Personalized cancer diagnosis

1. Business Problem

1.1. Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training_variants.zip and training_text.zip from Kaggle.

Context:

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

Problem statement:

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

1.2. Source/Useful Links

Some articles and reference blogs about the problem statement

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

1.3. Real-world/Business objectives and constraints.

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

2. Machine Learning Problem Formulation

2.1. Data

2.1.1. Data Overview

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

2.1.2. Example Data Point

training variants

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

...

training_text

ID, Text

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

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

2.2.1. Type of Machine Learning Problem

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

2.2.2. Performance Metric

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

Metric(s):

- · Multi class log-loss
- Confusion matrix

2.2.3. Machine Learing Objectives and Constraints

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

Constraints:

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

2.3. Train, CV and Test Datasets

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

3. Exploratory Data Analysis

```
In [1]: import pandas as pd
        import matplotlib.pyplot as plt
        import re
        import time
        import warnings
        import numpy as np
        from nltk.corpus import stopwords
        from sklearn.decomposition import TruncatedSVD
        from sklearn.preprocessing import normalize
        from sklearn.feature extraction.text import CountVectorizer
        from sklearn.manifold import TSNE
        import seaborn as sns
        from sklearn.neighbors import KNeighborsClassifier
        from sklearn.metrics import confusion matrix
        from sklearn.metrics.classification import accuracy score, log loss
        from sklearn.feature extraction.text import TfidfVectorizer
        from sklearn.linear model import SGDClassifier
        from imblearn.over sampling import SMOTE
        from collections import Counter
        from scipy.sparse import hstack
        from sklearn.multiclass import OneVsRestClassifier
        from sklearn.svm import SVC
        from sklearn.model selection import StratifiedKFold
        from collections import Counter, defaultdict
        from sklearn.calibration import CalibratedClassifierCV
        from sklearn.naive bayes import MultinomialNB
        from sklearn.naive bayes import GaussianNB
        from sklearn.model selection import train test split
        from sklearn.model selection import GridSearchCV
        import math
        from sklearn.metrics import normalized mutual info score
        from sklearn.ensemble import RandomForestClassifier
        warnings.filterwarnings("ignore")
        from mlxtend.classifier import StackingClassifier
        from sklearn import model selection
        from sklearn.linear model import LogisticRegression
```

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

```
In [2]: data = pd.read_csv('C:\\Users\\admin\\Downloads\\training_variants')
    print('Number of data points : ', data.shape[0])
    print('Number of features : ', data.shape[1])
    print('Features : ', data.columns.values)
    data.head()
```

Number of data points : 3321 Number of features : 4

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

Out[2]:

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

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

Fields are

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

3.1.2. Reading Text Data

```
In [3]: # note the seprator in this file
         data text =pd.read csv("C:\\Users\\admin\\Downloads\\training text",sep="\|\|"
         ,engine="python",names=["ID","TEXT"],skiprows=1)
         print('Number of data points : ', data_text.shape[0])
         print('Number of features : ', data_text.shape[1])
         print('Features : ', data_text.columns.values)
         data text.head()
         Number of data points : 3321
         Number of features : 2
         Features : ['ID' 'TEXT']
Out[3]:
             ID
                                                    TEXT
          0
             0
                 Cyclin-dependent kinases (CDKs) regulate a var...
          1
             1
                   Abstract Background Non-small cell lung canc...
             2
                   Abstract Background Non-small cell lung canc...
          2
             3 Recent evidence has demonstrated that acquired...
                Oncogenic mutations in the monomeric Casitas B...
```

3.1.3. Preprocessing of text

```
In [4]: # Loading stop words from nltk library
        stop words = set(stopwords.words('english'))
        def nlp_preprocessing(total_text, index, column):
            if type(total text) is not int:
                 string = ""
                # replace every special char with space
                total_text = re.sub('[^a-zA-Z0-9\n]', ' ', total_text)
                # replace multiple spaces with single space
                total_text = re.sub('\s+',' ', total_text)
                # converting all the chars into lower-case.
                total text = total text.lower()
                for word in total_text.split():
                # if the word is a not a stop word then retain that word from the data
                     if not word in stop words:
                        string += word + " "
                data text[column][index] = string
```

```
PersonalizedCancerDiagnosis
In [5]: | #text processing stage.
         start time = time.clock()
         for index, row in data text.iterrows():
              if type(row['TEXT']) is str:
                  nlp_preprocessing(row['TEXT'], index, 'TEXT')
              else:
                  print("there is no text description for id:",index)
         print('Time took for preprocessing the text :',time.clock() - start time,
         "seconds")
         there is no text description for id: 1109
         there is no text description for id: 1277
         there is no text description for id: 1407
         there is no text description for id: 1639
         there is no text description for id: 2755
         Time took for preprocessing the text: 268.8862924314848 seconds
In [6]: #merging both gene variations and text data based on ID
         result = pd.merge(data, data text,on='ID', how='left')
         result.head()
Out[6]:
                                                                                    TEXT
             ID
                   Gene
                                 Variation Class
             0 FAM58A Truncating Mutations
                                              1
                                                   cyclin dependent kinases cdks regulate variety...
             1
                   CBL
                                   W802*
                                              2
                                                   abstract background non small cell lung cancer...
          1
             2
                   CBL
                                   Q249E
                                                   abstract background non small cell lung cancer...
          2
                                              2
          3
             3
                   CBL
                                   N454D
                                              3 recent evidence demonstrated acquired uniparen...
                   CBL
                                    L399V
                                              4 oncogenic mutations monomeric casitas b lineag...
         result[result.isnull().any(axis=1)]
In [7]:
Out[7]:
```

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

```
In [8]: | result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Varia
        tion']
```

In [9]: result[result['ID']==1109]

Out[9]:

	ID	Gene	Variation	Class	TEXT
1109	1109	FANCA	S1088F	1	FANCA S1088F

3.1.4. Test, Train and Cross Validation Split

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

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

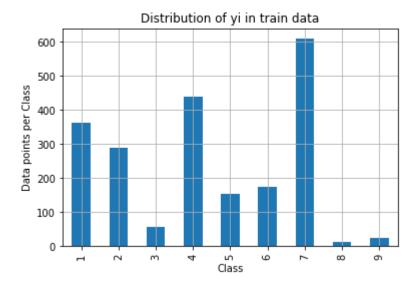
```
In [11]: print('Number of data points in train data:', train_df.shape[0])
    print('Number of data points in test data:', test_df.shape[0])
    print('Number of data points in cross validation data:', cv_df.shape[0])

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

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

```
In [12]: # it returns a dict, keys as class labels and values as the number of data
          points in that class
         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.a
         rgsort.html
         # -(train class distribution.values): the minus sign will give us in decrea
         sing order
         sorted_yi = np.argsort(-train_class_distribution.values)
         for i in sorted vi:
             print('Number of data points in class', i+1, ':',train class distributi
         on.values[i], '(', np.round((train_class_distribution.values[i]/train_df.sh
         ape[0]*100), 3), '%)')
         print('-'*80)
         my colors = 'rgbkymc'
         test class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in test data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.a
         rasort.html
         # -(train class distribution.values): the minus sign will give us in decrea
         sing order
         sorted yi = np.argsort(-test class distribution.values)
         for i in sorted yi:
             print('Number of data points in class', i+1, ':',test_class_distributio
         n.values[i], '(', np.round((test class distribution.values[i]/test df.shape
         [0]*100), 3), '%)')
         print('-'*80)
         my colors = 'rgbkymc'
         cv class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in cross validation data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.a
         rgsort.html
         # -(train class distribution.values): the minus sign will give us in decrea
```

```
sing order
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',cv_class_distribution.
values[i], '(', np.round((cv_class_distribution.values[i]/cv_df.shape[0]*10
0), 3), '%)')
```



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

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

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

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

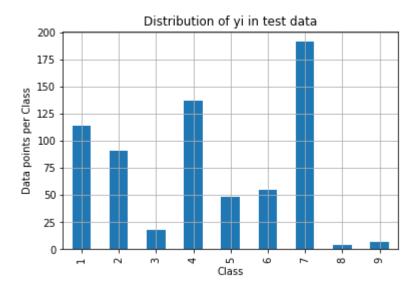
Number of data points in class 6 : 176 ( 8.286 %)

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

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

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

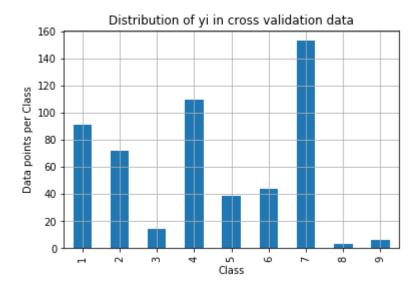
Number of data points in class 8 : 12 ( 0.565 %)
```



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

diliber of data points in class o . + (0.002 %)

- - -



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

3.2 Prediction using a 'Random' Model

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

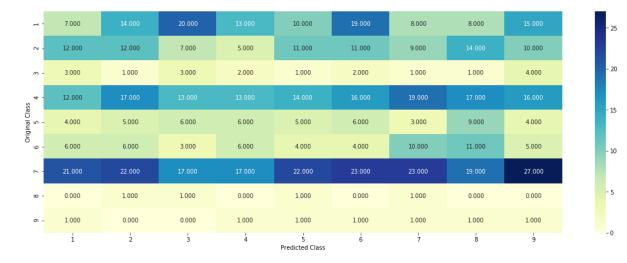
```
In [13]: # This function plots the confusion matrices given y_i, y_i_hat.
          def plot confusion matrix(test y, predict y):
              C = confusion matrix(test y, predict y)
              \# C = 9,9 \text{ matrix}, \text{ each cell } (i,j) \text{ represents number of points of class}
           i are predicted class j
              A = (((C.T)/(C.sum(axis=1))).T)
              #divid each element of the confusion matrix with the sum of elements in
           that column
              # C = [[1, 2],
              # [3, 4]]
              # C.T = [[1, 3],
                       [2, 411]
              # C.sum(axis = 1) axis=0 corresonds to columns and axis=1 corresponds
           to rows in two diamensional array
              # C.sum(axix = 1) = [[3, 7]]
              \# ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
                                           [2/3, 4/7]]
              \# ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]]
                                          [3/7, 4/7]]
              # sum of row elements = 1
              B = (C/C.sum(axis=0))
              #divid each element of the confusion matrix with the sum of elements in
           that row
              \# C = [[1, 2],
                    [3, 4]]
              # C.sum(axis = 0) axis=0 corresonds to columns and axis=1 corresponds
           to rows in two diamensional array
              # C.sum(axix = 0) = [[4, 6]]
              \# (C/C.sum(axis=0)) = \lceil \lceil 1/4, 2/6 \rceil,
                                      [3/4, 4/6]]
              labels = [1,2,3,4,5,6,7,8,9]
              # representing A in heatmap format
              print("-"*20, "Confusion matrix", "-"*20)
              plt.figure(figsize=(20,7))
              sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels
          , yticklabels=labels)
              plt.xlabel('Predicted Class')
              plt.ylabel('Original Class')
              plt.show()
              print("-"*20, "Precision matrix (Column Sum=1)", "-"*20)
              plt.figure(figsize=(20,7))
              sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels
          , yticklabels=labels)
              plt.xlabel('Predicted Class')
              plt.ylabel('Original Class')
              plt.show()
              # representing B in heatmap format
              print("-"*20, "Recall matrix (Row sum=1)", "-"*20)
              plt.figure(figsize=(20,7))
```

```
sns.heatmap(A, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels
, yticklabels=labels)
  plt.xlabel('Predicted Class')
  plt.ylabel('Original Class')
  plt.show()
```

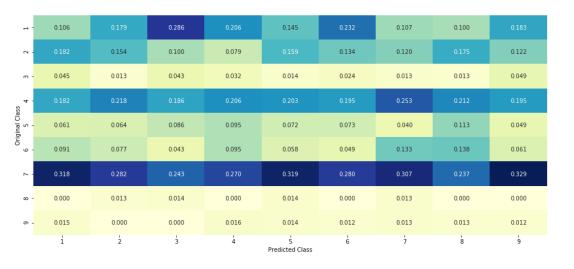
In [14]: # we need to generate 9 numbers and the sum of numbers should be 1 # one solution is to genarate 9 numbers and divide each of the numbers by thei r sum # ref: https://stackoverflow.com/a/18662466/4084039 test data len = test df.shape[0] cv_data_len = cv_df.shape[0] # we create a output array that has exactly same size as the CV data cv predicted y = np.zeros((cv data len,9)) for i in range(cv_data_len): rand probs = np.random.rand(1,9) cv_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0]) print("Log loss on Cross Validation Data using Random Model",log_loss(y_cv,cv_ predicted y, eps=1e-15)) # Test-Set error. #we create a output array that has exactly same as the test data test_predicted_y = np.zeros((test_data_len,9)) for i in range(test data len): rand probs = np.random.rand(1,9) test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0]) print("Log loss on Test Data using Random Model",log loss(y test,test predicte d_y, eps=1e-15)) predicted y =np.argmax(test predicted y, axis=1) plot confusion matrix(y test, predicted y+1)

Log loss on Cross Validation Data using Random Model 2.467459274823523 Log loss on Test Data using Random Model 2.491713215993295

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



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



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



3.3 Univariate Analysis

0.30

0.24

- 0.18

-0.12

-0.00

- 0.20

-0.15

-0.10

- 0.05

```
In [15]: # code for response coding with Laplace smoothing.
         # alpha: used for laplace smoothing
         # feature: ['gene', 'variation']
         # df: ['train_df', 'test_df', 'cv_df']
         # algorithm
         # Consider all unique values and the number of occurances of given feature
          in train data dataframe
         # build a vector (1*9) , the first element = (number of times it occured in
          class1 + 10*alpha / number of time it occurred in total data+90*alpha)
         # qv dict is like a look up table, for every gene it store a (1*9) represen
         tation of it
         # for a value of feature in df:
         # if it is in train data:
         # we add the vector that was stored in 'gv dict' look up table to 'gv fea'
         # if it is not there is train:
         # we add [1/9, 1/9, 1/9, 1/9,1/9, 1/9, 1/9, 1/9] to '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
             #
                       BRCA2
                                   75
                       PTEN
                                   69
             #
             #
                       KIT
                                   61
             #
                       BRAF
                                   60
             #
                       ERBB2
                                   47
                       PDGFRA
                                   46
                       ...}
             # print(train df['Variation'].value counts())
             # output:
             # {
                                                         63
             # Truncating Mutations
             # Deletion
                                                         43
             # Amplification
                                                         43
             # Fusions
                                                         22
             # Overexpression
                                                          3
                                                          3
             # E17K
             # Q61L
                                                          3
             # S222D
                                                          2
             # P130S
                                                          2
             # ...
             # }
             value count = train df[feature].value counts()
             # qv dict : Gene Variation Dict, which contains the probability array f
         or each gene/variation
             gv dict = dict()
             # denominator will contain the number of time that particular feature o
```

```
ccured in whole data
   for i, denominator in value_count.items():
       # vec will contain (p(yi==1/Gi) probability of gene/variation belon
as to perticular class
       # vec is 9 diamensional vector
       vec = []
       for k in range(1,10):
           # print(train_df.loc[(train_df['Class']==1) & (train_df['Gene']
== 'BRCA1')])
                     ID
                         Gene
                                          Variation Class
           # 2470 2470 BRCA1
                                             S1715C
           # 2486 2486 BRCA1
                                             S1841R
                                                         1
           # 2614 2614 BRCA1
                                                M1R
                                                         1
           # 2432 2432 BRCA1
                                             L1657P
                                                         1
           # 2567 2567 BRCA1
                                                         1
                                             T1685A
           # 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[featu
re]==i)]
           # cls cnt.shape[0](numerator) will contain the number of time t
hat particular feature occured in whole data
           vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alp
ha))
       # we are adding the gene/variation to the dict as key and vec as va
Lue
       gv_dict[i]=vec
   return gv_dict
# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
   # print(qv dict)
         { 'BRCA1': [0.20075757575757575, 0.037878787878788, 0.0681818181
81818177, 0.13636363636363635, 0.25, 0.193181818181818, 0.037878787878787
88, 0.03787878787878788, 0.0378787878787878],
          'TP53': [0.32142857142857145, 0.061224489795918366, 0.0612244897
95918366, 0.27040816326530615, 0.061224489795918366, 0.066326530612244902,
0.051020408163265307, 0.051020408163265307, 0.056122448979591837],
          'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.06
81818181818177, 0.0681818181818177, 0.0625, 0.34659090909090912, 0.062
5, 0.056818181818181816],
           'BRCA2': [0.1333333333333333, 0.060606060606060608, 0.060606060
606060608, 0.078787878787878782, 0.13939393939394, 0.34545454545454546,
0.060606060606060608, 0.060606060606060608, 0.060606060606060608],
          'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389
937106917, 0.46540880503144655, 0.075471698113207544, 0.062893081761006289,
0.069182389937106917, 0.062893081761006289, 0.062893081761006289],
          'KIT': [0.066225165562913912, 0.25165562913907286, 0.07284768211
9205295, 0.072847682119205295, 0.066225165562913912, 0.066225165562913912,
0.27152317880794702, 0.066225165562913912, 0.066225165562913912],
          'BRAF': [0.0666666666666666666, 0.179999999999999, 0.0733333333
3333334, 0.073333333333333334, 0.09333333333333338, 0.080000000000000002,
```

```
}
   gv_dict = get_gv_fea_dict(alpha, feature, df)
   # value count is similar in get gv fea dict
   value count = train df[feature].value counts()
   # gv_fea: Gene_variation feature, it will contain the feature for each
feature value in the data
   gv fea = []
   # for every feature values in the given data frame we will check if it
is there in the train data then we will add the feature to av fea
   # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to gv_fea
   for index, row in df.iterrows():
       if row[feature] in dict(value count).keys():
           gv_fea.append(gv_dict[row[feature]])
       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

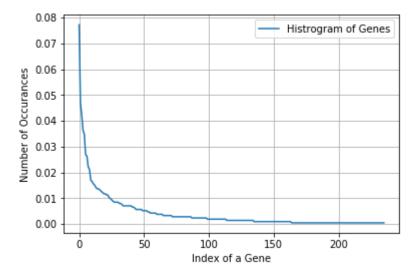
Q2. How many categories are there and How they are distributed?

