# Personalized cancer diagnosis

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# 1. Business Problem

# 1.1. Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training\_variants.zip and training\_text.zip from Kaggle.

#### Context:

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

#### Problem statement:

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

### 1.2. Source/Useful Links

Some articles and reference blogs about the problem statement

- 1. <a href="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</a>)
- 2. <a href="https://www.youtube.com/watch?v=UwbuW7oK8rk">https://www.youtube.com/watch?v=UwbuW7oK8rk</a>)
- 3. <a href="https://www.youtube.com/watch?v=qxXRKVompl8">https://www.youtube.com/watch?v=qxXRKVompl8</a>)

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

### 2.1.2. Example Data Point

#### training\_variants

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

• • •

#### training text

ID, Text

0||Cyclin-dependent kinases (CDKs) regulate a variety of fundamental cellular processes. CDK10 stands out as one of the last orphan CDKs for which no activating cyclin has been identified and no kinase activity revealed. Previous work has shown that CDK10 silencing increases ETS2 (v-ets erythroblastosis virus E26 oncogene homolog 2)-driven activation of the MAPK pathway, which confers tamoxifen resistance to breast cancer cells. The precise mechanisms by which CDK10 modulates ETS2 activity, and more generally the functions of CDK10, remain elusive. Here we demonstrate that CDK10 is a cyclin-dependent kinase by identifying cyclin M as an activating cyclin. Cyclin M, an orphan cyclin, is the product of FAM58A, whose mutations cause STAR syndrome, a human developmental anomaly whose features include toe syndactyly, telecanthus, and anogenital and renal malformations. We show that STAR syndrome-associated cyclin M mutants are unable to interact with CDK10. Cyclin M silencing phenocopies CDK10 silencing in increasing c-Raf and in conferring tamoxifen resistance to breast cancer cells. CDK10/cyclin M phosphorylates ETS2 in vitro, and in cells it positively controls ETS2 degradation by the proteasome. ETS2 protein levels are increased in cells derived from a STAR patient, and this increase is attributable to decreased cyclin M levels. Altogether, our results reveal an additional regulatory mechanism for ETS2, which plays key roles in cancer and development. They also shed light on the molecular mechanisms underlying STAR syndrome. Cyclindependent 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)

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 collections import Counter
        from scipy.sparse import hstack
        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 sklearn import model_selection
        from imblearn.over sampling import SMOTE
        from mlxtend.classifier import StackingClassifier
```

from sklearn.linear\_model import LogisticRegression
from sklearn.multiclass import OneVsRestClassifier

In [2]: data = pd.read\_csv('training\_variants.csv')
 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

In [3]: data.shape

Out[3]: (3321, 4)

Out[4]: ID 6
Gene 7
Variation 6
Class 6
dtype: int64

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

### **Reading Text Data**

```
In [5]: # note the seprator in this file
    data_text =pd.read_csv("training_text.csv",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[5]:

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

```
In [6]: # replacing na values in college with No college
data_text["TEXT"].fillna("No Value", inplace = True)
```

```
In [7]: # check the null value in data_text
    data_text.isnull().sum()

Out[7]: ID     0
     TEXT     0
```

### 3.1.3. Preprocessing of text

dtype: int64

```
In [8]: # Loading stop words from nltk library
        stop words = set(stopwords.words('english'))
        def nlp preprocessing(total text, index, column):
            if type(total text) is not int:
                string = ""
                # replace every special char with space
                total text = re.sub('[^a-zA-Z0-9\n]', ' ', total_text)
                # replace multiple spaces with single space
                total text = re.sub('\s+',' ', total text)
                # converting all the chars into lower-case.
                total text = total text.lower()
                for word in total text.split():
                # if the word is a not a stop word then retain that word from the data
                    if not word in stop words:
                        string += word + " "
                data text[column][index] = string
```

```
In [9]: #text processing stage.
    start_time = time.clock()
    for index, row in data_text.iterrows():
        if type(row['TEXT']) is str:
            nlp_preprocessing(row['TEXT'], index, 'TEXT')
        else:
            print("there is no text description for id:",index)
        print('Time took for preprocessing the text :',time.clock() - start_time, "seconds")
```

Time took for preprocessing the text : 249.68624421411303 seconds

```
In [10]: #merging both gene_variations and text data based on ID
    result = pd.merge(data,data_text,on= 'ID',how = 'left')
    result.head()
```

Out[10]:

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

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

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

```
In [11]: y_true = result['Class'].values
    result['Gene'] = result['Gene'].str.replace('\s+','_')
    result['Variation'] = result['Variation'].str.replace('\s+','_')

# split the data into test and train by maintaining same distribution of output variable 'y_true' [stratify=y_true]
    X_train, test_df, y_train, y_test = train_test_split(result, y_true, stratify=y_true, test_size=0.2)
# split the train data into train and cross validation by maintaining same distribution of output variable 'y_train'
    [stratify=y_train]
    train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train, stratify=y_train, test_size=0.2)
```

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

```
In [12]: 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])

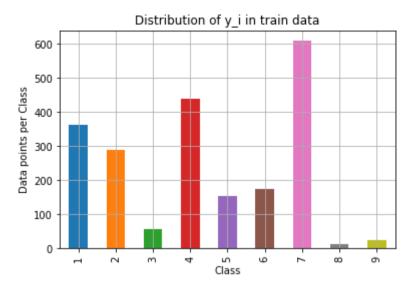
Number of data points in train data: 2124
    Number of data points in test data: 665
    Number of data points in cross validation data: 532
```

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

```
In [13]: # it returns a dict, keys as class labels and values as the number of data points in that class
         train class distribution = train df['Class'].value counts().sortlevel()
         test class distribution = test df['Class'].value counts().sortlevel()
         cv class distribution = cv df['Class'].value counts().sortlevel()
         my colors = ['r','g','b','k','y','m','c']
         train class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.vlabel('Data points per Class')
         plt.title('Distribution of v i in train data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
         # -(train class distribution.values): the minus sign will give us in decreasing order
         sorted vi = np.argsort(-train class distribution.values)
         for i in sorted vi:
              print('Number of data points in class', i+1, ':',train class distribution.values[i], '(', np.round((train class di
         stribution.values[i]/train df.shape[0]*100), 3), '%)')
              #ends
         print('-'*80)
         my colors = ['r','g','b','k','y','m','c']
         test class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of y i in test data')
         plt.grid()
         plt.show()
          sorted yi = np.argsort(-test class distribution.values)
          for i in sorted vi:
              print('Number of data points in class', i+1, ':',test class distribution.values[i], '(', np.round((test class dist
         ribution.values[i]/test df.shape[0]*100), 3), '%)')
              #ends
         print('-'*80)
         my_colors = ['r','g','b','k','y','m','c']
         cv class distribution.plot(kind='bar')
```

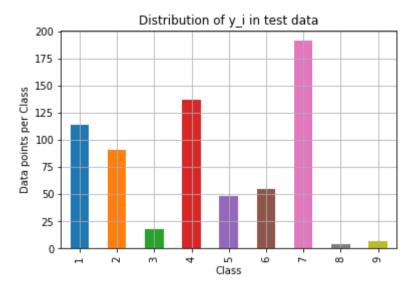
```
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of y_i in cross validation data')
plt.grid()
plt.show()

sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',cv_class_distribution.values[i], '(', np.round((cv_class_distribution.values[i]/cv_df.shape[0]*100), 3), '%)')
```



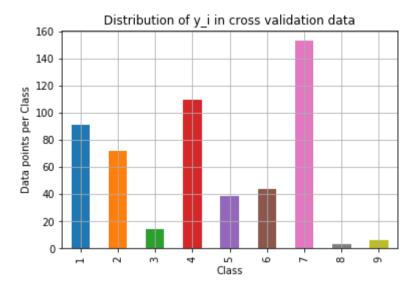
```
Number of data points in class 7 : 609 ( 28.672 %)
Number of data points in class 4 : 439 ( 20.669 %)
Number of data points in class 1 : 363 ( 17.09 %)
Number of data points in class 2 : 289 ( 13.606 %)
Number of data points in class 6 : 176 ( 8.286 %)
Number of data points in class 5 : 155 ( 7.298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

-----



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

------



```
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 [35]: # This function plots the confusion matrices given y i, y i hat.
          def plot confusion matrix(test y, predict y):
             C = confusion matrix(test y, predict y)
             \# C = 9,9 matrix, each cell (i,j) represents number of points of class i are predicted class j
             A = (((C.T)/(C.sum(axis=1))).T)
             #divid each element of the confusion matrix with the sum of elements in that column
             \# C = [[1, 2],
                   [3, 4]]
             # C.T = [[1, 3],
                       [2, 4]]
              # C.sum(axis = 1) axis=0 corresponds to columns and axis=1 corresponds to rows in two diamensional array
             # C.sum(axix = 1) = [[3, 7]]
             \# ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
                                          [2/3, 4/7]]
              # ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]]
                                         [3/7, 4/7]]
              # sum of row elements = 1
              B = (C/C.sum(axis=0))
              #divid each element of the confusion matrix with the sum of elements in that row
             \# C = [[1, 2],
                    [3, 4]]
             # C.sum(axis = 0) axis=0 corresonds to columns and axis=1 corresponds to rows in two diamensional array
              # C.sum(axix = 0) = [[4, 6]]
             \# (C/C.sum(axis=0)) = [[1/4, 2/6],
                                     [3/4, 4/6]]
             labels = [1,2,3,4,5,6,7,8,9]
             # representing C 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()
             # representing B in heatmap format FOR PRECISION
              print("-"*20, "Precision matrix (Columm 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 A in heatmap format FOR RECALL
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 [16]: # we need to generate 9 numbers and the sum of numbers should be 1
# one solution is to genarate 9 numbers and divide each of the numbers by their sum
# ref: https://stackoverflow.com/a/18662466/4084039

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

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))
```

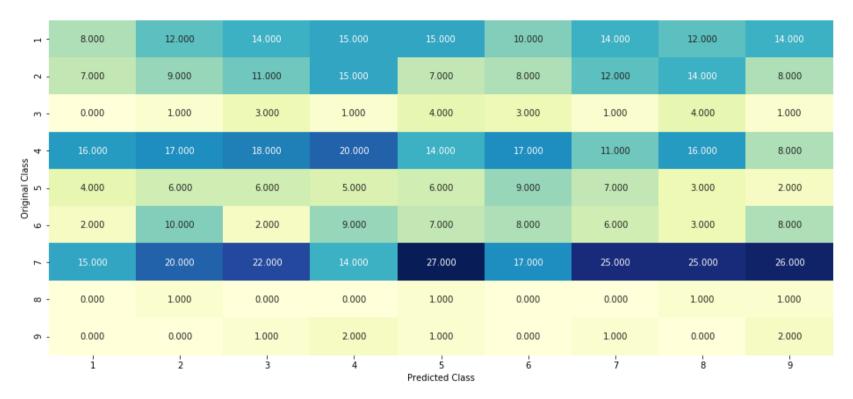
Log loss on Cross Validation Data using Random Model 2.4827779901832203

```
In [17]: # Test-Set error.
#we create a output array that has exactly same as the test data
test_predicted_y = np.zeros((test_data_len,9))
for i in range(test_data_len):
    rand_probs = np.random.rand(1,9)
    test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Test Data using Random Model",log_loss(y_test,test_predicted_y, eps=1e-15))
```

Log loss on Test Data using Random Model 2.543907507426031

In [18]: predicted\_y =np.argmax(test\_predicted\_y, axis=1)
 plot\_confusion\_matrix(y\_test, predicted\_y+1)

#### ----- Confusion matrix -----



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

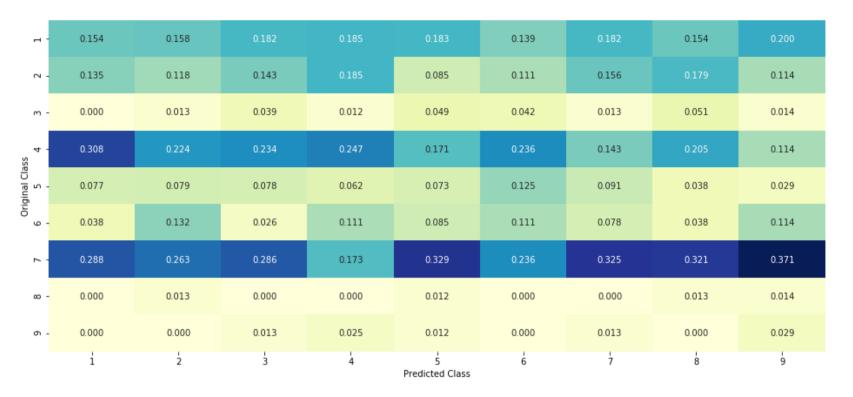
- 25

- 20

- 15

- 10

-0



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

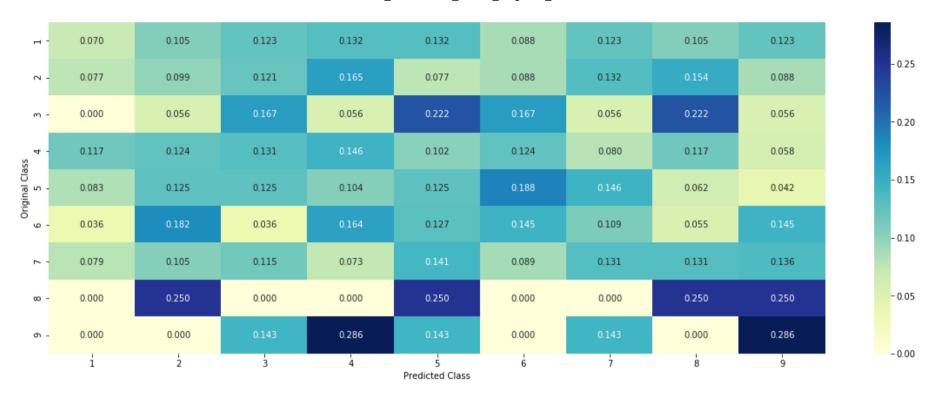
- 0.32

-0.24

-0.16

- 0.08

- 0.00



# 3.3 Univariate Analysis

