Personalized cancer diagnosis

1. Business Problem

1.1. Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training_variants.zip and training_text.zip from Kaggle.

Context:

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

Problem statement:

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

1.2. Source/Useful Links

Some articles and reference blogs about the problem statement

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

1.3. Real-world/Business objectives and constraints.

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

2. Machine Learning Problem Formulation

2.1. Data

2.1.1. Data Overview

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

2.1.2. Example Data Point

training variants

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

training_text

ID, Text

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

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

2.2.1. Type of Machine Learning Problem

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

2.2.2. Performance Metric

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

Metric(s):

- · Multi class log-loss
- Confusion matrix

2.2.3. Machine Learing Objectives and Constraints

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

Constraints:

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

2.3. Train, CV and Test Datasets

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

3. Exploratory Data Analysis

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

D:\Anaconda3\lib\site-packages\sklearn\utils\deprecation.py:144: FutureWarnin g: The sklearn.metrics.classification module is deprecated in version 0.22 a nd will be removed in version 0.24. The corresponding classes / functions sho uld instead be imported from sklearn.metrics. Anything that cannot be imported from sklearn.metrics is now part of the private API.

warnings.warn(message, FutureWarning)

D:\Anaconda3\lib\site-packages\sklearn\externals\six.py:31: FutureWarning: The module is deprecated in version 0.21 and will be removed in version 0.23 since we've dropped support for Python 2.7. Please rely on the official version of six (https://pypi.org/project/six/).

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

D:\Anaconda3\lib\site-packages\sklearn\utils\deprecation.py:144: FutureWarnin g: The sklearn.neighbors.base module is deprecated in version 0.22 and will be removed in version 0.24. The corresponding classes / functions should inst ead be imported from sklearn.neighbors. Anything that cannot be imported from sklearn.neighbors is now part of the private API.

warnings.warn(message, FutureWarning)

D:\Anaconda3\lib\site-packages\sklearn\externals\joblib__init__.py:15: Futur eWarning: sklearn.externals.joblib is deprecated in 0.21 and will be removed in 0.23. Please import this functionality directly from joblib, which can be installed with: pip install joblib. If this warning is raised when loading pi ckled models, you may need to re-serialize those models with scikit-learn 0.2 1+.

warnings.warn(msg, category=FutureWarning)

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

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

Number of data points : 3321

Number of features: 4

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

Out[2]: _

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

```
In [3]: data.shape
Out[3]: (3321, 4)
```

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

Fields are

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

3.1.2. Reading Text Data

```
In [4]: # note the seprator in this file
    data_text =pd.read_csv("training/training_text",sep="\|\|",engine="python",nam
    es=["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[4]:

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

3.1.3. Preprocessing of text

```
In [5]: # 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 [6]: #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, "sec onds")
```

```
there is no text description for id: 1109
there is no text description for id: 1277
there is no text description for id: 1407
there is no text description for id: 1639
there is no text description for id: 2755
Time took for preprocessing the text : 220.5662871749492 seconds
```

In [7]: #merging both gene_variations and text data based on ID
 result = pd.merge(data, data_text,on='ID', how='left')
 result.head()

Out[7]:

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

In [8]: result[result.isnull().any(axis=1)]

Out[8]:

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

In [9]: result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Varia
tion']

In [10]: result[result['ID']==1109]

Out[10]:

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

3.1.4. Test, Train and Cross Validation Split

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

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

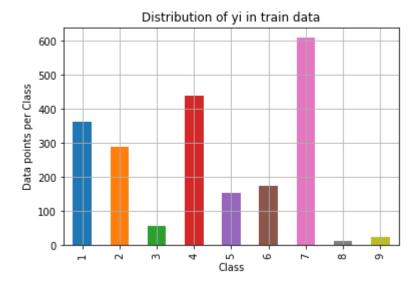
```
In [12]: print('Number of data points in train data:', train_df.shape[0])
    print('Number of data points in test data:', test_df.shape[0])
    print('Number of data points in cross validation data:', cv_df.shape[0])

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
```

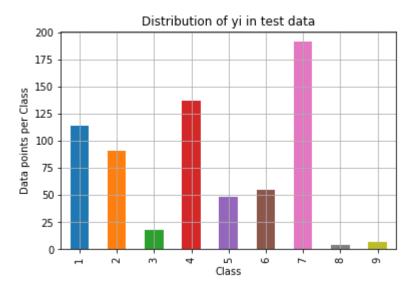
3.1.4.2. Distribution of y_i's in Train, Test and Cross Validation datasets

```
In [13]: # it returns a dict, keys as class labels and values as the number of data poi
         nts in that class
         train class distribution = train df['Class'].value counts().sortlevel()
         test class distribution = test df['Class'].value counts().sortlevel()
         cv class distribution = cv df['Class'].value counts().sortlevel()
         my_colors = 'rgbkymc'
         train class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in train data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.args
         ort.html
         # -(train class distribution.values): the minus sign will give us in decreasin
         g order
         sorted yi = np.argsort(-train class distribution.values)
         for i in sorted vi:
             print('Number of data points in class', i+1, ':',train_class_distribution.
         values[i], '(', np.round((train_class_distribution.values[i]/train_df.shape[0]
         *100), 3), '%)')
         print('-'*80)
         my colors = 'rgbkymc'
         test class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in test data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.args
         ort.html
         # -(train class distribution.values): the minus sign will give us in decreasin
         g order
         sorted yi = np.argsort(-test class distribution.values)
         for i in sorted yi:
             print('Number of data points in class', i+1, ':',test_class_distribution.v
         alues[i], '(', np.round((test class distribution.values[i]/test df.shape[0]*10
         0), 3), '%)')
         print('-'*80)
         my colors = 'rgbkymc'
         cv class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.vlabel('Data points per Class')
         plt.title('Distribution of yi in cross validation data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.args
         ort.html
         # -(train class distribution.values): the minus sign will give us in decreasin
```

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



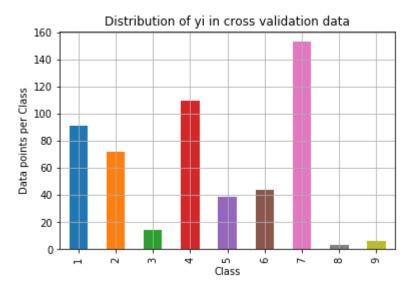
```
Number of data points in class 7 : 609 ( 28.672 %) Number of data points in class 4 : 439 ( 20.669 %) Number of data points in class 1 : 363 ( 17.09 %) Number of data points in class 2 : 289 ( 13.606 %) Number of data points in class 6 : 176 ( 8.286 %) Number of data points in class 5 : 155 ( 7.298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



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

.-----

_ _ _



```
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.

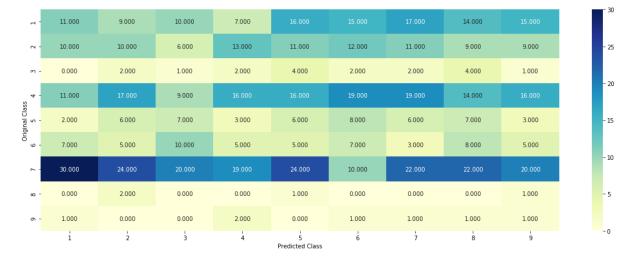
```
In [14]: # This function plots the confusion matrices given y i, y i hat.
         def plot_confusion_matrix(test_y, predict_y):
             C = confusion matrix(test y, predict y)
             \# C = 9,9 matrix, each cell (i,j) represents number of points of class i a
         re predicted class j
             A = (((C.T)/(C.sum(axis=1))).T)
             #divid each element of the confusion matrix with the sum of elements in th
         at column
             \# C = [[1, 2],
                   [3, 4]]
             # C.T = [[1, 3],
                       [2, 4]]
             # C.sum(axis = 1) axis=0 corresonds to columns and axis=1 corresponds to
          rows in two diamensional array
             # C.sum(axix = 1) = [[3, 7]]
             \# ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
                                          [2/3, 4/7]]
             \# ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]
                                          [3/7, 4/7]]
             # sum of row elements = 1
             B = (C/C.sum(axis=0))
             #divid each element of the confusion matrix with the sum of elements in th
         at row
             \# C = [[1, 2],
                   [3, 4]]
             # C.sum(axis = 0) axis=0 corresonds to columns and axis=1 corresponds to
          rows in two diamensional array
             # C.sum(axix = 0) = [[4, 6]]
             \# (C/C.sum(axis=0)) = [[1/4, 2/6],
                                     [3/4, 4/6]]
             labels = [1,2,3,4,5,6,7,8,9]
             # representing A in heatmap format
             print("-"*20, "Confusion matrix", "-"*20)
             plt.figure(figsize=(20,7))
             sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, y
         ticklabels=labels)
             plt.xlabel('Predicted Class')
             plt.ylabel('Original Class')
             plt.show()
             print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
             plt.figure(figsize=(20,7))
             sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, y
         ticklabels=labels)
             plt.xlabel('Predicted Class')
             plt.ylabel('Original Class')
             plt.show()
             # representing B in heatmap format
             print("-"*20, "Recall matrix (Row sum=1)", "-"*20)
             plt.figure(figsize=(20,7))
```

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

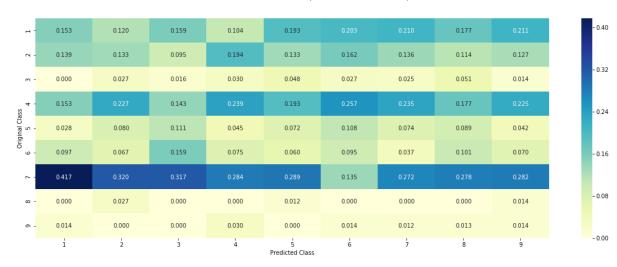
In [15]: # we need to generate 9 numbers and the sum of numbers should be 1 # one solution is to genarate 9 numbers and divide each of the numbers by thei r sum # ref: https://stackoverflow.com/a/18662466/4084039 test_data_len = test_df.shape[0] cv_data_len = cv_df.shape[0] # we create a output array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

Log loss on Cross Validation Data using Random Model 2.5062271926893938 Log loss on Test Data using Random Model 2.4869298665993456

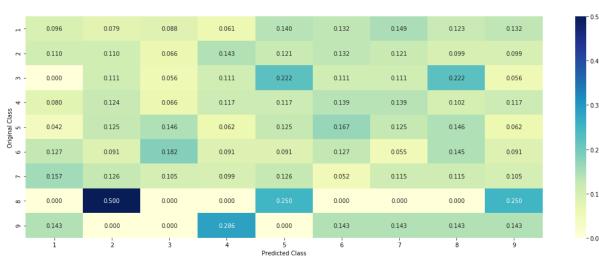




----- Precision matrix (Columm Sum=1) ------



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



3.3 Univariate Analysis

```
In [16]: # 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 cl
         ass1 + 10*alpha / number of time it occurred in total data+90*alpha)
         # qv dict is like a look up table, for every gene it store a (1*9) representat
         ion 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 'gv_fea'
         # return 'gv_fea'
         # get qv 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
                                    47
             #
                       ERBB2
             #
                       PDGFRA
                                    46
                        ...}
             # print(train_df['Variation'].value_counts())
             # output:
             # {
                                                         63
             # Truncating Mutations
             # Deletion
                                                         43
             # Amplification
                                                         43
             # Fusions
                                                         22
             # Overexpression
                                                          3
                                                          3
             # E17K
             # Q61L
                                                          3
             # S222D
                                                          2
             # P130S
                                                          2
             # ...
             # }
             value count = train df[feature].value counts()
             # qv dict : Gene Variation Dict, which contains the probability array for
          each gene/variation
             gv_dict = dict()
             # denominator will contain the number of time that particular feature occu
```

```
red 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')])
                                          Variation Class
                     ID
                          Gene
           # 2470 2470 BRCA1
                                              S1715C
           # 2486 2486 BRCA1
                                              S1841R
                                                         1
           # 2614 2614 BRCA1
                                                M1R
                                                         1
           # 2432 2432 BRCA1
                                              L1657P
                                                         1
           # 2567 2567 BRCA1
                                              T1685A
                                                         1
           # 2583 2583 BRCA1
                                             E1660G
                                                         1
           # 2634 2634 BRCA1
                                             W1718L
                                                         1
           # cls_cnt.shape[0] will return the number of rows
           cls cnt = train df.loc[(train df['Class']==k) & (train df[feature]
==i)]
           # cls cnt.shape[0](numerator) will contain the number of time that
particular feature occured in whole data
           vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha
))
       # we are adding the gene/variation to the dict as key and vec as value
       gv dict[i]=vec
   return gv_dict
# Get Gene variation feature
def get gv feature(alpha, feature, df):
   # print(qv dict)
         {'BRCA1': [0.20075757575757575, 0.037878787878788, 0.0681818181818
18177, 0.136363636363635, 0.25, 0.193181818181818, 0.0378787878787878, 0.
03787878787878788, 0.03787878787878788],
           'TP53': [0.32142857142857145, 0.061224489795918366, 0.0612244897959
18366, 0.27040816326530615, 0.061224489795918366, 0.066326530612244902, 0.0510
20408163265307, 0.051020408163265307, 0.056122448979591837],
           'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.06818
1818181818177, 0.068181818181818177, 0.0625, 0.34659090909090912, 0.0625, 0.05
6818181818181816],
           'BRCA2': [0.1333333333333333, 0.060606060606060608, 0.060606060606
060608, 0.078787878787878782, 0.13939393939394, 0.34545454545454546, 0.06060
6060606060608, 0.060606060606060608, 0.060606060606060608],
           'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937
106917, 0.46540880503144655, 0.075471698113207544, 0.062893081761006289, 0.069
182389937106917, 0.062893081761006289, 0.062893081761006289],
           'KIT': [0.066225165562913912, 0.25165562913907286, 0.07284768211920
5295, 0.072847682119205295, 0.066225165562913912, 0.066225165562913912, 0.2715
2317880794702, 0.066225165562913912, 0.066225165562913912],
           'BRAF': [0.066666666666666666, 0.179999999999999, 0.073333333333
33334, 0.07333333333333334, 0.09333333333333338, 0.08000000000000000, 0.299
#
   #
```