```
In [16]:
         unique_genes = train_df['Gene'].value_counts()
          print('Number of Unique Genes :', unique_genes.shape[0])
          # the top 10 genes that occured most
          print(unique_genes.head(10))
         Number of Unique Genes: 236
         BRCA1
                    164
         TP53
                    100
         EGFR
                     90
                     77
         BRCA2
         PTEN
                     74
         KIT
                     57
         BRAF
                     56
         ERBB2
                     47
         ALK
                     45
         PDGFRA
                     36
         Name: Gene, dtype: int64
```

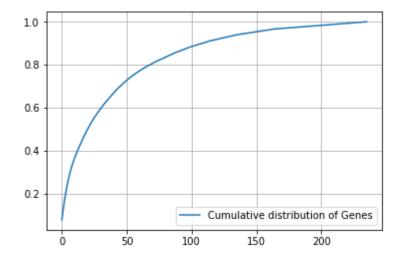
```
In [17]: print("Ans: There are", unique_genes.shape[0] ,"different categories of genes
    in the train data, and they are distibuted as follows",)
```

Ans: There are 236 different categories of genes in the train data, and they are distibuted as follows

```
In [18]: s = sum(unique_genes.values);
h = unique_genes.values/s;
plt.plot(h, label="Histrogram of Genes")
plt.xlabel('Index of a Gene')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



```
In [19]: c = np.cumsum(h)
    plt.plot(c,label='Cumulative distribution of Genes')
    plt.grid()
    plt.legend()
    plt.show()
```



Q3. How to featurize this Gene feature?

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

- 1. One hot Encoding
- 2. Response coding

We will choose the appropriate featurization based on the ML model we use. For this problem of multi-class classification with categorical features, one-hot encoding is better for Logistic regression while response coding is better for Random Forests.

```
In [20]: #response-coding of the Gene feature
         # alpha is used for laplace smoothing
         alpha = 1
         # train gene feature
         train gene feature responseCoding = np.array(get gv feature(alpha, "Gene", tra
         in df))
         # test gene feature
         test gene feature responseCoding = np.array(get gv feature(alpha, "Gene", test
         df))
         # cross validation gene feature
         cv gene feature responseCoding = np.array(get gv feature(alpha, "Gene", cv df
         ))
In [21]:
         print("train gene feature responseCoding is converted feature using respone co
         ding method. The shape of gene feature:", train_gene_feature_responseCoding.sh
         ape)
         train gene feature responseCoding is converted feature using respone coding m
         ethod. The shape of gene feature: (2124, 9)
         # one-hot encoding of Gene feature.
In [22]:
         gene vectorizer = TfidfVectorizer()
         train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gen
         test gene feature onehotCoding = gene vectorizer.transform(test df['Gene'])
         cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
In [23]: | train_df['Gene'].head()
Out[23]: 688
                 CDKN2A
         946
                 PDGFRB
         2491
                  BRCA1
         2717
                   BRAF
         995
                   TSC1
         Name: Gene, dtype: object
```

In [24]: gene_vectorizer.get_feature_names()

```
Out[24]: ['abl1',
            'acvr1',
            'ago2',
            'akt1',
            'akt2',
            'akt3',
            'alk',
            'apc',
            'ar',
            'araf',
            'arid1a',
            'arid1b',
            'arid2',
            'atm',
            'atr',
            'atrx',
            'aurka',
            'aurkb',
            'b2m',
            'bap1',
            'bcl10',
            'bcl2l11',
            'bcor',
            'braf',
            'brca1',
            'brca2',
            'brip1',
            'btk',
            'card11',
            'carm1',
            'casp8',
            'cbl',
            'ccnd1',
            'ccnd2',
            'ccnd3',
            'ccne1',
            'cdh1',
            'cdk12',
            'cdk4',
            'cdk8',
            'cdkn1a',
            'cdkn1b',
            'cdkn2a',
            'cdkn2b',
            'cdkn2c',
            'cebpa',
            'chek2',
            'cic',
            'crebbp',
            'ctcf',
            'ctnnb1',
            'ddr2',
            'dicer1',
            'dnmt3a',
            'dnmt3b',
            'dusp4',
            'egfr',
```

'eif1ax', 'elf3', 'ep300', 'epas1', 'epcam', 'erbb2', 'erbb3', 'erbb4', 'ercc2', 'ercc3', 'ercc4', 'erg', 'esr1', 'etv1', 'etv6', 'ewsr1', 'ezh2', 'fam58a', 'fanca', 'fat1', 'fbxw7', 'fgf3', 'fgf4', 'fgfr1', 'fgfr2', 'fgfr3', 'fgfr4', 'flt1', 'flt3', 'foxa1', 'fox12', 'foxo1', 'foxp1', 'fubp1', 'gata3', 'gli1', 'gna11', 'gnaq', 'gnas', 'h3f3a', 'hla', 'hnf1a', 'hras', 'idh1', 'idh2', 'igf1r', 'ikzf1', 'il7r', 'inpp4b', 'jak1', 'jak2', 'kdm5a', 'kdm5c', 'kdm6a', 'kdr', 'keap1',

'kit',

'kmt2a', 'kmt2b', 'kmt2c', 'kmt2d', 'knstrn', 'kras', 'lats1', 'lats2', 'map2k1', 'map2k2', 'map2k4', 'map3k1', 'mapk1', 'med12', 'mef2b', 'men1', 'met', 'mga', 'mlh1', 'mpl', 'msh2', 'msh6', 'mtor', 'myc', 'mycn', 'myd88', 'myod1', 'ncor1', 'nf1', 'nf2', 'nfe212', 'nfkbia', 'nkx2', 'notch1', 'notch2', 'npm1', 'nras', 'nsd1', 'ntrk1', 'ntrk2', 'ntrk3', 'nup93', 'pak1', 'pax8', 'pbrm1', 'pdgfra', 'pdgfrb', 'pik3ca', 'pik3cb', 'pik3cd', 'pik3r1', 'pik3r2', 'pik3r3', 'pim1', 'pms1', 'pms2',

'pole',

```
'ppm1d',
'ppp2r1a',
'ppp6c',
'prdm1',
'pten',
'ptpn11',
'ptprd',
'ptprt',
'rab35',
'rac1',
'rad21',
'rad50',
'rad51b',
'rad51c',
'rad51d',
'raf1',
'rara',
'rasa1',
'rb1',
'rbm10',
'ret',
'rheb',
'rhoa',
'rictor',
'rit1',
'ros1',
'rras2',
'runx1',
'rxra',
'sdhb',
'sdhc',
'setd2',
'sf3b1',
'shq1',
'smad2',
'smad3',
'smad4',
'smarca4',
'smarcb1',
'smo',
'sos1',
'sox9',
'spop',
'src',
'srsf2',
'stat3',
'stk11',
'tcf712',
'tert',
'tet1',
'tet2',
'tgfbr1',
'tgfbr2',
'tmprss2',
'tp53',
'tp53bp1',
'tsc1',
```

```
'tsc2',
'u2af1',
'vhl',
'whsc1',
'whsc1l1',
'xpo1',
'xrcc2',
'yap1']

In [25]: print("train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature:", train_gene_feature_onehotCoding.shape)

train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature: (2124, 236)
```

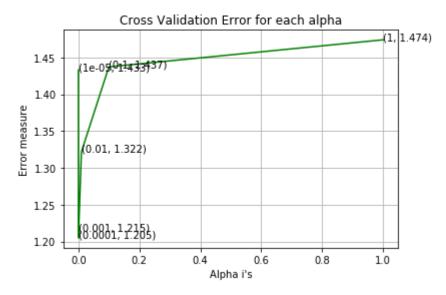
Q4. How good is this gene feature in predicting y_i?

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 [26]: | alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
         # read more about SGDClassifier() at http://scikit-learn.org/stable/module
         s/generated/sklearn.linear model.SGDClassifier.html
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fi
         t intercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learni
         ng_rate='optimal', eta0=0.0, power_t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         astic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link:
         #-----
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
             clf.fit(train gene feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train gene feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv gene feature onehotCoding)
             cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_
         , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, pr
         edict y, labels=clf.classes , eps=1e-15))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i
         1))
         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', rand
         om state=42)
         clf.fit(train gene feature onehotCoding, y train)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_gene_feature_onehotCoding, y_train)
         predict_y = sig_clf.predict_proba(train_gene_feature_onehotCoding)
         print('For values of best alpha = ', alpha[best_alpha], "The train log loss
          is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
```

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

```
For values of alpha = 1e-05 The log loss is: 1.4330459357840406
For values of alpha = 0.0001 The log loss is: 1.2049931344184501
For values of alpha = 0.001 The log loss is: 1.2145841560553023
For values of alpha = 0.01 The log loss is: 1.3217895993760151
For values of alpha = 0.1 The log loss is: 1.4371401277366276
For values of alpha = 1 The log loss is: 1.4739301360246393
```



```
For values of best alpha = 0.0001 The train log loss is: 1.0567878366928105
For values of best alpha = 0.0001 The cross validation log loss is: 1.204993
1344184501
For values of best alpha = 0.0001 The test log loss is: 1.1952885509217699
```

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

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

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

print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(cv_coverage/cv_df.shape[0])*100)

Q6. How many data points in Test and CV datasets are covered by the 236 genes in train dataset?
Ans
1. In test data 646 out of 665 : 97.14285714285714
2. In cross validation data 520 out of 532 : 97.74436090225564
```

3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it?

Ans. Variation is a categorical variable

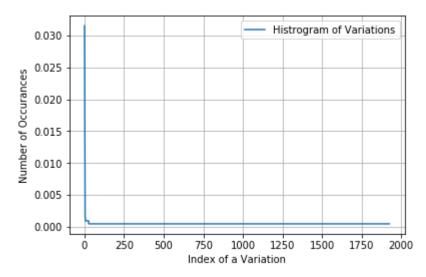
Q8. How many categories are there?

```
unique_variations = train_df['Variation'].value_counts()
In [28]:
         print('Number of Unique Variations :', unique variations.shape[0])
         # the top 10 variations that occured most
         print(unique variations.head(10))
         Number of Unique Variations: 1925
         Truncating Mutations
                                  67
         Deletion
                                  49
         Amplification
                                  41
         Fusions
                                  21
         Overexpression
                                   3
                                   3
         G12V
                                   2
         P130S
         G12A
                                   2
                                   2
         T58I
         A146V
         Name: Variation, dtype: int64
         print("Ans: There are", unique variations.shape[0] ,"different categories of v
In [29]:
         ariations in the train data, and they are distibuted as follows",)
```

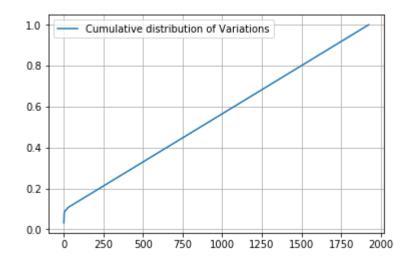
Ans: There are 1925 different categories of variations in the train data, and

they are distibuted as follows

```
In [30]: 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()
```







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 [32]: # alpha is used for laplace smoothing
    alpha = 1
    # train gene feature
    train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train_df))
    # test gene feature
    test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", test_df))
    # cross validation gene feature
    cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", cv_df))
In [33]: print("train_variation_feature_responseCoding is a converted feature using the
```

In [33]: print("train_variation_feature_responseCoding is a converted feature using the
 response coding method. The shape of Variation feature:", train_variation_fea
 ture_responseCoding.shape)

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

```
In [34]: # one-hot encoding of variation feature.
    variation_vectorizer = TfidfVectorizer()
    train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variation'])
    test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
    cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])
```

In [35]: print("train_variation_feature_onehotEncoded is converted feature using the on
 ne-hot encoding method. The shape of Variation feature:", train_variation_feat
 ure_onehotCoding.shape)

train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding 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 [36]: | alpha = [10 ** x for x in range(-5, 1)]
         # read more about SGDClassifier() at http://scikit-learn.org/stable/module
         s/generated/sklearn.linear model.SGDClassifier.html
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fi
         t intercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learni
         ng_rate='optimal', eta0=0.0, power_t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])
Fit linear model with Stoch
         astic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         #-----
         # video link:
         #-----
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
             clf.fit(train variation feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train variation feature onehotCoding, y train)
             predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes
         , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, pr
         edict_y, labels=clf.classes_, eps=1e-15))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_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', rand
         om state=42)
         clf.fit(train variation feature onehotCoding, y train)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train variation feature onehotCoding, y train)
         predict y = sig clf.predict proba(train variation feature onehotCoding)
```

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

```
For values of alpha = 1e-05 The log loss is: 1.7133634867662357

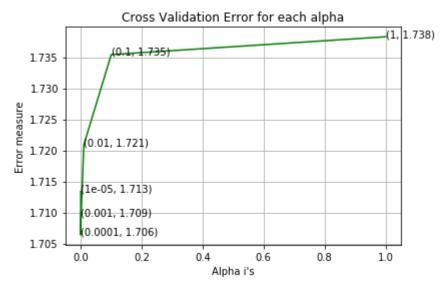
For values of alpha = 0.0001 The log loss is: 1.7063928606105725

For values of alpha = 0.001 The log loss is: 1.70942893628625

For values of alpha = 0.01 The log loss is: 1.7208702466850165

For values of alpha = 0.1 The log loss is: 1.735413103985182

For values of alpha = 1 The log loss is: 1.738277015675633
```



For values of best alpha = 0.0001 The train log loss is: 0.7423323962986081 For values of best alpha = 0.0001 The cross validation log loss is: 1.706392 8606105725 For values of best alpha = 0.0001 The test log loss is: 1.7076499771369058