```
In [14]: # 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 occu
          rred in total data+90*alpha)
         # qv dict is like a look up table, for every gene it store a (1*9) representation of it
         # for a value of feature in df:
         # if it is in train data:
         # we add the vector that was stored in 'qv dict' look up table to 'qv fea'
         # if it is not there is train:
         # we add [1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9] to 'qv fea'
          # return 'av 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:
              # {
             # Truncating_Mutations
                                                         63
              # Deletion
                                                         43
              # Amplification
                                                         43
              # Fusions
                                                         22
                                                          3
              # Overexpression
```

```
# E17K
                                                3
    # Q61L
                                                3
                                                2
    # S222D
    # P130S
                                                2
    # ...
    # }
   value count = train df[feature].value counts()
    # av dict : Gene Variation Dict, which contains the probability array for each gene/variation
   gv dict = dict()
   # denominator will contain the number of time that particular feature occured in whole data
   for i, denominator in value count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticular class
        # vec is 9 diamensional vector
        vec = []
        for k in range(1,10):
            # print(train df.loc[(train df['Class']==1) & (train df['Gene']=='BRCA1')])
                      ID Gene
                                            Variation Class
            # 2470
                   2470 BRCA1
                                               S1715C
            # 2486 2486 BRCA1
                                               S1841R
                                                          1
            # 2614 2614 BRCA1
                                                  M1R
            # 2432 2432 BRCA1
                                               L1657P
                                                          1
            # 2567 2567 BRCA1
                                               T1685A
                                                          1
            # 2583 2583 BRCA1
                                               E1660G
                                                          1
            # 2634 2634 BRCA1
                                               W1718L
            # cls cnt.shape[0] will return the number of rows
            cls cnt = train df.loc[(train df['Class']==k) & (train df[feature]==i)]
            # cls cnt.shape[0](numerator) will contain the number of time that particular feature occured in whole dat
а
            vec.append((cls cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
        # we are adding the gene/variation to the dict as key and vec as value
        gv dict[i]=vec
    return gv dict
# Get Gene variation feature
def get gv feature(alpha, feature, df):
    # print(qv dict)
          {'BRCA1': [0.20075757575757575, 0.037878787878788, 0.0681818181818177, 0.13636363636363635, 0.25, 0.1931
```

```
'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 0.27040816326530615, 0.0612244897
95918366, 0.066326530612244902, 0.051020408163265307, 0.051020408163265307, 0.056122448979591837],
          'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.0681818181818177, 0.068181818181818177, 0.0
625, 0.34659090909090912, 0.0625, 0.056818181818181816],
          'BRCA2': [0.1333333333333333, 0.060606060606060608, 0.0606060606060608, 0.078787878787878782, 0.13939393
93939394, 0.345454545454545, 0.060606060606060608, 0.0606060606060608, 0.0606060606060608],
          'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 0.46540880503144655, 0.075471698
113207544, 0.062893081761006289, 0.069182389937106917, 0.062893081761006289, 0.062893081761006289],
          'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.072847682119205295, 0.0662251655
62913912, 0.066225165562913912, 0.27152317880794702, 0.066225165562913912, 0.066225165562913912],
          'BRAF': [0.0666666666666666666, 0.179999999999999, 0.073333333333334, 0.073333333333334, 0.093333333
333333338. 0.080000000000000000, 0.29999999999999, 0.066666666666666, 0.0666666666666666],
   gv dict = get gv fea dict(alpha, feature, df)
   # value count is similar in get qv fea dict
   value count = train df[feature].value counts()
   # qv 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 gv 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([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
             qv 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 + 10alpha) / (denominator + 90alpha)

### 3.2.1 Univariate Analysis on Gene Feature

### Q1. Gene, What type of feature it is?

Ans. Gene is a categorical variable

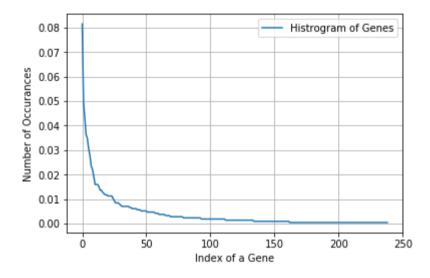
#### Q2. How many categories are there and How they are distributed?

```
In [18]: unique genes = train df['Gene'].value counts()
          print('Number of Unique Genes :', unique genes.shape[0])
          # the top 10 genes that occured most
          print(unique genes.head(10))
          Number of Unique Genes: 233
          BRCA1
                    170
          TP53
                    103
          EGFR
                     95
          PTEN
                      85
          BRCA2
                      83
          KIT
                      63
          BRAF
                      59
          ERBB2
                      51
          PIK3CA
                      39
          PDGFRA
                      36
          Name: Gene, dtype: int64
In [129]: print("Ans: There are", unique genes.shape[0], "different categories of genes in the train data, and they are distibut
          ed as follows",)
```

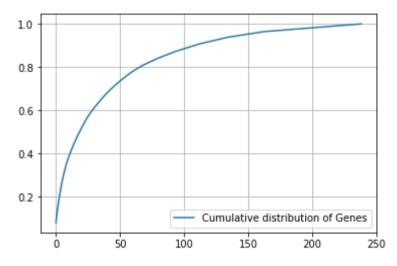
Ans: There are 239 different categories of genes in the train data, and they are distibuted as follows

file:///C:/Users/Ravi%20Krishna/Ravi Personalized Cancer Diagnosis Final.html

```
In [130]: 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 [131]: 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

- 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 [15]: #response-coding of the Gene feature
    # alpha is used for laplace smoothing
    alpha = 1
    # train gene feature
    train_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", train_df))
    # test gene feature
    test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", test_df))
# cross validation gene feature
    cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", cv_df))
In [21]: print("train_gene_feature_responseCoding is converted feature using respone coding method. The shape of gene feature:"
    , train_gene_feature_responseCoding is converted feature using respone coding method. The shape of gene feature: (2124,)
```

### **Assignment Section**

9)

- 1. Task 1. Use TfidfVectorizer for all models
- 2. Task 2, Use top 1000 words for tfidf
- 3. Task 3, Apply Logistic regression with CountVectorizer Features, including both unigrams and bigrams
- 4. Task 4, Apply feature engineering that gives log loss less than 1
- 1. Task 1, Use TfidfVectorizer for all models

```
In [26]: # one-hot encoding of Gene feature.
gene_vectorizer = TfidfVectorizer(ngram_range=(1,1))#unigrams
train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gene'])
test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gene'])
cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
```

```
In [20]: train_df['Gene'].head(10)
Out[20]: 2153
                  PTEN
         1773
                 XRCC2
         2882
                 BRCA2
         2538
                 BRCA1
         1306
                  MLH1
         249
                  EGFR
         107
                  MSH6
         146
                  EGFR
         1035
                  TSC2
         2414
                 PTPRD
         Name: Gene, dtype: object
```

In [25]: gene\_vectorizer.get\_feature\_names()

```
Out[25]: ['abl1',
           'acvr1',
           'ago2',
           'akt1',
           'akt2',
           'akt3',
           'alk',
           'apc',
           'ar',
           'araf',
           'arid1a',
           'arid1b',
           'arid2',
           'arid5b',
           'asxl1',
           'atm',
           'atrx',
           'aurka',
           'aurkb',
           'axl',
           'b2m',
           'bap1',
           'bard1',
           'bcl2',
           'bcl2l11',
           'bcor',
           'braf',
           'brca1',
           'brca2',
           'brd4',
           'brip1',
           'btk',
           'card11',
           'carm1',
           'casp8',
           'cbl',
           'ccnd1',
           'ccnd2',
           'ccnd3',
           'ccne1',
           'cdh1',
```

```
'cdk12',
'cdk4',
'cdk6',
'cdkn1a',
'cdkn1b',
'cdkn2a',
'cdkn2b',
'cdkn2c',
'chek2',
'cic',
'crebbp',
'ctcf',
'ctla4',
'ctnnb1',
'ddr2',
'dicer1',
'dnmt3a',
'dnmt3b',
'dusp4',
'egfr',
'eif1ax',
'elf3',
'ep300',
'epas1',
'epcam',
'erbb2',
'erbb3',
'erbb4',
'ercc2',
'ercc3',
'ercc4',
'erg',
'errfi1',
'esr1',
'etv1',
'etv6',
'ewsr1',
'ezh2',
'fanca',
'fancc',
'fat1',
'fbxw7',
```

```
'fgfr1',
'fgfr2',
'fgfr3',
'fgfr4',
'flt1',
'flt3',
'foxa1',
'fox12',
'foxo1',
'fubp1',
'gata3',
'gli1',
'gnas',
'h3f3a',
'hist1h1c',
'hla',
'hnf1a',
'hras',
'idh1',
'idh2',
'igf1r',
'ikzf1',
'il7r',
'inpp4b',
'jak1',
'jak2',
'jun',
'kdm5c',
'kdm6a',
'kdr',
'keap1',
'kit',
'kmt2a',
'kmt2b',
'kmt2c',
'knstrn',
'kras',
'lats2',
'map2k1',
'map2k2',
'map2k4',
'map3k1',
```

```
'mapk1',
'mdm4',
'med12',
'mef2b',
'men1',
'met',
'mga',
'mlh1',
'mpl',
'msh2',
'msh6',
'mtor',
'myc',
'mycn',
'myd88',
'ncor1',
'nf1',
'nf2',
'nfe212',
'nfkbia',
'nkx2',
'notch1',
'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',
'ptch1',
'pten',
'ptpn11',
'ptprd',
'ptprt',
'rab35',
'rac1',
'rad21',
'rad50',
'rad51b',
'rad51c',
'raf1',
'rasa1',
'rb1',
'rbm10',
'ret',
'rheb',
'rhoa',
'rictor',
'rit1',
'ros1',
'runx1',
'rxra',
'rybp',
'sdhb',
'sdhc',
'setd2',
'sf3b1',
'shoc2',
'shq1',
'smad2',
'smad3',
'smad4',
'smarca4',
'smarcb1',
'smo',
```

```
'sos1',
'sox9',
'spop',
'src',
'srsf2',
'stat3',
'stk11',
'tert',
'tet1',
'tet2',
'tgfbr1',
'tgfbr2',
'tmprss2',
'tp53',
'tp53bp1',
'tsc1',
'tsc2',
'u2af1',
'vhl',
'xpo1',
'xrcc2',
'yap1']
```

# **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/modules/generated/sklearn.linear model.SGDClassifi
         er.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=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 Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         cv log error array = []
         for i in alpha:
             clf = SGDClassifier(loss='log',penalty='l2',alpha = i,random state=42)
             clf.fit(train gene feature onehotCoding,y train)
             sig clf = CalibratedClassifierCV(clf,method='sigmoid')
             sig clf.fit(train gene feature onehotCoding,y train)
             predict_y = sig_clf.predict_proba(cv_gene feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.4277066483293113

For values of alpha = 0.0001 The log loss is: 1.2458590683769941

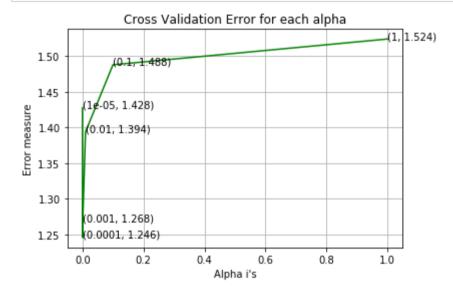
For values of alpha = 0.001 The log loss is: 1.2680504025912644

For values of alpha = 0.01 The log loss is: 1.393989020517406

For values of alpha = 0.1 The log loss is: 1.487952520014476

For values of alpha = 1 The log loss is: 1.5240757891010241
```

```
In [27]: 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()
```



```
In [28]: best alpha = np.argmin(cv log error array)
         clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
         clf.fit(train gene feature onehotCoding, y train)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train gene feature onehotCoding, v train)
Out[28]: CalibratedClassifierCV(base estimator=SGDClassifier(alpha=0.0001, average=False, class weight=None,
                early stopping=False, epsilon=0.1, eta0=0.0, fit intercept=True,
                11 ratio=0.15, learning rate='optimal', loss='log', max iter=None,
                n iter=None, n iter no change=5, n jobs=None, penalty='12',
                power t=0.5, random state=42, shuffle=True, tol=None,
                validation fraction=0.1, verbose=0, warm start=False),
                     cv='warn', method='sigmoid')
In [29]: 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(v train, predict v, labels=clf.classes , eps=1e-15))
         predict y = sig clf.predict proba(cv gene feature onehotCoding)
         print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",
               log loss(v cv, predict v, 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 best alpha = 0.0001 The train log loss is: 1.043717620447401
         For values of best alpha = 0.0001 The cross validation log loss is: 1.2458590683769941
         For values of best alpha = 0.0001 The test log loss is: 1.236494812986371
```

**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 [32]: 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 232 genes in train dataset? Ans

- 1. In test data 646 out of 665 : 97.14285714285714
- 2. In cross validation data 515 out of 532 : 96.80451127819549

## 3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it?

**Ans.** Variation is a categorical variable

Q8. How many categories are there?

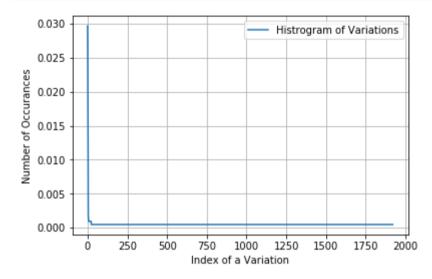
```
In [33]: unique_variations = train_df['Variation'].value_counts()
    print('Number of Unique Variations :', unique_variations.shape[0])
# the top 10 variations that occured most
    print(unique_variations.head(10))
```

Number of Unique Variations: 1921 Truncating Mutations 63 Deletion 52 Amplification 46 Fusions 24 G12V **Overexpression** T58I ETV6-NTRK3 Fusion P130S 2 061H Name: Variation, dtype: int64

In [34]: print("Ans: There are", unique\_variations.shape[0] ,"different categories of variations in the train data, and they ar
e distibuted as follows",)

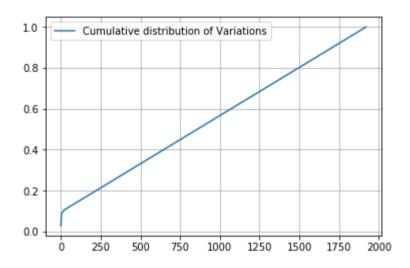
Ans: There are 1921 different categories of variations in the train data, and they are distibuted as follows

```
In [35]: s = sum(unique_variations.values);
h = unique_variations.values/s;
plt.plot(h, label="Histrogram of Variations")
plt.xlabel('Index of a Variation')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



```
In [36]: c = np.cumsum(h)
    print(c)
    plt.plot(c,label='Cumulative distribution of Variations')
    plt.grid()
    plt.legend()
    plt.show()
```

[0.02966102 0.05414313 0.07580038 ... 0.99905838 0.99952919 1.



