0029]]
          Actual Class : 2
          66 Text feature [10] present in test data point [True]
          Out of the top 500 features 1 are present in query point
```

### 4.3.2. Without Class balancing

#### 4.3.2.1. Hyper paramter tuning

```
In [247]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gener
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit inte
          # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_ra
          # 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 Grad
          \# predict(X) Predict class labels for samples in X.
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/le
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight])
Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict proba(X) Posterior probabilities of classification
          # video link:
          alpha = [10 ** x for x in range(-6, 1)]
          cv log error array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier(alpha=i, penalty='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_,
              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_st
```

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

for alpha = 1e-06

Log Loss: 1.136482140857177

for alpha = 1e-05

Log Loss : 1.0368376251084792

for alpha = 0.0001

Log Loss: 0.9938234479054255

for alpha = 0.001

Log Loss: 1.1143680745282043

for alpha = 0.01

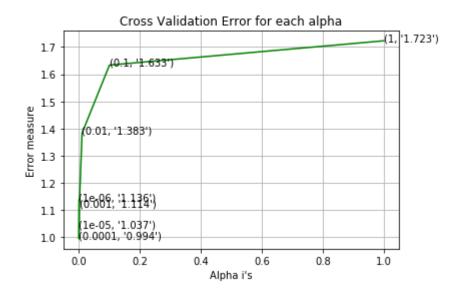
Log Loss: 1.3829721405841202

for alpha = 0.1

Log Loss: 1.6334785650563497

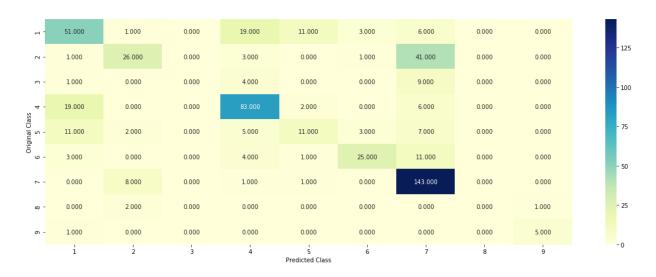
for alpha = 1

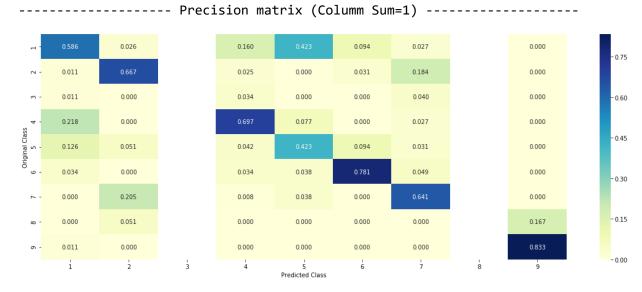
Log Loss: 1.722956626558638



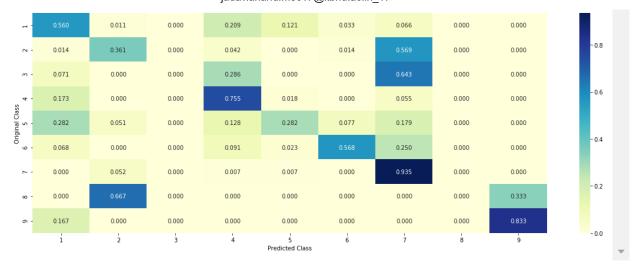
For values of best alpha = 0.0001 The train log loss is: 0.37658416351640145
For values of best alpha = 0.0001 The cross validation log loss is: 0.99382344
79054255
For values of best alpha = 0.0001 The test log loss is: 1.0852118785249474

### 4.3.2.2. Testing model with best hyper parameters





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



#### 4.3.2.3. Feature Importance, Correctly Classified point