```
gv dict = get gv fea dict(alpha, feature, df)
   # value_count is similar in get_gv_fea_dict
   value_count = train_df[feature].value_counts()
   # qv fea: Gene variation feature, it will contain the feature for each fea
ture 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])
             gv fea.append([-1,-1,-1,-1,-1,-1,-1,-1])
   return gv fea
```

when we caculate the probability of a feature belongs to any particular class, we apply laplace smoothing
• (numerator + 10*alpha) / (denominator + 90*alpha)

3.2.1 Univariate Analysis on Gene Feature

Q1. Gene, What type of feature it is?

Ans. Gene is a categorical variable

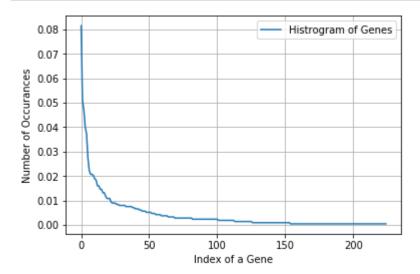
Q2. How many categories are there and How they are distributed?

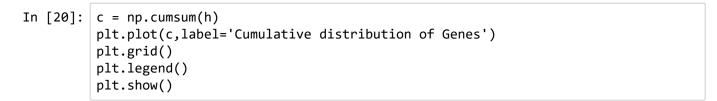
```
In [17]:
         unique genes = train df['Gene'].value counts()
          print('Number of Unique Genes :', unique genes.shape[0])
          # the top 10 genes that occured most
          print(unique_genes.head(10))
         Number of Unique Genes: 225
         BRCA1
                    173
         TP53
                    108
                    100
         EGFR
         PTEN
                     85
                     79
         BRCA2
         KIT
                     58
         BRAF
                     47
         PDGFRA
                     44
         ERBB2
                     44
         ALK
                     43
         Name: Gene, dtype: int64
```

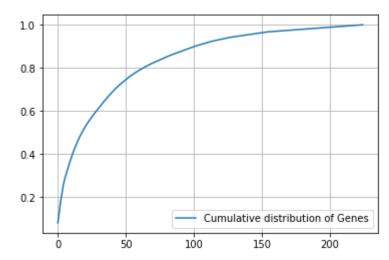
In [18]: print("Ans: There are", unique_genes.shape[0] ,"different categories of genes
 in the train data, and they are distibuted as follows",)

Ans: There are 225 different categories of genes in the train data, and they are distibuted as follows

```
In [19]: s = sum(unique_genes.values);
h = unique_genes.values/s;
plt.plot(h, label="Histrogram of Genes")
plt.xlabel('Index of a Gene')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```







Q3. How to featurize this Gene feature?

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

- 1. One hot Encoding
- 2. Response 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 [21]: #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 [22]: print("train_gene_feature_responseCoding is converted feature using respone co ding method. The shape of gene feature:", train_gene_feature_responseCoding.sh ape)
print("test_gene_feature_responseCoding is converted feature using respone cod ing method. The shape of test feature:", test_gene_feature_responseCoding.shap e)
print("cv_gene_feature_responseCoding is converted feature using respone codin g method. The shape of cv feature:", cv_gene_feature_responseCoding.shape)

train_gene_feature_responseCoding is converted feature using respone coding m ethod. The shape of gene feature: (2124, 9) test_gene_feature_responseCoding is converted feature using respone coding me thod. The shape of test feature: (665, 9) cv_gene_feature_responseCoding is converted feature using respone coding meth od. The shape of cv feature: (532, 9)

```
In [23]: # one-hot encoding of Gene feature.
    gene_vectorizer = TfidfVectorizer()
    train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gen e'])
    test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gene'])
    cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
```

```
In [24]: train_df['Gene'].head()
```

Out[24]: 2998 KIT 2848 BRCA2

1799 AR 383 TP53 2722 BRAF

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',
            'asx12',
            'atm',
            'atr',
            'atrx',
            'aurka',
            'aurkb',
            'axin1',
            'b2m',
            'bap1',
            'bard1',
            'bcl10',
            'bcl2l11',
            'bcor',
            'braf',
            'brca1',
            'brca2',
            'brd4',
            'brip1',
            'btk',
            'card11',
            'carm1',
            'casp8',
            'cbl',
            'ccnd1',
            'ccnd2',
            'ccnd3',
            'cdh1',
            'cdk12',
            'cdk4',
            'cdk6',
            'cdk8',
            'cdkn1a',
            'cdkn1b',
            'cdkn2a',
            'cdkn2b',
            'cdkn2c',
            'chek2',
            'cic',
            'crebbp',
            'ctcf',
            'ctnnb1',
            'ddr2',
```

'dicer1', 'dnmt3a', 'dnmt3b', 'egfr', 'eif1ax', 'elf3', 'ep300', 'epas1', 'epcam', 'erbb2', 'erbb3', 'erbb4', 'ercc2', 'ercc4', 'erg', 'esr1', 'etv1', 'etv6', 'ewsr1', 'ezh2', 'fanca', 'fancc', 'fat1', 'fbxw7', 'fgf19', 'fgf3', 'fgfr1', 'fgfr2', 'fgfr3', 'fgfr4', 'flt3', 'foxa1', 'foxp1', 'gata3', 'gli1', 'gna11', 'gnas', 'h3f3a', 'hist1h1c', 'hla', 'hnf1a', 'hras', 'idh1', 'idh2', 'igf1r', 'il7r', 'inpp4b', 'jak1', 'jak2', 'kdm5a', 'kdm5c', 'kdm6a', 'kdr', 'keap1', 'kit', 'kmt2a', 'kmt2b',

'kmt2d', 'knstrn', 'kras', 'lats2', 'map2k1', 'map2k2', 'map2k4', 'map3k1', 'mapk1', 'med12', 'mef2b', 'met', 'mga', 'mlh1', 'mpl', 'msh2', 'msh6', 'mtor', 'myc', 'mycn' 'myd88', 'ncor1', 'nf1', 'nf2', 'nfe212', 'nfkbia', 'nkx2', 'notch1', 'notch2', 'npm1', 'nras', 'nsd1', 'ntrk1', 'ntrk2', 'nup93', 'pak1', 'pax8', 'pdgfra', 'pdgfrb', 'pik3ca', 'pik3cb', 'pik3cd', 'pik3r1', 'pik3r2', 'pim1', 'pms1', 'pms2', 'pole', 'ppm1d', 'ppp2r1a', 'ppp6c', 'prdm1', 'ptch1', 'pten', 'ptpn11', 'ptprd',

'kmt2c',

'ptprt', 'rab35', 'rac1', 'rad21', 'rad50', 'rad51b', 'rad51c', 'rad51d', 'rad541', 'raf1', 'rasa1', 'rb1', 'rbm10', 'ret', 'rheb', 'rhoa', 'rit1', 'ros1', 'runx1', 'rxra', 'sdhc', 'sf3b1', 'shq1', 'smad2', 'smad3', 'smad4', 'smarca4', 'smarcb1', 'smo', 'sos1', 'sox9', 'spop', 'src', 'srsf2', 'stag2', 'stat3', 'stk11', 'tert', 'tet2', 'tgfbr1', 'tgfbr2', 'tmprss2', 'tp53', 'tp53bp1', 'tsc1', 'tsc2', 'u2af1', 'vhl', 'whsc1', 'whsc1l1', 'xpo1', 'xrcc2',

'yap1']

In [26]: print("train_gene_feature_onehotCoding is converted feature using one-hot enco
 ding method. The shape of gene feature:", train_gene_feature_onehotCoding.shap
 e)

train_gene_feature_onehotCoding is converted feature using one-hot encoding m ethod. The shape of gene feature: (2124, 224)

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 [27]: alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/qe
         nerated/sklearn.linear model.SGDClassifier.html
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max_iter=None, tol=None.
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning
         rate='optimal', eta0=0.0, power_t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])      Fit linear model with Stochast
         ic Gradient Descent.
         # predict(X)
                        Predict class labels for samples in X.
         #-----
         # video link:
         #-----
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
             clf.fit(train gene_feature_onehotCoding, y_train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train gene feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv gene feature onehotCoding)
             cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, e
         ps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predi
         ct 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 gene feature onehotCoding, y train)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train gene feature onehotCoding, y train)
         predict_y = sig_clf.predict_proba(train_gene_feature_onehotCoding)
         print('For values of best alpha = ', alpha[best alpha], "The train log loss i
         s:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
         predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
```

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

```
For values of alpha = 1e-05 The log loss is: 1.2540111267947311

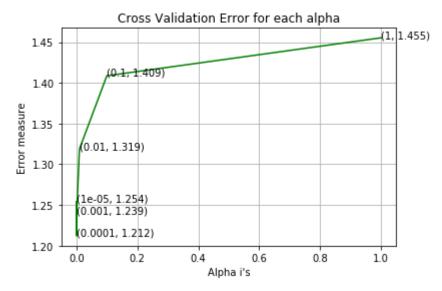
For values of alpha = 0.0001 The log loss is: 1.2120950763061806

For values of alpha = 0.001 The log loss is: 1.239000589887041

For values of alpha = 0.01 The log loss is: 1.3186440894440317

For values of alpha = 0.1 The log loss is: 1.408721964712307

For values of alpha = 1 The log loss is: 1.4553525134680059
```



```
For values of best alpha = 0.0001 The train log loss is: 0.9858999925424323
For values of best alpha = 0.0001 The cross validation log loss is: 1.212095
0763061806
For values of best alpha = 0.0001 The test log loss is: 1.1945034241197496
```

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 [28]: 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 225 genes in train dataset?

Ans

- 1. In test data 638 out of 665 : 95.93984962406014
- 2. In cross validation data 507 out of 532 : 95.30075187969925

3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it?

Ans. Variation is a categorical variable

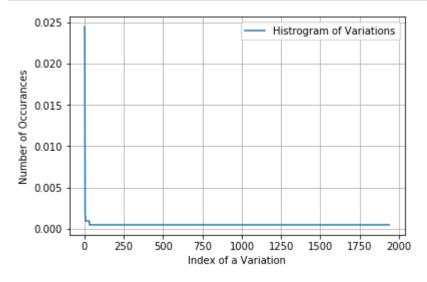
Q8. How many categories are there?

```
unique_variations = train_df['Variation'].value_counts()
In [29]:
         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: 1939
         Truncating_Mutations
                                  52
                                  50
         Deletion
         Amplification
                                  41
         Fusions
                                  15
         Overexpression
                                   4
         Q61L
                                   3
         Q61R
                                   2
         Y64A
         R170W
                                   2
         E330K
         Name: Variation, dtype: int64
```

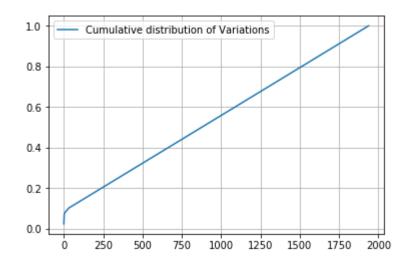
In [30]: print("Ans: There are", unique_variations.shape[0] ,"different categories of v
ariations in the train data, and they are distibuted as follows",)

Ans: There are 1939 different categories of variations in the train data, and they are distibuted as follows

```
In [31]: s = sum(unique_variations.values);
h = unique_variations.values/s;
plt.plot(h, label="Histrogram of Variations")
plt.xlabel('Index of a Variation')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```







Q9. How to featurize this Variation feature?

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

- 1. One hot Encoding
- 2. Response coding

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

```
In [33]: # 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 [34]: print("train_variation_feature_responseCoding is a converted feature using the response coding method. The shape of Variation feature:", train_variation_feature_responseCoding.shape)

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

- In [35]: # one-hot encoding of variation feature.
 variation_vectorizer = TfidfVectorizer()
 train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variation'])
 test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
 cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])

train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method. The shape of Variation feature: (2124, 1973)

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

Let's build a model just like the earlier!

```
In [37]: | alpha = [10 ** x for x in range(-5, 1)]
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/qe
         nerated/sklearn.linear model.SGDClassifier.html
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning
         rate='optimal', eta0=0.0, power_t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])      Fit linear model with Stochast
         ic Gradient Descent.
         # predict(X)
                        Predict class labels for samples in X.
         #-----
         # video link:
         #-----
         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_, e
         ps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predi
         ct_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 variation feature onehotCoding, y train)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_variation_feature_onehotCoding, y_train)
         predict y = sig clf.predict proba(train variation feature onehotCoding)
         print('For values of best alpha = ', alpha[best alpha], "The train log loss i
```

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

```
For values of alpha = 1e-05 The log loss is: 1.6955477942667168

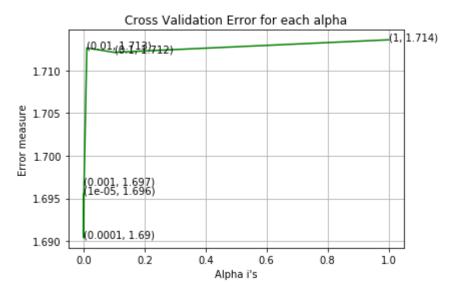
For values of alpha = 0.0001 The log loss is: 1.6903773117608554

For values of alpha = 0.001 The log loss is: 1.6965718919110084

For values of alpha = 0.01 The log loss is: 1.7126152285050742

For values of alpha = 0.1 The log loss is: 1.7121025941256351

For values of alpha = 1 The log loss is: 1.7135711277220442
```