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

Q12. How many data points are covered by total 1925 genes in test and cross
    validation data sets?
    Ans
    1. In test data 73 out of 665 : 10.977443609022556
    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 prediciting y i?
- 5. Is the text feature stable across train, test and CV datasets?

```
In [39]:
         import math
         #https://stackoverflow.com/a/1602964
         def get text responsecoding(df):
             text feature responseCoding = np.zeros((df.shape[0],9))
             for i in range(0,9):
                 row index = 0
                 for index, row in df.iterrows():
                     sum prob = 0
                     for word in row['TEXT'].split():
                          sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(total
         dict.get(word,0)+90)))
                     text_feature_responseCoding[row_index][i] = math.exp(sum_prob/1
         en(row['TEXT'].split()))
                     row index += 1
             return text feature responseCoding
```

```
In [40]: | # building a CountVectorizer with all the words that occured minimum 3 times i
         n train data
         text vectorizer = TfidfVectorizer(min df=3,max features=1000)
         train text feature onehotCoding = text vectorizer.fit transform(train df['TEX
         T'])
         # 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 return
         s (1*number of features) vector
         train text fea counts = train text feature onehotCoding.sum(axis=0).A1
         # zip(list(text_features),text_fea_counts) will zip a word with its number of
          times it occured
         text fea dict = dict(zip(list(train text features),train text fea counts))
         print("Total number of unique words in train data :", len(train text features
         ))
         # one-hot encoding of Gene feature.
         gene vectorizer = TfidfVectorizer()
         train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gen
         test gene feature onehotCoding = gene vectorizer.transform(test df['Gene'])
         cv gene feature onehotCoding = gene vectorizer.transform(cv df['Gene'])
```

Total number of unique words in train data : 1000

```
In [41]: | 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 [42]: #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 [44]: # don't forget to normalize every feature
 train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding, a
 xis=0)

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

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

In [46]: # Number of words for a given frequency.
print(Counter(sorted_text_occur))

Counter({253.85472592979377: 1, 183.61315598541483: 1, 134.31328155390688: 1, 131.42058010117685: 1, 131.37452553001935: 1, 118.64949007951357: 1, 117.6151 4405964607: 1, 117.4842593947599: 1, 108.78267856452527: 1, 108.5682414600171 2: 1, 106.74270143925446: 1, 90.81367880274159: 1, 90.5961552973477: 1, 82.40 829302305777: 1, 81.44954123294214: 1, 80.05741213654336: 1, 79.8476798177453 3: 1, 79.03529147903217: 1, 77.79731353734692: 1, 76.84905284286371: 1, 75.45 753982392108: 1, 75.30476575942032: 1, 71.54022524569686: 1, 70.376042141475 7: 1, 68.80946517189231: 1, 67.8648497135477: 1, 66.99858509571406: 1, 65.000 89234226651: 1, 64.4994979092931: 1, 64.48339428373531: 1, 64.22615208347595: 1, 64.0695401704742: 1, 62.40330828692051: 1, 61.85172383226394: 1, 61.464505 86846852: 1, 60.21434604133533: 1, 57.67073243156497: 1, 56.68992818531152: 1, 56.675335732710174: 1, 52.05014833469474: 1, 50.247046378325614: 1, 49.689 596070229165: 1, 49.16069461304344: 1, 47.894625007429546: 1, 47.680522724000 09: 1, 47.629160743771735: 1, 47.14234960756658: 1, 46.01537197330936: 1, 45. 48687032548178: 1, 44.71128918598107: 1, 44.053050187498336: 1, 43.7342498417 3358: 1, 43.30242601252255: 1, 43.229421950546346: 1, 43.15180697991381: 1, 4 2.85843927307464: 1, 42.30386028387075: 1, 42.185538218165156: 1, 42.15504656 4230204: 1, 42.07128584379701: 1, 41.51099956603417: 1, 41.41522850116809: 1, 41.33780450664496: 1, 41.32926373513186: 1, 40.095283494183526: 1, 40.0441663 91715116: 1, 39.98992846138894: 1, 39.45686279215865: 1, 39.341366256091845: 1, 38.83324658486234: 1, 38.51652280555914: 1, 38.340903813880296: 1, 38.1991 5115487085: 1, 37.548203756727126: 1, 37.4464021443145: 1, 36.79797586704470 5: 1, 36.61007360138737: 1, 36.41420644450772: 1, 36.31143674705824: 1, 35.96 056092875907: 1, 35.55234088425858: 1, 35.35009724272548: 1, 34.811428122244 5: 1, 34.79245594811209: 1, 34.59398410202698: 1, 34.32026974591977: 1, 34.10 4981365332364: 1, 34.03874462334645: 1, 33.896027508946894: 1, 33.61471764092 626: 1, 33.46999074650181: 1, 33.0282863722076: 1, 33.017832129935286: 1, 32. 91696287606172: 1, 32.8689336139438: 1, 32.670248170982326: 1, 32.62507774300 3985: 1, 32.32284376084956: 1, 31.998335485344448: 1, 31.93452084629748: 1, 3 1.82158252828258: 1, 31.633985149728886: 1, 31.62283189217166: 1, 31.60530015 0755323: 1, 31.60351912271884: 1, 31.59565102401618: 1, 31.416866591354232: 1, 31.310718058170842: 1, 31.258469028325248: 1, 31.231025456199344: 1, 31.22 192394021683: 1, 31.154442825408033: 1, 31.129145989675095: 1, 30.96122435970 4765: 1, 30.918180267140663: 1, 30.856349584786578: 1, 30.790579512148827: 1, 30.644717161843854: 1, 30.614764406877455: 1, 30.604680774783084: 1, 30.29455 1603061034: 1, 30.291388997104757: 1, 30.27394044634792: 1, 30.04844589248926 6: 1, 29.64016128294162: 1, 29.51855109143011: 1, 29.36061881947653: 1, 29.30 0426946080755: 1, 29.257088537672317: 1, 28.9630384222879: 1, 28.789105009542 386: 1, 28.37401769052743: 1, 27.938364366963338: 1, 27.8774046853039: 1, 27. 834050413603318: 1, 27.791870460209886: 1, 27.756402999568962: 1, 27.68650914 5258533: 1, 27.500964308711133: 1, 27.359436614034692: 1, 27.2622892708659: 1, 26.979290594271063: 1, 26.958456133544598: 1, 26.787594077164805: 1, 26.75 5061259218973: 1, 26.351168258749375: 1, 26.28931850717165: 1, 26.26762405306 0494: 1, 26.031948714679245: 1, 26.021916969679967: 1, 26.010377008055727: 1, 25.904920193257546: 1, 25.75477387078562: 1, 25.67385649995869: 1, 25.6731226 44889784: 1, 25.64215995891992: 1, 25.519891604641074: 1, 25.359686098995844: 1, 25.312097388178678: 1, 25.00127806537085: 1, 24.92463508286752: 1, 24.9121 54031072717: 1, 24.82558507395981: 1, 24.81658918800779: 1, 24.71213138623944 5: 1, 24.67814689037456: 1, 24.534286341134855: 1, 24.47770874394808: 1, 24.4 6183712302472: 1, 24.422328383498677: 1, 24.397546861205853: 1, 24.3736370097 48013: 1, 24.131079633355235: 1, 24.11500582328209: 1, 24.09087623525415: 1, 24.044049388024042: 1, 24.033824553651254: 1, 24.026485634527695: 1, 24.00027 205448451: 1, 23.989130747511783: 1, 23.74674628383244: 1, 23.56582602202909 3: 1, 23.546873257649448: 1, 23.40696297956194: 1, 23.3681187254458: 1, 23.22 8484378142277: 1, 23.212878028078205: 1, 23.191097300262424: 1, 23.1397231858 0417: 1, 23.032335073931474: 1, 22.954162279314893: 1, 22.852128063832524: 1, 22.807278833768162: 1, 22.805505784777445: 1, 22.752918365524955: 1, 22.72505

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```
In [47]: | # Train a Logistic regression+Calibration model using text features whicha
          re on-hot encoded
         alpha = [10 ** x for x in range(-5, 1)]
         # read more about SGDClassifier() at http://scikit-learn.org/stable/module
         s/generated/sklearn.linear_model.SGDClassifier.html
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fi
         t_intercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learni
         ng_rate='optimal', eta0=0.0, power_t=0.5,
         # class_weight=None, warm_start=False, average=False, n_iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])
Fit linear model with Stoch
         astic Gradient Descent.
         # predict(X)
                      Predict class labels for samples in X.
         #-----
         # video link:
         cv_log_error_array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train_text_feature_onehotCoding, y_train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train text feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv text feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes
         , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, pr
         edict_y, labels=clf.classes_, eps=1e-15))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
             ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i
         1))
         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', rand
         om state=42)
         clf.fit(train_text_feature_onehotCoding, y_train)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train text feature onehotCoding, y train)
```

```
predict_y = sig_clf.predict_proba(train_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss
is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validati
on log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss
is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.1247373975259722

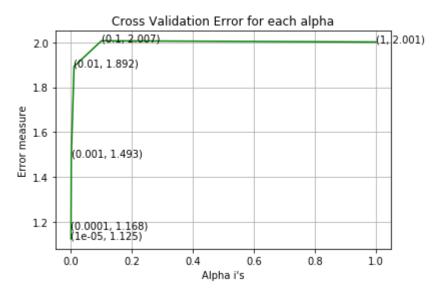
For values of alpha = 0.0001 The log loss is: 1.1684605363001976

For values of alpha = 0.001 The log loss is: 1.492688662666901

For values of alpha = 0.01 The log loss is: 1.8923232486472448

For values of alpha = 0.1 The log loss is: 2.006500608840076

For values of alpha = 1 The log loss is: 2.0012330027725733
```



```
For values of best alpha = 1e-05 The train log loss is: 0.7894093294625585
For values of best alpha = 1e-05 The cross validation log loss is: 1.1247373
975259722
For values of best alpha = 1e-05 The test log loss is: 1.1062789750449955
```

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

Ans. Yes, it seems like!

```
In [48]: def get_intersec_text(df):
    df_text_vec = TfidfVectorizer(min_df=3,max_features=1000)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

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

94.1 % of word of test data appeared in train data 93.4 % of word of Cross Validation appeared in train data

4. Machine Learning Models

```
In [50]: #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 bel
        ongs to each class
            print("Log loss :",log_loss(test_y, sig_clf.predict_proba(test_x)))
            # calculating the number of data points that are misclassified
            print("Number of mis-classified points :", np.count_nonzero((pred_y- test_y))/test_y.shape[0])
            plot_confusion_matrix(test_y, pred_y)
In [51]: def report_log_loss(train_x, train_y, test_x, test_y, clf):

**Clf fit(train_x, train_y)**

**Clf fit(tr
```

```
In [51]: 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 [52]: # 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]
                      ves no = True if word == gene else False
                      if yes no:
                          word present += 1
                          print(i, "Gene feature [{}] present in test data point [{}]".f
         ormat(word,yes_no))
                 elif (v < fea1 len+fea2 len):</pre>
                      word = var vec.get feature names()[v-(fea1 len)]
                      yes no = True if word == var else False
                      if yes no:
                          word present += 1
                          print(i, "variation feature [{}] present in test data point [
         {}]".format(word,yes no))
                 else:
                      word = text vec.get feature names()[v-(fea1 len+fea2 len)]
                      yes_no = True if word in text.split() else False
                      if yes_no:
                          word present += 1
                          print(i, "Text feature [{}] present in test data point [{}]".f
         ormat(word,yes no))
             print("Out of the top ",no_features," features ", word_present, "are prese
         nt in query point")
```

Stacking the three types of features

```
In [53]: # merging gene, variance and text features
         # building train, test and cross validation data sets
         \# \ a = [[1, 2],
                [3, 4]]
         #b = [[4, 5],
                [6, 7]]
          + hstack(a, b) = [[1, 2, 4, 5], 
                          [ 3, 4, 6, 7]]
         train gene var onehotCoding = hstack((train gene feature onehotCoding,train
         variation feature onehotCoding))
         test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_va
         riation feature onehotCoding))
         cv gene var onehotCoding = hstack((cv gene feature onehotCoding,cv variatio
         n_feature_onehotCoding))
         train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text_feat
         ure onehotCoding)).tocsr()
         train y = np.array(list(train df['Class']))
         test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_feature
          onehotCoding)).tocsr()
         test y = np.array(list(test df['Class']))
         cv x onehotCoding = hstack((cv gene var onehotCoding, cv text feature oneho
         tCoding)).tocsr()
         cv_y = np.array(list(cv_df['Class']))
         train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCodin
         g,train variation feature responseCoding))
         test gene var responseCoding = np.hstack((test gene feature responseCoding,
         test variation feature responseCoding))
         cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_v
         ariation feature responseCoding))
         train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_te
         xt feature responseCoding))
         test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_
         feature responseCoding))
         cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_featur
         e responseCoding))
```

```
In [54]: print("One hot encoding features :")
         print("(number of data points * number of features) in train data = ", train x
         onehotCoding.shape)
         print("(number of data points * number of features) in test data = ", test x o
         nehotCoding.shape)
         print("(number of data points * number of features) in cross validation data
          =", cv x onehotCoding.shape)
         One hot encoding features :
         (number of data points * number of features) in train data = (2124, 3198)
         (number of data points * number of features) in test data = (665, 3198)
         (number of data points * number of features) in cross validation data = (532,
         3198)
In [55]: print(" Response encoding features :")
         print("(number of data points * number of features) in train data = ", train x
         responseCoding.shape)
         print("(number of data points * number of features) in test data = ", test x r
         esponseCoding.shape)
         print("(number of data points * number of features) in cross validation data
          =", cv x responseCoding.shape)
          Response encoding features :
         (number of data points * number of features) in train data = (2124, 27)
         (number of data points * number of features) in test data = (665, 27)
         (number of data points * number of features) in cross validation data = (532,
         27)
```

4.1. Base Line Model

4.1.1. Naive Bayes

4.1.1.1. Hyper parameter tuning

```
In [56]: # find more about Multinomial Naive base function here http://scikit-learn.
         org/stable/modules/generated/sklearn.naive bayes.MultinomialNB.html
         # default paramters
         # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=
         None)
         # some of methods of MultinomialNB()
         # fit(X, y[, sample weight]) Fit Naive Bayes classifier according to X,
         # predict(X) Perform classification on an array of test vectors X.
         # predict_log_proba(X) Return log-probability estimates for the test vecto
         r X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-onli
         ne/lessons/naive-bayes-algorithm-1/
         # -----
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/st
         able/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='s
         igmoid', cv=3)
         #
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample_weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-onli
         ne/lessons/naive-bayes-algorithm-1/
         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.clas
         ses_, eps=1e-15))
             # to avoid rounding error while multiplying probabilites we use log-pro
         bability estimates
             print("Log Loss :",log loss(cv y, sig clf probs))
         fig, ax = plt.subplots()
         ax.plot(np.log10(alpha), cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv_log_error_array
```

```
[i]))
plt.grid()
plt.xticks(np.log10(alpha))
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = MultinomialNB(alpha=alpha[best alpha])
clf.fit(train_x_onehotCoding, train_y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss
is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validati
on log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss
 is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-05