```
In [249]:
          clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_st
          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_on
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df[
          Predicted Class: 2
          Predicted Class Probabilities: [[0.0699 0.7681 0.0158 0.0219 0.0228 0.0342 0.05
          19 0.0083 0.0072]]
          Actual Class : 2
          Out of the top 500 features 0 are present in query point
```

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

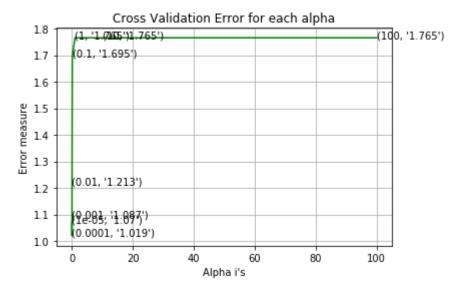
```
In [250]:
          test point index = 100
          no feature = 500
          predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_one))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df[
          Predicted Class : 7
          Predicted Class Probabilities: [[0.0119 0.1755 0.0479 0.0108 0.0613 0.0049 0.68
          19 0.0032 0.0025]]
          Actual Class : 2
          92 Text feature [10] present in test data point [True]
          Out of the top 500 features 1 are present in query point
```

# 4.4. Linear Support Vector Machines

### 4.4.1. Hyper paramter tuning

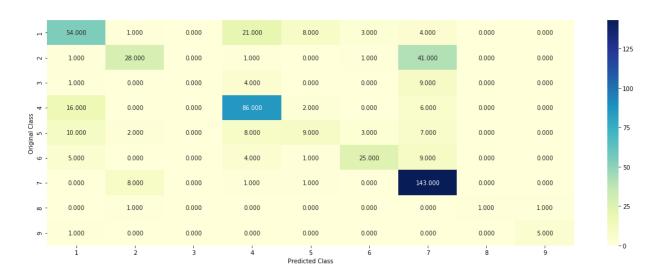
```
In [251]: # read more about support vector machines with linear kernals here http://scikit
          # -----
          # default parameters
          # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, pro
          # cache size=200, class weight=None, verbose=False, max iter=-1, decision function
          # Some of methods of SVM()
          # fit(X, y, [sample weight]) Fit the SVM model according to the given training
          \# predict(X) Perform classification on samples in X.
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/le
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
          # 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='h;
              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_,
              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='1
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:"
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",
וחו. ר = דה-מס
Log Loss: 1.0698822969097057
for C = 0.0001
Log Loss: 1.0193858139473322
for C = 0.001
Log Loss: 1.0872484058054963
for C = 0.01
Log Loss: 1.2134336253066649
for C = 0.1
Log Loss: 1.6951515535703288
for C = 1
Log Loss: 1.7651671192013214
for C = 10
Log Loss: 1.765165253959348
for C = 100
Log Loss: 1.765166614339717
```

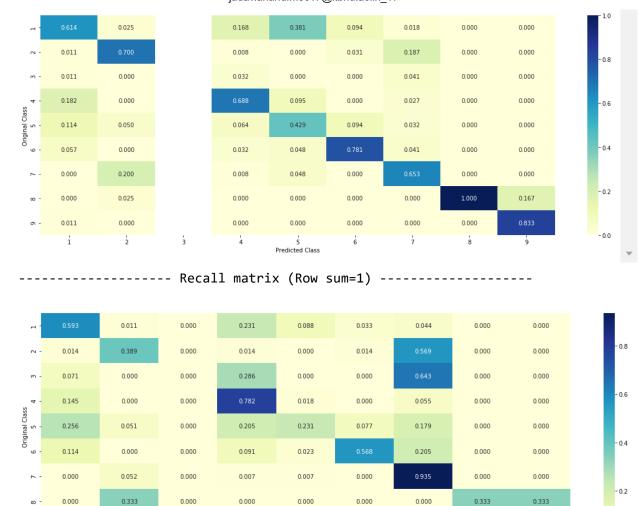


For values of best alpha = 0.0001 The train log loss is: 0.3063108332430362
For values of best alpha = 0.0001 The cross validation log loss is: 1.01938581
39473322
For values of best alpha = 0.0001 The test log loss is: 1.1181703217284822

### 4.4.2. Testing model with best hyper parameters



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



0.000

0.000

0.000

0.333

-0.0

# 4.3.3. Feature Importance

0.000

0.000

í

#### 4.3.3.1. For Correctly classified point

0.000

0.000

0.000

0.000

0.000

0.000

Predicted Class

0.000

0.000

```
In [253]: | clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', random
          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 on
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df[
          Predicted Class: 2
          Predicted Class Probabilities: [[0.0418 0.7849 0.0179 0.0223 0.0472 0.021 0.05
          17 0.0076 0.0057]]
          Actual Class : 2
          Out of the top 500 features 0 are present in query point
```

#### 4.3.3.2. For Incorrectly classified point

```
In [254]:
          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_one))
          print("Actual Class :", test y[test point index])
          indices = np.argsort(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df[
          Predicted Class: 7
          Predicted Class Probabilities: [[0.0299 0.144 0.0357 0.0376 0.0621 0.0041 0.68
          01 0.0037 0.0028]]
          Actual Class : 2
          313 Text feature [10] present in test data point [True]
          464 Text feature [11] present in test data point [True]
          Out of the top 500 features 2 are present in query point
```

### 4.5 Random Forest Classifier

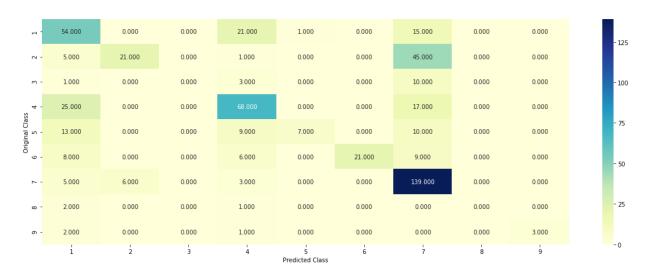
## 4.5.1. Hyper paramter tuning (With One hot Encoding)