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

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

- 1. One hot Encoding
- 2. Response coding

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

```
In [16]: # 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 [38]: print("train variation feature responseCoding is a converted feature using the response coding method. The shape of Va
         riation feature: ", train variation feature responseCoding.shape)
         train variation feature responseCoding is a converted feature using the response coding method. The shape of Variatio
         n feature: (2124, 9)
In [28]: # one-hot encoding of variation feature.
         variation vectorizer = TfidfVectorizer(ngram range=(1,1))
         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'])
```

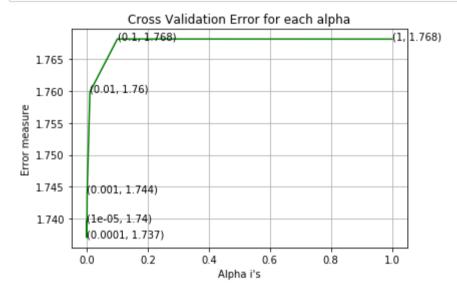
### **Q10.** How good is this Variation feature in predicting y i?

Let's build a model just like the earlier!

```
In [40]: | \text{alpha} = [10 ** x \text{ for } x \text{ in } range(-5, 1)] |
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SGDClassifi
          er.html
          # -----
          # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=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 Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         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(v cv, predict v, labels=clf.classes , eps=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.7396563641234508
For values of alpha = 0.0001 The log loss is: 1.7370313404242068
For values of alpha = 0.001 The log loss is: 1.7440809096266048
For values of alpha = 0.01 The log loss is: 1.7598369532967972
For values of alpha = 0.1 The log loss is: 1.7681377406463816
For values of alpha = 1 The log loss is: 1.7681269672786877
```

```
In [41]: 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()
```



```
In [42]: best alpha = np.argmin(cv log error array)
         clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
         clf.fit(train variation feature onehotCoding, y train)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train variation feature onehotCoding, v train)
Out[42]: CalibratedClassifierCV(base estimator=SGDClassifier(alpha=0.0001, average=False, class weight=None,
                early stopping=False, epsilon=0.1, eta0=0.0, fit intercept=True,
                11 ratio=0.15, learning rate='optimal', loss='log', max iter=None,
                n iter=None, n iter no change=5, n jobs=None, penalty='12',
                power t=0.5, random state=42, shuffle=True, tol=None,
                validation fraction=0.1, verbose=0, warm start=False),
                     cv='warn', method='sigmoid')
In [43]: 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(v train, predict v, labels=clf.classes , eps=1e-15))
         predict y = sig clf.predict proba(cv variation feature onehotCoding)
         print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",
               log loss(v cv, predict v, 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 best alpha = 0.0001 The train log loss is: 0.6920637989525468
         For values of best alpha = 0.0001 The cross validation log loss is: 1.7370313404242068
         For values of best alpha = 0.0001 The test log loss is: 1.7214012496402096
```

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

Q12. How many data points are covered by total 1921 genes in test and cross validation data sets? Ans

- 1. In test data 69 out of 665 : 10.37593984962406
- 2. In cross validation data 44 out of 532 : 8.270676691729323

#### 3.2.3 Univariate Analysis on Text Feature

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

```
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/len(row['TEXT'].split()))
                  row_index += 1
                  return text_feature_responseCoding
```

```
In [19]: # building a CountVectorizer with all the words that occured minimum 3 times in train data
    text_vectorizer = TfidfVectorizer(min_df=3,ngram_range=(1,1),max_features=2000)
    train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
    # getting all the feature names (words)
    train_text_features= text_vectorizer.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).
# A1 will sum every row and returns (1*number of 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 [20]: 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 [21]: #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 [52]: #https://stackoverflow.com/a/2258273/4084039
    sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambda x: x[1] , reverse=True))
    sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))
```

In [53]: # Number of words for a given frequency.
print(Counter(sorted\_text\_occur))

Counter({207.02733506161096: 1, 139.43965395835238: 1, 123.59372391819772: 1, 109.42257777788723: 1, 99.8506854678345 4: 1, 96.55480011903177: 1, 95.52386119013462: 1, 95.30624606406973: 1, 94.37631614906044: 1, 89.33510884988704: 1, 8 5.81518295101024: 1, 77.29038635783971: 1, 76.35742670209501: 1, 74.72520345134006: 1, 72.23123366133166: 1, 71.21857 60548949: 1, 65.17344301236898: 1, 64.46236595245013: 1, 64.22916323071577: 1, 63.647806497780394: 1, 61.162427022487 46: 1, 61.044274187137006: 1, 56.91851281239383: 1, 55.6331310634885: 1, 55.581586188304755: 1, 55.120617487644544: 1, 54.90952484048327: 1, 54.14641792492305: 1, 53.40068655970865: 1, 52.676958926775235: 1, 52.383904388637056: 1, 5 2.10085639498383: 1, 51.519940811851164: 1, 51.25364636251695: 1, 49.32555075541631: 1, 48.1386722821889: 1, 47.81297 19735249: 1, 46.65292310429546: 1, 45.6689721490592: 1, 45.53383564346477: 1, 45.292669197368234: 1, 43.8294271712204 2: 1, 43.38696654220223: 1, 43.31212880485689: 1, 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3.4062741583274905: 1, 3.405899411672747: 1, 3.39500183115 2265: 1, 3.392682418926099: 1, 3.389151720539676: 1, 3.387968106473728: 1, 3.3854317175504387: 1, 3.383978502040268: 1, 3.383226357988007: 1, 3.38215072066649: 1, 3.366005685020408: 1, 3.3592028403086487: 1, 3.358645778896409: 1, 3.35 70042277521854: 1, 3.3526881911427884: 1, 3.347950927641227: 1, 3.3292199661706334: 1, 3.3214342336907343: 1, 3.32017 93744475063: 1, 3.298443515494985: 1, 3.2974354859758304: 1, 3.2908244981154042: 1, 3.278189880826381: 1, 3.274793583 53746: 1, 3.2742469379030292: 1, 3.270491260255584: 1, 3.269951784969656: 1, 3.2674068541548693: 1, 3.26541491639953: 1, 3.2617388360412303: 1, 3.2433902363649247: 1, 3.241263615851571: 1, 3.2405163482328097: 1, 3.235427356137531: 1, 3.216877888463073: 1, 3.211115364069015: 1, 3.1933024778752572: 1, 3.1783043872566634: 1, 3.165941164707314: 1, 3.142 2925766702425: 1, 3.1405622982101993: 1, 3.133323712979683: 1, 3.1138329653340575: 1, 3.0898249558513373: 1, 3.088974 588545892: 1, 3.0755440471911704: 1, 3.039692972867657: 1, 3.02120945938044: 1, 3.0124523669885868: 1, 2.961710279871 1232: 1, 2.901222599832102: 1, 2.900070591304457: 1, 2.885951170385234: 1, 2.8129760785470572: 1, 2.79185913547278: 1, 2.3275233508278275: 1, 2.196538903293827: 1})

```
In [54]: # 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/modules/generated/sklearn.linear model.SGDClassifi
         er.html
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=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 Stochastic Gradient Descent.
         # predict(X) Predict class labels for samples in X.
         #-----
         # video Link:
         #-----
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train text feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train text feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv text feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict y, labels=clf.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', random_state=42)
clf.fit(train_text_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_onehotCoding, y_train)

predict_y = sig_clf.predict_proba(train_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_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: 1.2473217402069148

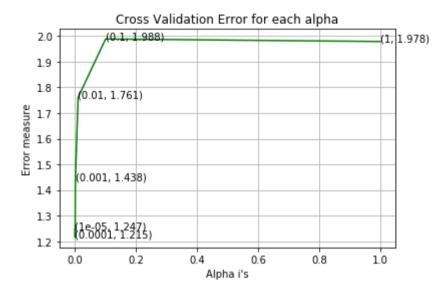
For values of alpha = 0.0001 The log loss is: 1.2150164429100236

For values of alpha = 0.001 The log loss is: 1.4378365557150556

For values of alpha = 0.01 The log loss is: 1.7606492005525152

For values of alpha = 0.1 The log loss is: 1.9882939583239234

For values of alpha = 1 The log loss is: 1.978436136642287
```



```
For values of best alpha = 0.0001 The train log loss is: 0.7620156539138682

For values of best alpha = 0.0001 The cross validation log loss is: 1.2150164429100236

For values of best alpha = 0.0001 The test log loss is: 1.0541686735272682
```

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

Ans. Yes, it seems like!

```
In [55]: def get_intersec_text(df):
    df_text_vec = TfidfVectorizer(min_df=3)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_fea = df_text_vec.get_feature_names()

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

In [56]: len1,len2 = get_intersec_text(test_df)
    print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data")
    len1,len2 = get_intersec_text(cv_df)
    print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train data")
6.89 % of word of test data appeared in train data
```

### 4. Machine Learning Models

7.571 % of word of Cross Validation appeared in train data

```
In [33]: #Data preparation for ML models.

#Misc. functionns for ML models

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

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

```
In [60]: 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 [38]: # 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,ngram range=(1,2))
              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 [{}]".format(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 ves 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 [{}]".format(word,yes no))
              print("Out of the top ",no_features," features ", word_present, "are present in query point")
```

```
In [29]: # STACKING TECHNIQUE
         # 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 variation feature onehotCoding))
         cv gene var onehotCoding = hstack((cv gene feature onehotCoding,
                                             cv variation feature onehotCoding))
         train x onehotCoding = hstack((train gene var onehotCoding,
                                         train text feature onehotCoding)).tocsr()
         train y = np.array(list(train df['Class']))
         test_x_onehotCoding = hstack((test_gene_var_onehotCoding,
                                        test text feature onehotCoding)).tocsr()
         test y = np.array(list(test df['Class']))
         cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding,
                                      cv text feature onehotCoding)).tocsr()
         cv y = np.array(list(cv df['Class']))
         train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,
                                                     train_variation_feature_responseCoding))
```

```
test gene var responseCoding = np.hstack((test gene feature responseCoding,
                                                   test variation feature responseCoding))
         cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,
                                                 cv variation feature responseCoding))
         train x responseCoding = np.hstack((train_gene_var_responseCoding,
                                             train text feature responseCoding))
         test x responseCoding = np.hstack((test gene var responseCoding,
                                            test text feature responseCoding))
         cv x responseCoding = np.hstack((cv gene var responseCoding,
                                           cv text feature responseCoding))
In [64]: print("One hot encoding features :")
         print("(number of data points * number of features) in train data = ", train_x_onehotCoding.shape)
         print("(number of data points * number of features) in test data = ", test x onehotCoding.shape)
         print("(number of data points * number of features) in cross validation data =", cv x onehotCoding.shape)
         One hot encoding features :
         (number of data points * number of features) in train data = (2124, 4183)
         (number of data points * number of features) in test data = (665, 4183)
         (number of data points * number of features) in cross validation data = (532, 4183)
In [65]: 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 responseCoding.shape)
         print("(number of data points * number of features) in cross validation data =", cv x responseCoding.shape)
          Response encoding features :
         (number of data points * number of features) in train data = (2124, 27)
         (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)
```

## Feature engineering on one hot encoded features

```
In [30]: train_x_onehotCodingFE=np.sqrt(train_x_onehotCoding)
         test x onehotCodingFE=np.sqrt(test x onehotCoding)
         cv x onehotCodingFE=np.sqrt(cv x onehotCoding)
In [67]: print("One hot encoding of features engineered features:")
         print("(number of data points * number of features) in train data = ", train x onehotCodingFE.shape)
         print("(number of data points * number of features) in test data = ", test x onehotCodingFE.shape)
         print("(number of data points * number of features) in cross validation data =", cv x onehotCodingFE.shape)
         One hot encoding of features engineered features:
         (number of data points * number of features) in train data = (2124, 4183)
         (number of data points * number of features) in test data = (665, 4183)
         (number of data points * number of features) in cross validation data = (532, 4183)
In [68]: 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_responseCoding.shape)
         print("(number of data points * number of features) in cross validation data =", cv x responseCoding.shape)
          Response encoding features :
         (number of data points * number of features) in train data = (2124, 27)
         (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 Naive base

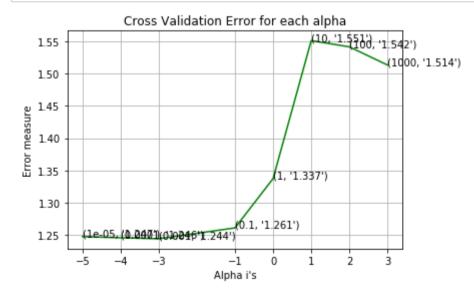
#### 4.1.1.1. Hyper parameter tuning

```
In [87]: # 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, v[, sample weight]) Fit Naive Bayes classifier according to X, v
         # predict(X) Perform classification on an array of test vectors X.
         # predict log proba(X) Return log-probability estimates for the test vector X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-algorithm-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.
         CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/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.classes , eps=1e-15))
```

```
# to avoid rounding error while multiplying probabilites we use log-probability estimates
print("for alpha = {} -----> Log Loss {}". format(i,log_loss(cv_y, sig_clf_probs)))
```

```
for alpha = 1e-05 ----> Log Loss 1.247491669245583 for alpha = 0.0001 ----> Log Loss 1.245679898704893 for alpha = 0.001 ----> Log Loss 1.2441355187830807 for alpha = 0.1 ----> Log Loss 1.260936037804692 for alpha = 1 ----> Log Loss 1.3374229086968037 for alpha = 10 ----> Log Loss 1.5513543842990123 for alpha = 100 ----> Log Loss 1.5416812684522725 for alpha = 1000 ----> Log Loss 1.513511114653115
```

```
In [88]: 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()
```



```
In [89]: 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)
Out[89]: CalibratedClassifierCV(base estimator=MultinomialNB(alpha=0.001, class prior=None, fit prior=True),
                     cv='warn', method='sigmoid')
In [90]:
         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=c
         lf.classes , eps=1e-15))
         predict y = sig clf.predict proba(cv x onehotCoding)
         print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, predict y,
         labels=clf.classes_, eps=1e-15))
         predict y = sig clf.predict proba(test x onehotCoding)
         print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss(y test, predict y, labels=clf
          .classes , eps=1e-15))
         For values of best alpha = 0.001 The train log loss is: 0.5635743875020112
         For values of best alpha = 0.001 The cross validation log loss is: 1.2441355187830807
         For values of best alpha = 0.001 The test log loss is: 1.169423133287461
```