Log Loss: 1.2121675202969273

for alpha = 0.0001

Log Loss: 1.2114320662173117

for alpha = 0.001

Log Loss: 1.21020483263532

for alpha = 0.1

Log Loss: 1.260445134193953

for alpha = 1

Log Loss: 1.3429752823187375

for alpha = 10

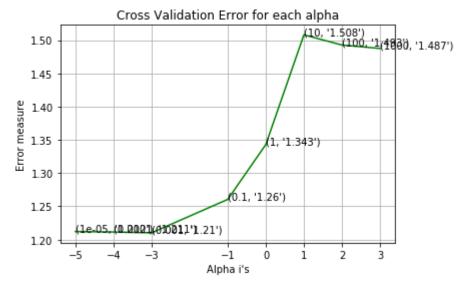
Log Loss: 1.5079178909241846

for alpha = 100

Log Loss: 1.4925606745817082

for alpha = 1000

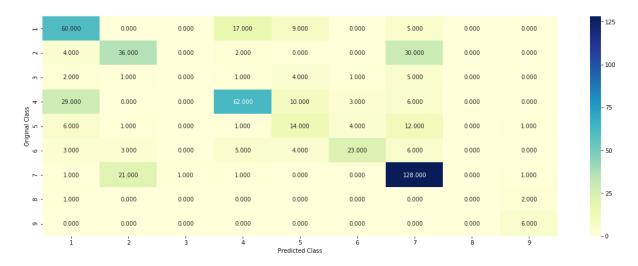
Log Loss: 1.487397594355744

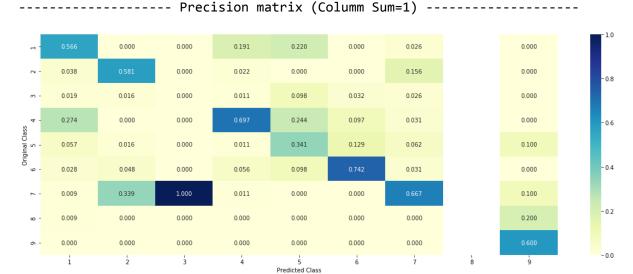


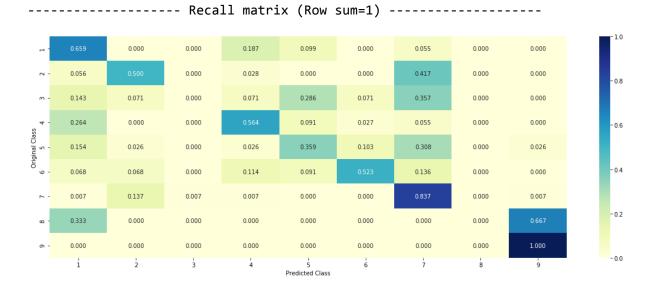
For values of best alpha = 0.001 The train log loss is: 0.532888131953395 For values of best alpha = 0.001 The cross validation log loss is: 1.2102048 3263532 For values of best alpha = 0.001 The test log loss is: 1.181352005765107

4.1.1.2. Testing the model with best hyper paramters

In [57]: # find more about Multinomial Naive base function here http://scikit-learn.or q/stable/modules/generated/sklearn.naive bayes.MultinomialNB.html # default paramters # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=Non e) # 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 Χ. # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/ lessons/naive-bayes-algorithm-1/ # find more about CalibratedClassifierCV here at http://scikit-learn.org/stabl e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html # -----# default paramters # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm oid', cv=3) # some of the methods of CalibratedClassifierCV() # fit(X, y[, sample weight]) Fit the calibrated model # get_params([deep]) Get parameters for this estimator. # predict(X) Predict the target of new samples. # predict proba(X) Posterior probabilities of classification clf = MultinomialNB(alpha=alpha[best alpha]) clf.fit(train x onehotCoding, train y) sig_clf = CalibratedClassifierCV(clf, method="sigmoid") sig_clf.fit(train_x_onehotCoding, train_y) sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding) # to avoid rounding error while multiplying probabilites we use log-probabilit v estimates print("Log Loss :",log_loss(cv_y, sig_clf_probs)) print("Number of missclassified point :", np.count_nonzero((sig_clf.predict(cv x onehotCoding)- cv y))/cv y.shape[0]) plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray()))







4.1.1.3. Feature Importance, Correctly classified point

```
In [58]: | test point index = 1
         no feature = 100
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x
         onehotCoding[test_point_index]),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.0625 0.049 0.0105 0.0687 0.0296 0.0286 0.
         7442 0.0046 0.0023]]
         Actual Class: 7
         36 Text feature [114] present in test data point [True]
         49 Text feature [117] present in test data point [True]
         60 Text feature [130] present in test data point [True]
         74 Text feature [11] present in test data point [True]
         79 Text feature [110] present in test data point [True]
         99 Text feature [106] present in test data point [True]
         Out of the top 100 features 6 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

```
In [59]: | test_point_index = 100
         no feature = 100
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test point index]),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.063 0.0668 0.0133 0.0646 0.0308 0.0298 0.
         7244 0.0048 0.002411
         Actual Class : 7
         74 Text feature [11] present in test data point [True]
         Out of the top 100 features 1 are present in query point
```

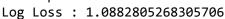
4.2. K Nearest Neighbour Classification

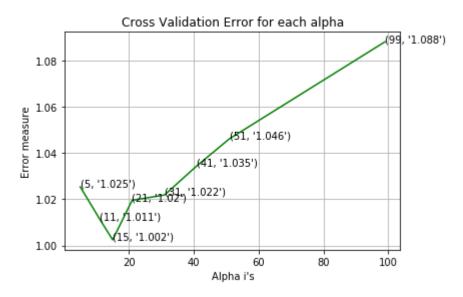
4.2.1. Hyper parameter tuning

```
In [83]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stabl
         e/modules/generated/sklearn.neighbors.KNeighborsClassifier.html
         # -----
         # default parameter
         # KNeighborsClassifier(n neighbors=5, weights='uniform', algorithm='auto',
         leaf size=30, p=2,
         # 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-onli
         ne/lessons/k-nearest-neighbors-geometric-intuition-with-a-toy-example-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/st
         able/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='s
         igmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         #-----
         # video link:
         alpha = [5, 11, 15, 21, 31, 41, 51, 99]
         cv log error array = []
         for i in alpha:
             print("for alpha =", i)
             clf = KNeighborsClassifier(n neighbors=i)
             clf.fit(train_x_responseCoding, train_y)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train x responseCoding, train y)
             sig clf probs = sig clf.predict proba(cv x responseCoding)
             cv log error array.append(log loss(cv y, sig clf probs, labels=clf.clas
         ses_, eps=1e-15))
             # to avoid rounding error while multiplying probabilites we use log-pro
         bability estimates
             print("Log Loss :",log loss(cv y, sig clf probs))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
             ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
         plt.title("Cross Validation Error for each alpha")
```

```
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x responseCoding, train y)
predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss
is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validati
on log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss
 is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

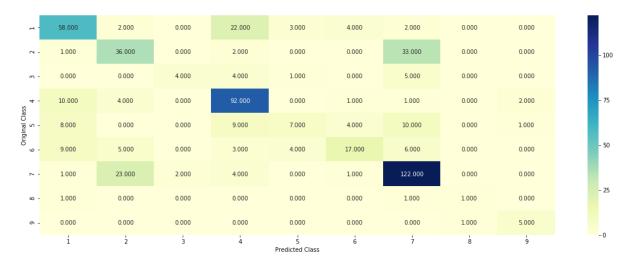
for alpha = 5Log Loss: 1.0254040126027122 for alpha = 11Log Loss: 1.0114376021287863 for alpha = 15Log Loss: 1.002444969002307 for alpha = 21Log Loss: 1.0195860069386846 for alpha = 31Log Loss: 1.02188287913295 for alpha = 41Log Loss: 1.0345527745182799 for alpha = 51Log Loss: 1.0462259378800565 for alpha = 99



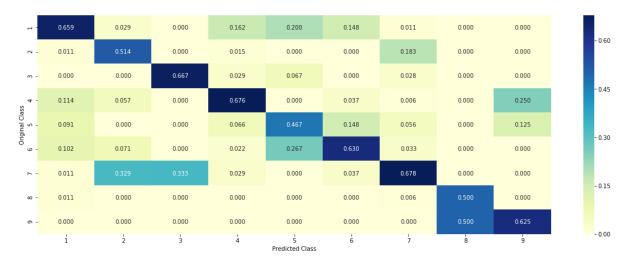


For values of best alpha = 15 The train log loss is: 0.6955823832520973 For values of best alpha = 15 The cross validation log loss is: 1.0024449690 02307 For values of best alpha = 15 The test log loss is: 1.0994540919206754

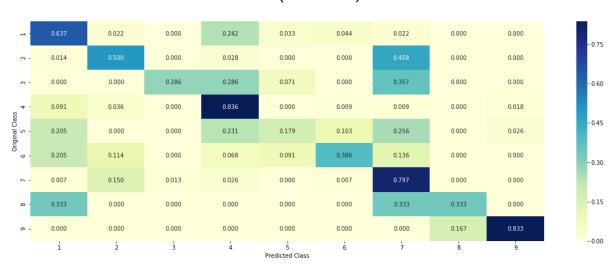
4.2.2. Testing the model with best hyper paramters







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



4.2.3. Sample Query point -1

```
In [85]: | clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
         clf.fit(train x responseCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x responseCoding, train y)
         test_point_index = 1
         predicted cls = sig clf.predict(test x responseCoding[0].reshape(1,-1))
         print("Predicted Class :", predicted cls[0])
         print("Actual Class :", test_y[test_point_index])
         neighbors = clf.kneighbors(test_x_responseCoding[test_point_index].reshape(1,
         -1), alpha[best alpha])
         print("The ",alpha[best_alpha]," nearest neighbours of the test points belongs
          to classes",train_y[neighbors[1][0]])
         print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
         Predicted Class: 4
         Actual Class : 1
         The 15 nearest neighbours of the test points belongs to classes [1 1 1 1 4
         4 4 4 1 1 1 1 1 1 1 1
         Fequency of nearest points : Counter({1: 11, 4: 4})
```

4.2.4. Sample Query Point-2

```
In [86]: | 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].reshap
         e(1,-1)
         print("Predicted Class :", predicted_cls[0])
         print("Actual Class :", test_y[test_point_index])
         neighbors = clf.kneighbors(test x responseCoding[test point index].reshape(1,
         -1), alpha[best alpha])
         print("the k value for knn is",alpha[best alpha],"and the nearest neighbours o
         f the test points belongs to classes",train_y[neighbors[1][0]])
         print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
         Predicted Class: 2
         Actual Class: 2
         the k value for knn is 15 and the nearest neighbours of the test points belon
         gs to classes [2 2 2 2 2 2 2 1 2 2 7 2 2 8 2]
         Fequency of nearest points : Counter({2: 12, 1: 1, 7: 1, 8: 1})
```

4.3. Logistic Regression

4.3.1. With Class balancing

4.3.1.1. Hyper paramter tuning

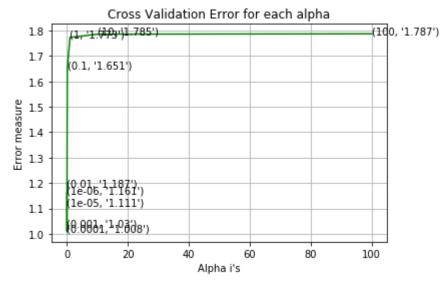
```
In [87]: | # read more about SGDClassifier() at http://scikit-learn.org/stable/module
         s/generated/sklearn.linear_model.SGDClassifier.html
         # ------
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fi
         t_intercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learni
         ng rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         astic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-onli
         ne/lessons/geometric-intuition-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/st
         able/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='s
         igmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         #-----
         # video link:
         alpha = [10 ** x for x in range(-6, 3)]
         cv log error array = []
         for i in alpha:
            print("for alpha =", i)
            clf = SGDClassifier(class weight='balanced', alpha=i, penalty='12', los
         s='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.clas
         ses_, eps=1e-15))
            # to avoid rounding error while multiplying probabilites we use log-pro
         bability estimates
            print("Log Loss :",log_loss(cv_y, sig_clf_probs))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
```

```
ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penal
ty='12', loss='log', random_state=42)
clf.fit(train_x_onehotCoding, train_y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss
is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validati
on log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss
is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-06Log Loss: 1.1606135137247384 for alpha = 1e-05Log Loss: 1.1114105288260316 for alpha = 0.0001Log Loss: 1.0080198815848118 for alpha = 0.001Log Loss: 1.030198911248978 for alpha = 0.01Log Loss: 1.1871596843655539 for alpha = 0.1Log Loss: 1.6508501605551202 for alpha = 1Log Loss: 1.772762870119923 for alpha = 10Log Loss: 1.7854754264378672

for alpha = 100

Log Loss: 1.7869227091967115



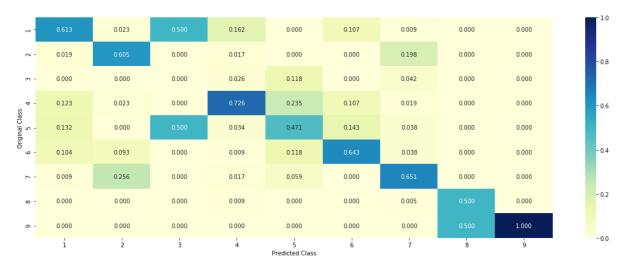
For values of best alpha = 0.0001 The train log loss is: 0.45414080100555276 For values of best alpha = 0.0001 The cross validation log loss is: 1.008019 8815848118 For values of best alpha = 0.0001 The test log loss is: 1.085766661069436

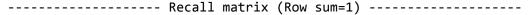
4.3.1.2. Testing the model with best hyper paramters

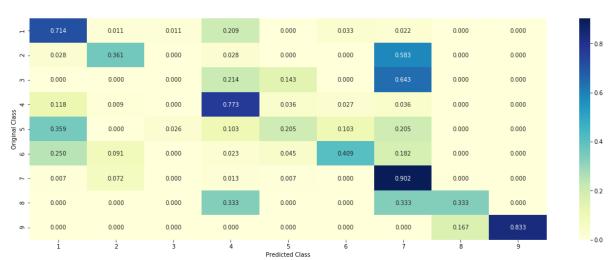
In [88]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge nerated/sklearn.linear model.SGDClassifier.html # -----# default parameters # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i ntercept=True, max_iter=None, tol=None, # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_ rate='optimal', eta0=0.0, power t=0.5, # class weight=None, warm start=False, average=False, n iter=None) # some of methods # fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochast ic Gradient Descent. # predict(X) Predict class labels for samples in X. # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/ lessons/geometric-intuition-1/ #----clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty= '12', loss='log', random state=42) predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCo ding, cv_y, clf)











4.3.1.3. Feature Importance

```
In [89]: 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], ye
         s_no])
                  incresingorder ind += 1
             print(word present, "most importent features are present in our query poin
         t")
             print("-"*50)
             print("The features that are most importent of the ",predicted cls[0]," cl
             print (tabulate(tabulte list, headers=["Index", 'Feature name', 'Present or
          Not']))
```

4.3.1.3.1. Correctly Classified point

```
In [90]: # from tabulate import tabulate
         clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty=
         '12', loss='log', random_state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test d
         f['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index],
         no_feature)
         Predicted Class: 1
         Predicted Class Probabilities: [[7.133e-01 1.200e-03 7.000e-04 2.500e-01 4.10
         0e-03 1.200e-03 2.830e-02
           7.000e-04 4.000e-04]]
         Actual Class: 1
         479 Text feature [01] present in test data point [True]
         493 Text feature [12] present in test data point [True]
         Out of the top 500 features 2 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

```
In [91]: test point index = 100
         no feature = 500
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x
         onehotCoding[test_point_index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index],
         no feature)
         Predicted Class: 2
         Predicted Class Probabilities: [[3.140e-01 6.162e-01 1.200e-03 3.500e-03 8.50
         0e-03 7.800e-03 4.290e-02
           5.600e-03 4.000e-04]]
         Actual Class : 2
         205 Text feature [100] present in test data point [True]
         256 Text feature [007] present in test data point [True]
         498 Text feature [130] present in test data point [True]
         Out of the top 500 features 3 are present in query point
```