```
In [255]: # -----
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
          # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max lea
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random stat
          # class weight=None)
          # Some of methods of RandomForestClassifier()
          # fit(X, y, [sample weight]) Fit the SVM model according to the given training
          \# 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/le
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
          # 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
                  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.class
                  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_l
          plt.title("Cross Validation Error for each alpha")
```

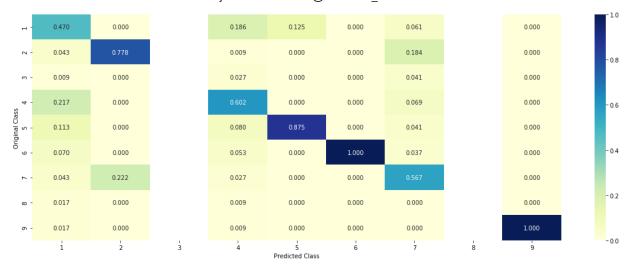
```
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='g
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train 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
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross values")
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log
for n_estimators = 100 and max depth =
Log Loss: 1.2123898639923436
for n estimators = 100 and max depth =
Log Loss: 1.2079599488392754
for n estimators = 200 and max depth =
Log Loss: 1.198475205032409
for n estimators = 200 and max depth = 10
Log Loss: 1.2010852612150646
for n estimators = 500 and max depth =
Log Loss: 1.1872142079564816
for n estimators = 500 and max depth = 10
Log Loss: 1.196300214483638
for n estimators = 1000 and max depth = 5
Log Loss: 1.1841425171896085
for n estimators = 1000 and max depth =
Log Loss: 1.1919204507234764
for n estimators = 2000 and max depth = 5
Log Loss: 1.1837999271630917
for n estimators = 2000 and max depth =
Log Loss: 1.1905664396534934
For values of best estimator = 2000 The train log loss is: 0.8939627894440503
For values of best estimator = 2000 The cross validation log loss is: 1.183799
9271630917
For values of best estimator = 2000 The test log loss is: 1.2623306496209639
```

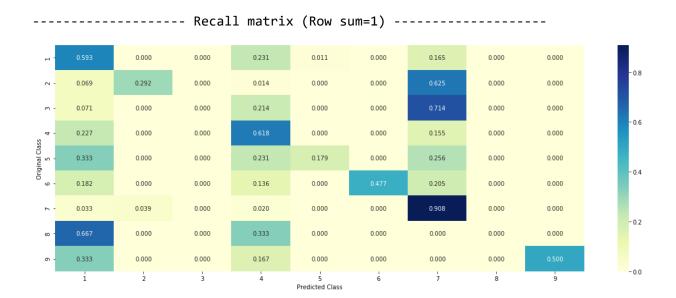
# 4.5.2. Testing model with best hyper parameters (One Hot Encoding)

```
In [256]:
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
          # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max lea
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random sta
          # class_weight=None)
          # Some of methods of RandomForestClassifier()
          # fit(X, y, [sample weight])
                                        Fit the SVM model according to the given training
                          Perform classification on samples in X.
          # predict(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/les
          clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='g
          predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding)
```



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





# 4.5.3. Feature Importance

#### 4.5.3.1. Correctly Classified point

```
In [257]: # test_point_index = 10
    clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='g.
    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_one 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])

Predicted Class : 2
```

#### 4.5.3.2. Inorrectly Classified point

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

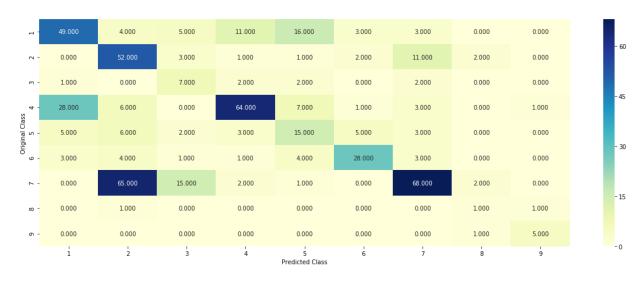
```
In [259]: # -----
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
          # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max lea
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random stat
          # class weight=None)
          # Some of methods of RandomForestClassifier()
          # fit(X, y, [sample weight]) Fit the SVM model according to the given training
          \# 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/les
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
          # 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
                  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.class
                  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_l
          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='g
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 lo
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The cross valida"
predict y = sig clf.predict proba(test x responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The test log los
for n_estimators = 10 and max depth =
Log Loss: 2.086875645592438
for n estimators = 10 and max depth =
Log Loss: 1.657743511320897
for n_estimators = 10 and max depth =
Log Loss: 1.5346621771119413
for n estimators = 10 and max depth =
                                      10
Log Loss: 1.7465073792602968
for n estimators = 50 and max depth =
Log Loss: 1.6660379753142083
for n_estimators = 50 and max depth =
Log Loss: 1.4642083057356599
for n estimators = 50 and max depth =
Log Loss: 1.33386874914904
for n estimators = 50 and max depth =
Log Loss: 1.6129944300444556
for n estimators = 100 and max depth = 2
Log Loss: 1.5067387343673515
for n estimators = 100 and max depth =
Log Loss: 1.4431070930095704
for n estimators = 100 and max depth =
Log Loss: 1.2990703795958765
for n_estimators = 100 and max depth =
Log Loss: 1.5681175089890185
for n estimators = 200 and max depth =
Log Loss: 1.5458662668211995
for n estimators = 200 and max depth = 3
Log Loss: 1.441997159468693
for n estimators = 200 and max depth =
Log Loss: 1.3882248733842144
for n_estimators = 200 and max depth =
Log Loss: 1.6077148634769651
for n estimators = 500 and max depth =
Log Loss: 1.5837982259371914
for n estimators = 500 and max depth =
Log Loss: 1.4756831763741975
for n_estimators = 500 and max depth =
Log Loss: 1.418354940420824
```

```
for n_estimators = 500 and max depth = 10
Log Loss : 1.6487332065239972
for n_estimators = 1000 and max depth = 2
Log Loss : 1.5641483252214516
for n_estimators = 1000 and max depth = 3
Log Loss : 1.47874883985345
for n_estimators = 1000 and max depth = 5
Log Loss : 1.4049997063196757
for n_estimators = 1000 and max depth = 10
Log Loss : 1.6377662246080875
For values of best alpha = 100 The train log loss is: 0.0660813739997366
For values of best alpha = 100 The cross validation log loss is: 1.299070379
5958758
For values of best alpha = 100 The test log loss is: 1.3516019428735186
```

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