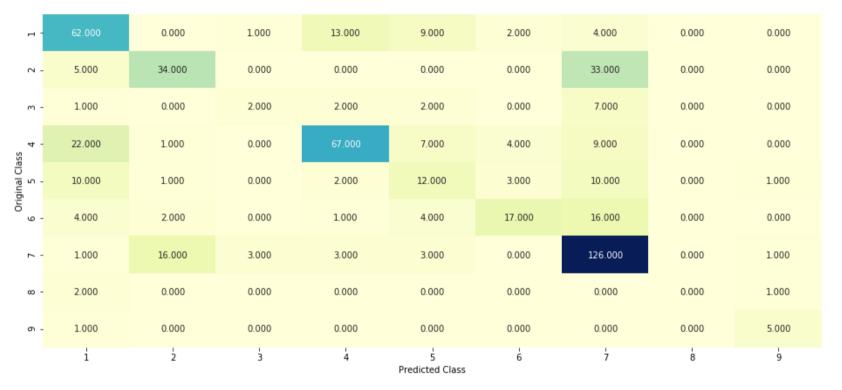
## 4.1.1.2. Testing the model with best hyper paramters

In [91]: # 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, v[, sample weight]) Fit Naive Bayes classifier according to X, v# predict(X) Perform classification on an array of test vectors X. # predict log proba(X) Return log-probability estimates for the test vector X. # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-algorithm-1/ # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration. CalibratedClassifierCV.html # -----# default paramters # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3) # some of the methods of CalibratedClassifierCV() # fit(X, y[, sample weight]) Fit the calibrated model # get params([deep]) Get parameters for this estimator. # predict(X) Predict the target of new samples. # predict proba(X) Posterior probabilities of classification # ----clf = MultinomialNB(alpha=alpha[best alpha]) clf.fit(train x onehotCoding, train y) sig clf = CalibratedClassifierCV(clf, method="sigmoid") sig clf.fit(train x onehotCoding, train y) sig clf probs = sig clf.predict proba(cv x onehotCoding) # to avoid rounding error while multiplying probabilites we use log-probability estimates print("Log Loss :",log loss(cv y, sig clf probs)) print("Number of missclassified point :", np.count nonzero((sig clf.predict(cv x onehotCoding)- cv y))/cv y.shape[0]) plot confusion matrix(cv y, sig clf.predict(cv x onehotCoding.toarray()))

Log Loss: 1.2441355187830807

Number of missclassified point : 0.3890977443609023

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



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

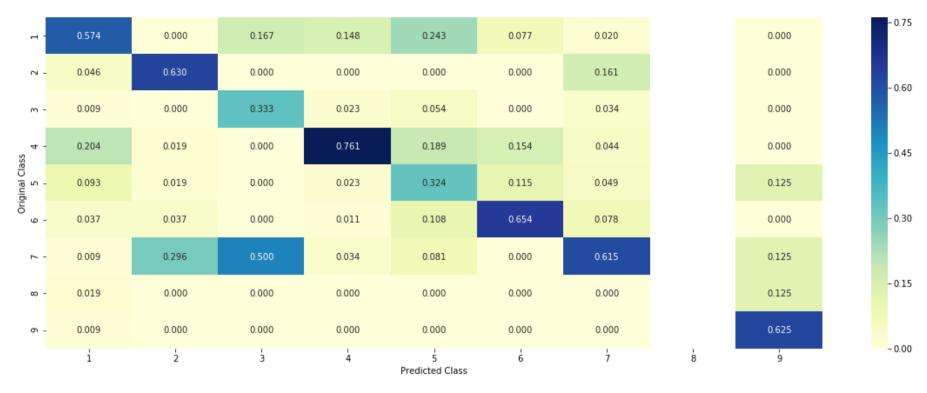
- 100

- 75

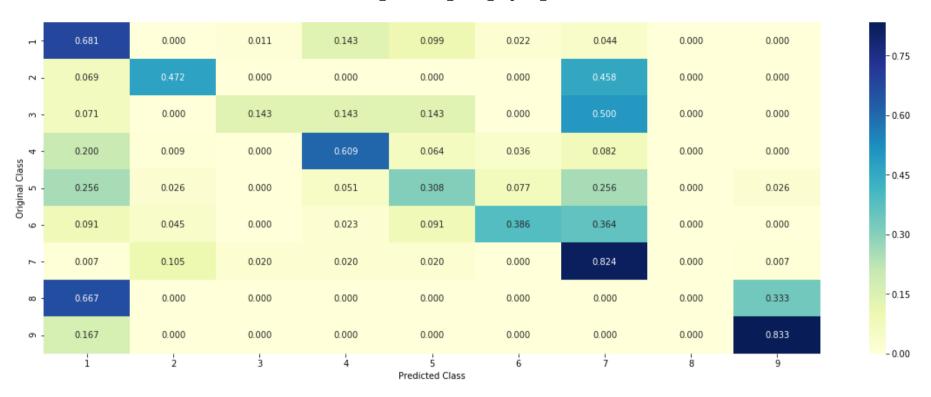
- 50

- 25

-0



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



## 4.1.1.3. Feature Importance, Correctly classified point

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

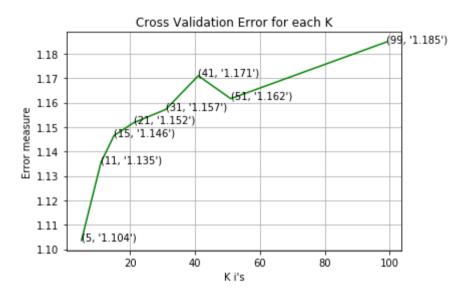
# 4.2. K Nearest Neighbour Classification

# 4.2.1. Hyper parameter tuning

```
In [95]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KNeig
         hborsClassifier.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-online/lessons/k-nearest-neighbors-geometric-in
         tuition-with-a-toy-example-1/
         #-----
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.
         CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         # video link:
         #-----
         alpha = [5, 11, 15, 21, 31, 41, 51, 99]
         cv log error array = []
         for i in alpha:
            #print("for k = ", i)
            clf = KNeighborsClassifier(n neighbors=i)
            clf.fit(train x responseCoding, train y)
            sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train x responseCoding, train y)
```

```
sig clf probs = sig clf.predict proba(cv x responseCoding)
    cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("for k ={} ----> Log Loss{}".format(i,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 K")
plt.xlabel("K 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 K = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y, labels=clf.c
lasses , eps=1e-15))
predict y = sig clf.predict proba(cv x responseCoding)
print('For values of best K = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, predict y, labe
ls=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x responseCoding)
print('For values of best K = ', alpha[best alpha], "The test log loss is:",log loss(y test, predict y, labels=clf.cla
sses , eps=1e-15))
```

```
for k =5 ----> Log Loss1.103553232412858
for k =11 ----> Log Loss1.1354767313405498
for k =15 ----> Log Loss1.1464716858088795
for k =21 ----> Log Loss1.1517313740448434
for k =31 ----> Log Loss1.157241154697575
for k =41 ----> Log Loss1.1710274581174727
for k =51 ----> Log Loss1.1616512338351952
for k =99 ----> Log Loss1.1848451161994125
```



```
For values of best K = 5 The train log loss is: 0.47513289626445343
For values of best K = 5 The cross validation log loss is: 1.103553232412858
For values of best K = 5 The test log loss is: 1.0587913365269643
```

## 4.2.2. Testing the model with best hyper paramters

Log loss : 1.103553232412858

Number of mis-classified points : 0.38345864661654133

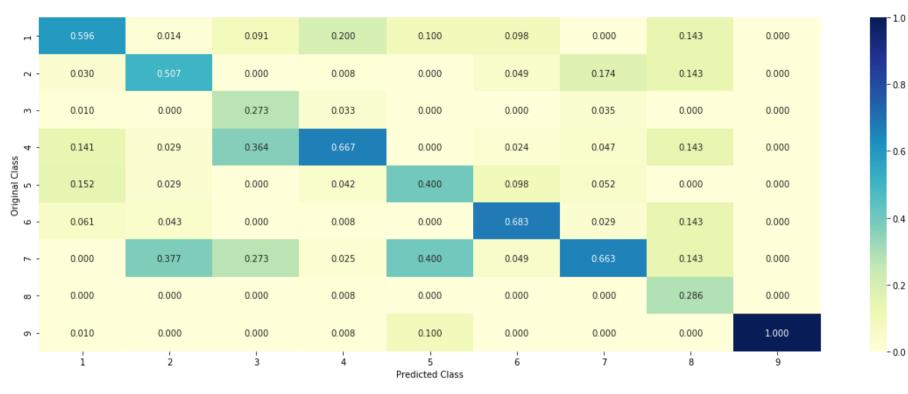
----- Confusion matrix -----

59.000     1.000     1.000     24.000     1.000     4.000     0.000     1.000        3.000     35.000     0.000     1.000     0.000     2.000     30.000     1.000	0.000
N - 3.000 35.000 0.000 1.000 0.000 2.000 30.000 1.000	
	0.000
m - 1.000 0.000 3.000 4.000 0.000 0.000 6.000 0.000	
4 -     14.000     2.000     4.000     80.000     0.000     1.000     8.000     1.000	0.000
Note of the last o	0.000
φ - 6.000 3.000 0.000 1.000 0.000 28.000 5.000 1.000	0.000
► - 0.000 26.000 3.000 3.000 4.000 2.000 114.000 1.000	0.000
∞ - 0.000 0.000 0.000 1.000 0.000 0.000 0.000 2.000	0.000
on - 1.000 0.000 0.000 1.000 1.000 0.000 0.000 0.000	3.000
1 2 3 4 5 6 7 8 Predicted Class	9

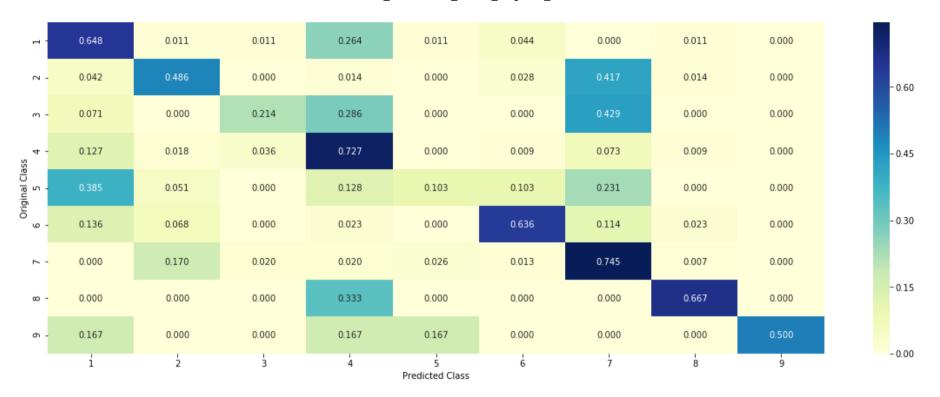
----- Precision matrix (Columm Sum=1) -----

- 20

-0



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



```
In [97]: 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]]))
```

The 5 nearest neighbours of the test points belongs to classes [4 4 4 4 4]

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

Predicted Class : 1
Actual Class : 7

## 4.2.4. Sample Query Point-2 for KNN

```
In [98]: clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
         clf.fit(train x responseCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x responseCoding, train y)
         test point index = 100
         predicted cls = sig clf.predict(test x responseCoding[test point index].reshape(1,-1))
         print("Predicted Class :", predicted cls[0])
         print("Actual Class :", test_y[test_point_index])
         neighbors = clf.kneighbors(test x responseCoding[test point index].reshape(1, -1), alpha[best alpha])
         print("the k value for knn is",alpha[best alpha], "and the nearest neighbours of the test points belongs to classes",tr
         ain v[neighbors[1][0]])
         print("Fequency of nearest points :",Counter(train v[neighbors[1][0]]))
         Predicted Class: 7
         Actual Class: 7
         the k value for knn is 5 and the nearest neighbours of the test points belongs to classes [5 7 7 1 7]
         Fequency of nearest points : Counter({7: 3, 5: 1, 1: 1})
```

# Task 3: Apply Logistic Regression with count vectorizer with unigram and bigram

## 4.3. Logistic Regression

In [26]: #Making one hot encoding features for logistic regression model by count vectorizer using unigram and bigram # one-hot encoding of Gene feature gene vectorizer LR = CountVectorizer() train gene feature onehotCoding LR = gene vectorizer LR.fit transform(train df['Gene']) test gene feature onehotCoding LR = gene vectorizer LR.transform(test df['Gene']) cv gene feature onehotCoding LR = gene vectorizer LR.transform(cv df['Gene']) # one-hot encoding of variation feature. variation vectorizer LR = CountVectorizer() train variation feature onehotCoding LR = variation vectorizer LR.fit transform(train df['Variation']) test variation feature onehotCoding LR = variation vectorizer LR.transform(test df['Variation']) cv variation feature onehotCoding LR = variation vectorizer LR.transform(cv df['Variation']) #one-hot encoding for Text feature text vectorizer LR = CountVectorizer(min df=3,ngram range=(1, 2)) train text feature onehotCoding LR = text vectorizer LR.fit transform(train df['TEXT']) train text feature onehotCoding LR = normalize(train text feature onehotCoding LR ,axis=0) test text feature onehotCoding LR = text vectorizer LR.transform(test df['TEXT']) test text feature onehotCoding LR = normalize(test text feature onehotCoding LR ,axis=0) cv text feature onehotCoding LR = text vectorizer LR.transform(cv df['TEXT']) cv text feature onehotCoding LR = normalize(cv text feature onehotCoding LR ,axis=0) #stacking all the features(gene, vartions, text of one-hot encoded) train gene var onehotCoding LR = hstack((train gene feature onehotCoding LR , train variation feature onehotCoding LR)) test\_gene\_var\_onehotCoding\_LR = hstack((test\_gene\_feature\_onehotCoding\_LR,test variation feature onehotCoding\_LR)) cv gene var onehotCoding LR = hstack((cv gene feature onehotCoding LR,cv variation feature onehotCoding LR)) train x onehotCoding LR = hstack((train gene var onehotCoding LR, train text feature onehotCoding LR)).tocsr() train y = np.array(list(train df['Class'])) test x onehotCoding LR = hstack((test gene var onehotCoding LR, test text feature onehotCoding LR)).tocsr() test y = np.array(list(test df['Class'])) cv\_x\_onehotCoding\_LR = hstack((cv\_gene\_var\_onehotCoding\_LR, cv\_text\_feature\_onehotCoding\_LR)).tocsr() cv y = np.array(list(cv df['Class'])) print("One hot encoding features :") print("(number of data points \* number of features) in train data = ", train x onehotCoding LR.shape)

```
print("(number of data points * number of features) in test data = ", test_x_onehotCoding_LR.shape)
print("(number of data points * number of features) in cross validation data =", cv_x_onehotCoding_LR.shape)
```

```
One hot encoding features:

(number of data points * number of features) in train data = (2124, 759560)

(number of data points * number of features) in test data = (665, 759560)

(number of data points * number of features) in cross validation data = (532, 759560)
```