For values of best alpha = 0.0001 The train log loss is: 0.6900581252091896
For values of best alpha = 0.0001 The cross validation log loss is: 1.690377
3117608554
For values of best alpha = 0.0001 The test log loss is: 1.7027076929439666

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 [38]: print("Q12. How many data points are covered by total ", unique_variations.sha
    pe[0], " genes in test and cross validation data sets?")
    test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
    cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'])))].s
    hape[0]
    print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(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 1939 genes in test and cross
```

Q12. How many data points are covered by total 1939 genes in test and cross validation data sets?

Ans

- 1. In test data 76 out of 665 : 11.428571428571429
- 2. In cross validation data 59 out of 532 : 11.090225563909774

3.2.3 Univariate Analysis on Text Feature

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

```
In [40]:
         import math
         #https://stackoverflow.com/a/1602964
         def get text responsecoding(df):
             text feature responseCoding = np.zeros((df.shape[0],9))
             for i in range(0,9):
                  row index = 0
                 for index, row in df.iterrows():
                      sum prob = 0
                      for word in row['TEXT'].split():
                          sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(total_di
         ct.get(word,0)+90)))
                      text feature responseCoding[row index][i] = math.exp(sum prob/len(
         row['TEXT'].split()))
                      row index += 1
             return text feature responseCoding
```

Total number of unique words in train data : 3000

```
In [42]: | 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 [43]: #response coding of text features
 train_text_feature_responseCoding = get_text_responsecoding(train_df)
 test_text_feature_responseCoding = get_text_responsecoding(test_df)
 cv_text_feature_responseCoding = get_text_responsecoding(cv_df)
- In [44]: # https://stackoverflow.com/a/16202486
 # we convert each row values such that they sum to 1
 train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train
 _text_feature_responseCoding.sum(axis=1)).T
 test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_responseCoding.sum(axis=1)).T
 cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.sum(axis=1)).T
- In [45]: # don't forget to normalize every feature
 train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding, a
 xis=0)

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

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

```
In [46]: #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 [47]: # Number of words for a given frequency.
print(Counter(sorted_text_occur))

Counter({193.87177083533788: 1, 127.28309351290949: 1, 123.9516369205886: 1, 95.27634367108831: 1, 89.49135585896761: 1, 88.45930440253197: 1, 87.76525239 990544: 1, 82.71406689968998: 1, 82.30785911801122: 1, 80.93104160221537: 1, 78.18050812460085: 1, 76.53874053412723: 1, 73.26940924075917: 1, 73.11228364 820379: 1, 68.55171974419262: 1, 62.968953418572504: 1, 59.55562691755885: 1, 59.510612038449665: 1, 59.1312029163687: 1, 58.710685016121815: 1, 54.9615870 39993695: 1, 53.50305936525071: 1, 52.75427793736526: 1, 50.009559714074165: 1, 49.319185747759235: 1, 48.574687892104016: 1, 48.431909215092396: 1, 47.85 8275167061656: 1, 47.29853833934683: 1, 47.09753485344249: 1, 46.685476140911 18: 1, 46.633634991667: 1, 46.39696865552379: 1, 46.12490703291477: 1, 44.349 5023026693: 1, 43.75740487272057: 1, 42.39872058071737: 1, 42.04550958731254: 1, 41.852064292591606: 1, 41.69793644078394: 1, 41.236905830027645: 1, 38.768 32817970881: 1, 38.36146652266362: 1, 38.28310233781683: 1, 38.18379421696625 5: 1, 37.19653306267872: 1, 36.73446706081922: 1, 35.35206271696007: 1, 35.30 4245996714904: 1, 34.827951309150414: 1, 34.780114553426515: 1, 34.0698445848 9117: 1, 33.92291938153465: 1, 33.9041744517319: 1, 33.89854120904206: 1, 32. 942589686711024: 1, 32.737986458638595: 1, 32.7064445822106: 1, 32.6018996433 4747: 1, 32.34950914849501: 1, 32.15076175713733: 1, 31.84663263110182: 1, 3 1.816163172959843: 1, 31.537507132038073: 1, 31.465391384465065: 1, 31.404846 060824234: 1, 31.179353318734737: 1, 31.04579669688957: 1, 30.93285688129221: 1, 30.88685889973828: 1, 30.384306328324268: 1, 30.025024180905522: 1, 29.770 49631673016: 1, 29.05573376031132: 1, 28.64883117005774: 1, 28.06417342315510 4: 1, 28.010170657849454: 1, 27.970425044562244: 1, 27.820646515406946: 1, 2 7.803149904907784: 1, 27.182720099938887: 1, 27.149771188392343: 1, 26.727076 375650906: 1, 26.517874815548407: 1, 26.38186325191481: 1, 26.14252933000759: 1, 26.115156805921895: 1, 25.79741421789772: 1, 25.639982812347817: 1, 25.611 866816098853: 1, 25.584730069851364: 1, 25.536882700841442: 1, 25.32969356052 2813: 1, 25.29846431435189: 1, 25.29668307254763: 1, 25.236628476995605: 1, 2 4.55330129720298: 1, 24.494726724436862: 1, 24.341945191668792: 1, 24.1582531 1610082: 1, 24.14330860512465: 1, 24.12679440864085: 1, 24.086753080561554: 1, 23.82946234270497: 1, 23.821917601049005: 1, 23.712575922538772: 1, 23.545 73826737324: 1, 23.47870478753906: 1, 23.387292663136407: 1, 23.3775328814707 07: 1, 23.340693666195193: 1, 23.268320701511172: 1, 23.18263950738593: 1, 2 3.155641711161437: 1, 22.950608103298716: 1, 22.857600219823762: 1, 22.813696 116894942: 1, 22.77032918483672: 1, 22.675767248823774: 1, 22.64985415296104 4: 1, 22.645705311908795: 1, 22.586473868991188: 1, 22.36137565698606: 1, 22. 287709101263392: 1, 22.09056389506355: 1, 22.00807404739081: 1, 21.6787732558 21426: 1, 21.640104608349674: 1, 21.584191346543385: 1, 21.577724201250284: 1, 21.52389504676622: 1, 21.470735472247632: 1, 21.444506386428763: 1, 21.418 982053153037: 1, 21.395844854374257: 1, 21.359828044008662: 1, 21.27975089268 496: 1, 21.223390604842685: 1, 21.19860023804342: 1, 20.851213292892687: 1, 2 0.745877206617475: 1, 20.52753789104859: 1, 20.523727758778954: 1, 20.4891284 8544538: 1, 20.33910766828922: 1, 20.167470548830185: 1, 20.154769057058118: 1, 20.06852057701836: 1, 20.03566976446402: 1, 19.862797219185435: 1, 19.8451 9935472838: 1, 19.76158558931519: 1, 19.742694582458224: 1, 19.64712471458678 4: 1, 19.46151857851957: 1, 19.24653259411346: 1, 19.245469968784846: 1, 19.1 54599758222854: 1, 19.14895836489851: 1, 19.112079013412984: 1, 19.0459202834 70775: 1, 18.960873782331557: 1, 18.93364273704337: 1, 18.721558286760274: 1, 18.62943376782954: 1, 18.595130187655258: 1, 18.44946480649205: 1, 18.4111557 86653406: 1, 18.359536652868297: 1, 18.35848275111671: 1, 18.248329827819315: 1, 18.09490245683486: 1, 18.084199487822094: 1, 18.044819361193397: 1, 17.990 12332399031: 1, 17.949204085379215: 1, 17.934923217489583: 1, 17.884234630584 78: 1, 17.872702364320283: 1, 17.74758945302231: 1, 17.703948332579003: 1, 1 7.637613373092826: 1, 17.585836455695883: 1, 17.56794413494214: 1, 17.4886831 3947405: 1, 17.45907203010106: 1, 17.38980471286387: 1, 17.335336445756194: 1, 17.317338515621095: 1, 17.287297644762898: 1, 17.274407813691397: 1, 17.22 8776800765267: 1, 17.189025493079217: 1, 17.080053051256744: 1, 17.0269961198

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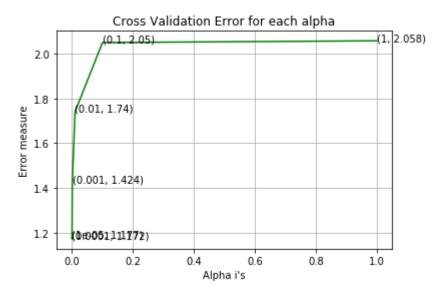
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In [48]: # Train a Logistic regression+Calibration model using text features whicha re
          on-hot encoded
         alpha = [10 ** x for x in range(-5, 1)]
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/qe
         nerated/sklearn.linear_model.SGDClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning
         rate='optimal', eta0=0.0, power_t=0.5,
         # class_weight=None, warm_start=False, average=False, n_iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochast
         ic Gradient Descent.
         # predict(X)
                        Predict class labels for samples in X.
         #-----
         # video link:
         #-----
         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 , e
         ps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predi
         ct_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 i
s:",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 i
s:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
For values of alpha = 1e-05 The log loss is: 1.1766143372443885
For values of alpha = 0.0001 The log loss is: 1.1722123562885514
For values of alpha = 0.001 The log loss is: 1.4235495836242769
For values of alpha = 0.01 The log loss is: 1.7403384840951115
For values of alpha = 0.1 The log loss is: 2.0500092667630945
For values of alpha = 1 The log loss is: 2.0578269884956337
```



```
For values of best alpha = 0.0001 The train log loss is: 0.6423746250903991
For values of best alpha = 0.0001 The cross validation log loss is: 1.172212
3562885514
For values of best alpha = 0.0001 The test log loss is: 1.1586735910532906
```

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

Ans. Yes, it seems like!

```
In [49]: def get_intersec_text(df):
    df_text_vec = TfidfVectorizer(min_df=5, max_features=3000)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

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

93.7 % of word of test data appeared in train data 92.733 % of word of Cross Validation appeared in train data

4. Machine Learning Models

```
In [51]: #Data preparation for ML models.

#Misc. functionns for ML models

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

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

```
In [52]: 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 [53]: # this function will be used just for naive bayes
         # for the given indices, we will print the name of the features
         # and we will check whether the feature present in the test point text or not
         def get impfeature names(indices, text, gene, var, no features):
             gene count vec = CountVectorizer()
             var_count_vec = CountVectorizer()
             text count vec = CountVectorizer(min df=3)
             gene vec = gene count vec.fit(train df['Gene'])
             var_vec = var_count_vec.fit(train_df['Variation'])
             text vec = text count vec.fit(train df['TEXT'])
             fea1_len = len(gene_vec.get_feature_names())
             fea2 len = len(var count vec.get feature names())
             word present = 0
             for i,v in enumerate(indices):
                  if (v < fea1 len):</pre>
                      word = gene_vec.get_feature_names()[v]
                      yes_no = True if word == gene else False
                      if yes no:
                          word present += 1
                          print(i, "Gene feature [{}] present in test data point [{}]".f
         ormat(word,yes_no))
                 elif (v < fea1 len+fea2 len):</pre>
                      word = var vec.get_feature_names()[v-(fea1_len)]
                      yes no = True if word == var else False
                      if yes no:
                          word present += 1
                          print(i, "variation feature [{}] present in test data point [
         {}]".format(word,yes_no))
                 else:
                      word = text vec.get feature names()[v-(fea1 len+fea2 len)]
                      yes_no = True if word in text.split() else False
                      if yes_no:
                          word present += 1
                          print(i, "Text feature [{}] present in test data point [{}]".f
         ormat(word,yes no))
             print("Out of the top ",no_features," features ", word_present, "are prese
         nt in query point")
```

Stacking the three types of features

```
In [54]: # 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 va
         riation feature onehotCoding))
         test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_varia
         tion feature onehotCoding))
         cv gene var onehotCoding = hstack((cv gene feature onehotCoding,cv variation f
         eature 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_on
         ehotCoding)).tocsr()
         test_y = np.array(list(test_df['Class']))
         cv x onehotCoding = hstack((cv gene var onehotCoding, cv text feature onehotCo
         ding)).tocsr()
         cv_y = np.array(list(cv_df['Class']))
         train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,t
         rain variation feature responseCoding))
         test gene var responseCoding = np.hstack((test gene feature responseCoding,tes
         t variation feature responseCoding))
         cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_vari
         ation 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 fea
         ture responseCoding))
         cv x responseCoding = np.hstack((cv gene var responseCoding, cv text feature r
```

esponseCoding))

```
In [55]: print("One hot encoding features :")
         print("(number of data points * number of features) in train data = ", train x
         onehotCoding.shape)
         print("(number of data points * number of features) in test data = ", test x o
         nehotCoding.shape)
         print("(number of data points * number of features) in cross validation data
          =", cv x onehotCoding.shape)
         One hot encoding features :
         (number of data points * number of features) in train data = (2124, 5197)
         (number of data points * number of features) in test data = (665, 5197)
         (number of data points * number of features) in cross validation data = (532,
         5197)
In [56]: print(" Response encoding features :")
         print("(number of data points * number of features) in train data = ", train x
         responseCoding.shape)
         print("(number of data points * number of features) in test data = ", test_x_r
         esponseCoding.shape)
         print("(number of data points * number of features) in cross validation data
          =", cv x responseCoding.shape)
          Response encoding features :
         (number of data points * number of features) in train data = (2124, 27)
         (number of data points * number of features) in test data = (665, 27)
         (number of data points * number of features) in cross validation data = (532,
         27)
```

Feature Engineering on one-hot encoded features

```
In [57]: train_x_onehotCodingFE=np.sqrt(train_x_onehotCoding)
    test_x_onehotCodingFE=np.sqrt(test_x_onehotCoding)
    cv_x_onehotCodingFE=np.sqrt(cv_x_onehotCoding)
```