```
In [260]:
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
          # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max lea
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random sta
          # class_weight=None)
          # Some of methods of RandomForestClassifier()
          # fit(X, y, [sample weight])
                                        Fit the SVM model according to the given training
                          Perform classification on samples in X.
          # predict(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/les
          clf = RandomForestClassifier(max depth=max depth[int(best alpha%4)], n estimator
          predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_responseCoding)
```



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



## 4.5.5. Feature Importance

#### 4.5.5.1. Correctly Classified point

```
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='g
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()
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_re
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:
        print("Text is important feature")
Predicted Class: 2
Predicted Class Probabilities: [[0.0537 0.6091 0.0948 0.0424 0.0226 0.0391 0.04
49 0.0747 0.0188]]
Actual Class: 2
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Gene is important feature
Text is important feature
Variation is important feature
Text is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

Gene is important feature

#### 4.5.5.2. Incorrectly Classified point

```
In [262]:
          test point index = 100
          predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape()
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x re
          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: 3
          Predicted Class Probabilities: [[0.0135 0.3142 0.3264 0.0183 0.0231 0.0274 0.23
          89 0.0275 0.0108]]
          Actual Class : 2
          Variation is important feature
          Variation is important feature
          Variation is important feature
          Variation is important feature
          Gene is important feature
          Variation is important feature
          Variation is important feature
          Text is important feature
          Text is important feature
          Gene is important feature
          Text is important feature
          Text is important feature
          Gene is important feature
          Text is important feature
          Gene is important feature
          Variation is important feature
          Gene is important feature
          Gene is important feature
          Text is important feature
          Variation is important feature
          Text is important feature
          Variation is important feature
          Text is important feature
          Text is important feature
          Gene is important feature
          Gene is important feature
          Gene is important feature
```

## 4.7 Stack the models

## 4.7.1 testing with hyper parameter tuning

```
In [263]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gene
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit inte
          # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_ra
          # 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 Grad
          \# predict(X) Predict class labels for samples in X.
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/le
          # read more about support vector machines with linear kernals here http://scikit
          # default parameters
          # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, pro
          # cache size=200, class weight=None, verbose=False, max iter=-1, decision function
          # Some of methods of SVM()
          # fit(X, y, [sample weight]) Fit the SVM model according to the given training
          \# predict(X) Perform classification on samples in X.
          # ------
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/le
          # read more about support vector machines with linear kernals here http://scikit
          # -----
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
          # min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random stat
          # class weight=None)
          # Some of methods of RandomForestClassifier()
          # fit(X, y, [sample weight]) Fit the SVM model according to the given training
          \# 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/les
          # -----
          clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class_weight='balance')
          clf1.fit(train_x_onehotCoding, train_y)
          sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
```

```
clf2 = SGDClassifier(alpha=1, penalty='12', loss='hinge', class weight='balanced
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.predic
sig_clf2.fit(train_x_onehotCoding, train_y)
print("Support vector machines: Log Loss: %0.2f" % (log loss(cv y, sig clf2.pred
sig_clf3.fit(train_x_onehotCoding, train_y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba(c))
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_cl
    sclf.fit(train x onehotCoding, train y)
    print("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" % (i
    log error =log loss(cv y, sclf.predict proba(cv x onehotCoding))
    if best_alpha > log_error:
        best alpha = log error
Support vector machines : Log Loss: 1.77
Naive Bayes : Log Loss: 1.24
Stacking Classifer: for the value of alpha: 0.000100 Log Loss: 1.817
Stacking Classifer: for the value of alpha: 0.001000 Log Loss: 1.714
Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.344
Stacking Classifer: for the value of alpha: 0.100000 Log Loss: 1.289
Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.656
Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 2.036
```