## 4.3.1. With Class balancing

#### 4.3.1.1. Hyper paramter tuning

```
In [101]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.SGDClassifi
          er.html
          # -----
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=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 Stochastic Gradient Descent.
          \# predict(X) Predict class labels for samples in X.
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
          #-----
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.
          CalibratedClassifierCV.html
          # -----
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample weight]) Fit the calibrated model
          # get params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict proba(X) Posterior probabilities of classification
          # video link:
          #-----
          alpha = [10 ** x for x in range(-6, 3)]
          cv log error array = []
          for i in alpha:
             print("for alpha =", i)
             clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='12', loss='log', random_state=42)
             clf.fit(train_x_onehotCoding_LR, train_y)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_x_onehotCoding_LR, train_y)
             sig clf probs = sig clf.predict proba(cv x onehotCoding LR)
```

```
cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.vlabel("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', random state=42)
clf.fit(train x onehotCoding LR, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding LR, train y)
predict v = sig clf.predict proba(train x onehotCoding LR)
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 LR)
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 LR)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",
      log loss(v test, predict v, labels=clf.classes , eps=1e-15))
```

for alpha = 1e-06

Log Loss: 1.526971311207314

for alpha = 1e-05

Log Loss: 1.5386623502716792

for alpha = 0.0001

Log Loss: 1.5266915853209928

for alpha = 0.001

Log Loss: 1.4522367672319636

for alpha = 0.01

Log Loss: 1.1628639564707144

for alpha = 0.1

Log Loss: 1.1899739328129815

for alpha = 1

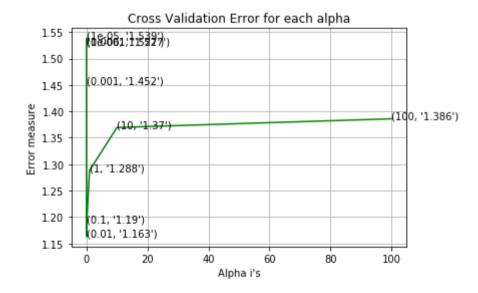
Log Loss : 1.287797395891601

for alpha = 10

Log Loss: 1.3695018048796566

for alpha = 100

Log Loss: 1.3859080701489557



For values of best alpha = 0.01 The train log loss is: 0.8765083328319367 For values of best alpha = 0.01 The cross validation log loss is: 1.1628639564707144

For values of best alpha = 0.01 The test log loss is: 1.1952757829548217

## 4.3.1.2. Testing the model with best hyper paramters

Log loss : 1.1628639564707144

Number of mis-classified points : 0.38721804511278196

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

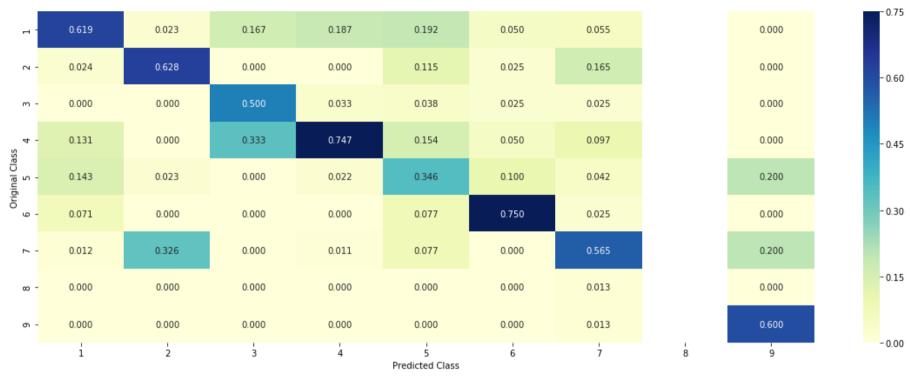
ra -	52.000	1.000	1.000	17.000	5.000	2.000	13.000	0.000	0.000
7 -	2.000	27.000	0.000	0.000	3.000	1.000	39.000	0.000	0.000
m -	0.000	0.000	3.000	3.000	1.000	1.000	6.000	0.000	0.000
- 4 -	11.000	0.000	2.000	68.000	4.000	2.000	23.000	0.000	0.000
Original Class	12.000	1.000	0.000	2.000	9.000	4.000	10.000	0.000	1.000
Ori	6.000	0.000	0.000	0.000	2.000	30.000	6.000	0.000	0.000
۲ -	1.000	14.000	0.000	1.000	2.000	0.000	134.000	0.000	1.000
ω -	0.000	0.000	0.000	0.000	0.000	0.000	3.000	0.000	0.000
o -	0.000	0.000	0.000	0.000	0.000	0.000	3.000	0.000	3.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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

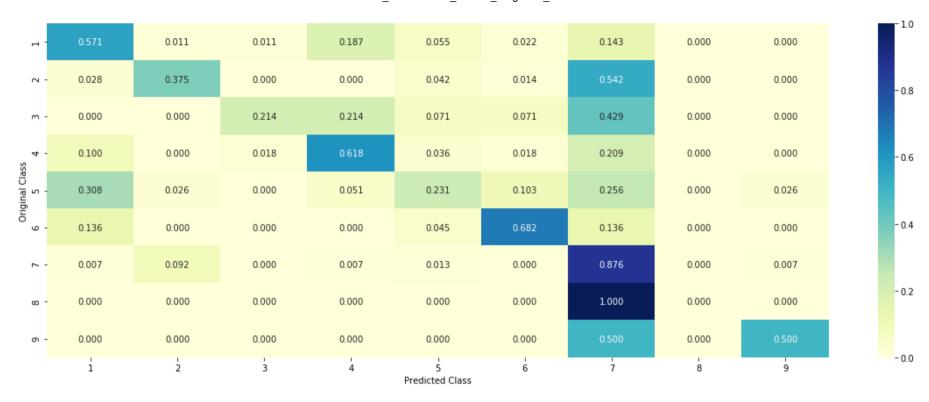
- 50

- 25

-0



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



# 4.3.1.3. Feature Importance

```
In [103]: # 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 LR(indices, text, gene, var, no features):
              gene count vec = CountVectorizer()
              var count vec = CountVectorizer()
              text count vec = CountVectorizer(ngram range=(1, 2))
              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 count 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 [{}]".format(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 ves 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 [{}]".format(word,yes no))
              print("Out of the top ", no features," features ", word present, "are present in query point")
```

#### 4.3.1.3.1. Correctly Classified point

```
In [104]: train x onehotCoding.shape
          train v.shape
Out[104]: (2124,)
In [105]: clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
          clf.fit(train x onehotCoding LR,train y)
          test point index =1
          no feature = 500
          predicted_cls = sig_clf.predict(test_x_onehotCoding_LR[test_point_index])
          print("Predicted Class :", predicted cls[0])
          print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding LR[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 LR(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test
          df['Variation'].iloc[test point index], no feature)
          Predicted Class: 4
          Predicted Class Probabilities: [[0.0694 0.2297 0.0146 0.4883 0.0361 0.011 0.1338 0.0108 0.0063]]
          Actual Class : 7
          261 Text feature [carcinomas] present in test data point [True]
          Out of the top 500 features 1 are present in query point
```

## 4.3.1.3.2. Incorrectly Classified point

```
In [107]: test_point_index = 100
    no_feature = 100
    predicted_cls = sig_clf.predict(test_x_onehotCoding_LR[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding_LR[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_LR(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index], no_feature)

Predicted Class : 7
    Predicted Class : 7
    Predicted Class : 7
    Out of the top 100 features 0 are present in query point
```

## 4.3.2. Without Class balancing

### 4.3.2.1. Hyper paramter tuning

```
In [108]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SGDClassifi
         er.html
          # -----
          # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=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 Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
          #-----
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.
         CalibratedClassifierCV.html
          # -----
          # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
          # video link:
          #-----
         alpha = [10 ** x for x in range(-6, 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_LR, train_y)
             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train x onehotCoding LR, train y)
```

```
sig clf probs = sig clf.predict proba(cv x onehotCoding LR)
    cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.vlabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)# here we have not written clas
s weight='balanced'
clf.fit(train x_onehotCoding_LR, train_y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding LR, train y)
predict y = sig clf.predict proba(train x onehotCoding LR)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y, labels=c
lf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x onehotCoding LR)
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_LR)
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: 1.4665532137033077

for alpha = 1e-05

Log Loss: 1.4685171825273864

for alpha = 0.0001

Log Loss: 1.477599201777331

for alpha = 0.001

Log Loss: 1.4435520394153087

for alpha = 0.01

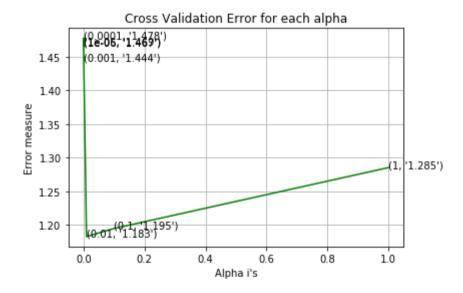
Log Loss: 1.1829103454047591

for alpha = 0.1

Log Loss: 1.1948630032134728

for alpha = 1

Log Loss: 1.2853418476335345



For values of best alpha = 0.01 The train log loss is: 0.8886156253613645 For values of best alpha = 0.01 The cross validation log loss is: 1.1829103454047591

For values of best alpha = 0.01 The test log loss is: 1.2225456836748452

## 4.3.2.2. Testing model with best hyper parameters

Log loss : 1.1829103454047591

Number of mis-classified points : 0.40225563909774437

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

_									
<b>-</b> -	51.000	1.000	0.000	19.000	3.000	2.000	15.000	0.000	0.000
- 2	2.000	25.000	0.000	0.000	1.000	1.000	42.000	1.000	0.000
m -	0.000	0.000	2.000	4.000	0.000	1.000	7.000	0.000	0.000
- 4 -	11.000	0.000	0.000	71.000	3.000	2.000	23.000	0.000	0.000
Original Class 5	14.000	1.000	0.000	6.000	3.000	3.000	12.000	0.000	0.000
oric	7.000	5.000	0.000	1.000	1.000	24.000	6.000	0.000	0.000
۲-	1.000	12.000	0.000	1.000	1.000	0.000	138.000	0.000	0.000
∞ -	0.000	0.000	0.000	0.000	0.000	0.000	3.000	0.000	0.000
o -	0.000	0.000	0.000	0.000	0.000	0.000	2.000	0.000	4.000
	i	2	3	4	5 Predicted Class	6	7	8	9

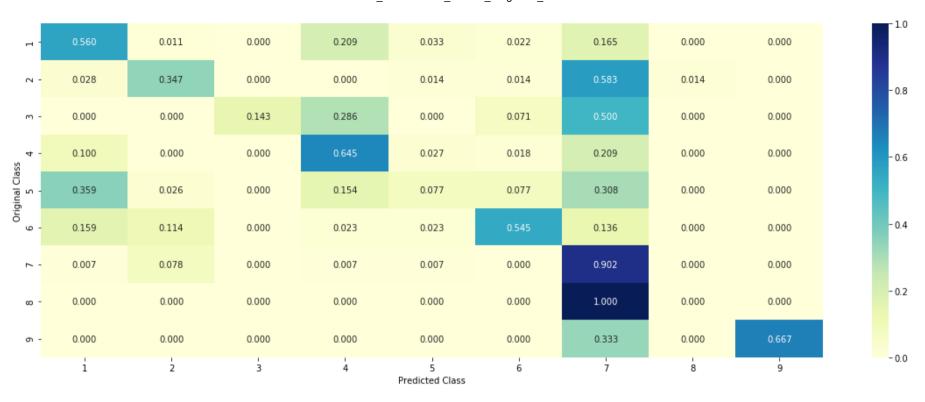
----- Precision matrix (Columm Sum=1) -----

- 25

-0



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



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

```
In [110]: clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
    clf.fit(train_x_onehotCoding_LR,train_y)
    test_point_index = 1
    no_feature = 500
    predicted_cls = sig_clf.predict(test_x_onehotCoding_LR[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding_LR[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_LR(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index], no_feature)

Predicted Class : 4
```

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

```
In [111]: test_point_index = 100
    no_feature = 500
    predicted_cls = sig_clf.predict(test_x_onehotCoding_LR[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding_LR[test_point_index]),4))
    print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
    get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_point_index],test_df
    ['Variation'].iloc[test_point_index], no_feature)