4.1. Base Line Model

4.1.1. Naive Bayes

4.1.1.1. Hyper parameter tuning

```
In [58]: # find more about Multinomial Naive base function here http://scikit-learn.or
         q/stable/modules/generated/sklearn.naive bayes.MultinomialNB.html
         # -----
         # default paramters
         # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=Non
         e)
         # some of methods of MultinomialNB()
         # fit(X, y[, sample weight]) Fit Naive Bayes classifier according to X, y
         \# predict(X) Perform classification on an array of test vectors X.
         # predict log proba(X) Return log-probability estimates for the test vector
         Χ.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
         lessons/naive-bayes-algorithm-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stabl
         e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm
         oid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         # -----
         # 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-probab
         ility estimates
             print("Log Loss :",log_loss(cv_y, sig_clf_probs))
         fig, ax = plt.subplots()
         ax.plot(np.log10(alpha), cv_log_error_array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
             ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv log error array[i
         ]))
```

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

for alpha = 1e-05

Log Loss: 1.2442427651450625

for alpha = 0.0001

Log Loss: 1.2454826518681834

for alpha = 0.001

Log Loss: 1.2423007584053438

for alpha = 0.1

Log Loss: 1.2656989120604816

for alpha = 1

Log Loss: 1.3155405657141117

for alpha = 10

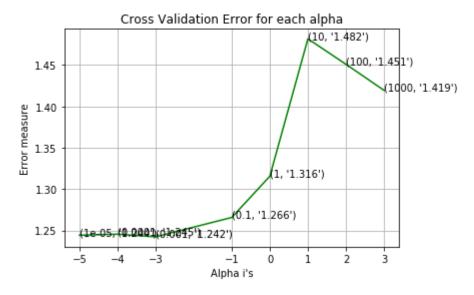
Log Loss: 1.4817120025323702

for alpha = 100

Log Loss: 1.4509086811280916

for alpha = 1000

Log Loss: 1.4194057044076456



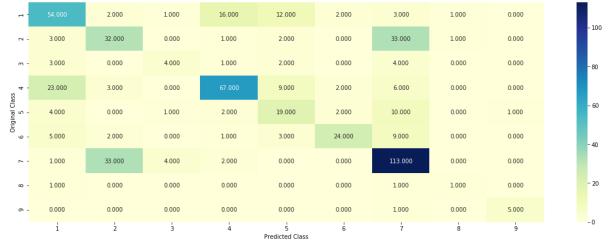
For values of best alpha = 0.001 The train log loss is: 0.5827010882734858
For values of best alpha = 0.001 The cross validation log loss is: 1.2423007
584053438
For values of best alpha = 0.001 The test log loss is: 1.2647146781626806

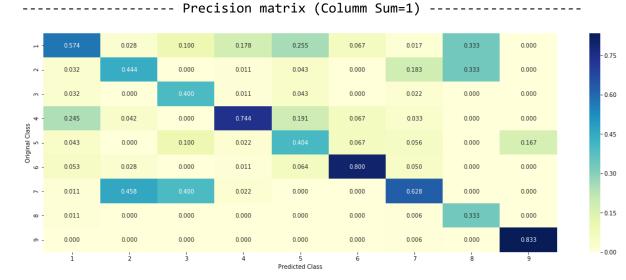
4.1.1.2. Testing the model with best hyper paramters

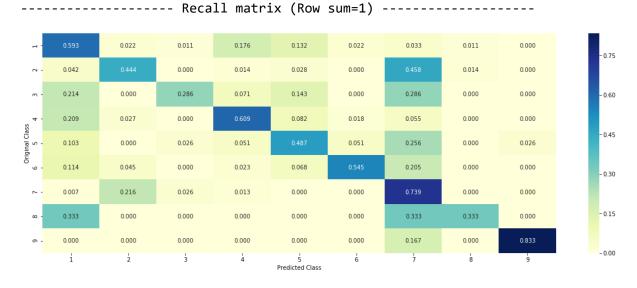
In [59]: # find more about Multinomial Naive base function here http://scikit-learn.or q/stable/modules/generated/sklearn.naive bayes.MultinomialNB.html # -----# default paramters # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=Non e) # some of methods of MultinomialNB() # fit(X, y[, sample weight]) Fit Naive Bayes classifier according to X, y # predict(X) Perform classification on an array of test vectors X. # predict log proba(X) Return log-probability estimates for the test vector Χ. # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/ lessons/naive-bayes-algorithm-1/ # find more about CalibratedClassifierCV here at http://scikit-learn.org/stabl e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html # -----# default paramters # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm oid', cv=3) # some of the methods of CalibratedClassifierCV() # fit(X, y[, sample weight]) Fit the calibrated model # get_params([deep]) Get parameters for this estimator. # predict(X) Predict the target of new samples. # predict proba(X) Posterior probabilities of classification clf = MultinomialNB(alpha=alpha[best alpha]) clf.fit(train x onehotCoding, train y) sig_clf = CalibratedClassifierCV(clf, method="sigmoid") sig_clf.fit(train_x_onehotCoding, train_y) sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding) # to avoid rounding error while multiplying probabilites we use log-probabilit v estimates print("Log Loss :",log_loss(cv_y, sig_clf_probs)) print("Number of missclassified point :", np.count_nonzero((sig_clf.predict(cv x onehotCoding)- cv y))/cv y.shape[0]) plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray()))

Log Loss: 1.2423007584053438

Number of missclassified point: 0.40037593984962405
------ Confusion matrix ------







4.1.1.3. Feature Importance, Correctly classified point

```
In [60]: 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(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.0811 0.0627 0.0133 0.0758 0.0384 0.0401 0.
         679 0.0055 0.0042]]
         Actual Class : 7
         Out of the top 100 features 0 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

```
In [61]: test point index = 100
         no feature = 100
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x
         onehotCoding[test point index]),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
         Predicted Class: 2
         Predicted Class Probabilities: [[0.0718 0.6318 0.0143 0.0814 0.0412 0.0434 0.
         1057 0.0059 0.0045]]
         Actual Class: 2
         Out of the top 100 features 0 are present in query point
```

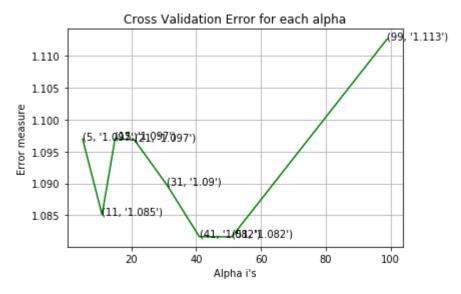
4.2. K Nearest Neighbour Classification

4.2.1. Hyper parameter tuning

```
In [62]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/m
         odules/generated/sklearn.neighbors.KNeighborsClassifier.html
         # -----
         # default parameter
         # KNeighborsClassifier(n neighbors=5, weights='uniform', algorithm='auto', lea
         f_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-intuition-with-a-toy-example-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stabl
         e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm
         oid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         #-----
         # video link:
         #-----
         alpha = [5, 11, 15, 21, 31, 41, 51, 99]
         cv log error array = []
         for i in alpha:
            print("for alpha =", i)
            clf = KNeighborsClassifier(n neighbors=i)
            clf.fit(train_x_responseCoding, train_y)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train x responseCoding, train y)
            sig clf probs = sig clf.predict proba(cv x responseCoding)
            cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes
         _, eps=1e-15))
            # to avoid rounding error while multiplying probabilites we use log-probab
         ility estimates
            print("Log Loss :",log loss(cv y, sig clf probs))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv_log_error_array,3)):
            ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
         plt.title("Cross Validation Error for each alpha")
```

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

```
for alpha = 5
Log Loss: 1.0969303646472561
for alpha = 11
Log Loss: 1.0851016136985003
for alpha = 15
Log Loss: 1.0970109480905619
for alpha = 21
Log Loss: 1.0967950051940067
for alpha = 31
Log Loss: 1.0897571502715409
for alpha = 41
Log Loss: 1.0816610736908696
for alpha = 51
Log Loss: 1.081632841418107
for alpha = 99
Log Loss: 1.1126261578804915
```



For values of best alpha = 51 The train log loss is: 0.8691792565078065

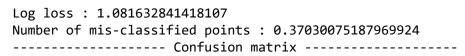
For values of best alpha = 51 The cross validation log loss is: 1.0816328414

18107

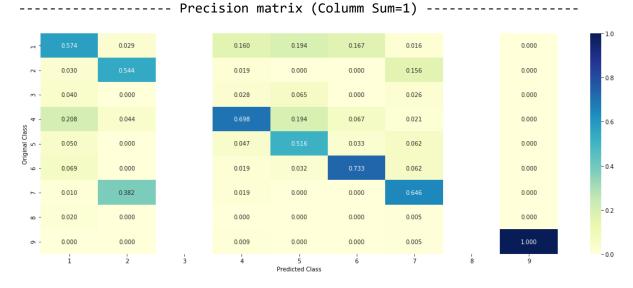
For values of best alpha = 51 The test log loss is: 1.0883792266791434

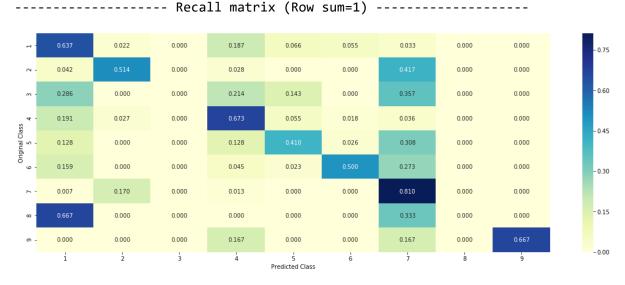
4.2.2. Testing the model with best hyper paramters

In [63]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/m odules/generated/sklearn.neighbors.KNeighborsClassifier.html # ------# default parameter # KNeighborsClassifier(n neighbors=5, weights='uniform', algorithm='auto', lea f_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-intuition-with-a-toy-example-1/ clf = KNeighborsClassifier(n neighbors=alpha[best alpha]) predict_and_plot_confusion_matrix(train_x_responseCoding, train_y, cv_x_respon seCoding, cv_y, clf)









4.2.3. Sample Query point -1

```
In [64]: | clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
         clf.fit(train x responseCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x responseCoding, train y)
         test point index = 1
         predicted cls = sig clf.predict(test x responseCoding[0].reshape(1,-1))
         print("Predicted Class :", predicted cls[0])
         print("Actual Class :", test_y[test_point_index])
         neighbors = clf.kneighbors(test_x_responseCoding[test_point_index].reshape(1,
         -1), alpha[best alpha])
         print("The ",alpha[best_alpha]," nearest neighbours of the test points belongs
         to classes",train_y[neighbors[1][0]])
         print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
        Predicted Class: 1
        Actual Class: 7
        The 51 nearest neighbours of the test points belongs to classes [7 6 1 6 1
        2 2 7 7 4 7 7 7 7 7 7 7 7 1
        Fequency of nearest points : Counter({7: 28, 2: 10, 1: 7, 6: 5, 4: 1})
```

4.2.4. Sample Query Point-2

```
clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)
test point index = 100
predicted cls = sig clf.predict(test x responseCoding[test point index].reshap
print("Predicted Class :", predicted_cls[0])
print("Actual Class :", test_y[test_point_index])
neighbors = clf.kneighbors(test x responseCoding[test point index].reshape(1,
-1), alpha[best alpha])
print("the k value for knn is",alpha[best alpha],"and the nearest neighbours o
f the test points belongs to classes",train_y[neighbors[1][0]])
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
Predicted Class: 2
Actual Class : 2
the k value for knn is 51 and the nearest neighbours of the test points belon
277727
 2 2 2 2 2 7 7 2 2 2 7 7 2 7]
Fequency of nearest points : Counter({2: 41, 7: 10})
```

4.3. Logistic Regression

With Count Vectorizer and Unigram and bigram

```
In [66]: # 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['Gen
         e'])
         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_transfor
         m(train df['Variation'])
         test variation feature onehotCoding lr = variation vectorizer lr.transform(tes
         t df['Variation'])
         cv_variation_feature_onehotCoding_lr = variation_vectorizer_lr.transform(cv_df
         ['Variation'])
         text vectorizer lr = CountVectorizer(ngram range=(1, 4))
         train text feature onehotCoding lr = text vectorizer lr.fit transform(train df
         ['TEXT'])
         # don't forget to normalize every feature
         train text feature onehotCoding lr = normalize(train text feature onehotCoding
         _lr, axis=0)
         test text feature onehotCoding lr = text vectorizer lr.transform(test df['TEX
         test text feature onehotCoding lr = normalize(test text feature onehotCoding l
         r, axis=0)
         cv text feature onehotCoding lr = text vectorizer lr.transform(cv df['TEXT'])
         # don't forget to normalize every feature
         cv_text_feature_onehotCoding_lr = normalize(cv_text_feature_onehotCoding_lr, a
         xis=0)
```

stacking all the features(gene, vartions, text of one-hot encoded)

```
In [67]: 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']))
```

```
In [68]: 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_o
    nehotCoding_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, 1191560 9)

(number of data points * number of features) in test data = (665, 11915609)

(number of data points * number of features) in cross validation data = (532, 11915609)
```

4.3.1. With Class balancing

4.3.1.1. Hyper paramter tuning

```
In [69]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge
         nerated/sklearn.linear_model.SGDClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_
         rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])   Fit linear model with Stochast
         ic Gradient Descent.
                       Predict class labels for samples in X.
         # predict(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/stabl
         e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm
         oid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         #-----
         # 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-probab
         ility estimates
             print("Log Loss :",log_loss(cv_y, sig_clf_probs))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
```

```
ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty=
'12', loss='log', 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 y = sig clf.predict proba(train x onehotCoding lr)
print('For values of best alpha = ', alpha[best alpha], "The train log loss i
s:",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 i
s:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-06
Log Loss : 1.8201104916799518
for alpha = 1e-05
Log Loss : 1.6203771586952185
for alpha = 0.0001