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

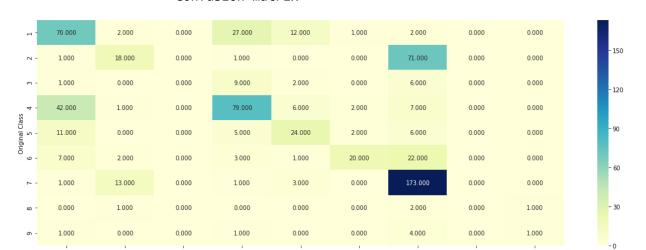
```
In [264]: lr = LogisticRegression(C=0.1)
    sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_class:
    sclf.fit(train_x_onehotCoding, train_y)

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

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

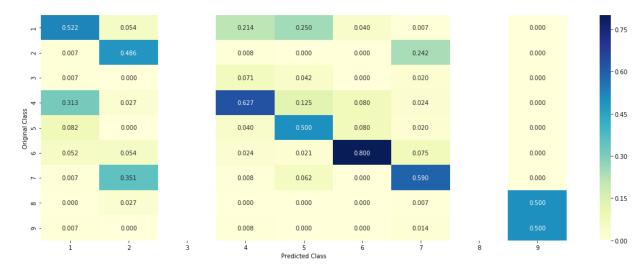
log_error = log_loss(test_y, sclf.predict_proba(test_x_onehotCoding))
    print("Log loss (test) on the stacking classifier :",log_error)

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



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

Predicted Class



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



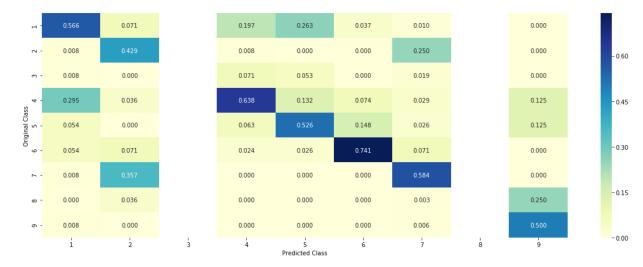
## 4.7.3 Maximum Voting classifier

#### In [265]:

#Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingCl
from sklearn.ensemble import VotingClassifier
vclf = VotingClassifier(estimators=[('lr', sig\_clf1), ('svc', sig\_clf2), ('rf', vclf.fit(train\_x\_onehotCoding,train\_y)
print("Log loss (train) on the VotingClassifier:", log\_loss(train\_y, vclf.predict\_print("Log loss (CV) on the VotingClassifier:", log\_loss(cv\_y, vclf.predict\_probiprint("Log loss (test) on the VotingClassifier:", log\_loss(test\_y, vclf.predict\_print("Number of missclassified point:", np.count\_nonzero((vclf.predict(test\_x\_oplot\_confusion\_matrix(test\_y=test\_y, predict\_y=vclf.predict(test\_x\_onehotCoding))



#### 





## 5. Assignments

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

WE WILL BE TRAINING 2 MODELS OF LOGISTIC REGRESSION WITHout BALANCED CLASS WEIGHT

- 1.MODEL TRAINED WITH FEATURES WITHOUT PERFORMING ANY FEATURE ENGINEERING
- 2.MODEL TRAINED WITH FEATURES BY PERFORMING FEATURE ENGINEERING TECHNIQUES
- 2.1-TEXT\_DATA-TFIDF VECTORIZATION
- 2.2-MEAN ENCODING FOR OF GENE AND VARIATION features

```
jadav.anand.mec17@itbhu.ac.in_17
 In [0]: | train df.columns
         var_train=train_df['Variation'].values;
         var test=test df['Variation'].values;
         var cv=cv df['Variation'].values
         gene_train=train_df['Gene'].values;
          gene_test=test_df['Gene'].values;
         gene_cv=cv_df['Gene'].values
         text_train=train_df['TEXT'].values;
         text test=test df['TEXT'].values;
          text_cv=cv_df['TEXT'].values
 In [0]:
         from sklearn.feature_extraction.text import CountVectorizer
         vectorizer=CountVectorizer(min df=10,ngram range=(1, 2))
         var_train=vectorizer.fit_transform(var_train)
         var test=vectorizer.transform(var test)
         var_cv=vectorizer.transform(var_cv)
         gene train=vectorizer.fit transform(gene train)
          gene test=vectorizer.transform(gene test)
         gene_cv=vectorizer.transform(gene_cv)
         text_train=vectorizer.fit_transform(text_train)
         text_test=vectorizer.transform(text_test)
         text cv=vectorizer.transform(text cv)
 In [0]:
         from scipy.sparse import hstack
         data_train=hstack([var_train,gene_train,text_train]).tocsr()
          data_test=hstack([var_test,gene_test,text_test]).tocsr()
          data cv=hstack([var cv,gene cv,text cv]).tocsr()
In [19]: | print(data_train.shape)
          print(data test.shape)
         print(data_cv.shape)
          (2124, 235934)
```

(665, 235934) (532, 235934)