4.3.2. Without Class balancing

4.3.2.1. Hyper paramter tuning

```
In [92]: # read more about SGDClassifier() at http://scikit-learn.org/stable/module
         s/generated/sklearn.linear_model.SGDClassifier.html
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fi
         t_intercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learni
         ng_rate='optimal', eta0=0.0, power_t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         astic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-onli
         ne/lessons/geometric-intuition-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/st
         able/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='s
         igmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample_weight])
Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         # video link:
         alpha = [10 ** x for x in range(-6, 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.clas
         ses_, eps=1e-15))
             print("Log Loss :",log_loss(cv_y, sig_clf_probs))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
             ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
         plt.grid()
```

```
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', rand
om state=42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss
is:",log loss(y train, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validati
on log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss
is:",log loss(y test, predict y, labels=clf.classes , eps=1e-15))
```

for alpha = 1e-06

Log Loss: 1.1489024799541627

for alpha = 1e-05

Log Loss: 1.1369452931007258

for alpha = 0.0001

Log Loss: 1.0439245420295757

for alpha = 0.001

Log Loss: 1.137345428345129

for alpha = 0.01

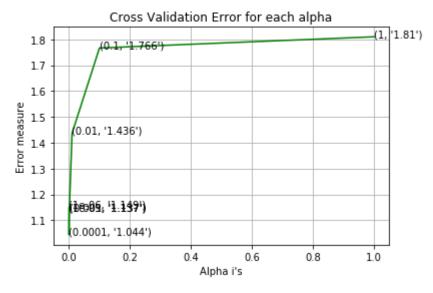
Log Loss: 1.4364673945364395

for alpha = 0.1

Log Loss: 1.7663719394560455

for alpha = 1

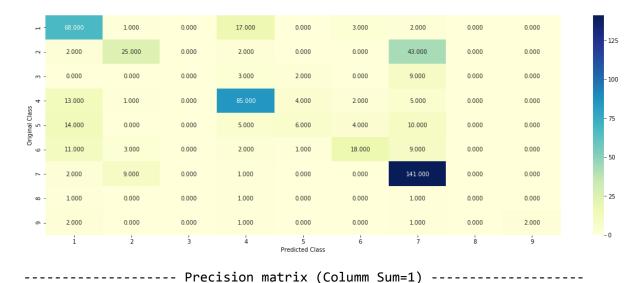
Log Loss: 1.809640751267211

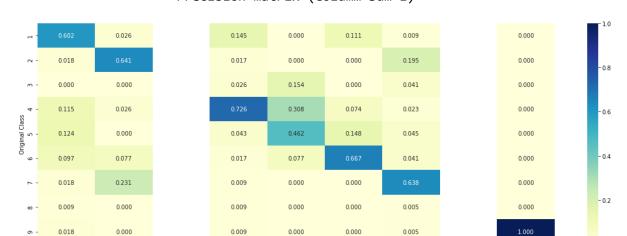


For values of best alpha = 0.0001 The train log loss is: 0.4449326181903318 For values of best alpha = 0.0001 The cross validation log loss is: 1.043924 5420295757 For values of best alpha = 0.0001 The test log loss is: 1.1144306955241083

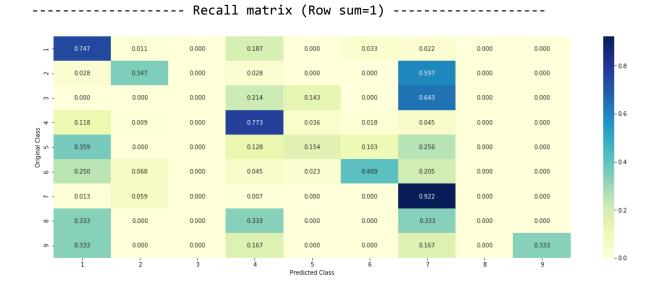
4.3.2.2. Testing model with best hyper parameters

In [93]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge nerated/sklearn.linear model.SGDClassifier.html # -----# default parameters # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i ntercept=True, max_iter=None, tol=None, # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_ rate='optimal', eta0=0.0, power t=0.5, # class weight=None, warm start=False, average=False, n iter=None) # some of methods # fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochast ic Gradient Descent. # predict(X) Predict class labels for samples in X. # video link: #----clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42) predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCo ding, cv_y, clf)





Predicted Class



4.3.2.3. Feature Importance, Correctly Classified point

-0.0

```
In [94]: clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random
         state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         no feature = 500
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x
         onehotCoding[test point index]),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
         Predicted Class: 1
         Predicted Class Probabilities: [[6.841e-01 1.000e-03 6.000e-04 2.733e-01 3.20
         0e-03 1.000e-03 3.660e-02
           1.000e-04 1.000e-04]]
         Actual Class: 1
         478 Text feature [12] present in test data point [True]
         Out of the top 500 features 1 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

```
In [95]: | test point index = 100
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test_point_index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test d
         f['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index],
         no feature)
         Predicted Class: 2
         Predicted Class Probabilities: [[3.297e-01 6.050e-01 1.400e-03 3.800e-03 8.00
         0e-03 8.200e-03 4.120e-02
           2.500e-03 1.000e-04]]
         Actual Class : 2
         199 Text feature [100] present in test data point [True]
         252 Text feature [007] present in test data point [True]
         Out of the top 500 features 2 are present in query point
```

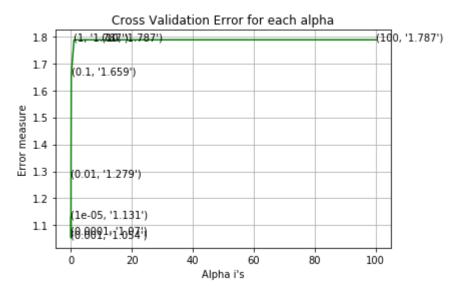
4.4. Linear Support Vector Machines

4.4.1. Hyper paramter tuning

```
In [96]: # read more about support vector machines with linear kernals here http://s
         cikit-learn.org/stable/modules/generated/sklearn.svm.SVC.html
         # default parameters
         # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=Tru
         e, probability=False, tol=0.001,
         # cache size=200, class weight=None, verbose=False, max iter=-1, decision f
         unction shape='ovr', random state=None)
         # Some of methods of SVM()
         aining data.
                     Perform classification on samples in X.
         # predict(X)
         # -----
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-onli
         ne/lessons/mathematical-derivation-copy-8/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/st
         able/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='s
         igmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         #----
         # video link:
         alpha = [10 ** x for x in range(-5, 3)]
         cv log error array = []
         for i in alpha:
            print("for C =", i)
              clf = SVC(C=i,kernel='linear',probability=True, class_weight='balance
         d')
            clf = SGDClassifier( class weight='balanced', alpha=i, penalty='12', lo
         ss='hinge', random state=42)
            clf.fit(train x onehotCoding, train y)
            sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train x onehotCoding, train y)
            sig clf probs = sig clf.predict proba(cv x onehotCoding)
            cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.clas
         ses_, eps=1e-15))
            print("Log Loss :",log_loss(cv_y, sig_clf_probs))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
```

```
ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
# clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced')
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penal
ty='12', loss='hinge', random_state=42)
clf.fit(train x onehotCoding, train y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss
is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validati
on log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss
 is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

for C = 1e-05Log Loss: 1.1305189006522445 for C = 0.0001Log Loss: 1.0704526192304331 for C = 0.001Log Loss: 1.0535154592796154 for C = 0.01Log Loss: 1.27927436726999 for C = 0.1Log Loss: 1.659327426281127 for C = 1Log Loss: 1.7873552689367513 for C = 10Log Loss: 1.7873964859737401 for C = 100Log Loss: 1.7873965282492525



For values of best alpha = 0.001 The train log loss is: 0.6100553816346953

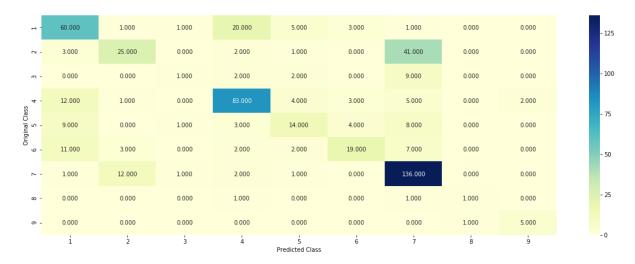
For values of best alpha = 0.001 The cross validation log loss is: 1.0535154

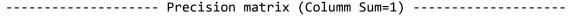
592796154

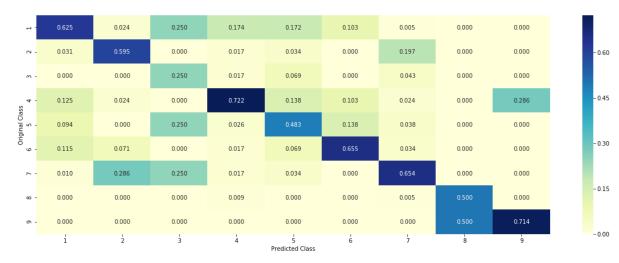
For values of best alpha = 0.001 The test log loss is: 1.1570737313499444

4.4.2. Testing model with best hyper parameters

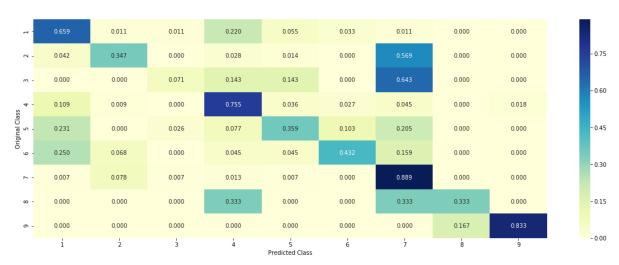
In [97]: # read more about support vector machines with linear kernals here http://scik it-learn.org/stable/modules/generated/sklearn.svm.SVC.html # default parameters # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001, # cache size=200, class weight=None, verbose=False, max iter=-1, decision func tion shape='ovr', random state=None) # Some of methods of SVM() ing data. # predict(X) Perform classification on samples in X. # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/ lessons/mathematical-derivation-copy-8/ # clf = SVC(C=alpha[best alpha],kernel='linear',probability=True, class weight = 'balanced') clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', rando m state=42,class weight='balanced') predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCod ing, cv y, clf)











4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

```
In [98]: clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', rando
         m state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         # test point index = 100
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test_point_index]),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no_feature)
         Predicted Class : 1
         Predicted Class Probabilities: [[0.6621 0.0038 0.0034 0.2389 0.0105 0.0061 0.
         0734 0.0009 0.0011]]
         Actual Class: 1
         436 Text feature [12] present in test data point [True]
         Out of the top 500 features 1 are present in query point
```

4.3.3.2. For Incorrectly classified point

```
In [99]: | test point index = 100
         no feature = 500
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index],
         no feature)
         Predicted Class: 2
         Predicted Class Probabilities: [[0.3658 0.4821 0.0096 0.0135 0.0168 0.0172 0.
         0887 0.0046 0.0017]]
         Actual Class : 2
         195 Text feature [100] present in test data point [True]
         380 Text feature [007] 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)

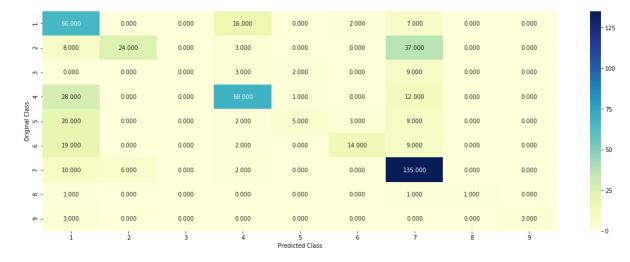
```
In [100]: # -----
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qin
          i', max depth=None, min samples split=2,
          # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', ma
          x_leaf_nodes=None, min_impurity_decrease=0.0,
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, rando
          m state=None, verbose=0, warm start=False,
          # class weight=None)
          # Some of methods of RandomForestClassifier()
          aining data.
          # predict(X)
                        Perform classification on samples in X.
          \# predict proba (X) Perform classification on samples in X.
          # some of attributes of RandomForestClassifier()
          # feature_importances_ : array of shape = [n_features]
          # The feature importances (the higher, the more important the feature).
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-onli
          ne/Lessons/random-forest-and-their-construction-2/
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/st
          able/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='s
          igmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight]) Fit the calibrated model
          # get params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          # video link:
          alpha = [100, 200, 500, 1000, 2000]
          max depth = [5, 10]
          cv log error array = []
          for i in alpha:
              for j in max_depth:
                  print("for n_estimators =", i,"and max depth = ", j)
                  clf = RandomForestClassifier(n estimators=i, criterion='gini', max
          depth=j, random state=42, n jobs=-1)
                  clf.fit(train x onehotCoding, train y)
                  sig clf = CalibratedClassifierCV(clf, method="sigmoid")
                  sig_clf.fit(train_x_onehotCoding, train_y)
                  sig clf probs = sig clf.predict proba(cv x onehotCoding)
                  cv log error array.append(log loss(cv y, sig clf probs, labels=clf.
          classes_, eps=1e-15))
```

```
print("Log Loss :",log_loss(cv_y, sig_clf_probs))
'''fiq, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel
()
ax.plot(features, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[int(i/2)],max_depth[int(i%2)],str(txt)), (features
[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criteri
on='gini', max depth=max depth[int(best alpha%2)], random state=42, n jobs=
-1)
clf.fit(train_x_onehotCoding, train_y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The tra
in log loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-1
5))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cro
ss validation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_,
eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The tes
t log loss is:",log loss(y test, predict y, labels=clf.classes , eps=1e-15
))
```

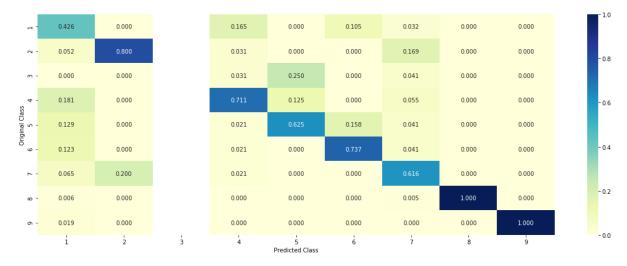
```
for n_{estimators} = 100 and max depth = 5
Log Loss: 1.2197473597430186
for n_estimators = 100 and max depth =
Log Loss: 1.2545533786251462
for n estimators = 200 and max depth = 5
Log Loss: 1.2115629351379342
for n_estimators = 200 and max depth = 10
Log Loss: 1.245005728263018
for n_estimators = 500 and max depth = 5
Log Loss: 1.2051687599657477
for n estimators = 500 and max depth = 10
Log Loss: 1.226881295568145
for n estimators = 1000 and max depth = 5
Log Loss: 1.2024090061217978
for n_estimators = 1000 and max depth = 10
Log Loss: 1.2256288509371314
for n_estimators = 2000 and max depth = 5
Log Loss: 1.1977331525635675
for n estimators = 2000 and max depth = 10
Log Loss: 1.226825408244335
For values of best estimator = 2000 The train log loss is: 0.862688610335302
For values of best estimator = 2000 The cross validation log loss is: 1.1977
331525635675
For values of best estimator = 2000 The test log loss is: 1.2328726593828045
```

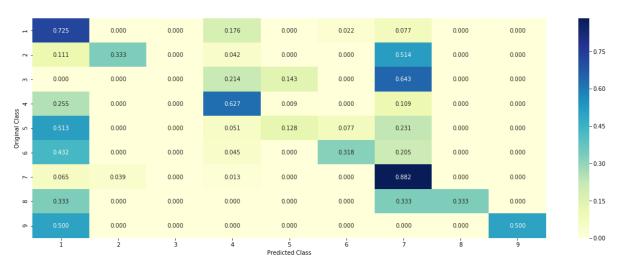
4.5.2. Testing model with best hyper parameters (One Hot Encoding)

```
In [101]:
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qin
          i', max depth=None, min samples split=2,
          # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', ma
          x_leaf_nodes=None, min_impurity_decrease=0.0,
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, rando
          m state=None, verbose=0, warm start=False,
          # class weight=None)
          # Some of methods of RandomForestClassifier()
          aining data.
          # predict(X)
                       Perform classification on samples in X.
          \# predict proba (X) Perform classification on samples in X.
          # some of attributes of RandomForestClassifier()
          # feature_importances_ : array of shape = [n_features]
          # The feature importances (the higher, the more important the feature).
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-onli
          ne/Lessons/random-forest-and-their-construction-2/
          clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criteri
          on='gini', max depth=max depth[int(best alpha%2)], random state=42, n jobs=
          -1)
          predict and plot confusion matrix(train x onehotCoding, train y,cv x onehot
          Coding,cv_y, clf)
```









4.5.3. Feature Importance

4.5.3.1. Correctly Classified point