Log Loss: 1.5875493680791593

for alpha = 0.001

Log Loss: 1.403376474810247

for alpha = 0.01

Log Loss: 1.2423272309940365

for alpha = 0.1

Log Loss: 1.2401531939506085

for alpha = 1

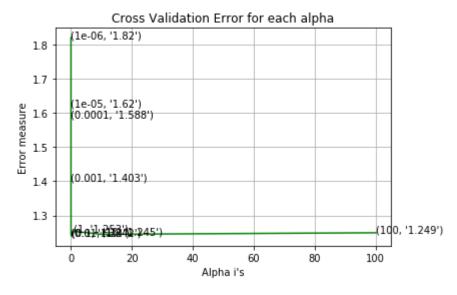
Log Loss: 1.2532748766119728

for alpha = 10

Log Loss: 1.244574367442384

for alpha = 100

Log Loss: 1.2491176828345538

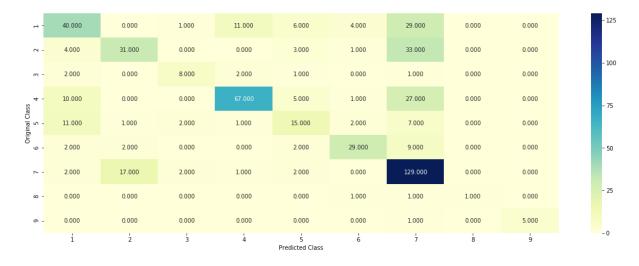


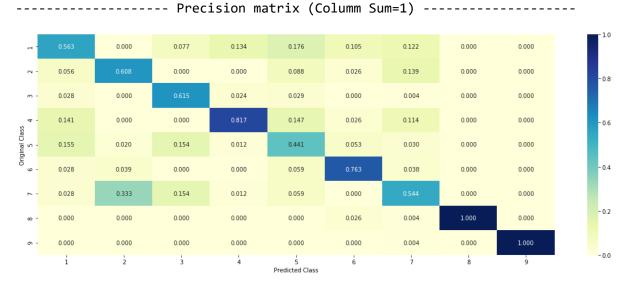
For values of best alpha = 0.1 The train log loss is: 0.5540673088073816 For values of best alpha = 0.1 The cross validation log loss is: 1.240153193 9506085

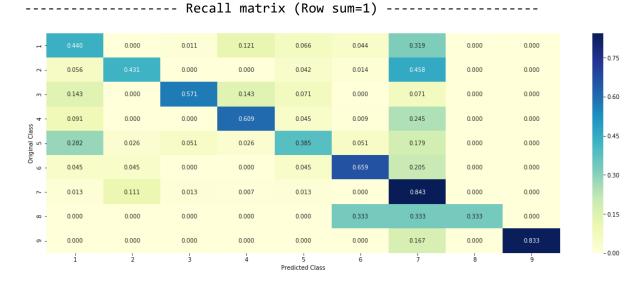
For values of best alpha = 0.1 The test log loss is: 1.2425756049800392

4.3.1.2. Testing the model with best hyper paramters

```
In [70]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge
         nerated/sklearn.linear_model.SGDClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_
         rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])   Fit linear model with Stochast
         ic Gradient Descent.
         # predict(X)
                        Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
         lessons/geometric-intuition-1/
         #-----
         clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty=
         '12', loss='log', random state=42)
         predict_and_plot_confusion_matrix(train_x_onehotCoding_lr, train_y, cv_x_oneho
         tCoding lr, cv y, clf)
```







4.3.1.3. Feature Importance

```
In [71]:
         #def get imp feature names(text, indices, removed ind = []):
              word present = 0
         #
              tabulte list = []
              incresingorder ind = 0
         #
              for i in indices:
                   if i < train_gene_feature_onehotCoding.shape[1]:</pre>
                       tabulte list.append([incresingorder ind, "Gene", "Yes"])
                   elif i< 18:
                       tabulte list.append([incresingorder ind, "Variation", "Yes"])
                   if ((i > 17) & (i not in removed_ind)) :
                      word = train text features[i]
                      yes_no = True if word in text.split() else False
                       if yes_no:
                           word present += 1
                       tabulte list.append([incresingorder ind,train text features[i], y
         es_no])
                   incresingorder ind += 1
              print(word_present, "most importent features are present in our query poi
         nt")
              print("-"*50)
              print("The features that are most importent of the ",predicted cls[0]," c
              print (tabulate(tabulte list, headers=["Index", 'Feature name', 'Present o
         r Not']))
         # this function will be used just for naive bayes
         # for the given indices, we will print the name of the features
         # and we will check whether the feature present in the test point text or not
         def get impfeature names(indices, text, gene, var, no features):
             gene count vec = TfidfVectorizer()
             var count vec = TfidfVectorizer()
             text_count_vec = TfidfVectorizer(ngram_range=(1, 4))
             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):
                      word = gene_vec.get_feature_names()[v]
                      yes no = True if word == gene else False
                      if yes no:
                          word_present += 1
                          print(i, "Gene feature [{}] present in test data point [{}]".f
         ormat(word,yes_no))
                 elif (v < fea1 len+fea2 len):</pre>
                      word = var vec.get feature names()[v-(fea1 len)]
                      yes no = True if word == var else False
                      if yes no:
                          word_present += 1
                          print(i, "variation feature [{}] present in test data point [
         {}]".format(word,yes_no))
```

```
else:
    word = text_vec.get_feature_names()[v-(fea1_len+fea2_len)]
    yes_no = True if word in text.split() else False
    if yes_no:
        word_present += 1
        print(i, "Text feature [{}] present in test data point [{}]".f

ormat(word,yes_no))

print("Out of the top ",no_features," features ", word_present, "are present in query point")
```

4.3.1.3.1. Correctly Classified point

```
In [72]: # 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 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(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
```

4.3.1.3.2. Incorrectly Classified point

```
In [73]: 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(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
    print("-"*50)
    get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index],
    no_feature)
```

Predicted Class : 2 Predicted Class Probabilities: [[0.0122 0.9412 0.0022 0.0096 0.006 0.003 0. 0185 0.005 0.0024]] Actual Class: 2 32 Text feature [wild] present in test data point [True] 33 Text feature [type] present in test data point [True] 36 Text feature [predicted] present in test data point [True] 38 Text feature [results] present in test data point [True] 41 Text feature [whereas] present in test data point [True] 43 Text feature [acid] present in test data point [True] 44 Text feature [used] present in test data point [True] 46 Text feature [amino] present in test data point [True] 47 Text feature [likely] present in test data point [True] 49 Text feature [determine] present in test data point [True] 50 Text feature [sequence] present in test data point [True] 54 Text feature [expected] present in test data point [True] 61 Text feature [data] present in test data point [True] 62 Text feature [thus] present in test data point [True] 63 Text feature [whether] present in test data point [True] 64 Text feature [although] present in test data point [True] 65 Text feature [shown] present in test data point [True] 66 Text feature [showed] present in test data point [True] 67 Text feature [previously] present in test data point [True] 68 Text feature [introduction] present in test data point [True] 70 Text feature [indicate] present in test data point [True] 72 Text feature [therefore] present in test data point [True] 73 Text feature [independent] present in test data point [True] 76 Text feature [containing] present in test data point [True] 77 Text feature [additional] present in test data point [True] 82 Text feature [also] present in test data point [True] 84 Text feature [mutant] present in test data point [True] 85 Text feature [using] present in test data point [True] 86 Text feature [addition] present in test data point [True] 87 Text feature [either] present in test data point [True] 88 Text feature [provide] present in test data point [True] 90 Text feature [well] present in test data point [True] 93 Text feature [indicated] present in test data point [True] 95 Text feature [result] present in test data point [True] 102 Text feature [found] present in test data point [True] 103 Text feature [changes] present in test data point [True] 105 Text feature [analysis] present in test data point [True] 112 Text feature [full] present in test data point [True] 113 Text feature [important] present in test data point [True] 115 Text feature [analyzed] present in test data point [True] 116 Text feature [critical] present in test data point [True] 117 Text feature [mutations] present in test data point [True] 118 Text feature [proteins] present in test data point [True] 119 Text feature [one] present in test data point [True] 121 Text feature [50] present in test data point [True] 124 Text feature [may] present in test data point [True] 125 Text feature [associated] present in test data point [True] 127 Text feature [domain] present in test data point [True] 130 Text feature [possible] present in test data point [True] 134 Text feature [resulting] present in test data point [True] 137 Text feature [assays] present in test data point [True] 138 Text feature [methods] present in test data point [True]

```
139 Text feature [directly] present in test data point [True]
141 Text feature [reduced] present in test data point [True]
146 Text feature [change] present in test data point [True]
147 Text feature [lower] present in test data point [True]
148 Text feature [figure] present in test data point [True]
151 Text feature [based] present in test data point [True]
152 Text feature [form] present in test data point [True]
153 Text feature [expressed] present in test data point [True]
156 Text feature [fact] present in test data point [True]
159 Text feature [cells] present in test data point [True]
160 Text feature [known] present in test data point [True]
161 Text feature [substitutions] present in test data point [True]
163 Text feature [note] present in test data point [True]
164 Text feature [highly] present in test data point [True]
166 Text feature [vitro] present in test data point [True]
168 Text feature [however] present in test data point [True]
170 Text feature [binding] present in test data point [True]
179 Text feature [levels] present in test data point [True]
181 Text feature [several] present in test data point [True]
184 Text feature [identified] present in test data point [True]
189 Text feature [performed] present in test data point [True]
193 Text feature [effects] present in test data point [True]
194 Text feature [mutation] present in test data point [True]
195 Text feature [represent] present in test data point [True]
196 Text feature [general] present in test data point [True]
197 Text feature [10] present in test data point [True]
198 Text feature [table] present in test data point [True]
199 Text feature [cancer] present in test data point [True]
201 Text feature [contribute] present in test data point [True]
204 Text feature [reported] present in test data point [True]
205 Text feature [members] present in test data point [True]
209 Text feature [indicates] present in test data point [True]
210 Text feature [residues] present in test data point [True]
213 Text feature [approximately] present in test data point [True]
214 Text feature [least] present in test data point [True]
217 Text feature [suggested] present in test data point [True]
221 Text feature [could] present in test data point [True]
227 Text feature [presence] present in test data point [True]
230 Text feature [30] present in test data point [True]
238 Text feature [would] present in test data point [True]
239 Text feature [different] present in test data point [True]
241 Text feature [genetic] present in test data point [True]
242 Text feature [cause] present in test data point [True]
245 Text feature [respectively] present in test data point [True]
247 Text feature [large] present in test data point [True]
248 Text feature [within] present in test data point [True]
249 Text feature [absence] present in test data point [True]
254 Text feature [derived] present in test data point [True]
255 Text feature [comparison] present in test data point [True]
259 Text feature [25] present in test data point [True]
265 Text feature [selected] present in test data point [True]
267 Text feature [predict] present in test data point [True]
270 Text feature [obtained] present in test data point [True]
274 Text feature [taken] present in test data point [True]
277 Text feature [26] present in test data point [True]
290 Text feature [available] present in test data point [True]
293 Text feature [possibility] present in test data point [True]
```

```
296 Text feature [confirmed] present in test data point [True]
301 Text feature [fold] present in test data point [True]
303 Text feature [studies] present in test data point [True]
304 Text feature [even] present in test data point [True]
305 Text feature [except] present in test data point [True]
306 Text feature [24] present in test data point [True]
310 Text feature [position] present in test data point [True]
311 Text feature [allows] present in test data point [True]
315 Text feature [present] present in test data point [True]
320 Text feature [identify] present in test data point [True]
321 Text feature [support] present in test data point [True]
322 Text feature [given] present in test data point [True]
324 Text feature [observation] present in test data point [True]
331 Text feature [approach] present in test data point [True]
332 Text feature [forms] present in test data point [True]
333 Text feature [cell] present in test data point [True]
336 Text feature [strong] present in test data point [True]
341 Text feature [yet] present in test data point [True]
342 Text feature [according] present in test data point [True]
345 Text feature [caused] present in test data point [True]
348 Text feature [relevant] present in test data point [True]
349 Text feature [specific] present in test data point [True]
350 Text feature [include] present in test data point [True]
352 Text feature [useful] present in test data point [True]
359 Text feature [frequently] present in test data point [True]
362 Text feature [significantly] present in test data point [True]
365 Text feature [similarly] present in test data point [True]
375 Text feature [recently] present in test data point [True]
378 Text feature [remaining] present in test data point [True]
384 Text feature [35] present in test data point [True]
385 Text feature [allow] present in test data point [True]
387 Text feature [low] present in test data point [True]
389 Text feature [grown] present in test data point [True]
391 Text feature [many] present in test data point [True]
397 Text feature [single] present in test data point [True]
400 Text feature [standard] present in test data point [True]
403 Text feature [model] present in test data point [True]
404 Text feature [assessment] present in test data point [True]
409 Text feature [little] present in test data point [True]
415 Text feature [proposed] present in test data point [True]
418 Text feature [resulted] present in test data point [True]
420 Text feature [including] present in test data point [True]
424 Text feature [detected] present in test data point [True]
425 Text feature [assessed] present in test data point [True]
435 Text feature [involved] present in test data point [True]
436 Text feature [less] present in test data point [True]
437 Text feature [basis] present in test data point [True]
441 Text feature [exception] present in test data point [True]
452 Text feature [structural] present in test data point [True]
453 Text feature [high] present in test data point [True]
458 Text feature [panel] present in test data point [True]
459 Text feature [impair] present in test data point [True]
463 Text feature [40] present in test data point [True]
466 Text feature [combined] present in test data point [True]
476 Text feature [difficult] present in test data point [True]
478 Text feature [31] present in test data point [True]
483 Text feature [published] present in test data point [True]
```

```
484 Text feature [comprehensive] present in test data point [True]
487 Text feature [abrogate] present in test data point [True]
489 Text feature [reduction] present in test data point [True]
496 Text feature [relatively] present in test data point [True]
497 Text feature [29] present in test data point [True]
499 Text feature [might] present in test data point [True]
Out of the top 500 features 172 are present in query point
```