```
In [172]:
          cv values=[]
          alpha=[10 ** x for x in range(-5, 5)]
          for c in tqdm(alpha):
            print("for alpha =", c)
            lr = LogisticRegression(random state=0, C=c,class weight='balanced',n jobs=-1)
            clf=CalibratedClassifierCV(base_estimator=lr,method='sigmoid')
            clf.fit(data train,y train)
            pre cv=clf.predict proba(data cv)
            print(c,log loss(y cv, pre cv))
            cv_values.append(log_loss(y_cv, pre_cv))
          print(alpha,cv values)
          print(len(alpha),len(cv_values))
          print(type(cv_values))
          fig, ax = plt.subplots()
          ax.plot(alpha, cv values,c='g')
          for i, t in enumerate(np.round(cv_values,3)):
            ax.annotate((alpha[i],str(t)), (alpha[i],cv_values[i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()
            0%|
                         | 0/10 [00:00<?, ?it/s]
          for alpha = 1e-05
           10%|
                         | 1/10 [04:18<38:46, 258.53s/it]
          1e-05 1.307704760189509
          for alpha = 0.0001
           20%
                         | 2/10 [08:33<34:19, 257.42s/it]
          0.0001 1.2837278442535625
          for alpha = 0.001
           30%|
                         | 3/10 [12:43<29:46, 255.15s/it]
          0.001 1.2948793444371294
          for alpha = 0.01
           40%
                         4/10 [16:50<25:16, 252.72s/it]
          0.01 1.482630497950825
          for alpha = 0.1
           50%|
                         | 5/10 [20:54<20:50, 250.06s/it]
          0.1 1.5182725411359548
          for alpha = 1
```

60%| 60%| 6/10 [24:58<16:33, 248.46s/it]

1 1.5230694403732323

for alpha = 10

10 1.5235605057949146

for alpha = 100

80%| | | 8/10 [33:12<08:14, 247.45s/it]

100 1.5231432546278938

for alpha = 1000

90%| 90%| 9/10 [37:16<04:06, 246.55s/it]

1000 1.5230428598845918

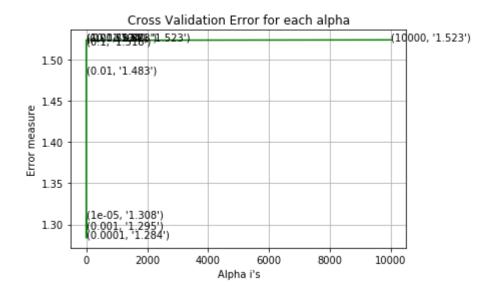
for alpha = 10000

100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%|

10000 1.523460007982243

10 10

<class 'list'>



#### from above graph best value for C=0.001

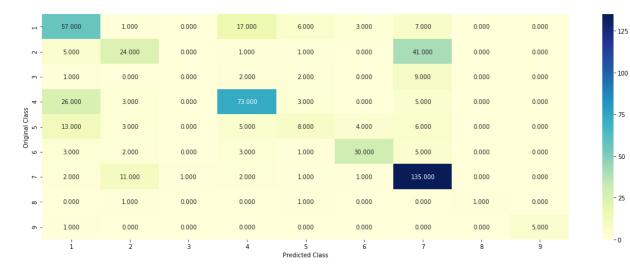
```
In [271]: | 1 = LogisticRegression(random_state=0, C=0.001,class_weight='balanced',n_jobs=-1
          clf=CalibratedClassifierCV(base estimator=1, method='sigmoid')
          clf.fit(data_train,y_train)
          pre_test=clf.predict_proba(data_test)
          print("Log Loss value for the test data is ",log_loss(y_test, pre_test))
```

Log Loss value for the test data is 1.3722961595858407

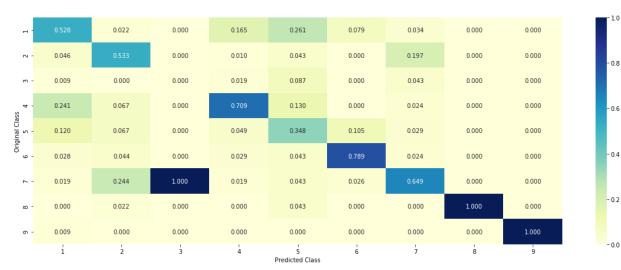
In [274]: | predict\_and\_plot\_confusion\_matrix(data\_train, y\_train,data\_cv,y\_cv, clf)

Log loss: 1.0824708168768304 Number of mis-classified points: 0.37406015037593987

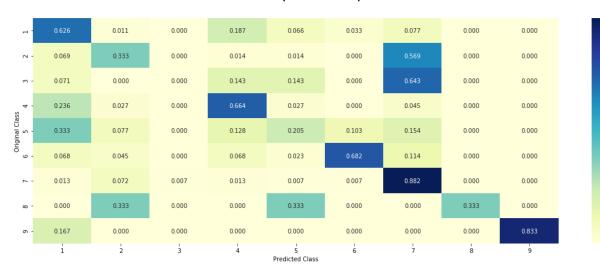
Confusion matrix -----



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



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



- 0.4

- 0.2

- 0.75

- 0.60

0.45

- 0.30

-0.15

-0.00

# Now we will do feature engineering on all the 3 features so that we get a loss less than 1

We will select top 5000 features using idf values from text data and vectorize them using TFIDF vectorizer

```
In [15]:
         from sklearn.feature extraction.text import TfidfVectorizer
         vectorizer_tfidf_text= TfidfVectorizer( min_df=10, max_features=5000)
         vectorizer tfidf text.fit(train df["TEXT"])
         text tfidf train = vectorizer tfidf text.transform(train df["TEXT"])
         text tfidf test = vectorizer tfidf text.transform(test df["TEXT"])
         text tfidf cv = vectorizer tfidf text.transform(cv df["TEXT"])
         print("Shape of matrix after one hot encoding ",text_tfidf_train.shape)
         print("Shape of matrix after one hot encoding ",text_tfidf_test.shape)
         print("Shape of matrix after one hot encoding ",text tfidf cv.shape)
         Shape of matrix after one hot encoding (2124, 5000)
         Shape of matrix after one hot encoding (665, 5000)
         Shape of matrix after one hot encoding (532, 5000)
In [38]:
         print(var_train.shape)
         print(gene_train.shape)
         print(text_train.shape)
         print(var_test.shape)
         print(gene_test.shape)
         print(text test.shape)
         print(var cv.shape)
         print(gene_cv.shape)
         print(text cv.shape)
          (2124, 5)
         (2124, 55)
         (2124, 222813)
         (665, 5)
         (665, 55)
          (665, 222813)
         (532, 5)
         (532, 55)
         (532, 222813)
 In [0]:
         vargen train=pd.DataFrame()
         vargen test=pd.DataFrame()
         vargen cv=pd.DataFrame()
         We will combine 2 features in single column
         vargen_train['var_gene']=train_df['Variation']+' '+train_df['Gene']
 In [0]:
         vargen_test['var_gene']=test_df['Variation']+' '+test_df['Gene']
         vargen cv['var gene']=cv df['Variation']+' '+cv df['Gene']
```