```
In [102]: | # test_point_index = 10
          clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion=
          'gini', max_depth=max_depth[int(best_alpha%2)], random_state=42, n_jobs=-1)
          clf.fit(train x onehotCoding, train y)
          sig clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(train_x_onehotCoding, train_y)
          test point index = 1
          no feature = 100
          predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
          onehotCoding[test_point_index]),4))
          print("Actual Class :", test y[test point index])
          indices = np.argsort(-clf.feature_importances_)
          print("-"*50)
          get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point ind
          ex],test df['Gene'].iloc[test point index],test df['Variation'].iloc[test poin
          t_index], no_feature)
          Predicted Class: 1
          Predicted Class Probabilities: [[0.4581 0.0275 0.0117 0.3406 0.0425 0.0389 0.
          0542 0.0067 0.019911
          Actual Class: 1
          51 Text feature [01] present in test data point [True]
          Out of the top 100 features 1 are present in query point
```

4.5.3.2. Inorrectly Classified point

```
In [103]:
          test point index = 100
          no feature = 100
          predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x
          onehotCoding[test_point_index]),4))
          print("Actuall Class :", test_y[test_point_index])
          indices = np.argsort(-clf.feature importances )
          print("-"*50)
          get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_point_ind
          ex],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index]
          t_index], no_feature)
          Predicted Class: 2
          Predicted Class Probabilities: [[0.2706 0.3429 0.014 0.0505 0.0491 0.043 0.
          1682 0.0533 0.0084]]
          Actuall Class : 2
          40 Text feature [016] present in test data point [True]
          51 Text feature [01] present in test data point [True]
          Out of the top 100 features 2 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

```
In [104]: # -----
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qin
          i', max depth=None, min samples split=2,
          # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', ma
          x_leaf_nodes=None, min_impurity_decrease=0.0,
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, rando
          m state=None, verbose=0, warm start=False,
          # class weight=None)
          # Some of methods of RandomForestClassifier()
          aining data.
          # predict(X)
                        Perform classification on samples in X.
          \# predict proba (X) Perform classification on samples in X.
          # some of attributes of RandomForestClassifier()
          # feature_importances_ : array of shape = [n_features]
          # The feature importances (the higher, the more important the feature).
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-onli
          ne/Lessons/random-forest-and-their-construction-2/
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/st
          able/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='s
          igmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight]) Fit the calibrated model
          # get params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          # video link:
          alpha = [10,50,100,200,500,1000]
          max depth = [2,3,5,10]
          cv log error array = []
          for i in alpha:
              for j in max_depth:
                  print("for n_estimators =", i,"and max depth = ", j)
                  clf = RandomForestClassifier(n estimators=i, criterion='gini', max
          depth=j, random state=42, n jobs=-1)
                 clf.fit(train x responseCoding, train y)
                 sig clf = CalibratedClassifierCV(clf, method="sigmoid")
                 sig_clf.fit(train_x_responseCoding, train_y)
                 sig clf probs = sig clf.predict proba(cv x responseCoding)
                  cv log error array.append(log loss(cv y, sig clf probs, labels=clf.
          classes_, eps=1e-15))
```

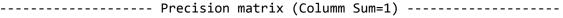
```
print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel
ax.plot(features, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[int(i/4)],max_depth[int(i%4)],str(txt)), (features
[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criteri
on='gini', max depth=max depth[int(best alpha%4)], random state=42, n jobs=
-1)
clf.fit(train_x_responseCoding, train_y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x responseCoding, train y)
predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The train 1
og loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best alpha/4)], "The cross v
alidation log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=
1e-15))
predict y = sig clf.predict proba(test x responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The test lo
g loss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

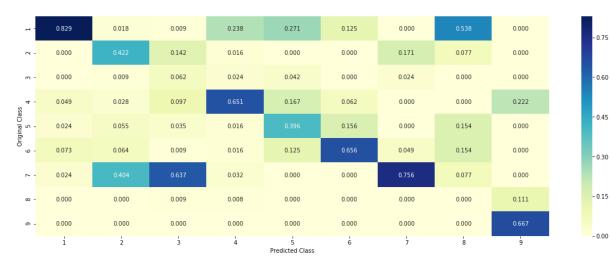
```
for n estimators = 10 and max depth = 2
Log Loss: 2.0739449723694237
for n_estimators = 10 and max depth = 3
Log Loss: 1.917175248913769
for n estimators = 10 and max depth = 5
Log Loss: 1.4849130320861939
for n estimators = 10 and max depth =
                                     10
Log Loss: 1.8515036146895019
for n_estimators = 50 and max depth =
Log Loss: 1.6980994399320763
for n estimators = 50 and max depth = 3
Log Loss: 1.4546012684762124
for n estimators = 50 and max depth = 5
Log Loss: 1.3652066289905578
for n_estimators = 50 and max depth = 10
Log Loss: 1.7137187273288592
for n estimators = 100 and max depth =
Log Loss: 1.5528883159699538
for n estimators = 100 and max depth = 3
Log Loss: 1.4711142034126652
for n_estimators = 100 and max depth =
Log Loss: 1.3394631195447033
for n estimators = 100 and max depth =
Log Loss: 1.6095756674027097
for n_estimators = 200 and max depth =
Log Loss: 1.600015478362364
for n estimators = 200 and max depth =
Log Loss: 1.4581907374982428
for n estimators = 200 and max depth = 5
Log Loss: 1.3939859621476538
for n_estimators = 200 and max depth =
Log Loss: 1.5961384874683142
for n estimators = 500 and max depth =
Log Loss: 1.6730148401917242
for n estimators = 500 and max depth =
Log Loss: 1.5441070633752967
for n_estimators = 500 and max depth =
Log Loss: 1.3899759720431726
for n estimators = 500 and max depth = 10
Log Loss: 1.6324415430949262
for n estimators = 1000 and max depth =
Log Loss: 1.6508458879057308
for n_estimators = 1000 and max depth = 3
Log Loss: 1.558795017418978
for n estimators = 1000 and max depth =
Log Loss: 1.3836282668889868
for n_estimators = 1000 and max depth = 10
Log Loss: 1.6108336152167182
For values of best alpha = 100 The train log loss is: 0.05745816213449988
For values of best alpha = 100 The cross validation log loss is: 1.339463119
5447033
For values of best alpha = 100 The test log loss is: 1.4474501410435336
```

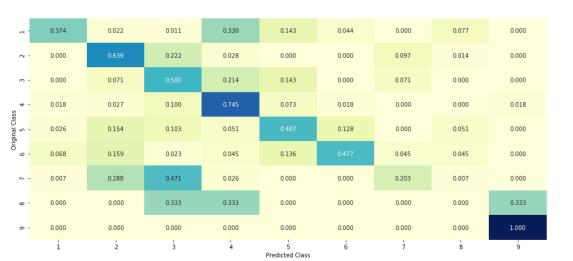
4.5.4. Testing model with best hyper parameters (Response Coding)

```
In [105]:
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', m
          ax depth=None, min samples split=2,
          # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max l
          eaf_nodes=None, min_impurity_decrease=0.0,
          # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random s
          tate=None, verbose=0, warm start=False,
          # class weight=None)
          # Some of methods of RandomForestClassifier()
          ing data.
          \# predict(X) Perform classification on samples in X.
          \# predict proba (X) Perform classification on samples in X.
          # some of attributes of RandomForestClassifier()
          # feature_importances_ : array of shape = [n_features]
          # The feature importances (the higher, the more important the feature).
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
          lessons/random-forest-and-their-construction-2/
          clf = RandomForestClassifier(max depth=max depth[int(best alpha%4)], n estimat
          ors=alpha[int(best alpha/4)], criterion='gini', max features='auto',random sta
          te=42)
          predict and plot confusion matrix(train x responseCoding, train y,cv x respons
          eCoding, cv y, clf)
```









4.5.5. Feature Importance

- 0.8

- 0.4

- 0.2

4.5.5.1. Correctly Classified point

```
In [106]: | clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion=
          'gini', max_depth=max_depth[int(best_alpha%4)], random_state=42, n_jobs=-1)
          clf.fit(train x responseCoding, train y)
          sig clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(train_x_responseCoding, train_y)
          test point index = 1
          no feature = 27
          predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshap
          e(1,-1)
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
          responseCoding[test point index].reshape(1,-1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.feature_importances_)
          print("-"*50)
          for i in indices:
              if i<9:
                  print("Gene is important feature")
              elif i<18:
                  print("Variation is important feature")
              else:
                  print("Text is important feature")
```

```
Predicted Class Probabilities: [[0.2354 0.0146 0.1212 0.4869 0.0288 0.0353 0.
0085 0.0337 0.0356]]
Actual Class : 1
_____
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
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.5.5.2. Incorrectly Classified point

Predicted Class: 4

```
In [107]: | test point index = 100
          predicted cls = sig clf.predict(test x responseCoding[test point index].reshap
          e(1,-1)
          print("Predicted Class :", predicted cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
          responseCoding[test_point_index].reshape(1,-1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.feature importances )
          print("-"*50)
          for i in indices:
              if i<9:
                   print("Gene is important feature")
              elif i<18:
                   print("Variation is important feature")
              else:
                   print("Text is important feature")
          Predicted Class: 2
          Predicted Class Probabilities: [[0.0336 0.522 0.0793 0.0372 0.0277 0.073 0.
          0782 0.0853 0.0638]]
          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
          Text is important feature
          Gene is important feature
          Text is important feature
          Text is important feature
          Gene is important feature
          Gene is important feature
          Variation is important feature
          Text is important feature
          Gene is important feature
          Variation is important feature
          Gene is important feature
          Text is important feature
          Text is important feature
          Gene is important feature
          Variation is important feature
```

4.7 Stack the models

Text is important feature Gene is important feature Gene is important feature

4.7.1 testing with hyper parameter tuning

```
In [108]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge
         nerated/sklearn.linear model.SGDClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit i
         ntercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_
         rate='optimal', eta0=0.0, power_t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         ic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
         lessons/geometric-intuition-1/
         # read more about support vector machines with linear kernals here http://scik
         it-learn.org/stable/modules/generated/sklearn.svm.SVC.html
         # default parameters
         # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True,
         probability=False, tol=0.001,
         # cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_func
         tion shape='ovr', random state=None)
         # Some of methods of SVM()
         ing data.
         \# predict(X) Perform classification on samples in X.
         # -----
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
         Lessons/mathematical-derivation-copy-8/
         # read more about support vector machines with linear kernals here http://scik
         it-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.
         html
         # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', m
         ax_depth=None, min_samples_split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max l
         eaf nodes=None, min impurity decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random s
         tate=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         ing data.
```

```
\# predict(X) Perform classification on samples in X.
# predict proba (X)
                       Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
lessons/random-forest-and-their-construction-2/
clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class weight='bala
nced', random state=0)
clf1.fit(train x onehotCoding, train y)
sig clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
clf2 = SGDClassifier(alpha=1, penalty='12', loss='hinge', class weight='balanc
ed', random state=0)
clf2.fit(train x onehotCoding, train y)
sig clf2 = CalibratedClassifierCV(clf2, method="sigmoid")
clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train x onehotCoding, train y)
sig_clf3 = CalibratedClassifierCV(clf3, method="sigmoid")
sig clf1.fit(train x onehotCoding, train y)
print("Logistic Regression : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf1.pred
ict_proba(cv_x_onehotCoding))))
sig clf2.fit(train x onehotCoding, train y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf2.p
redict proba(cv x onehotCoding))))
sig clf3.fit(train x onehotCoding, train y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba
(cv x onehotCoding))))
print("-"*50)
alpha = [0.0001, 0.001, 0.01, 0.1, 1, 10]
best alpha = 999
for i in alpha:
   lr = LogisticRegression(C=i)
   sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta
classifier=lr, use probas=True)
   sclf.fit(train x onehotCoding, train y)
   print("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" %
(i, log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))))
   log error =log loss(cv y, sclf.predict proba(cv x onehotCoding))
   if best alpha > log error:
        best_alpha = log_error
```

Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.357 Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.802

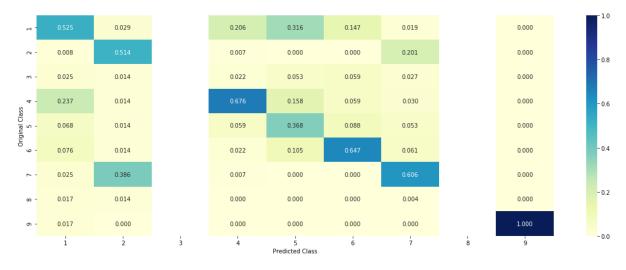
4.7.2 testing the model with the best hyper parameters

Log loss (train) on the stacking classifier: 0.5440122399697161 Log loss (CV) on the stacking classifier: 1.1536881218851502 Log loss (test) on the stacking classifier: 1.2323038106015556 Number of missclassified point: 0.4120300751879699

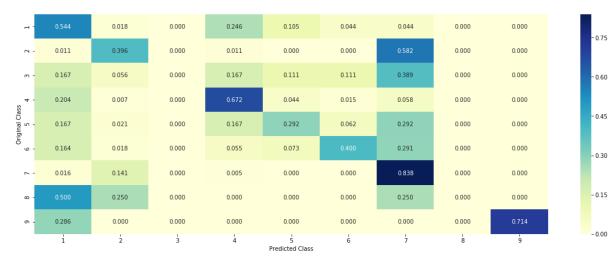
----- Confusion matrix ------



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



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



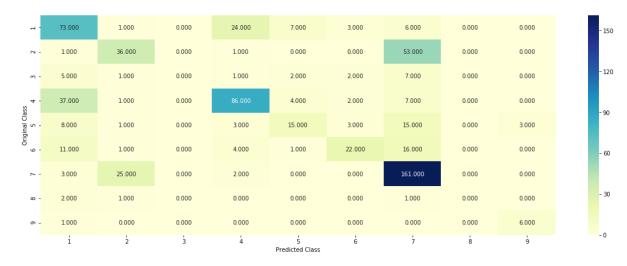
4.7.3 Maximum Voting classifier

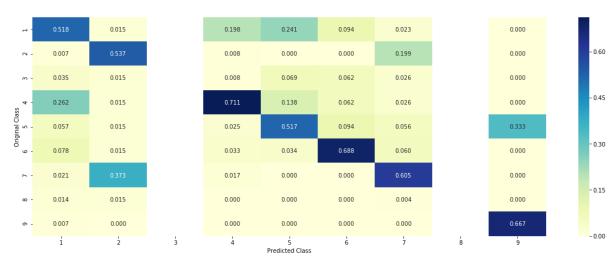
In [110]: #Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.Votin gClassifier.html from sklearn.ensemble import VotingClassifier vclf = VotingClassifier(estimators=[('lr', sig clf1), ('svc', sig clf2), ('rf' , sig_clf3)], voting='soft') vclf.fit(train_x_onehotCoding, train_y) print("Log loss (train) on the VotingClassifier :", log_loss(train_y, vclf.pre dict proba(train x onehotCoding))) print("Log loss (CV) on the VotingClassifier :", log_loss(cv_y, vclf.predict_p roba(cv_x_onehotCoding))) print("Log loss (test) on the VotingClassifier :", log loss(test y, vclf.predi ct_proba(test_x_onehotCoding))) print("Number of missclassified point :", np.count_nonzero((vclf.predict(test_ x onehotCoding) - test y))/test y.shape[0]) plot confusion matrix(test y=test y, predict y=vclf.predict(test x onehotCodin g))