Predicted Class : 7
    Predicted Class : 7
    Out of the top 500 features 0 are present in query point
```

Logistic Regression using TFIDF vectorizer with feature engineering features

In [112]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear\_model.SGDClassifi er.html alpha = [10 \*\* x for x in range(-6, 3)]cv log error array = [] for i in alpha: print("for alpha =", i) clf = SGDClassifier(class weight='balanced', alpha=i, penalty='12', loss='log', random state=42) clf.fit(train x onehotCodingFE, train y) sig clf = CalibratedClassifierCV(clf, method="sigmoid") sig clf.fit(train x onehotCodingFE, train y) sig clf probs = sig clf.predict proba(cv x onehotCodingFE) cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15)) # to avoid rounding error while multiplying probabilites we use log-probability estimates print("Log Loss :",log loss(cv y, sig clf probs)) fig, ax = plt.subplots() ax.plot(alpha, cv log error array,c='g') for i, txt in enumerate(np.round(cv log error array,3)): ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i])) plt.grid() plt.title("Cross Validation Error for each alpha") plt.xlabel("Alpha i's") plt.ylabel("Error measure") plt.show() best alpha = np.argmin(cv log error array) clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', random state=42) clf.fit(train\_x\_onehotCodingFE, train y) sig clf = CalibratedClassifierCV(clf, method="sigmoid") sig clf.fit(train x onehotCodingFE, train y) predict y = sig clf.predict proba(train x onehotCodingFE) print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y, labels=c lf.classes , eps=1e-15)) predict y = sig clf.predict proba(cv x onehotCodingFE) 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 onehotCodingFE)

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: 1.083821739016169

for alpha = 1e-05

Log Loss: 1.0868178423544974

for alpha = 0.0001

Log Loss: 1.0724055267477606

for alpha = 0.001

Log Loss: 1.032136557996591

for alpha = 0.01

Log Loss: 1.1088810097920543

for alpha = 0.1

Log Loss: 1.5367919152002336

for alpha = 1

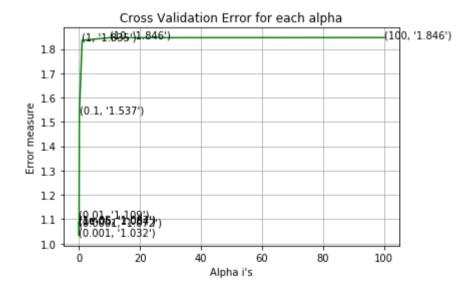
Log Loss: 1.835137915131387

for alpha = 10

Log Loss: 1.8459414645922774

for alpha = 100

Log Loss: 1.8464178871572867



For values of best alpha = 0.001 The train log loss is: 0.6123783471421275

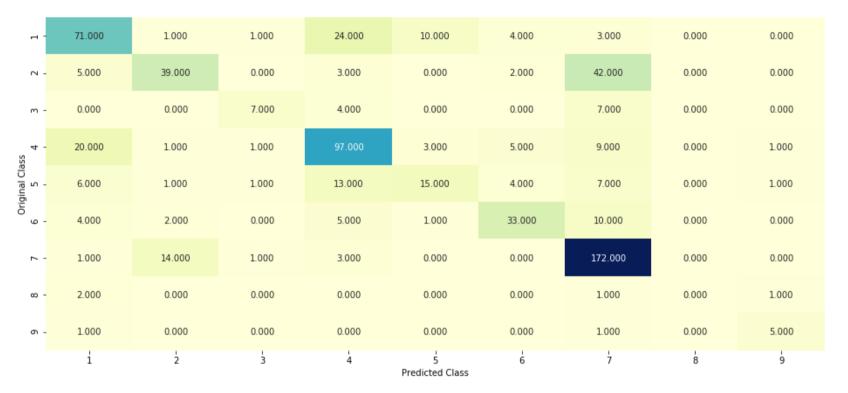
For values of best alpha = 0.001 The cross validation log loss is: 1.032136557996591

For values of best alpha = 0.001 The test log loss is: 0.9465105468033816

Log loss : 0.9465105468033816

Number of mis-classified points: 0.3398496240601504

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



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

- 150

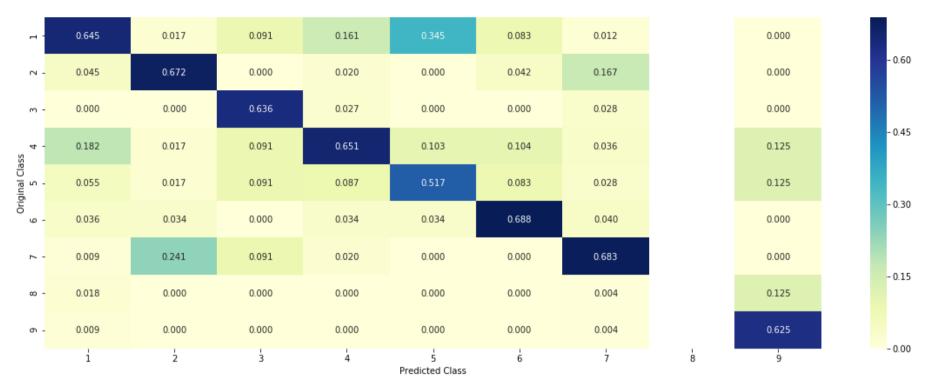
- 120

- 90

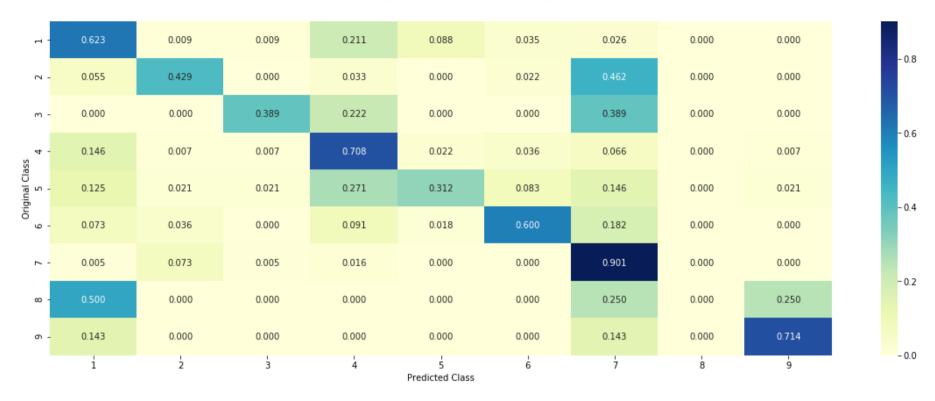
- 60

- 30

-0



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



# Obervation

We use logistic regression using TFIDF vectorizer for all three feature such as Gene, Variation, Text and implemented feature engineering as square root of vectorizer and found log-loss is 0.946 and misclassified points are 0.339

# **Correctly Classified points**

```
In [114]: # 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 = 100
    predicted_cls = sig_clf.predict((test_x_onehotCoding[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
    print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
    get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_point_index],test_df
    ['Variation'].iloc[test_point_index], no_feature)
```

Predicted Class: 4

Predicted Class Probabilities: [[0.1925 0.2022 0.0206 0.2945 0.0628 0.0752 0.1104 0.0051 0.0368]]

Actual Class: 7

Out of the top 100 features 0 are present in query point

#### **Incorrectly Classified point**

# 4.4. Linear Support Vector Machines

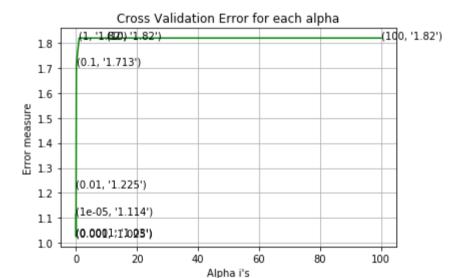
# 4.4.1. Hyper paramter tuning

In [31]: # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/generated/sk Learn.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 function shape='ovr', random state=None) # Some of methods of SVM() # fit(X, y, [sample weight]) Fit the SVM model according to the given training data. # predict(X) Perform classification on samples in X. # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathematical-derivation-copy-8/ # -----# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration. CalibratedClassifierCV.html # -----# default paramters # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3) # some of the methods of CalibratedClassifierCV() # fit(X, y[, sample weight]) Fit the calibrated model # get params([deep]) Get parameters for this estimator. # predict(X) Predict the target of new samples. # predict proba(X) Posterior probabilities of classification # video link: alpha = [10 \*\* x for x in range(-5, 3)]cv log error array = [] for i in alpha: print("for C =", i) clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced') clf = SGDClassifier( class weight='balanced', alpha=i, penalty='12', loss='hinge', random state=42) clf.fit(train x onehotCoding, train y) sig\_clf = CalibratedClassifierCV(clf, method="sigmoid") sig clf.fit(train x onehotCoding, train y)

```
sig clf probs = sig clf.predict proba(cv x onehotCoding)
    cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.vlabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
# clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced')
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='hinge', 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=c
lf.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 C = 1e-05
Log Loss : 1.1137049321264103
for C = 0.0001
Log Loss : 1.0295760364061246
for C = 0.001
Log Loss : 1.0251509418867966
for C = 0.01
Log Loss : 1.2248003696516199
for C = 0.1
Log Loss : 1.713120337856678
for C = 1
Log Loss : 1.8196045692242897
for C = 10
Log Loss : 1.819604484711596
for C = 100
```

Log Loss: 1.819604503074025



For values of best alpha = 0.001 The train log loss is: 0.5684338035686777

For values of best alpha = 0.001 The cross validation log loss is: 1.0251509418867966

For values of best alpha = 0.001 The test log loss is: 1.0064956595650647

# 4.4.2. Testing model with best hyper parameters

Log loss : 1.0251509418867966

Number of mis-classified points : 0.3233082706766917

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

_									
	62.000	2.000	0.000	17.000	6.000	1.000	3.000	0.000	0.000
2 -	0.000	39.000	0.000	1.000	1.000	1.000	30.000	0.000	0.000
m -	1.000	0.000	2.000	3.000	3.000	0.000	5.000	0.000	0.000
4 -	20.000	0.000	0.000	73.000	10.000	1.000	5.000	0.000	1.000
Original Class 5	2.000	1.000	2.000	3.000	19.000	1.000	11.000	0.000	0.000
Orig	4.000	2.000	1.000	2.000	4.000	25.000	6.000	0.000	0.000
۲ -	1.000	12.000	3.000	0.000	3.000	0.000	134.000	0.000	0.000
ω -	1.000	1.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000
თ -	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	6.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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

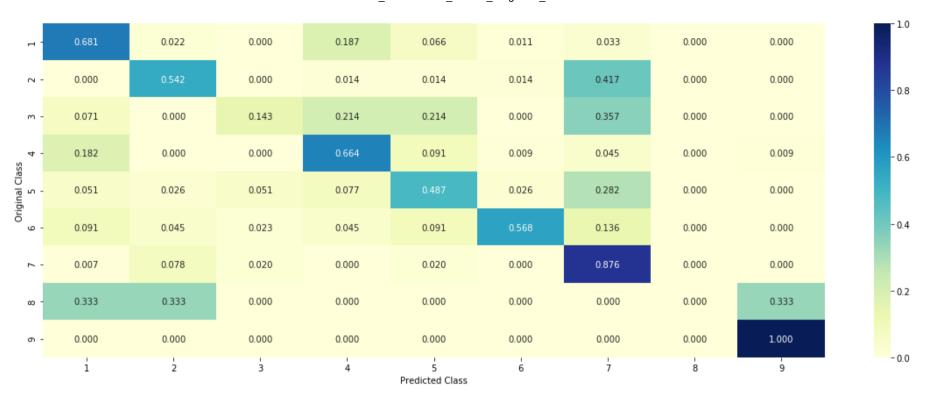
- 50

- 25

-0



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



# 4.3.3. Feature Importance

## 4.3.3.1. For Correctly classified point

```
In [39]: %%time
         clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', random state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         # test point index = 100
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test df
         ['Variation'].iloc[test point index], no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[2.850e-02 5.860e-02 3.400e-03 4.060e-02 2.640e-02 1.680e-02 8.221e-01
           4.000e-04 3.200e-0311
         Actual Class : 7
         Out of the top 500 features 0 are present in query point
         Wall time: 5min 39s
```

#### 4.3.3.2. For Incorrectly classified point

```
In [40]: %%time
         test_point_index = 100
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test df
         ['Variation'].iloc[test point index], no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.0525 0.1666 0.0012 0.0433 0.0501 0.0452 0.6352 0.0012 0.0047]]
         Actual Class : 7
         Out of the top 500 features 0 are present in query point
         Wall time: 5min 42s
```

### 4.5 Random Forest Classifier

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

```
In [41]: # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0.
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         \# predict proba (X) Perform classification on samples in X.
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their-construc
         tion-2/
         # -----
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.
         CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         # video link:
         #-----
         alpha = [100,200,500,1000,2000]
         max_depth = [5, 10]
         cv log error array = []
```

```
for i in alpha:
    for j in max depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, random state=42, 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))
'''fia. ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[int(i/2)],max depth[int(i%2)],str(txt)), (features[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', max depth=max depth[int(best alp
ha%2)], random state=42, n jobs=-1)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best estimator = ', alpha[int(best alpha/2)], "The train log loss is:",log loss(y train, predict
y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best estimator = ', alpha[int(best alpha/2)], "The cross validation log loss is:",log loss(y cv,
predict y, labels=clf.classes , eps=1e-15))
predict_y = sig_clf.predict_proba(test_x onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss is:",log_loss(y_test, predict_y,
labels=clf.classes , eps=1e-15))
```

```
for n estimators = 100 and max depth = 5
Log Loss: 1.2058062909738223
for n estimators = 100 and max depth = 10
Log Loss: 1.2515407256802213
for n_estimators = 200 and max depth = 5
Log Loss: 1.1919436833687997
for n estimators = 200 and max depth = 10
Log Loss: 1.2364559940525628
for n estimators = 500 and max depth = 5
Log Loss: 1.1929061303907207
for n estimators = 500 and max depth = 10
Log Loss: 1.231924935559586
for n estimators = 1000 and max depth = 5
Log Loss: 1.1909951282137456
for n estimators = 1000 and max depth = 10
Log Loss: 1.2253146194839353
for n estimators = 2000 and max depth = 5
Log Loss: 1.1901255319611563
for n estimators = 2000 and max depth = 10
Log Loss: 1.2224376301280562
For values of best estimator = 2000 The train log loss is: 0.8769144330158822
For values of best estimator = 2000 The cross validation log loss is: 1.1901255319611566
For values of best estimator = 2000 The test log loss is: 1.1516954354004543
```

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