```
In [0]:
    vargene_train=pd.DataFrame()
    vargene_test=pd.DataFrame()
    vargene_cv=pd.DataFrame()

In [0]:    var n train=pd.DataFrame()
```

## Feature engineering steps:

var\_n\_test=pd.DataFrame()
var n cv=pd.DataFrame()

- 1.We will count length for the combined var\_gene feature
- 2..We will select top 10 words from variation and gene andperform mean encoding i.e check if word is present in the row,if the word is is present 1 is appended else 0 is appended.
- 3.TDFIDF Vectorization for text and select 5000 best words

## mean encoding Variation feature

## Mean encoding Gene feature

text\_n\_cv=pd.DataFrame()

```
In [0]: count=pd.DataFrame()
    line=[]
    cnt_train=[]
    cnt_cv=[]
    cnt_cv=[]
    cnt_text_train=[]
    cnt_text_test=[]
    cnt_text_cv=[]
```

counting number of words in Var gene feature

```
In [53]:
         for i in vargen train['var gene']:
           for j in i:
              line.append(j)
           cnt train.append(len(line))
         for i in vargen_test['var_gene']:
           for j in i:
              line.append(i)
           cnt test.append(len(line))
         for i in vargen_cv['var_gene']:
           for j in i:
              line.append(j)
           cnt_cv.append(len(line))
          cnt train=pd.DataFrame(cnt train)
          cnt test=pd.DataFrame(cnt test)
          cnt_cv=pd.DataFrame(cnt_cv)
         print(cnt train.shape)
         print(cnt_test.shape)
          print(cnt_cv.shape)
          (2124, 1)
          (665, 1)
         (532, 1)
```

## Normalizing length of text

```
In [54]: from sklearn.preprocessing import Normalizer
    normalizer = Normalizer()
    normalizer.fit(cnt_train.values.reshape(-1,1))
    cnt_train = normalizer.transform(cnt_train.values.reshape(-1,1))
    cnt_cv = normalizer.transform(cnt_cv.values.reshape(-1,1))
    cnt_test = normalizer.transform(cnt_test.values.reshape(-1,1))
    print("After vectorizations")
    print(cnt_train.shape, y_train.shape)
    print(cnt_cv.shape, y_cv.shape)
    print(cnt_test.shape, y_test.shape)

After vectorizations
    (2124, 1) (2124,)
    (532, 1) (532,)
    (665, 1) (665,)
```

## Stacking the feature engineered features

```
In [0]: data_train_fe=hstack([var_train,gene_train,text_tfidf_train,var_n_train,gene_n_t
data_test_fe=hstack([var_test,gene_test,text_tfidf_test,var_n_test,gene_n_test,ci
data_cv_fe=hstack([var_cv,gene_cv,text_tfidf_cv,var_n_cv,gene_n_cv,cnt_cv]).tocs
In [57]: print(data_train_fe.shape)
print(data_test_fe.shape)
print(data_cv_fe.shape)

(2124, 5081)
(665, 5081)
(532, 5081)
```

Hyperparameter tuning using the CV\_data

```
In [58]:
         from tqdm import tqdm
         cv values=[]
         alpha=[10 ** x for x in range(-3, 7)]
         for c in tqdm(alpha):
           print("for alpha =", c)
           lr = LogisticRegression(random_state=0, C=c,n_jobs=-1)
           clf=CalibratedClassifierCV(base estimator=lr,method='sigmoid')
           clf.fit(data train fe,y train)
           pre_cv=clf.predict_proba(data_cv_fe)
           print(c,log_loss(y_cv, pre_cv))
           cv_values.append(log_loss(y_cv, pre_cv))
         print(alpha,cv values)
         print(len(alpha),len(cv_values))
         print(type(cv values))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv_values,c='g')
         for i, t in enumerate(np.round(cv values,3)):
           ax.annotate((alpha[i],str(t)), (alpha[i],cv_values[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
         plt.show()
           0%|
                        | 0/10 [00:00<?, ?it/s]
         for alpha = 0.001
          10%
                        | 1/10 [00:08<01:18, 8.69s/it]
         0.001 1.27309174912667
         for alpha = 0.01
          20%
                        | 2/10 [00:15<01:05, 8.22s/it]
         0.01 1.244138503182963
         for alpha = 0.1
          30%
                        | 3/10 [00:28<01:05, 9.42s/it]
         0.1 1.1315744489504467
         for alpha = 1
          40%
                        | 4/10 [00:49<01:17, 12.99s/it]
         1 0.9937219276589544
         for alpha = 10
          50%
                        | 5/10 [01:10<01:17, 15.41s/it]
         10 0.9385640085921434
         for alpha = 100
                        6/10 [01:31<01:08, 17.02s/it]
         100 1.0482154337714413
         for alpha = 1000
                        7/10 [01:52<00:55, 18.33s/it]
```