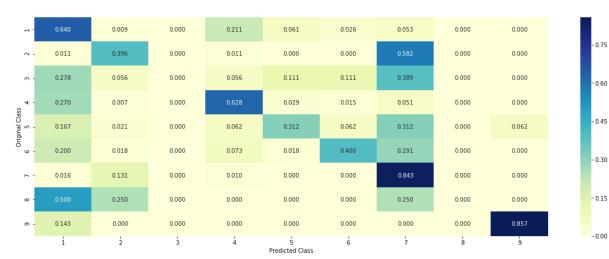
Log loss (train) on the VotingClassifier: 0.8300230398903303 Log loss (CV) on the VotingClassifier: 1.1831603660033636 Log loss (test) on the VotingClassifier: 1.2441864226666837

Number of missclassified point : 0.4

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







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

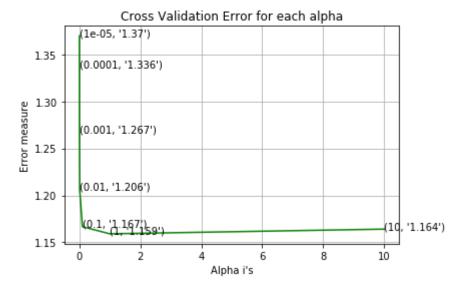
Logistic regression with CountVectorizer Features, including both unigrams and bigrams

```
In [60]: train df.columns
         train variation=train df['Variation'].values;test variation=test df['Variatio
         n'].values;cv variation=cv df['Variation'].values
         train_gene=train_df['Gene'].values;test_gene=test_df['Gene'].values;cv_gene=cv
          df['Gene'].values
         train_text=train_df['TEXT'].values;test_text=test_df['TEXT'].values;cv_text=cv
         df['TEXT'].values
         from sklearn.feature extraction.text import CountVectorizer
         encode=CountVectorizer(ngram range=(1, 2))
         train_variation=encode.fit_transform(train_variation);test_variation=encode.tr
         ansform(test variation);cv variation=encode.transform(cv variation)
         train gene=encode.fit transform(train gene); test gene=encode.transform(test ge
         ne);cv gene=encode.transform(cv gene)
         train variation=normalize(train variation,axis=0);test variation=normalize(tes
         t variation,axis=0);cv variation=normalize(cv variation,axis=0);
         train_gene=normalize(train_gene,axis=0);test_gene=normalize(test_gene,axis=0);
         cv_gene=normalize(cv_gene,axis=0);
         print(train gene.shape)
         print(train gene[1,:])
         print(train_variation.shape)
         print(train variation[100,:])
         train text=encode.fit transform(train text);test text=encode.transform(test te
         xt);cv text=encode.transform(cv text)
         train_text=normalize(train_text,axis=0);test_text=normalize(test_text,axis=0);
         cv text=normalize(cv text,axis=0)
         print(train_text.shape)
         (2124, 236)
           (0, 176)
                         0.23570226039551587
         (2124, 2058)
           (0, 1081)
                         1.0
         (2124, 2373961)
```

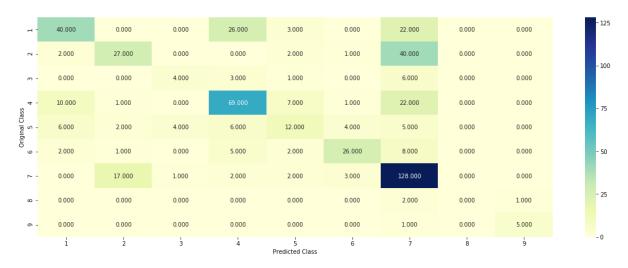
```
In [61]:
         from scipy.sparse import hstack
         print(train_variation.shape,train_gene.shape,train_text.shape)
         train data=hstack([train variation,train gene,train text]).tocsr()
         cv data=hstack([cv variation,cv gene,cv text]).tocsr()
         test data=hstack([test variation,test gene,test text]).tocsr()
         print(train_data.shape,cv_data.shape,test_data.shape)
         train y = y test
         test_y = y_test
         cv_y = y_cv
         (2124, 2058) (2124, 236) (2124, 2373961)
         (2124, 2376255) (532, 2376255) (665, 2376255)
In [63]: cv scores=[]
         alpha=[10 ** x for x in range(-5, 2)]
         for c in alpha:
             print("for alpha =", c)
             lr = LogisticRegression(random_state=0, C=c,class_weight='balanced',n_jobs
         =-1)
             clf=CalibratedClassifierCV(base estimator=lr,method='sigmoid')
             clf.fit(train data,y train)
             cv_op=clf.predict_proba(cv_data)
             print(c,log loss(y cv, cv op))
             cv_scores.append(log_loss(y_cv, cv_op))
         for alpha = 1e-05
         1e-05 1.3697693377839029
         for alpha = 0.0001
         0.0001 1.3360783630381698
         for alpha = 0.001
         0.001 1.267264941559578
         for alpha = 0.01
         0.01 1.2063816360415758
         for alpha = 0.1
         0.1 1.1667435762242009
         for alpha = 1
         1 1.1591281398367685
         for alpha = 10
         10 1.1641198594655746
```

```
In [64]: print(alpha,cv_scores)
    print(len(alpha),len(cv_scores))
    print(type(cv_scores))
    fig, ax = plt.subplots()
    ax.plot(alpha, cv_scores,c='g')
    for i, txt in enumerate(np.round(cv_scores,3)):
        ax.annotate((alpha[i],str(txt)), (alpha[i],cv_scores[i]))
    plt.grid()
    plt.title("Cross Validation Error for each alpha")
    plt.xlabel("Alpha i's")
    plt.ylabel("Error measure")
    plt.show()
```

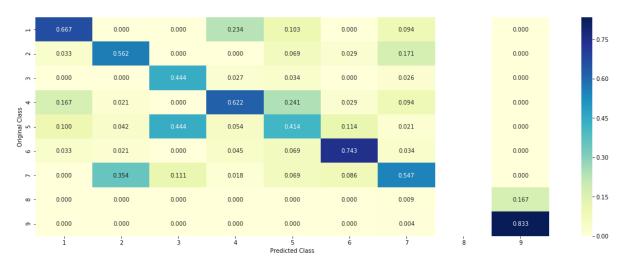
[1e-05, 0.0001, 0.001, 0.01, 0.1, 1, 10] [1.3697693377839029, 1.3360783630381 698, 1.267264941559578, 1.2063816360415758, 1.1667435762242009, 1.15912813983 67685, 1.1641198594655746] 7 7 <class 'list'>

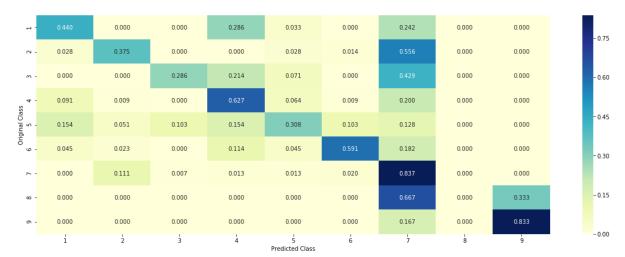


Log Loss value for the test data is(10) 1.1820860678013823







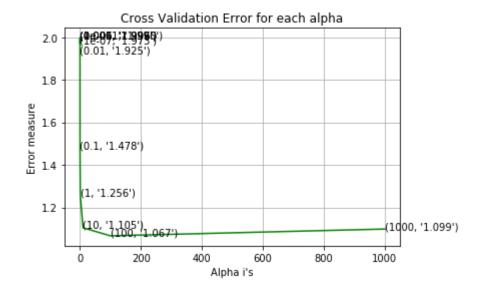


Logistic Regression with tf-idf vectorizer and top 1000 max features.

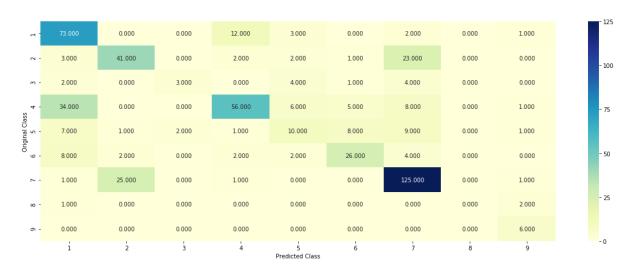
```
In [117]: | train df.columns
          train_variation=train_df['Variation'].values;test_variation=test_df['Variatio
          n'].values;cv variation=cv df['Variation'].values
          train gene=train df['Gene'].values;test gene=test df['Gene'].values;cv gene=cv
           df['Gene'].values
          train text=train df['TEXT'].values;test text=test df['TEXT'].values;cv text=cv
          _df['TEXT'].values
          encode=TfidfVectorizer(max features=1000)
          train variation=encode.fit transform(train variation);test variation=encode.tr
          ansform(test_variation);cv_variation=encode.transform(cv_variation)
          train gene=encode.fit transform(train gene); test gene=encode.transform(test ge
          ne);cv gene=encode.transform(cv gene)
          train variation=normalize(train variation,axis=0);test variation=normalize(tes
          t variation,axis=0);cv variation=normalize(cv variation,axis=0);
          train gene=normalize(train gene,axis=0);test gene=normalize(test gene,axis=0);
          cv gene=normalize(cv gene,axis=0);
          print(train_gene.shape)
          print(train gene[1,:])
          print(train variation.shape)
          print(train_variation[100,:])
          train_text=encode.fit_transform(train_text);test_text=encode.transform(test_te
          xt);cv text=encode.transform(cv text)
          train text=normalize(train text,axis=0);test text=normalize(test text,axis=0);
          cv text=normalize(cv text,axis=0)
          print(train text.shape)
          (2124, 236)
            (0, 176)
                           0.23570226039551587
          (2124, 1000)
                          1.0
            (0, 63)
          (2124, 1000)
In [118]:
          from scipy.sparse import hstack
          print(train_variation.shape,train_gene.shape,train_text.shape)
          train_data=hstack([train_variation,train_gene,train_text]).tocsr()
          cv data=hstack([cv variation,cv gene,cv text]).tocsr()
          test data=hstack([test variation,test gene,test text]).tocsr()
          print(train_data.shape,cv_data.shape,test_data.shape)
          train y = y test
          test_y = y_test
          cv_y = y_cv
          (2124, 1000) (2124, 236) (2124, 1000)
          (2124, 2236) (532, 2236) (665, 2236)
```

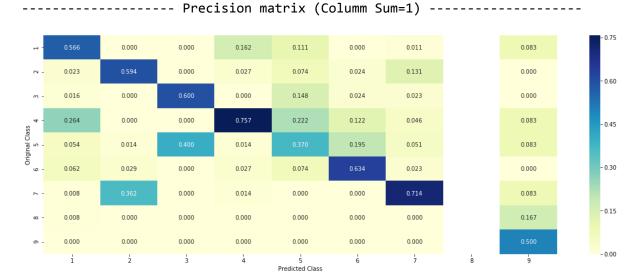
for alpha = 1e-071e-07 1.9726712835140503 for alpha = 1e-061e-06 1.995957643382 for alpha = 1e-051e-05 1.995996494451589 for alpha = 0.00010.0001 1.996034427257036 for alpha = 0.0010.001 1.9973098010071164 for alpha = 0.010.01 1.9247563289266012 for alpha = 0.10.1 1.4775939654330232 for alpha = 11 1.256027520547887 for alpha = 1010 1.104602796438512 for alpha = 100100 1.0668936060841459 for alpha = 10001000 1.0986756638305286

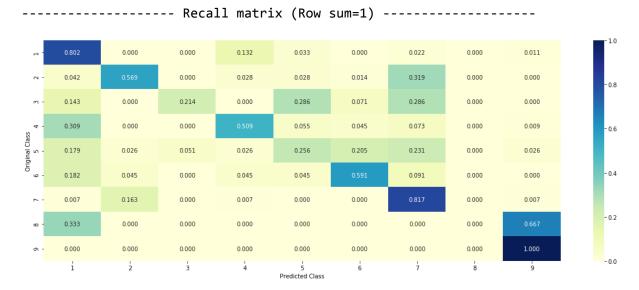
```
In [120]: print(alpha,cv_scores)
    print(len(alpha),len(cv_scores))
    print(type(cv_scores))
    fig, ax = plt.subplots()
    ax.plot(alpha, cv_scores,c='g')
    for i, txt in enumerate(np.round(cv_scores,3)):
        ax.annotate((alpha[i],str(txt)), (alpha[i],cv_scores[i]))
    plt.grid()
    plt.title("Cross Validation Error for each alpha")
    plt.xlabel("Alpha i's")
    plt.ylabel("Error measure")
    plt.show()
```



Log Loss value for the test data is(10) 1.0486989424144908





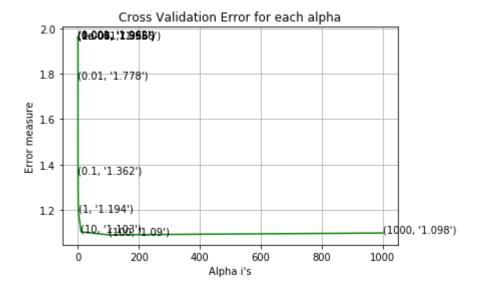


Logistic Regression with (1-4)ngrams and top 2000 features

```
In [101]: train df.columns
          train variation=train df['Variation'].values;test variation=test df['Variatio
          n'].values;cv_variation=cv_df['Variation'].values
          train gene=train df['Gene'].values;test gene=test df['Gene'].values;cv gene=cv
           df['Gene'].values
          train text=train df['TEXT'].values;test text=test df['TEXT'].values;cv text=cv
          df['TEXT'].values
          encode=TfidfVectorizer(ngram_range=(1, 4),max_features=2000)
          train variation=encode.fit transform(train variation); test variation=encode.tr
          ansform(test variation);cv variation=encode.transform(cv variation)
          train_gene=encode.fit_transform(train_gene);test_gene=encode.transform(test_ge
          ne);cv gene=encode.transform(cv gene)
          train variation=normalize(train variation,axis=0);test variation=normalize(tes
          t_variation,axis=0);cv_variation=normalize(cv_variation,axis=0);
          train gene=normalize(train gene,axis=0);test gene=normalize(test gene,axis=0);
          cv gene=normalize(cv gene,axis=0);
          print(train gene.shape)
          print(train_gene[1,:])
          print(train variation.shape)
          print(train_variation[100,:])
          train text=encode.fit transform(train text); test text=encode.transform(test te
          xt);cv text=encode.transform(cv text)
          train text=normalize(train text,axis=0);test text=normalize(test text,axis=0);
          cv text=normalize(cv text,axis=0)
          print(train_text.shape)
          (2124, 236)
            (0, 176)
                          0.23570226039551587
          (2124, 2000)
            (0, 1022)
                          1.0
          (2124, 2000)
In [102]:
          from scipy.sparse import hstack
          print(train variation.shape,train gene.shape,train text.shape)
          train data=hstack([train variation,train gene,train text]).tocsr()
          cv_data=hstack([cv_variation,cv_gene,cv_text]).tocsr()
          test_data=hstack([test_variation,test_gene,test_text]).tocsr()
          print(train_data.shape,cv_data.shape,test_data.shape)
          train_y = y_test
          test y = y test
          cv_y = y_cv
          (2124, 2000) (2124, 236) (2124, 2000)
          (2124, 4236) (532, 4236) (665, 4236)
```

```
for alpha = 1e-07
1e-07 1.9546053755901789
for alpha = 1e-06
1e-06 1.9553058499034912
for alpha = 1e-05
1e-05 1.9557262289822985
for alpha = 0.0001
0.0001 1.9564280674572203
for alpha = 0.001
0.001 1.9623893909124739
for alpha = 0.01
0.01 1.7784731918008843
for alpha = 0.1
0.1 1.3615658299544349
for alpha = 1
1 1.1943980965018823
for alpha = 10
10 1.1029507632799167
for alpha = 100
100 1.0899707293005236
for alpha = 1000
1000 1.0978931968556114
```