```
In [42]: # ------
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0.
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
                              Perform classification on samples in X.
         # predict proba (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-construc
         tion-2/
         # -----
         clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', max depth=max depth[int(best alp
         ha%2)], random state=42, n jobs=-1)
         predict and plot confusion matrix(train x onehotCoding, train y,cv x onehotCoding,cv y, clf)
```

Log loss : 1.1901255319611563

Number of mis-classified points : 0.43045112781954886

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

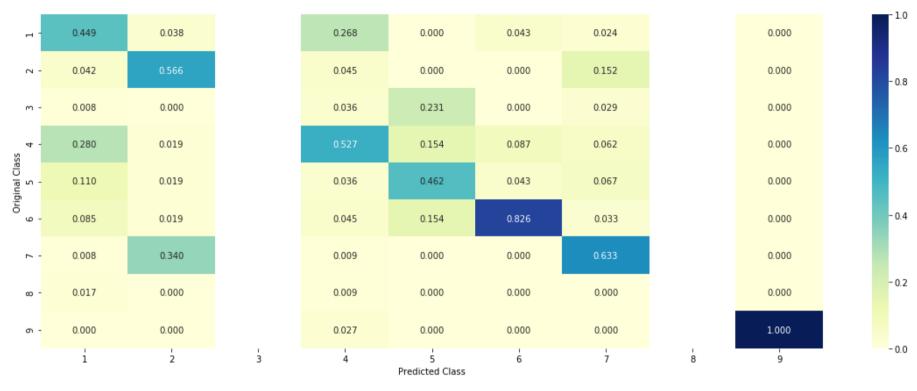
53.000	2.000	0.000	30.000	0.000	1.000	5.000	0.000	0.000
5.000	30.000	0.000	5.000	0.000	0.000	32.000	0.000	0.000
1.000	0.000	0.000	4.000	3.000	0.000	6.000	0.000	0.000
33.000	1.000	0.000	59.000	2.000	2.000	13.000	0.000	0.000
13.000	1.000	0.000	4.000	6.000	1.000	14.000	0.000	0.000
10.000	1.000	0.000	5.000	2.000	19.000	7.000	0.000	0.000
1.000	18.000	0.000	1.000	0.000	0.000	133.000	0.000	0.000
2.000	0.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	3.000	0.000	0.000	0.000	0.000	3.000
i	2	3	4	5 Predicted Class	6	7	8	9
	5.000 1.000 33.000 13.000 10.000 2.000 0.000	5.000     30.000       1000     0.000       33.000     1.000       13.000     1.000       10.000     1.000       1000     18.000       2.000     0.000       0.000     0.000	5.000     30.000     0.000       1.000     0.000     0.000       33.000     1.000     0.000       13.000     1.000     0.000       10.000     1.000     0.000       1.000     1.000     0.000       2.000     0.000     0.000       0.000     0.000     0.000       0.000     0.000     0.000	5.000     30.000     0.000     5.000       1.000     0.000     0.000     4.000       33.000     1.000     0.000     59.000       13.000     1.000     0.000     4.000       10.000     1.000     0.000     5.000       1000     18.000     0.000     1.000       2000     0.000     0.000     1.000       0.000     0.000     3.000	5.000     30.000     0.000     5.000     0.000       1.000     0.000     0.000     4.000     3.000       33.000     1.000     0.000     59.000     2.000       13.000     1.000     0.000     4.000     6.000       10.000     1.000     0.000     5.000     2.000       1     2     3     4     5	5.000     30.000     0.000     5.000     0.000     0.000       1.000     0.000     0.000     4.000     3.000     0.000       33.000     1.000     0.000     59.000     2.000     2.000       13.000     1.000     0.000     4.000     6.000     1.000       10.000     1.000     0.000     5.000     2.000     19.000       1000     18.000     0.000     1.000     0.000     0.000       2.000     0.000     0.000     1.000     0.000     0.000       1     2     3     4     5     6	5.000     30.000     0.000     5.000     0.000     0.000     32.000       1.000     0.000     0.000     4.000     3.000     0.000     6.000       33.000     1.000     0.000     59.000     2.000     2.000     13.000       13.000     1.000     0.000     4.000     6.000     1.000     14.000       10.000     1.000     0.000     5.000     2.000     19.000     7.000       1000     18.000     0.000     1.000     0.000     0.000     133.000       2000     0.000     0.000     1.000     0.000     0.000     0.000       1     2     3     4     5     6     7	5.000       30.000       0.000       5.000       0.000       0.000       32.000       0.000         1.000       0.000       0.000       4.000       3.000       0.000       6.000       0.000         33.000       1.000       0.000       59.000       2.000       2.000       13.000       0.000         13.000       1.000       0.000       4.000       6.000       1.000       14.000       0.000         10.000       1.000       0.000       5.000       2.000       19.000       7.000       0.000         1000       18.000       0.000       1.000       0.000       0.000       133.000       0.000         2000       0.000       0.000       1.000       0.000       0.000       0.000       0.000         1       2       3       4       5       6       7       8

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

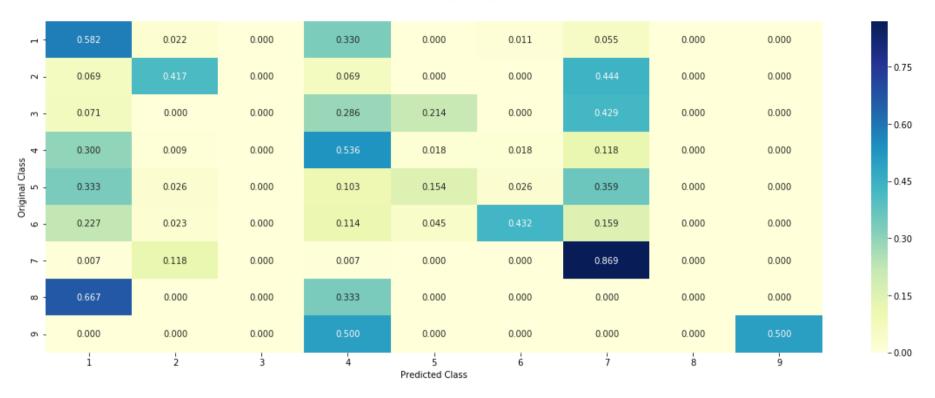
- 50

- 25

-0



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



# 4.5.3. Feature Importance

### 4.5.3.1. Correctly Classified point

```
In [43]: # test point index = 10
         clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', max depth=max depth[int(best alp
         ha%2)], random state=42, n jobs=-1)
         clf.fit(train x onehotCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x onehotCoding, train y)
         test point index = 1
         no feature = 100
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index]
         x],test df['Variation'].iloc[test point index], no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.0402 0.243 0.0169 0.0266 0.0372 0.0378 0.5922 0.0049 0.0011]]
```

### 4.5.3.2. Inorrectly Classified point

```
In [44]: test_point_index = 100
    no_feature = 100
    predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
    print("Actuall Class :", test_y[test_point_index])
    indices = np.argsort(-clf.feature_importances_)
    print("-"*50)
    get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index], no_feature)

Predicted Class : 7
    Predicted Class Probabilities: [[0.0126 0.3496 0.0134 0.0087 0.0284 0.0299 0.5538 0.0028 0.0007]]
    Actuall Class : 7
    Text feature [02] present in test data point [True]
    Out of the top 100 features 1 are present in query point
```

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

```
In [45]: # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0.
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         \# predict proba (X) Perform classification on samples in X.
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their-construc
         tion-2/
         # -----
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.
         CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         # video link:
         #-----
         alpha = [10,50,100,200,500,1000]
         max_depth = [2,3,5,10]
         cv log error array = []
```

```
for i in alpha:
    for j in max depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, random state=42, n jobs=-1)
        clf.fit(train x responseCoding, train y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig clf.fit(train x responseCoding, train y)
        sig clf probs = sig clf.predict proba(cv x responseCoding)
        cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
        print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[int(i/4)],max depth[int(i%4)],str(txt)), (features[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='gini', max depth=max depth[int(best alp
ha%4)], random state=42, n jobs=-1)
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x responseCoding, train y)
predict y = sig clf.predict proba(train x responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The train log loss is:",log_loss(y_train, predict_y, l
abels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x responseCoding)
print('For values of best alpha = ', alpha[int(best alpha/4)], "The cross validation log loss is:",log loss(y cv, pred
ict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The test log loss is:",log_loss(y_test, predict_y, lab
els=clf.classes , eps=1e-15))
```

for n estimators = 10 and max depth = 2 Log Loss: 2.121168855735514 for n estimators = 10 and max depth = 3Log Loss: 1.7006781420159711 for n estimators = 10 and max depth = 5 Log Loss: 1.4056412284730369 for n estimators = 10 and max depth = 10 Log Loss: 1.846864985390235 for n estimators = 50 and max depth = 2Log Loss: 1.7249999968157448 for n estimators = 50 and max depth = 3Log Loss: 1.4181305989462831 for n estimators = 50 and max depth = 5Log Loss: 1.3799630854936158 for n estimators = 50 and max depth = 10 Log Loss: 1.6843258779008994 for n estimators = 100 and max depth = 2 Log Loss: 1.5298875588579697 for n estimators = 100 and max depth = 3 Log Loss: 1.493488826646144 for n estimators = 100 and max depth = 5 Log Loss: 1.3828067200183298 for n estimators = 100 and max depth = 10 Log Loss: 1.6708934796553525 for n estimators = 200 and max depth = 2Log Loss: 1.5920252308990268 for n estimators = 200 and max depth = 3Log Loss: 1.5004105275348263 for n estimators = 200 and max depth = 5Log Loss: 1.429187775610955 for n estimators = 200 and max depth = 10 Log Loss: 1.6931047930156682 for n estimators = 500 and max depth = 2Log Loss: 1.7157244885551617 for n estimators = 500 and max depth = 3Log Loss: 1.5684045326602118 for n estimators = 500 and max depth = 5 Log Loss: 1.4044330656835644 for  $n_{estimators} = 500$  and max depth = 10Log Loss: 1.7490076493750095 for n\_estimators = 1000 and max depth = 2

```
Log Loss: 1.6706634299746126

for n_estimators = 1000 and max depth = 3

Log Loss: 1.5690344903579458

for n_estimators = 1000 and max depth = 5

Log Loss: 1.40981010845083

for n_estimators = 1000 and max depth = 10

Log Loss: 1.7223475342655636

For values of best alpha = 50 The train log loss is: 0.05278144175374067

For values of best alpha = 50 The cross validation log loss is: 1.3799630854936158

For values of best alpha = 50 The test log loss is: 1.3957894129939916
```

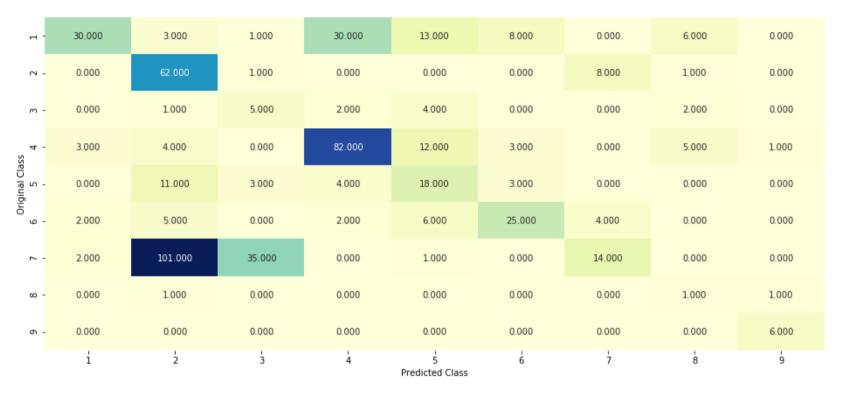
# 4.5.4. Testing model with best hyper parameters (Response Coding)

In [46]: # ------# default parameters # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2, # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0. # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False, # class weight=None) # Some of methods of RandomForestClassifier() # fit(X, y, [sample weight]) Fit the SVM model according to the given training data. # predict(X) Perform classification on samples in X. Perform classification on samples in X. # predict proba (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-construc tion-2/ # ----clf = RandomForestClassifier(max depth=max depth[int(best alpha%4)], n estimators=alpha[int(best alpha/4)], criterion ='gini', max features='auto', random state=42) predict and plot confusion matrix(train x responseCoding, train y,cv x responseCoding,cv y, clf)

Log loss: 1.379963085493616

Number of mis-classified points : 0.543233082706767

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



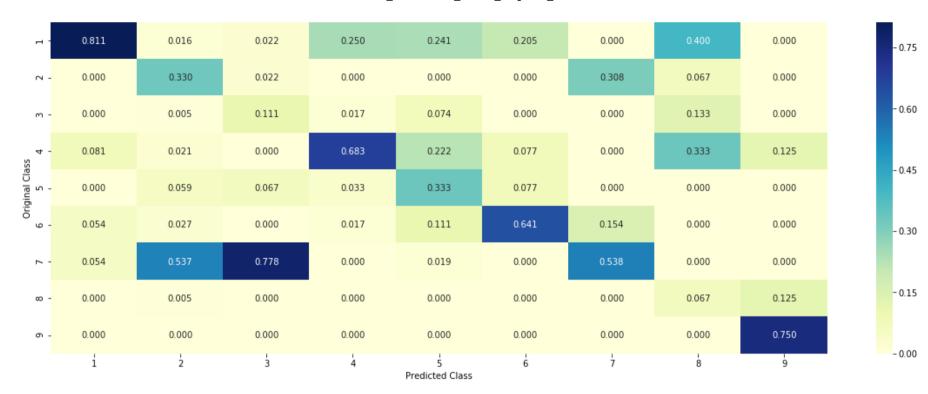
----- Precision matrix (Columm Sum=1) -----

- 80

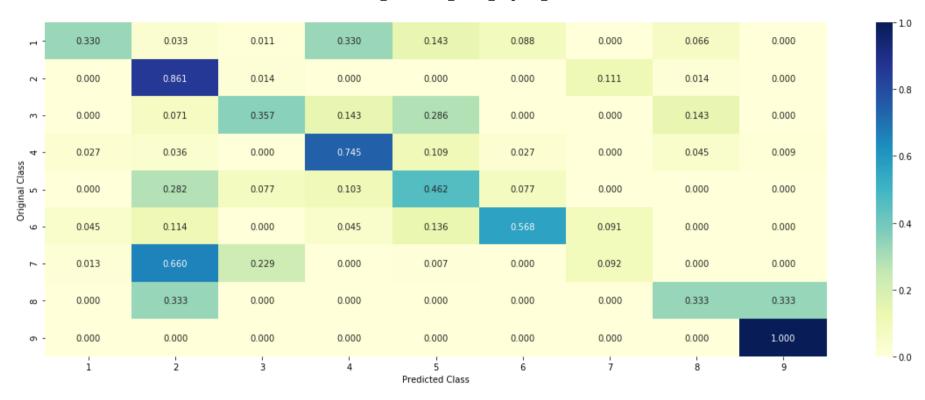
- 40

- 20

-0



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



## 4.5.5. Feature Importance

### 4.5.5.1. Correctly Classified point

In [47]: clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='gini', max depth=max depth[int(best alp ha%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 = 1no feature = 27 predicted cls = sig clf.predict(test x responseCoding[test point index].reshape(1,-1)) print("Predicted Class :", predicted cls[0]) print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x responseCoding[test point index].reshape (1,-1),4)print("Actual Class :", test y[test point index]) indices = np.argsort(-clf.feature importances ) print("-"\*50) for i in indices: **if** i<9: print("Gene is important feature") elif i<18: print("Variation is important feature") else: print("Text is important feature")