4.3.2. Without Class balancing

4.3.2.1. Hyper paramter tuning

```
In [74]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge
         nerated/sklearn.linear_model.SGDClassifier.html
         # ------
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_
         rate='optimal', eta0=0.0, power_t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])      Fit linear model with Stochast
         ic Gradient Descent.
                       Predict class labels for samples in X.
         # predict(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/stabl
         e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm
         oid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample_weight]) Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         # 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.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_
state=42)
clf.fit(train x onehotCoding 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 i
s:",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 i
s:",log_loss(y_test, predict y, labels=clf.classes , eps=1e-15))
```

for alpha = 1e-06

Log Loss: 1.774894857014709

for alpha = 1e-05

Log Loss: 1.5578290286106147

for alpha = 0.0001

Log Loss: 1.5544148761287524

for alpha = 0.001

Log Loss: 1.4115997798122784

for alpha = 0.01

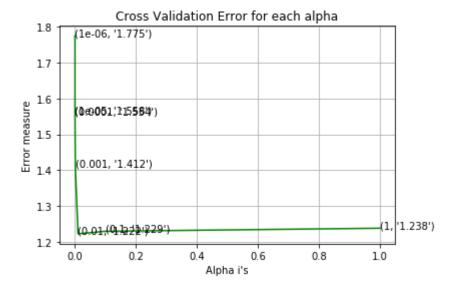
Log Loss: 1.2223735845597772

for alpha = 0.1

Log Loss: 1.2294773325874306

for alpha = 1

Log Loss: 1.2379790995332929

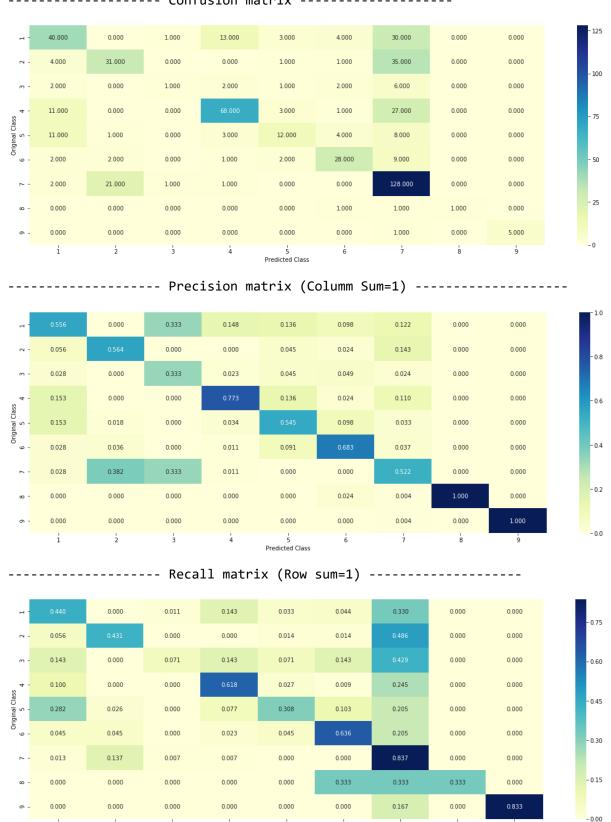


For values of best alpha = 0.01 The train log loss is: 0.6068200320716836 For values of best alpha = 0.01 The cross validation log loss is: 1.22237358 45597772

For values of best alpha = 0.01 The test log loss is: 1.235224292000013

4.3.2.2. Testing model with best hyper parameters

In [75]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge nerated/sklearn.linear_model.SGDClassifier.html # -----# default parameters # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i ntercept=True, max_iter=None, tol=None, # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_ rate='optimal', eta0=0.0, power t=0.5, # class_weight=None, warm_start=False, average=False, n_iter=None) # some of methods # fit(X, y[, coef_init, intercept_init, ...])
Fit linear model with Stochast ic Gradient Descent. # predict(X) Predict class labels for samples in X. # video link: #----clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42) predict_and_plot_confusion_matrix(train_x_onehotCoding_lr, train_y, cv_x_oneho tCoding_lr, cv_y, clf)



Predicted Class

4.3.2.3. Feature Importance, Correctly Classified point

```
In [76]: | 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(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
         Predicted Class : 7
         Predicted Class Probabilities: [[0.1797 0.1384 0.0365 0.1727 0.0877 0.0913 0.
         2744 0.0055 0.0138]]
```

4.3.2.4. Feature Importance, Inorrectly Classified point

```
In [77]: 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(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
         Predicted Class: 2
         Predicted Class Probabilities: [[0.0179 0.8893 0.0069 0.0126 0.0096 0.0048 0.
         0507 0.006 0.0022]]
         Actual Class : 2
         Out of the top 500 features 0 are present in query point
```

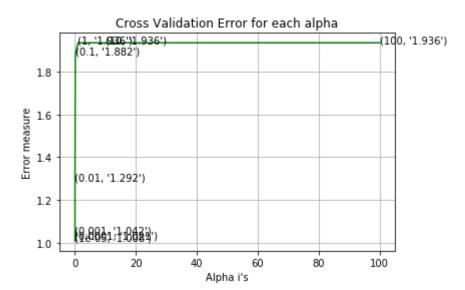
4.4. Linear Support Vector Machines

4.4.1. Hyper paramter tuning

In [78]: # read more about support vector machines with linear kernals here http://scik it-learn.org/stable/modules/generated/sklearn.svm.SVC.html # default parameters # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001, # cache size=200, class weight=None, verbose=False, max iter=-1, decision func tion shape='ovr', random state=None) # Some of methods of SVM() ing data. # predict(X) Perform classification on samples in X. # -----# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/ Lessons/mathematical-derivation-copy-8/ # find more about CalibratedClassifierCV here at http://scikit-learn.org/stabl e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html # default paramters # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm oid', cv=3) # some of the methods of CalibratedClassifierCV() # fit(X, y[, sample_weight]) Fit the calibrated model # get_params([deep]) Get parameters for this estimator. # predict(X) Predict the target of new samples. # predict_proba(X) Posterior probabilities of classification #----# 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 print("Log Loss :",log loss(cv y, sig clf probs)) fig, ax = plt.subplots() ax.plot(alpha, cv_log_error_array,c='g') for i, txt in enumerate(np.round(cv_log_error_array,3)): ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))

```
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
# clf = SVC(C=i,kernel='linear',probability=True, class_weight='balanced')
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty=
'12', loss='hinge', 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 i
s:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation
log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss i
s:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for C = 1e-05
Log Loss: 1.0084816711655122
for C = 0.0001
Log Loss: 1.0211186485835775
for C = 0.001
Log Loss: 1.0424249526918998
for C = 0.01
Log Loss: 1.2923698826699872
for C = 0.1
Log Loss: 1.8817742008573548
for C = 1
Log Loss: 1.9360273420627463
for C = 10
Log Loss: 1.9360251971882068
for C = 100
Log Loss: 1.9360242795186076
```



For values of best alpha = 1e-05 The train log loss is: 0.41723500769698235

For values of best alpha = 1e-05 The cross validation log loss is: 1.0084816

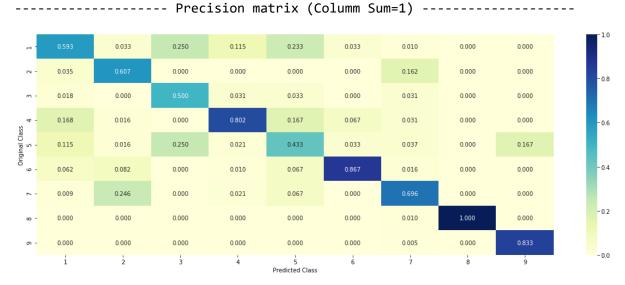
711655122

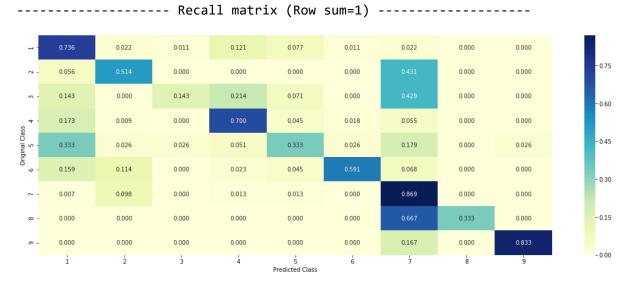
For values of best alpha = 1e-05 The test log loss is: 1.0867171998905403

4.4.2. Testing model with best hyper parameters

In [79]: # read more about support vector machines with linear kernals here http://scik it-learn.org/stable/modules/generated/sklearn.svm.SVC.html # default parameters # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001, # cache size=200, class weight=None, verbose=False, max iter=-1, decision func tion shape='ovr', random state=None) # Some of methods of SVM() ing data. # predict(X) Perform classification on samples in X. # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/ lessons/mathematical-derivation-copy-8/ # clf = SVC(C=alpha[best alpha],kernel='linear',probability=True, class weight ='balanced') clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', rando m state=42,class weight='balanced') predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCod ing, cv y, clf)







4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

```
In [80]: | clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', rando
         m state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         # test point index = 100
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test point index]),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-1*abs(clf.coef_))[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no_feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.1045 0.0585 0.0056 0.0072 0.0537 0.0231 0.
         7386 0.0079 0.0009]]
         Actual Class: 7
         Out of the top 500 features 0 are present in query point
```

4.3.3.2. For Incorrectly classified point

```
In [81]: 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(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no_feature)
         Predicted Class: 2
         Predicted Class Probabilities: [[6.760e-02 8.167e-01 1.300e-03 3.200e-03 5.61
         0e-02 1.910e-02 2.900e-02
           6.700e-03 3.000e-04]]
         Actual Class : 2
         Out of the top 500 features 0 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

```
In [82]: # ------
        # default parameters
        # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', m
        ax depth=None, min samples split=2,
        # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max l
        eaf_nodes=None, min_impurity_decrease=0.0,
        # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random s
        tate=None, verbose=0, warm start=False,
        # class weight=None)
        # Some of methods of RandomForestClassifier()
        ing data.
        \# predict(X) Perform classification on samples in X.
        \# predict proba (X) Perform classification on samples in X.
        # some of attributes of RandomForestClassifier()
        # feature_importances_ : array of shape = [n_features]
        # The feature importances (the higher, the more important the feature).
        # ------
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
        lessons/random-forest-and-their-construction-2/
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stabl
        e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
        # -----
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm
        oid', cv=3)
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample_weight]) Fit the calibrated model
        # get_params([deep]) Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
        # predict_proba(X) Posterior probabilities of classification
        #-----
        # 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 dep
        th=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.cla
        sses_, eps=1e-15))
```

```
print("Log Loss :",log_loss(cv_y, sig_clf_probs))
'''fiq, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel()
ax.plot(features, cv log error array,c='q')
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],c
v log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion=
'gini', max_depth=max_depth[int(best_alpha%2)], random_state=42, n_jobs=-1)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The train
log loss 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=1
e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test 1
og loss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for n_estimators = 100 and max depth = 5
Log Loss: 1.2281311521625655
for n estimators = 100 and max depth =
Log Loss: 1.2016759360832534
for n estimators = 200 and max depth = 5
Log Loss: 1.2175515228590474
for n estimators = 200 and max depth =
Log Loss: 1.1925979376924802
for n estimators = 500 and max depth = 5
Log Loss: 1.219568165490032
for n_estimators = 500 and max depth = 10
Log Loss: 1.1891083251834829
for n estimators = 1000 and max depth = 5
Log Loss: 1.215188954131631
for n estimators = 1000 and max depth = 10
Log Loss: 1.1871364831297526
for n estimators = 2000 and max depth = 5
Log Loss: 1.2146143588782397
for n_estimators = 2000 and max depth = 10
Log Loss: 1.1853708880800045
For values of best estimator = 2000 The train log loss is: 0.529806763228517
For values of best estimator = 2000 The cross validation log loss is: 1.1853
708880800042
For values of best estimator = 2000 The test log loss is: 1.18208984475796
```

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

```
In [83]:
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', m
         ax depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max l
         eaf_nodes=None, min_impurity_decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random s
         tate=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample_weight])
                                        Fit the SVM model according to the given train
         ing 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-construction-2/
         clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion=
         'gini', max depth=max depth[int(best alpha%2)], random state=42, n jobs=-1)
         predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCod
         ing,cv y, clf)
```

Log loss: 1.1853708880800045 Number of mis-classified points : 0.3890977443609023 ----- Confusion matrix -----5.000 7.000 0.000 13.000 1.000 0.000 0.000 0.000 29.000 100 4.000 38.000 0.000 1.000 0.000 0.000 0.000 5.000 - 80 5.000 4.000 4.000 1.000 0.000 1.000 0.000 0.000 0.000 3.000 0.000 3.000 5 Predicted Class Precision matrix (Columm Sum=1) ------0.081 0.134 0.000 0.027 0.000 0.010 0.017 0.000 0.052 0.125 0.000 0.027 0.210 0.070 0.250 0.036 0.049 0.6 0.118 0.023 0.052 0.036 0.044 0.000 0.034 0.070 0.041 0.022 0.034 0.302 0.041 0.000 0.000 0.008 0.012 0.000 0.000 0.005 0.000 0.000 0.000 0.000 0.000 0.000 0.016 1.000 - 0.0 5 Predicted Class Recall matrix (Row sum=1) 0.75 0.077 0.000 0.143 0.055 0.000 0.000 0.011 0.000 0.056 0.000 0.014 0.000 0.000 0.000 0.000 - 0.60 0.357 0.357 0.143 0.000 0.000 0.143 0.000 0.000 0.000 0.227 0.036 0.082 0.000 0.055 0.000 0.009 0.000 - 0.45 0.359 0.000 0.128 0.231 0.026 0.205 0.000 0.000 0.051

0.091

0.026

0.000

0.000

0.000

Predicted Class

0.000

0.000

0.333

4.5.3. Feature Importance

0.333

0.333

0.000

0.000

- 0.30

-0.15

-0.00

0.000

0.000

0.000

4.5.3.1. Correctly Classified point