```
1000 1.1010144397944943
for alpha = 10000
```

80%| | 8/10 [02:13<00:38, 19.15s/it]

10000 1.102444900198064 for alpha = 100000

90%| 90%| 9/10 [02:34<00:19, 19.65s/it]

100000 1.1052350566275917

for alpha = 1000000

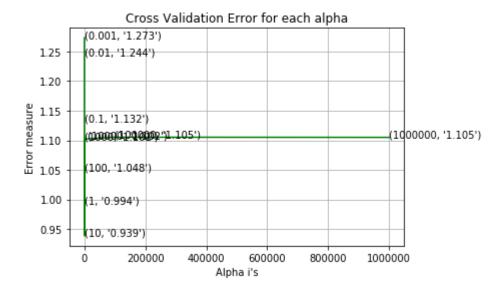
100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%| 100%|

1000000 1.104914598584836

[0.001, 0.01, 0.1, 1, 10, 100, 1000, 10000, 100000, 1000000] [1.27309174912667, 1.244138503182963, 1.1315744489504467, 0.9937219276589544, 0.9385640085921434, 1.0482154337714413, 1.1010144397944943, 1.102444900198064, 1.1052350566275917, 1.104914598584836]

10 10

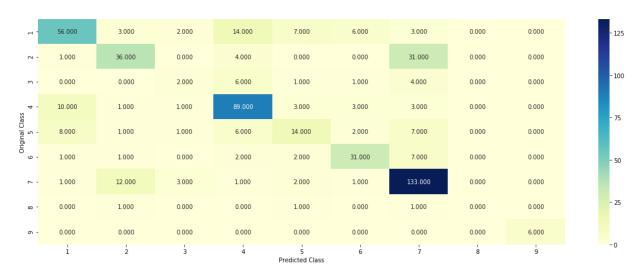
<class 'list'>



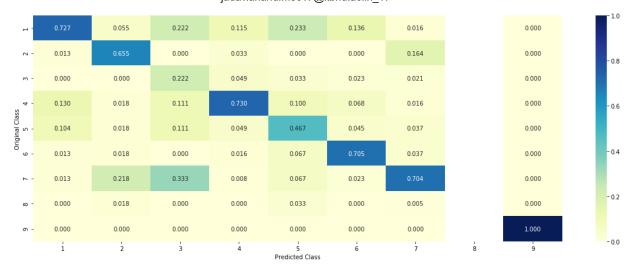
Using the best hyperparameter c=10

```
In [64]: l = LogisticRegression(random_state=0, C=10,n_jobs=-1)
    clf=CalibratedClassifierCV(base_estimator=l,method='sigmoid')
    clf.fit(data_train_fe,y_train)
    pre_test=clf.predict_proba(data_test_fe)
    print("Log Loss value for the test data is ",log_loss(y_test, pre_test))
```

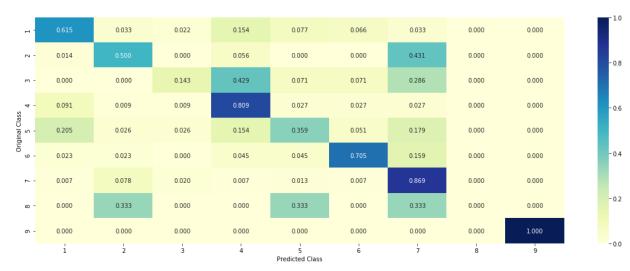
Log Loss value for the test data is 0.9887221971467367 Log loss: 0.9088807259280711 Number of mis-classified points: 0.3101503759398496 ------ Confusion matrix







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



In [69]: # Names of models

```
from prettytable import PrettyTable
model=['Naive Bayes ','KNN','Logistic Regression With Class balancing ','Logistic
train = [0.4446,0.5723,0.3820,0.3766,0.3066, 0.8939,0.3323,0.7116,0.6608,0.3762,0
test = [1.2911,1.1678,1.0949,1.0852,1.1182,1.2623,1.3509,1.2826,1.3516,1.3723,0.9
cv=[1.2405,1.0429,0.9949,0.9938,1.019,1.1837,1.2894,1.2176,1.2991,1.0824,0.9385]
mp = [40.9, 34.58, 34.77, 35.34, 34, 41.17, 42.11, 41.53, 45.67, 37.406, 31.01]
numbering=[1,2,3,4,5,6,7,8,9,10,11]
p = PrettyTable()
p.add column("S.NO.", numbering)
p.add_column("model", model)
p.add column("train",train)
p.add column("test",test)
p.add column("cv",cv)
p.add_column("% Misclassified Points",mp)
print(p)
                                                                    | train
  test
            cv | % Misclassified Points |
                            Naive Baves
                                                                    0.444
6 | 1.2911 | 1.2405 | 40.9
                                    KNN
                                                                    0.572
   2
3 | 1.1678 | 1.0429 | 34.58
                 Logistic Regression With Class balancing
                                                                   0.382
 1.0949 | 0.9949 | 34.77
                 Logistic Regression Without Class balancing
                                                                   0.376
6 | 1.0852 | 0.9938 | 35.34
                                 Linear SVM
                                                                   0.306
6 | 1.1182 | 1.019 |
                 Random Forest Classifier With One hot Encoding
                                                             0.893
9 | 1.2623 | 1.1837 |
                            41.17
                Random Forest Classifier With Response Coding
                                                                   0.332
3 | 1.3509 | 1.2894 | 42.11
                           Stack Models:LR+NB+SVM
                                                                   0.711
Maximum Voting classifier 8 | 1.3516 | 1.2991 | 45.67
6 | 1.2826 | 1.2176 |
                          41.53
                                                                    0.660
   10 | CountVectorizer Features, including both unigrams and bigrams | 0.376
2 | 1.3723 | 1.0824 | 37.406
   11 |
                          after feature engineering
                                                                    0.908
8 | 0.9887 | 0.9385 |
                           31.01
```

## **Conclusion:**

After performing feature engineering the loss for train test and cv are below 1.