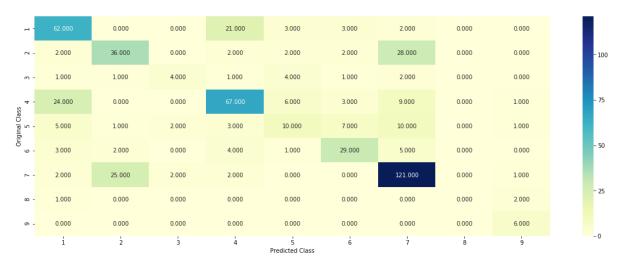
```
In [114]: print(alpha,cv_scores)
    print(len(alpha),len(cv_scores))
    print(type(cv_scores))
    fig, ax = plt.subplots()
    ax.plot(alpha, cv_scores,c='g')
    for i, txt in enumerate(np.round(cv_scores,3)):
        ax.annotate((alpha[i],str(txt)), (alpha[i],cv_scores[i]))
    plt.grid()
    plt.title("Cross Validation Error for each alpha")
    plt.xlabel("Alpha i's")
    plt.ylabel("Error measure")
    plt.show()
```



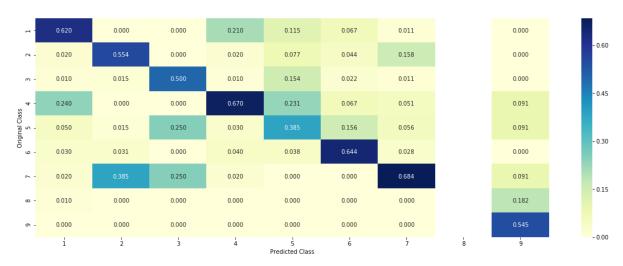
Log Loss value for the test data is(10) 0.9968369435179198

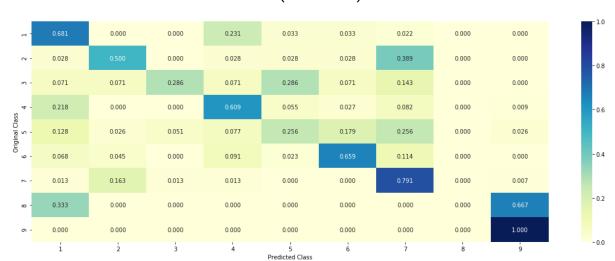
Log loss: 1.089630632796889

Number of mis-classified points : 0.37030075187969924









Stacking 3 features and using (1-4) ngrams with 2000 max_features in TF-IDF and using Logistic Regression

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

```
In [93]: alpha = 1

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

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

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

- In [94]: gene_vectorizer = TfidfVectorizer(ngram_range=(1, 3),max_features=2000)
 train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(x_train['Gene'
])
 test_gene_feature_onehotCoding = gene_vectorizer.transform(x_test['Gene'])
 cv_gene_feature_onehotCoding = gene_vectorizer.transform(x_cv['Gene'])
- In [95]: alpha = 1

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

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

 # cross validation gene feature
 cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", x_cv))
- In [96]: variation_vectorizer = TfidfVectorizer()
 train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(x_tr
 ain['Variation'])
 test_variation_feature_onehotCoding = variation_vectorizer.transform(x_test['V
 ariation'])
 cv_variation_feature_onehotCoding = variation_vectorizer.transform(x_cv['Variation'])

```
In [97]: | def extract dictionary paddle(cls text):
             dictionary = defaultdict(int)
             for index, row in cls text.iterrows():
                 for word in row['TEXT'].split():
                      dictionary[word] +=1
             return dictionary
         import math
         #https://stackoverflow.com/a/1602964
         def get text responsecoding(df):
             text feature responseCoding = np.zeros((df.shape[0],9))
             for i in range(0,9):
                  row index = 0
                 for index, row in df.iterrows():
                      sum prob = 0
                      for word in row['TEXT'].split():
                          sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(total_di
         ct.get(word,0)+90)))
                      text feature responseCoding[row index][i] = math.exp(sum prob/len(
         row['TEXT'].split()))
                      row index += 1
             return text feature responseCoding
```

```
In [98]: text_vectorizer = TfidfVectorizer(ngram_range=(1, 3),max_features=2000)
    train_text_feature_onehotCoding = text_vectorizer.fit_transform(x_train['TEXT'
])
    # getting all the feature names (words)
    train_text_features= text_vectorizer.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and return
    s (1*number of features) vector
    train_text_fea_counts = train_text_feature_onehotCoding.sum(axis=0).A1

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

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

Total number of unique words in train data : 2000

```
In [99]: dict list = []
          # dict_list =[] contains 9 dictoinaries each corresponds to a class
          for i in range(1,10):
              cls text = x train[x train['Class']==i]
              # build a word dict based on the words in that class
              dict_list.append(extract_dictionary_paddle(cls_text))
              # append it to dict list
          # dict list[i] is build on i'th class text data
          # total_dict is buid on whole training text data
          total dict = extract dictionary paddle(x train)
          confuse array = []
          for i in train text features:
              ratios = []
              \max val = -1
              for j in range(0,9):
                  ratios.append((dict_list[j][i]+10 )/(total_dict[i]+90))
              confuse array.append(ratios)
          confuse array = np.array(confuse array)
In [100]:
          train_text_feature_responseCoding = get_text_responsecoding(x_train)
          test_text_feature_responseCoding = get_text_responsecoding(x_test)
          cv text feature responseCoding = get text responsecoding(x cv)
          # https://stackoverflow.com/a/16202486
          # we convert each row values such that they sum to 1
          train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train
          text feature responseCoding.sum(axis=1)).T
          test text feature responseCoding = (test text feature responseCoding.T/test te
          xt feature responseCoding.sum(axis=1)).T
          cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_fea
          ture responseCoding.sum(axis=1)).T
In [101]: | test_text_feature_onehotCoding = text_vectorizer.transform(x_test['TEXT'])
          cv text feature onehotCoding = text vectorizer.transform(x cv['TEXT'])
In [102]: | gene_variation = []
          for gene in data['Gene'].values:
              gene_variation.append(gene)
          for variation in data['Variation'].values:
              gene variation.append(variation)
In [103]: | tfidfVectorizer = TfidfVectorizer(ngram range=(1, 3), max features=2000)
          text2 = tfidfVectorizer.fit transform(gene variation)
          gene variation features = tfidfVectorizer.get feature names()
          train_text = tfidfVectorizer.transform(x_train['TEXT'])
          test text = tfidfVectorizer.transform(x test['TEXT'])
          cv text = tfidfVectorizer.transform(x cv['TEXT'])
```

```
In [104]: train gene var onehotCoding = hstack((train gene feature onehotCoding,train
          _variation_feature_onehotCoding))
          test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_va
          riation feature onehotCoding))
          cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variatio
          n_feature_onehotCoding))
          # Adding the train text feature
          train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text))
          train_x_onehotCoding = hstack((train_x_onehotCoding, train_text_feature_one
          hotCoding)).tocsr()
          train_y = np.array(list(x_train['Class']))
          # Adding the test text feature
          test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text))
          test_x_onehotCoding = hstack((test_x_onehotCoding, test_text_feature_onehot
          Coding)).tocsr()
          test_y = np.array(list(x_test['Class']))
          # Adding the cv text feature
          cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text))
          cv_x_onehotCoding = hstack((cv_x_onehotCoding, cv_text_feature_onehotCoding)
          )).tocsr()
          cv_y = np.array(list(x_cv['Class']))
          train gene var responseCoding = np.hstack((train gene feature responseCodin
          g,train variation feature responseCoding))
          test gene var responseCoding = np.hstack((test gene feature responseCoding,
          test variation feature responseCoding))
          cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_v
          ariation feature responseCoding))
          train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_te
          xt_feature_responseCoding))
          test x responseCoding = np.hstack((test gene var responseCoding, test text
          feature responseCoding))
          cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_featur
          e responseCoding))
In [105]: | print("One hot encoding features :")
          print("(number of data points * number of features) in train data = ", train x
          onehotCoding.shape)
          print("(number of data points * number of features) in test data = ", test_x_o
          nehotCoding.shape)
          print("(number of data points * number of features) in cross validation data
           =", cv_x_onehotCoding.shape)
          One hot encoding features :
          (number of data points * number of features) in train data = (2124, 6188)
```

(number of data points * number of features) in test data = (665, 6188) (number of data points * number of features) in cross validation data = (532,

6188)

```
In [106]: print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train n_x_responseCoding.shape)
print("(number of data points * number of features) in test data = ", test_x_responseCoding.shape)
print("(number of data points * number of features) in cross validation dat a = ", cv_x_responseCoding.shape)
```

```
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, 27)
```

```
In [107]: | alpha = [10 ** x for x in range(-6, 2)]
          cv log error array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier(class weight='balanced', alpha=i, penalty='12', loss=
           'log', random_state=41)
              clf.fit(train x onehotCoding, train y)
              sig clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig clf.fit(train x onehotCoding, train y)
              sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
              cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes
          _, eps=1e-15))
              # to avoid rounding error while multiplying probabilites we use log-probab
          ility estimates
              print("Log Loss :",log loss(cv y, sig clf probs))
          fig, ax = plt.subplots()
          ax.plot(alpha, cv_log_error_array,c='g')
          for i, txt in enumerate(np.round(cv_log_error_array,3)):
              ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()
          best_alpha = np.argmin(cv_log_error_array)
          clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty=
          '12', loss='log',)
          clf.fit(train x onehotCoding, train y)
          sig clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig clf.fit(train x onehotCoding, train y)
          predict_y = sig_clf.predict_proba(train_x_onehotCoding)
          print('For values of best alpha = ',
                alpha[best alpha],
                "The train log loss is:",
                log loss(y train, predict y, labels=clf.classes , eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
          print('For values of best alpha = ',
                alpha[best alpha],
                "The cross validation log loss is:",
                log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
          predict_y = sig_clf.predict_proba(test_x_onehotCoding)
          print('For values of best alpha = ',
                alpha[best alpha], "The test log loss is:",
                log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-06

Log Loss: 1.1043497266852318

for alpha = 1e-05

Log Loss: 1.0701351426809702

for alpha = 0.0001

Log Loss: 0.9944815805808248

for alpha = 0.001

Log Loss: 1.033929211472418

for alpha = 0.01

Log Loss: 1.2364021988820038

for alpha = 0.1

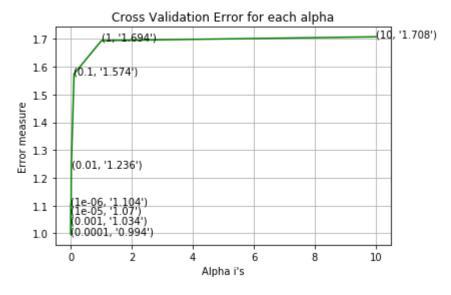
Log Loss: 1.5741336944624982

for alpha = 1

Log Loss: 1.6940041972753461

for alpha = 10

Log Loss: 1.707754812882125

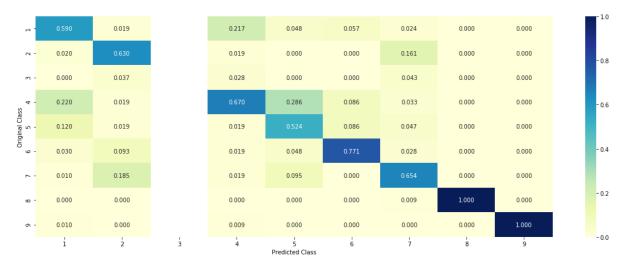


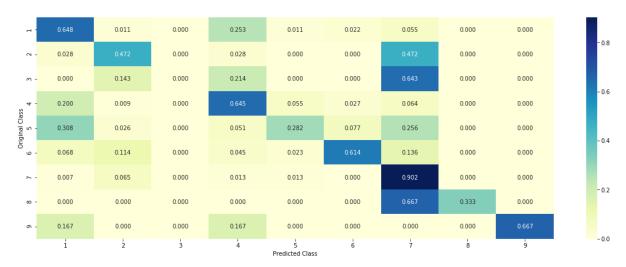
For values of best alpha = 0.0001 The train log loss is: 0.47122286805214036 For values of best alpha = 0.0001 The cross validation log loss is: 0.990483 0734953544

For values of best alpha = 0.0001 The test log loss is: 0.9996015940329241

59.000 1.000 0.000 23.000 1.000 2.000 5.000 0.000 0.000 125 34.000 2.000 34.000 0.000 2.000 0.000 0.000 0.000 0.000 0.000 2.000 0.000 3.000 0.000 0.000 9.000 0.000 0.000 100 22.000 1.000 0.000 6.000 3.000 7.000 0.000 0.000 12.000 2.000 11.000 3.000 10.000 1.000 0.000 0.000 27.000 3.000 5.000 0.000 2.000 1.000 6.000 0.000 0.000 - 50 138.000 1.000 10.000 0.000 2.000 2.000 0.000 0.000 0.000 - 25 0.000 0.000 0.000 0.000 0.000 0.000 2.000 1.000 0.000 0.000 0.000 1.000 0.000 1.000 Predicted Class

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





In []:

In	[]:	
In	[]:	
In	[]:	

```
In [111]:
          from prettytable import PrettyTable
          from termcolor import colored
          print(colored('Performance Table of Models with TFIDF vectorizer ','red'))
          x = PrettyTable()
          x.field names =["Models", "Train", "Test", "Misclassified(%)"]
          x.add row(["Naive Bayes (One hot coding)",0.52,1.26,0.36])
          x.add row(["KNN (Response)",0.69,1.09,0.35])
          x.add_row(["LR(Class balanced) one hot coding",0.45,1.08,0.34])
          x.add_row(["LR(Class unbalanced) one hot coding",0.44,1.11,0.35])
          x.add row(["Lr SVM one hot encoding",0.6,1.15,0.35])
          x.add_row(["Random Forest one hot coding",0.86,1.23,0.40])
          x.add row(["Random Forest Response coding",0.05,1.44,0.53])
          x.add_row(["Stacking classifier",0.54,1.23,0.41])
          x.add row(["Maximum Voting Classifier",0.83,1.24,0.4])
          x.add_row(["LR(Class balanced) CountVectorizer",0.45,1.08,0.34])
          x.add row(["LR(Class balanced) TF-IDF Vectorizer and top 1000 max features",1.
          09,1.04,0.36])
          x.add_row(["LR(Class balanced) TF-IDF Vectorizer and (1-4)ngrams and top 2000
           features",1.08,0.99,0.371)
          x.add row(["Stacking 3 features and using (1-4) ngrams with 2000 max features
           in TF-IDF \n and using Logistic Regression with class balancing", 0.47, 0.99, 0.
          35])
          print(x)
          print("\n")
```

Performance Table of Models with TFIDF vectorizer

```
Models
 | Train | Test | Misclassified(%) |
                        Naive Bayes (One hot coding)
 | 0.52 | 1.26 |
                       0.36
                               KNN (Response)
  0.69 | 1.09 |
                       0.35
                     LR(Class balanced) one hot coding
  0.45 | 1.08 |
                       0.34
                    LR(Class unbalanced) one hot coding
  0.44 | 1.11 |
                       0.35
                          Lr SVM one hot encoding
  0.6 | 1.15 |
                       0.35
                        Random Forest one hot coding
  0.86 | 1.23 |
                       0.4
                       Random Forest Response coding
  0.05 | 1.44 |
                            Stacking classifier
  0.54 | 1.23 |
                       0.41
                         Maximum Voting Classifier
    0.83 | 1.24 |
                     LR(Class balanced) CountVectorizer
    0.45 | 1.08 |
        LR(Class balanced) TF-IDF Vectorizer and top 1000 max features
    1.09 | 1.04 |
                       0.36
  LR(Class balanced) TF-IDF Vectorizer and (1-4)ngrams and top 2000 features
    1.08 | 0.99 |
                       0.37
Stacking 3 features and using (1-4) ngrams with 2000 max_features in TF-IDF
 | 0.47 | 0.99 |
              and using Logistic Regression with class balancing
-+----+
```

In []:	