```
In [84]: # test point index = 10
         clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion=
         'gini', max depth=max depth[int(best alpha%2)], random state=42, n jobs=-1)
         clf.fit(train x onehotCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x onehotCoding, train y)
         test point index = 1
         no feature = 100
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test_point_index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point ind
         ex],test df['Gene'].iloc[test point index],test df['Variation'].iloc[test poin
         t_index], no_feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.1483 0.2316 0.0227 0.1459 0.06
                                                                             0.0604 0.
         3133 0.0084 0.0094]]
         Actual Class: 7
         Out of the top 100 features 0 are present in query point
```

4.5.3.2. Inorrectly Classified point

```
In [85]: test_point_index = 100
         no feature = 100
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x
         onehotCoding[test point index]),4))
         print("Actuall Class :", test_y[test_point_index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point ind
         ex],test df['Gene'].iloc[test point index],test df['Variation'].iloc[test poin
         t index], no feature)
         Predicted Class: 2
         Predicted Class Probabilities: [[0.0374 0.8232 0.0112 0.0237 0.0305 0.0276 0.
         0379 0.0038 0.004711
         Actuall Class : 2
```

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

4.5.3. Hyper paramter tuning (With Response Coding)

```
In [86]: # ------
        # default parameters
        # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', m
        ax depth=None, min samples split=2,
        # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max l
        eaf_nodes=None, min_impurity_decrease=0.0,
        # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random s
        tate=None, verbose=0, warm start=False,
        # class weight=None)
        # Some of methods of RandomForestClassifier()
        ing data.
        \# predict(X) Perform classification on samples in X.
        \# predict proba (X) Perform classification on samples in X.
        # some of attributes of RandomForestClassifier()
        # feature_importances_ : array of shape = [n_features]
        # The feature importances (the higher, the more important the feature).
        # ------
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
        lessons/random-forest-and-their-construction-2/
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stabl
        e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
        # -----
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm
        oid', cv=3)
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample_weight]) Fit the calibrated model
        # get_params([deep]) Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
        # predict_proba(X) Posterior probabilities of classification
        #-----
        # 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 dep
        th=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.cla
        sses_, eps=1e-15))
```

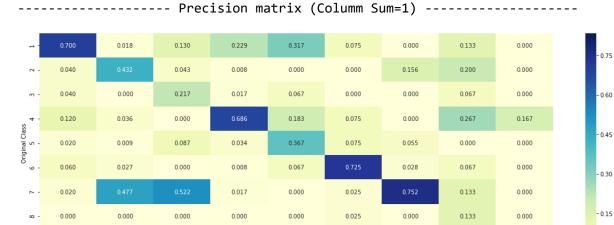
```
print("Log Loss :",log_loss(cv_y, sig_clf_probs))
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[int(i/4)],max depth[int(i%4)],str(txt)),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

```
for n estimators = 10 and max depth = 2
Log Loss: 2.061724756653649
for n estimators = 10 and max depth =
Log Loss: 1.7910329172541843
for n estimators = 10 and max depth = 5
Log Loss: 1.4895860644462515
for n estimators = 10 and max depth =
Log Loss: 1.6284775889672949
for n estimators = 50 and max depth =
Log Loss: 1.6817896209283998
for n_estimators = 50 and max depth =
Log Loss: 1.4416309015498987
for n_estimators = 50 and max depth = 5
Log Loss: 1.3743188677368006
for n estimators = 50 and max depth = 10
Log Loss: 1.6418261536253445
for n estimators = 100 and max depth =
Log Loss: 1.5642606651228206
for n_estimators = 100 and max depth =
Log Loss: 1.4474642777930014
for n estimators = 100 and max depth =
Log Loss: 1.296283409073802
for n estimators = 100 and max depth =
Log Loss: 1.707053409615415
for n_estimators = 200 and max depth =
Log Loss: 1.584006280908212
for n estimators = 200 and max depth =
Log Loss: 1.4596795181637647
for n estimators = 200 and max depth = 5
Log Loss: 1.3515525796758852
for n_estimators = 200 and max depth =
Log Loss: 1.67543766818155
for n estimators = 500 and max depth = 2
Log Loss: 1.6037968514884746
for n_estimators = 500 and max depth =
Log Loss: 1.491675068311772
for n_estimators = 500 and max depth =
Log Loss: 1.3527340554950347
for n estimators = 500 and max depth = 10
Log Loss: 1.6866252632477592
for n_estimators = 1000 and max depth =
Log Loss: 1.588058323618764
for n estimators = 1000 and max depth = 3
Log Loss: 1.5009066626880303
for n estimators = 1000 and max depth =
Log Loss: 1.354320213853695
for n_estimators = 1000 and max depth = 10
Log Loss: 1.6762314802392537
For values of best alpha = 100 The train log loss is: 0.0690817567521354
For values of best alpha = 100 The cross validation log loss is: 1.296283409
0738018
For values of best alpha = 100 The test log loss is: 1.2929752726522183
```

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

```
In [87]:
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', m
         ax depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max l
         eaf_nodes=None, min_impurity_decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random s
         tate=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample_weight])
                                        Fit the SVM model according to the given train
         ing 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-construction-2/
         clf = RandomForestClassifier(max depth=max depth[int(best alpha%4)], n estimat
         ors=alpha[int(best alpha/4)], criterion='gini', max features='auto',random sta
         te=42)
         predict and plot confusion matrix(train x responseCoding, train y,cv x respons
         eCoding, cv y, clf)
```





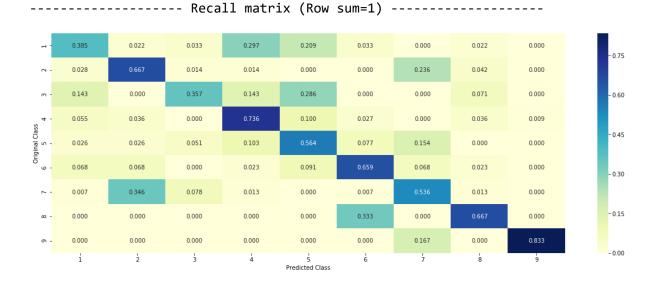
0.000

Predicted Class

0.000

0.000

0.009



4.5.5. Feature Importance

0.000

0.000

0.000

0.000

-0.00

4.5.5.1. Correctly Classified point

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

```
Predicted Class: 6
Predicted Class Probabilities: [[0.0682 0.167 0.1092 0.062 0.096 0.1889 0.
1747 0.0791 0.0547]]
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
Text is important feature
Variation is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Variation is important feature
Gene is important feature
Gene is important feature
Text is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
```

4.5.5.2. Incorrectly Classified point

Gene is important feature

```
In [89]: test point index = 100
         predicted cls = sig clf.predict(test x responseCoding[test point index].reshap
         e(1,-1)
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         responseCoding[test_point_index].reshape(1,-1)),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         for i in indices:
             if i<9:
                 print("Gene is important feature")
             elif i<18:
                 print("Variation is important feature")
             else:
                 print("Text is important feature")
         Predicted Class: 2
         Predicted Class Probabilities: [[0.0251 0.7726 0.0309 0.0272 0.017 0.035 0.
         0373 0.0286 0.0263]]
         Actual Class: 2
         Variation is important feature
         Variation is important feature
         Variation is important feature
         Variation is important feature
         Gene is important feature
         Variation is important feature
         Text is important feature
         Variation is important feature
         Text is important feature
         Gene is important feature
         Text is important feature
         Text is important feature
         Text is important feature
         Gene is important feature
         Variation is important feature
         Gene is important feature
         Gene is important feature
         Text is important feature
         Variation is important feature
         Gene is important feature
         Variation is important feature
         Text is important feature
         Text is important feature
         Text is important feature
```

4.7 Stack the models

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

4.7.1 testing with hyper parameter tuning

```
In [90]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge
         nerated/sklearn.linear_model.SGDClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_
         rate='optimal', eta0=0.0, power_t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])      Fit linear model with Stochast
         ic Gradient Descent.
                      Predict class labels for samples in X.
         # predict(X)
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
         lessons/geometric-intuition-1/
         # read more about support vector machines with linear kernals here http://scik
         it-learn.org/stable/modules/generated/sklearn.svm.SVC.html
         # default parameters
         # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True,
         probability=False, tol=0.001,
         # cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_func
         tion shape='ovr', random state=None)
         # Some of methods of SVM()
         ing data.
         \# predict(X) Perform classification on samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
         Lessons/mathematical-derivation-copy-8/
         # -----
         # read more about support vector machines with linear kernals here http://scik
         it-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.
         htmL
         # ------
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', m
         ax_depth=None, min_samples_split=2,
         # min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_l
         eaf nodes=None, min impurity decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random s
         tate=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample_weight])
Fit the SVM model according to the given train
         ing data.
```

```
\# predict(X) Perform classification on samples in X.
# predict proba (X)
                       Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
lessons/random-forest-and-their-construction-2/
# -----
clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class weight='bala
nced', random state=0)
clf1.fit(train x onehotCoding, train y)
sig clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
clf2 = SGDClassifier(alpha=1, penalty='12', loss='hinge', class weight='balanc
ed', random state=0)
clf2.fit(train x onehotCoding, train y)
sig clf2 = CalibratedClassifierCV(clf2, method="sigmoid")
clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train x onehotCoding, train y)
sig clf3 = CalibratedClassifierCV(clf3, method="sigmoid")
sig clf1.fit(train x onehotCoding, train y)
print("Logistic Regression : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf1.pred
ict_proba(cv_x_onehotCoding))))
sig clf2.fit(train x onehotCoding, train y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf2.p
redict proba(cv x onehotCoding))))
sig clf3.fit(train x onehotCoding, train y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba
(cv x onehotCoding))))
print("-"*50)
alpha = [0.0001, 0.001, 0.01, 0.1, 1, 10]
best alpha = 999
for i in alpha:
   lr = LogisticRegression(C=i)
   sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta
classifier=lr, use probas=True)
   sclf.fit(train x onehotCoding, train y)
   print("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" %
(i, log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))))
   log error =log loss(cv y, sclf.predict proba(cv x onehotCoding))
   if best alpha > log error:
        best_alpha = log_error
```

```
Logistic Regression: Log Loss: 1.09

Support vector machines: Log Loss: 1.94

Naive Bayes: Log Loss: 1.24

Stacking Classifer: for the value of alpha: 0.000100 Log Loss: 1.817

Stacking Classifer: for the value of alpha: 0.001000 Log Loss: 1.715

Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.320

Stacking Classifer: for the value of alpha: 0.100000 Log Loss: 1.243

Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.598
```

Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.977

4.7.2 testing the model with the best hyper parameters

```
In [91]: lr = LogisticRegression(C=0.1)
    sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_cla
    ssifier=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)

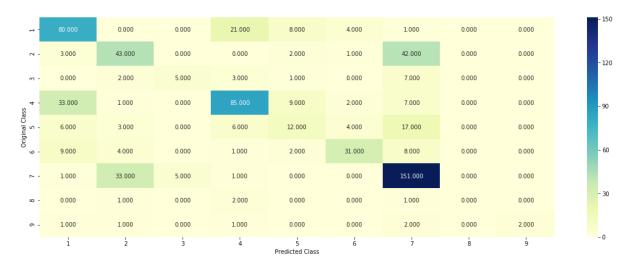
log_error = log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    print("Log loss (CV) on the stacking classifier :",log_error)

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

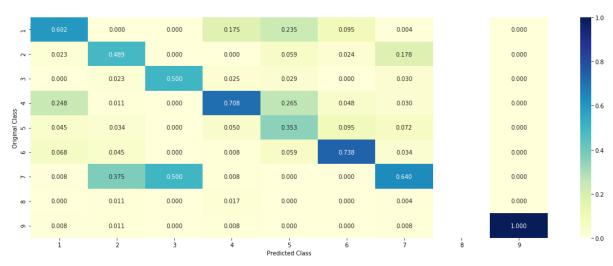
print("Number of missclassified point :", np.count_nonzero((sclf.predict(test_x_onehotCoding) - test_y))/test_y.shape[0])
    plot_confusion_matrix(test_y=test_y, predict_y=sclf.predict(test_x_onehotCoding))
```

Log loss (train) on the stacking classifier: 0.4597113477737592 Log loss (CV) on the stacking classifier: 1.2434078280255831 Log loss (test) on the stacking classifier: 1.2759942326172031 Number of missclassified point: 0.3849624060150376

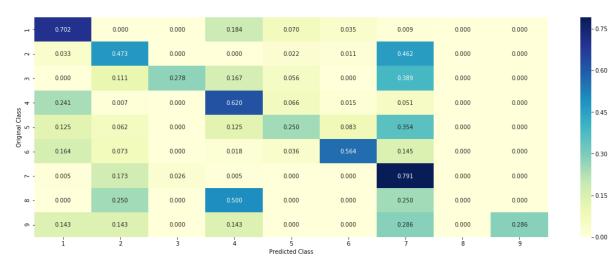
----- Confusion matrix



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

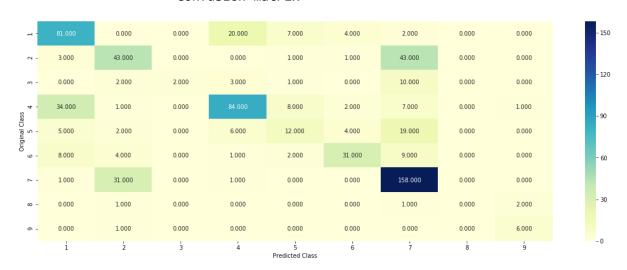


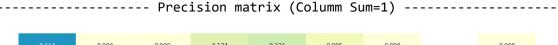
------ Recall matrix (Row sum=1) ---------