```
Predicted Class: 7
Predicted Class Probabilities: [[0.0022 0.0027 0.0025 0.0031 0.0013 0.0019 0.9838 0.0011 0.0014]]
Actual Class: 7
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
Variation is important feature
Gene is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Text is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Gene is important feature
```

### 4.7 Stack the models

### 4.7.1 testing with hyper parameter tuning

```
In [48]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SGDClassifi
         er.html
         # ------
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=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 Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
         #-----
         # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/generated/sk
         Learn.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 function shape='ovr', random state=None)
         # Some of methods of SVM()
         # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathematical-derivation-copy-8/
         # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/generated/sk
         Learn.ensemble.RandomForestClassifier.html
         # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='qini', max_depth=None, min_samples_split=2,
         # min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_impurity_decrease=0.
         # min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None, verbose=0, warm_start=False,
         # class weight=None)
```

```
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
\# predict(X) Perform classification on samples in X.
# predict proba (X)
                     Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their-construc
tion-2/
# -----
clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class weight='balanced', random state=0)
clf1.fit(train x onehotCoding, train y)
sig clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
clf2 = SGDClassifier(alpha=1, penalty='12', loss='hinge', class weight='balanced', random state=0)
clf2.fit(train x onehotCoding, train y)
sig clf2 = CalibratedClassifierCV(clf2, method="sigmoid")
clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train x onehotCoding, train y)
sig clf3 = CalibratedClassifierCV(clf3, method="sigmoid")
sig clf1.fit(train x onehotCoding, train y)
print("Logistic Regression : Log Loss: %0.2f" % (log loss(cv y, sig clf1.predict proba(cv x onehotCoding))))
sig clf2.fit(train x onehotCoding, train y)
print("Support vector machines : Log Loss: %0.2f" % (log loss(cv y, sig clf2.predict proba(cv x onehotCoding))))
sig clf3.fit(train x onehotCoding, train y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.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
```

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

In [49]: lr = LogisticRegression(C=0.1)
 sclf = StackingClassifier(classifiers=[sig\_clf1, sig\_clf2, sig\_clf3], meta\_classifier=lr, use\_probas=True)
 sclf.fit(train\_x\_onehotCoding, train\_y)

log\_error = log\_loss(train\_y, sclf.predict\_proba(train\_x\_onehotCoding))
 print("Log loss (train) on the stacking classifier :",log\_error)

log\_error = log\_loss(cv\_y, sclf.predict\_proba(cv\_x\_onehotCoding))
 print("Log loss (CV) on the stacking classifier :",log\_error)

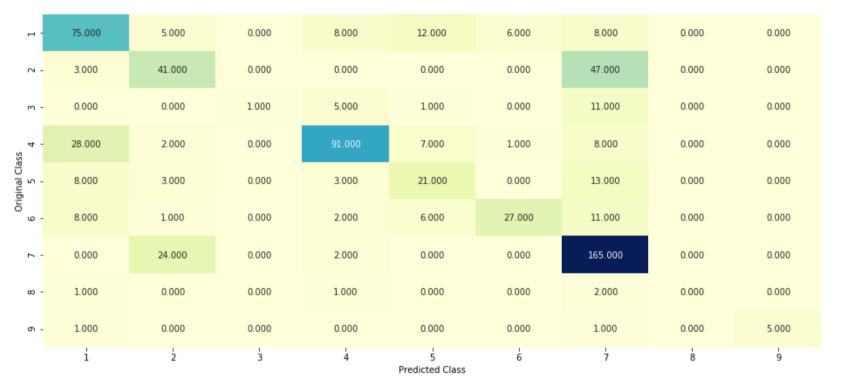
log\_error = log\_loss(test\_y, sclf.predict\_proba(test\_x\_onehotCoding))
 print("Log loss (test) on the stacking classifier :",log\_error)

print("Number of missclassified point :", np.count\_nonzero((sclf.predict(test\_x\_onehotCoding) - test\_y))/test\_y.shape[0])
 plot\_confusion\_matrix(test\_y=test\_y, predict\_y=sclf.predict(test\_x\_onehotCoding))

Log loss (train) on the stacking classifier: 0.5792511661131973 Log loss (CV) on the stacking classifier: 1.1125648572313287 Log loss (test) on the stacking classifier: 1.1409032736214493

Number of missclassified point : 0.3593984962406015

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



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

- 150

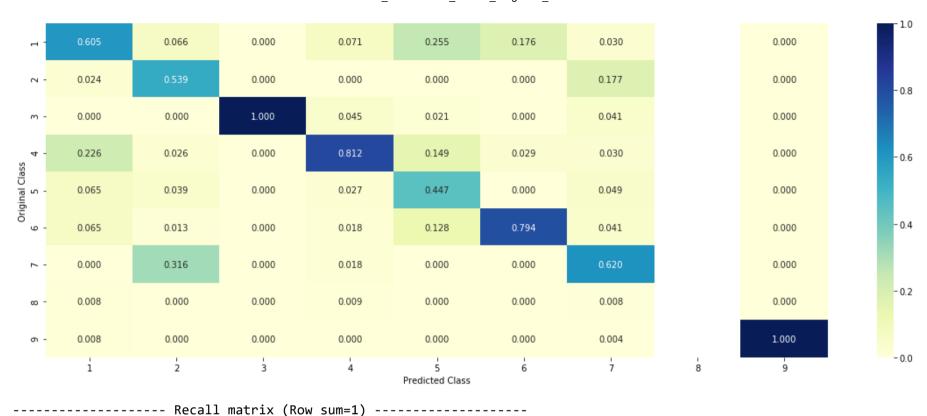
- 120

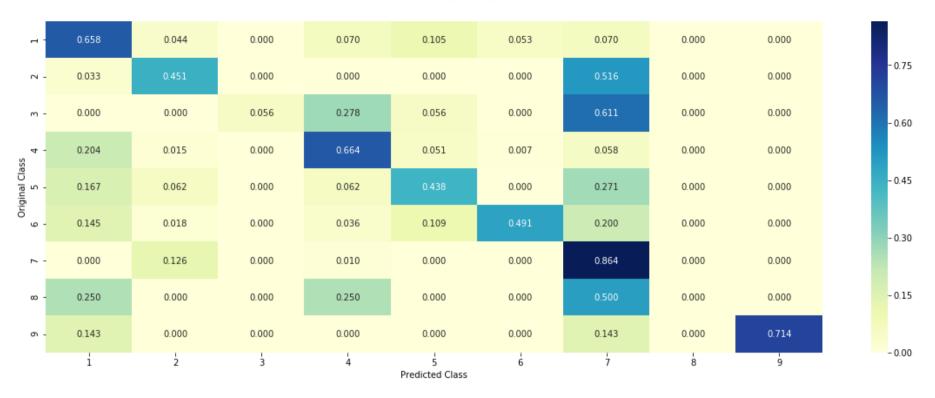
- 90

- 60

- 30

- 0





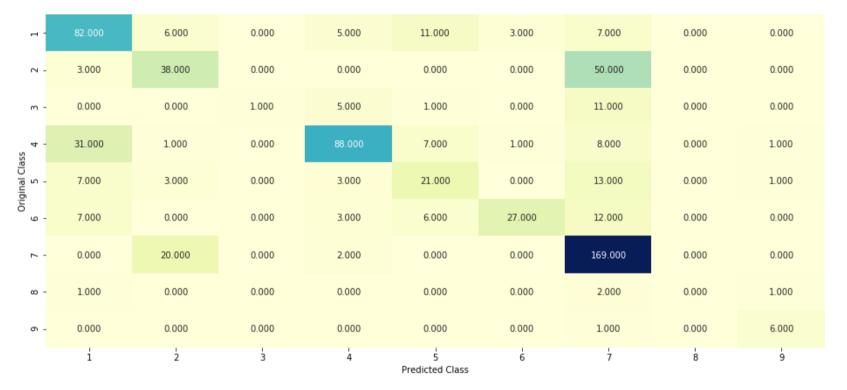
# 4.7.3 Maximum Voting classifier

In [50]: #Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassifier.html
 from sklearn.ensemble import VotingClassifier
 vclf = VotingClassifier(estimators=[('lr', sig\_clf1), ('svc', sig\_clf2), ('rf', sig\_clf3)], voting='soft')
 vclf.fit(train\_x\_onehotCoding, train\_y)
 print("Log loss (train) on the VotingClassifier :", log\_loss(train\_y, vclf.predict\_proba(train\_x\_onehotCoding)))
 print("Log loss (CV) on the VotingClassifier :", log\_loss(cv\_y, vclf.predict\_proba(cv\_x\_onehotCoding)))
 print("Log loss (test) on the VotingClassifier :", log\_loss(test\_y, vclf.predict\_proba(test\_x\_onehotCoding)))
 print("Number of missclassified point :", np.count\_nonzero((vclf.predict(test\_x\_onehotCoding) - test\_y))/test\_y.shape[0]
 ])
 plot\_confusion\_matrix(test\_y=test\_y, predict\_y=vclf.predict(test\_x\_onehotCoding))

Log loss (train) on the VotingClassifier : 0.8486513343697619 Log loss (CV) on the VotingClassifier : 1.1652193874731789 Log loss (test) on the VotingClassifier : 1.162165126025522

Number of missclassified point : 0.35037593984962406

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



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

- 150

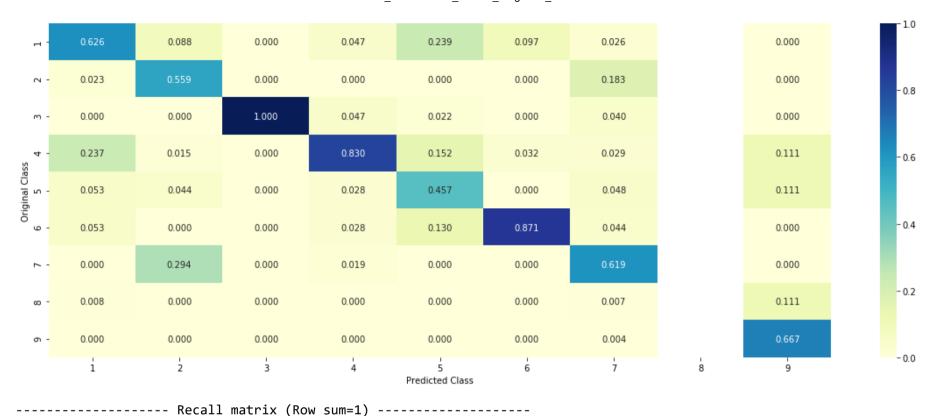
- 120

- 90

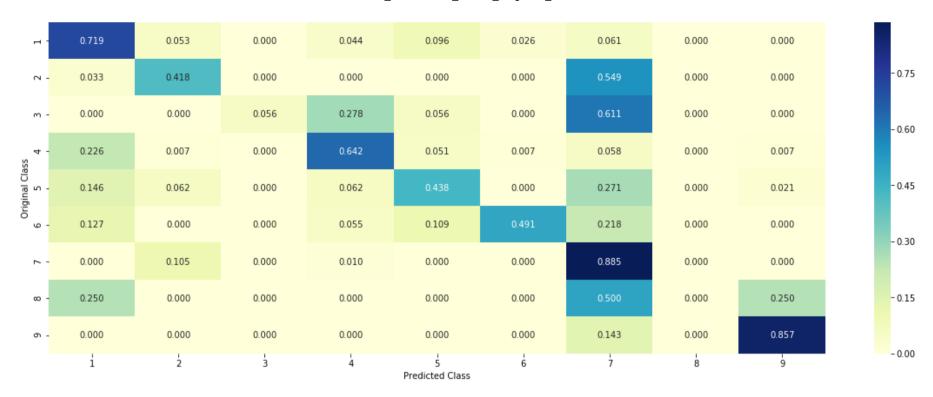
- 60

- 30

- 0



file:///C:/Users/Ravi%20Krishna/Ravi\_Personalized\_Cancer\_Diagnosis\_Final.html



**Analysis of Personalized Cancer Diagnosis Case Study** 

Model	Best Hyperparameters	Train error	CV error	Test error	Misclassified Points	Log - Loss
Naive Bayes + one-hot Encoding	alpha=0.001	0.563	1.244	1.169	38.9%	1.244
KNN + Response coding	K=5	0.475	1.03	1.058	38.3%	1.103
Logistic Regression unigram+bigram + class balance	alpha= 0.01	0.876	1.162	1.195	38.7%	1.16
Logistic Regression unigram+bigram + without class balance	alpha= 0.01	0.888	1.182	1.222	40.2%	1.18
Logistic Regression tfidf vectorizer(with 2000 max words)+FE(square root)	alpha= 0.001	0.612	1.032	0.946	33.9%	0.946
Linear SVM + one-hot encoding	alpha=0.0001	0.568	1.025	1.006	32.3%	1.025
Random Forest + one-hot encoding	best-estimators=2000	0.87	1.190	1.151	43.0%	1.190
Random Forest + one-hot encoding	alpha=50	0.052	1.379	1.395	54.3%	1.379
Stack Classifier(LR+LrSVM+NB)	alpha=0.10	0.579	1.112	1.140	35.9%	1.113
Maximum voting Classifier(LR+SVM+RF)	alpha=0.10	0.84	1.165	1.162	35.0%	1.113

#### **Observation**

- We did onehot encoding featurization for TfidfVectorizer() with 2000 features
- We accomplished onehot encoding for Logistic Regression models with un-igram and bi-gram
- On Logistic Regression model we did tfidf vectorizer with 2000 features and did Feature Engineering such as square root which have given log-loss 0.94. Using square root feature engineering we find the best model among all models.
- Second good model is Liner Support Vector Machine

---XXX---