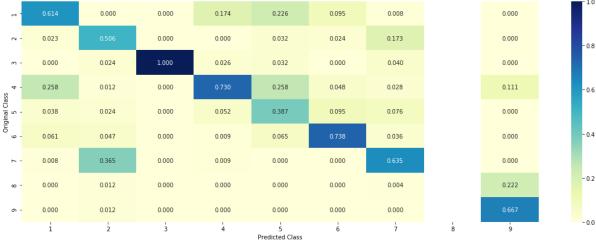


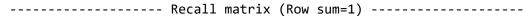
4.7.3 Maximum Voting classifier

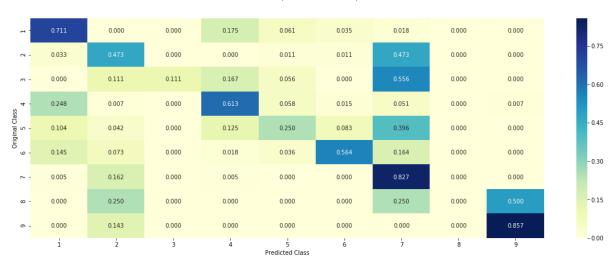
In [92]: #Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.Votin qClassifier.html from sklearn.ensemble import VotingClassifier vclf = VotingClassifier(estimators=[('lr', sig clf1), ('svc', sig clf2), ('rf' , sig_clf3)], voting='soft') vclf.fit(train_x_onehotCoding, train_y) print("Log loss (train) on the VotingClassifier :", log_loss(train_y, vclf.pre dict proba(train x onehotCoding))) print("Log loss (CV) on the VotingClassifier :", log_loss(cv_y, vclf.predict_p roba(cv_x_onehotCoding))) print("Log loss (test) on the VotingClassifier :", log_loss(test_y, vclf.predi ct_proba(test_x_onehotCoding))) print("Number of missclassified point :", np.count_nonzero((vclf.predict(test_ x onehotCoding)- test y))/test y.shape[0]) plot confusion matrix(test y=test y, predict y=vclf.predict(test x onehotCodin g))











Logistic Regression with feature engineering

```
In [93]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge
         nerated/sklearn.linear_model.SGDClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_
         rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])      Fit linear model with Stochast
         ic Gradient Descent.
                       Predict class labels for samples in X.
         # predict(X)
         #-----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/stabl
         e/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigm
         oid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get_params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict_proba(X) Posterior probabilities of classification
         #-----
         # 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 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-probab
         ility estimates
             print("Log Loss :",log_loss(cv_y, sig_clf_probs))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
```

```
ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty=
'12', loss='log', 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 i
s:",log_loss(y_train, predict_y, labels=clf.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 i
s:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-06

Log Loss: 1.051003134377265

for alpha = 1e-05

Log Loss: 1.0497192969426299

for alpha = 0.0001

Log Loss: 1.0177458951615523

for alpha = 0.001

Log Loss: 0.9901953437928124

for alpha = 0.01

Log Loss: 1.0748573283596188

for alpha = 0.1

Log Loss: 1.3966976110157225

for alpha = 1

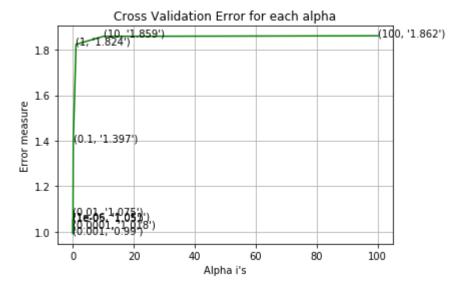
Log Loss: 1.8240950106014056

for alpha = 10

Log Loss: 1.8594408627142196

for alpha = 100

Log Loss: 1.8618215887417076

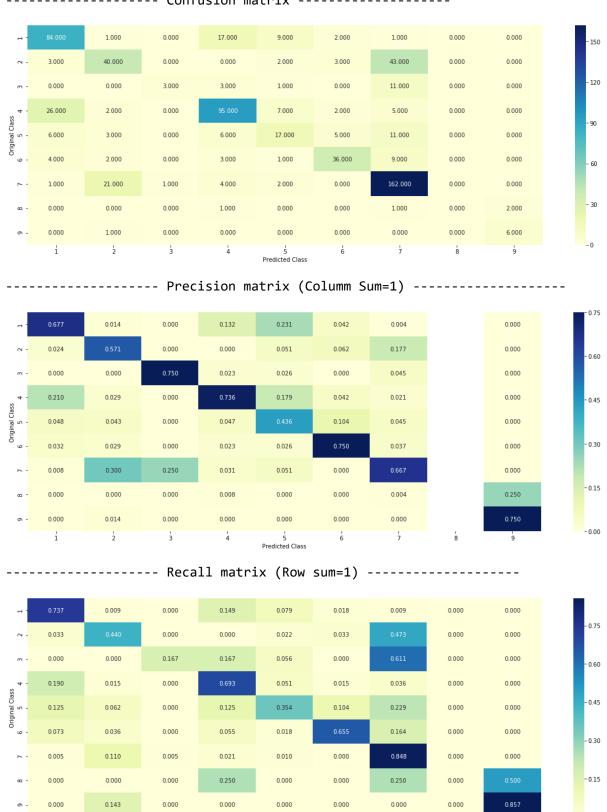


For values of best alpha = 0.001 The train log loss is: 0.5233614846923389
For values of best alpha = 0.001 The cross validation log loss is: 0.9901953
437928124

For values of best alpha = 0.001 The test log loss is: 0.9919153581128131

Testing model with best hyper parameters

```
In [94]:
        # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/ge
         nerated/sklearn.linear_model.SGDClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_i
         ntercept=True, max_iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_
         rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef_init, intercept_init, ...])      Fit linear model with Stochast
         ic Gradient Descent.
         # predict(X)
                        Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
         lessons/geometric-intuition-1/
         #-----
         clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty=
         '12', loss='log', random state=42)
         predict_and_plot_confusion_matrix(train_x_onehotCodingFE, train_y, test_x_oneh
         otCodingFE, test y, clf)
```



Predicted Class

Correctly Classified point

```
In [95]: # from tabulate import tabulate
         clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty=
         '12', loss='log', random state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test_point_index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test d
         f['Gene'].iloc[test point index],test df['Variation'].iloc[test point index],
         no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.1672 0.1572 0.0312 0.1138 0.1086 0.1003 0.
         2854 0.0065 0.0296]]
         Actual Class : 7
         Out of the top 500 features 0 are present in query point
```

Incorrectly Classified point

```
In [96]: test point index = 50
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_
         onehotCoding[test point index]),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test d
         f['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test_point_index],
         no_feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.108 0.2367 0.0246 0.1145 0.0527 0.1108 0.
         3173 0.0062 0.0291]]
         Actual Class : 7
```

Out of the top 500 features 0 are present in query point

Conclusion

ngram_range(1,3), min_df=3, max_features=1000 used and below is the output

result = result.append(pd.DataFrame([["LR with FE", 0.640, 0.975, 1.005, "36.3
9%", "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test

In [103]: result = pd.DataFrame(columns = ["Model", "Train Log-loss", "CV Log-loss", "Te st Log-loss", "No of Missclassified point", "Remarks"]) result = result.append(pd.DataFrame([["Naive Bayes", 0.693, 1.150, 1.247, "36. 09%", "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["KNN", 0.600, 0.990, 1.101, "33.08%", "B est Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-los s", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["LR - Class Balancing", 0.648, 1.136, 1. 172, "38.72%", "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-los s", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["LR -Without Class Balancing", 0.557, 1. 165, 1.181, "40.03%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["LR -SVM", 0.774, 1.106, 1.180, "33.08%" , "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log
-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["RF -With OHE", 0.862, 1.186, 1.208, "4 0.22%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Te st Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["RF -With RC", 0.066, 1.295, 1.339, "46. 80%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["Stacking Models", 0.686, 1.102, 1.254, "42.25%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["Max Voting Classifier", 0.914, 1.160, 1.235, "40.30%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"]))

Log-loss", "No of Missclassified point", "Remarks"]))

result.reset_index(drop = True, inplace = True)

result

Out[103]:

	Model	Train Log- loss	CV Log- loss	Test Log- loss	No of Missclassified point	Remarks
0	Naive Bayes	0.693	1.150	1.247	36.09%	Best Fit
1	KNN	0.600	0.990	1.101	33.08%	Best Fit
2	LR - Class Balancing	0.648	1.136	1.172	38.72%	Best Fit
3	LR -Without Class Balancing	0.557	1.165	1.181	40.03%	Over Fit
4	LR -SVM	0.774	1.106	1.180	33.08%	Best Fit
5	RF -With OHE	0.862	1.186	1.208	40.22%	Over Fit
6	RF -With RC	0.066	1.295	1.339	46.80%	Over Fit
7	Stacking Models	0.686	1.102	1.254	42.25%	Over Fit
8	Max Voting Classifier	0.914	1.160	1.235	40.30%	Over Fit
9	LR with FE	0.640	0.975	1.005	36.39%	Best Fit

In order to reduce test log loss to below 1, made changes as below

ngram_range(1,4), min_df=5, max_features=3000 we got minimum test log-loss is 0.991 and minimum misclassified points as 33.38% for LR with FE

In [104]:

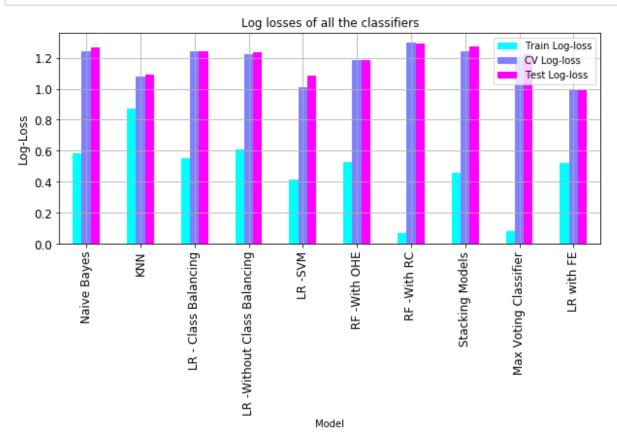
result = pd.DataFrame(columns = ["Model", "Train Log-loss", "CV Log-loss", "Te st Log-loss", "No of Missclassified point", "Remarks"]) result = result.append(pd.DataFrame([["Naive Bayes", 0.582, 1.242, 1.264, "40. 03%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["KNN", 0.869, 1.081, 1.088, "37.03%", "B est Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-los s", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["LR - Class Balancing", 0.554, 1.240, 1. 242, "38.90%", "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-los s", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["LR -Without Class Balancing", 0.606, 1. 222, 1.235, "40.97%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["LR -SVM", 0.417, 1.008, 1.086, "32.14%" , "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log
-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["RF -With OHE", 0.529, 1.185, 1.182, "3 8.90%", "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Te st Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["RF -With RC", 0.069, 1.296, 1.292, "41. 91%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["Stacking Models", 0.459, 1.243, 1.275, "38.49%", "Over Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["Max Voting Classifier", 0.082, 1.206, 1.224, "37.29%", "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result = result.append(pd.DataFrame([["LR with FE", 0.523, 0.990, 0.991, "33.3 8%", "Best Fit"]], columns = ["Model", "Train Log-loss", "CV Log-loss", "Test Log-loss", "No of Missclassified point", "Remarks"])) result.reset_index(drop = True, inplace = True) result

Out[104]:

	Model	Train Log- loss	CV Log- loss	Test Log- loss	No of Missclassified point	Remarks
0	Naive Bayes	0.582	1.242	1.264	40.03%	Over Fit
1	KNN	0.869	1.081	1.088	37.03%	Best Fit
2	LR - Class Balancing	0.554	1.240	1.242	38.90%	Best Fit
3	LR -Without Class Balancing	0.606	1.222	1.235	40.97%	Over Fit
4	LR -SVM	0.417	1.008	1.086	32.14%	Best Fit
5	RF -With OHE	0.529	1.185	1.182	38.90%	Best Fit
6	RF -With RC	0.069	1.296	1.292	41.91%	Over Fit
7	Stacking Models	0.459	1.243	1.275	38.49%	Over Fit
8	Max Voting Classifier	0.082	1.206	1.224	37.29%	Best Fit
9	LR with FE	0.523	0.990	0.991	33.38%	Best Fit

In [101]: bar_result = result.drop(["No of Missclassified point", "Remarks"], axis = 1)

```
In [102]: bar_result.plot(x = "Model", kind = "bar", figsize = (10, 4), grid = True, fon
    tsize = 12, colormap="cool")
    plt.title("Log losses of all the classifiers", fontsize = 12)
    plt.ylabel("Log-Loss", fontsize = 12)
    plt.show()
```



Summary

- 1. Applied all the models with tf-idf feature
- 2. Maximum 1000 words used
- 3. NB OHE is applied
- 4. KNN Response coding is applied
- 5. LR with count vectorizer and unigram and bigram and OHE is applied, with class balancing
- 6. LR with count vectorizer and unigram and bigram and OHE is applied, without class balancing
- 7. Lr SVM with class balancing with OHE is applied
- 8. RF with OHE
- 9. RF with response coding
- 10. stacking the models with OHE
- 11. Maximum voting classifier with OHE
- 12. LR with FE