Problem statement

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

Objective

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

Contraints

No low-latency requirement.

Interpretability is important.

Errors can be very costly.

Probability of a data-point belonging to each class is needed.

About files

there are 2 data files and both have one common col (id)

training_variants (ID , Gene, Variations, Class)

training_text (ID, Text)

```
# Multi class classification problem, data belongs to 9 different classes

# Performance Metric: (KPI)
#Multi class log-loss, bcoz we want results in probabilities
#Confusion matrix:
 #confusion, pre, rec gives us more visibility into what is happening in the different classes
 #what is actual, what your model predicted. Logloss only give you just one no.
```

```
import pandas as pd
import numpy as np
```

```
!gdown --id 1RmX5_q6D7rzoXD7nPUM_s8rKEf1KVMDi #training_text.zip download
!gdown --id 1bSQrw5WmDqqI8hBcr8Pflzatx4xCT0Ex #training_variants.zip download
```

```
/usr/local/lib/python3.7/dist-packages/gdown/cli.py:131: FutureWarning: Option `--id` was deprecated in version 4.3.1 and will be remove
  category=FutureWarning,
Downloading...
From: https://drive.google.com/uc?id=1RmX5_q6D7rzoXD7nPUM_s8rKEf1KVMDi
To: /content/training_text.zip
100% 63.9M/63.9M [00:00<00:00, 67.3MB/s]
/usr/local/lib/python3.7/dist-packages/gdown/cli.py:131: FutureWarning: Option `--id` was deprecated in version 4.3.1 and will be remove
  category=FutureWarning,
Downloading...
From: https://drive.google.com/uc?id=1bSQrw5WmDqqI8hBcr8Pflzatx4xCT0Ex
To: /content/training_variants.zip
100% 24.8k/24.8k [00:00<00:00, 28.5MB/s]
```

```
!unzip training_text.zip
```

```
Archive:  training_text.zip
  inflating: training_text
```

```
!unzip training_variants.zip
```

```
Archive:  training_variants.zip
  inflating: training_variants
```

```
#reading data
data = pd.read_csv('training_variants')
print('Number of data points : ', data.shape[0])
print('Number of features : ', data.shape[1])
print('Features : ', data.columns.values)

print(data.shape)
data.head()
```

```
Number of data points :  3321
Number of features :  4
Features :  ['ID' 'Gene' 'Variation' 'Class']
(3321, 4)
```

	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

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3321 entries, 0 to 3320
Data columns (total 4 columns):
 #   Column     Non-Null Count  Dtype 
---  ------     --------------  ----- 
 0   ID         3321 non-null   int64 
 1   Gene       3321 non-null   object
 2   Variation  3321 non-null   object
 3   Class      3321 non-null   int64 
dtypes: int64(2), object(2)
memory usage: 103.9+ KB
```

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 one of class this genetic mutation has been classified on

```
#checking output/dependent variable
print(list(data['Class'].unique()))
data.value_counts('Class')
```

```
[1, 2, 3, 4, 5, 6, 7, 8, 9]
Class
7    953
4    686
1    568
2    452
6    275
5    242
3     89
9     37
8     19
dtype: int64
```

Can say Imbalanced data

```
#Reading text file
# There is the seprator (between id and text, which is '||') in this file. So instead of comma seperator, we have ||
data_text =pd.read_csv("training_text",sep="\|\|",engine="python",names=["ID","TEXT"],skiprows=1)

print(data_text.shape)
print('Features : ', data_text.columns.values)      #data_text.columns.values, to know cols of the table
data_text.head()
```

```
(3321, 2)
Features :  ['ID' 'TEXT']
```

	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...

```
data_text.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3321 entries, 0 to 3320
Data columns (total 2 columns):
 #   Column  Non-Null Count  Dtype 
---  ------  --------------  ----- 
 0   ID      3321 non-null   int64 
 1   TEXT    3316 non-null   object
dtypes: int64(1), object(1)
memory usage: 52.0+ KB
```

Pre process text

text processing befor merge 2 files into one.

```
#copy code from course
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 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")
import six
import sys
sys.modules['sklearn.externals.six'] = six
from mlxtend.classifier import StackingClassifier
from sklearn import model_selection
from sklearn.linear_model import LogisticRegression
```

```
import nltk
nltk.download('stopwords')
```

```
[nltk_data] Downloading package stopwords to /root/nltk_data...
[nltk_data]   Unzipping corpora/stopwords.zip.
True
```

```
# 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
```

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

```
there is no text description for id: 1109
there is no text description for id: 1277
there is no text description for id: 1407
there is no text description for id: 1639
there is no text description for id: 2755
Time took for preprocessing the text : 31.911836 seconds
```

```
#merging two files
#merging both gene_variations(data) and text data based on ID
result = pd.merge(data, data_text, on='ID', how='left')  #pd.merge, left merge so data file has all columns
result.head()
```

	ID	Gene	Variation	Class	TEXT
0	0	FAM58A	Truncating Mutations	1	Cyclin-dependent kinases (CDKs) regulate a var...
1	1	CBL	W802*	2	Abstract Background Non-small cell lung canc...
2	2	CBL	Q249E	2	Abstract Background Non-small cell lung canc...
3	3	CBL	N454D	3	Recent evidence has demonstrated that acquired...
4	4	CBL	L399V	4	Oncogenic mutations in the monomeric Casitas B...

```
#checking null values
print(result.isnull().sum())
result[result.isnull().any(axis=1)]
#result.dropna(inplace=True), if wanna drop these 5 rows
```

```
ID           0
Gene         0
Variation    0
Class        0
TEXT         5
dtype: int64
```

	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

text col. has null vaues in 5 rows

```
# Handling missing values, can't use mean/median/mode in text data, decided not to drop as well.
#merging two cols to fill nan datapoint

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

```
#checking update
result[result['ID']==1639]
```

```
          ID  Gene   Variation  Class             TEXT
```

```
result.isnull().sum()
#now no missing value
```

```
ID           0
Gene         0
Variation    0
Class        0
TEXT         0
dtype: int64
```

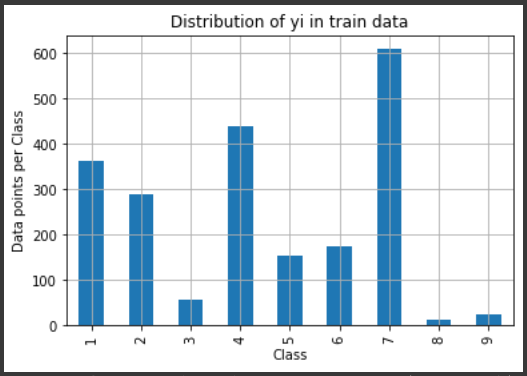
```
# splitting data into train, test, cv (64:20:16) and maintaining disb. of data in each split, to work ML models well
y_true = result['Class'].values
#resulting Gene & variation column will have underscores instead of whitespaces (replaced)
result.Gene = result.Gene.str.replace('\s+', '_')       #'\s' whitespace
result.Variation = result.Variation.str.replace('\s+', '_')

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

```
print('train data pts:', train_df.shape[0])
print('test data pts:', test_df.shape[0])
print('CV data pts:', cv_df.shape[0])
```

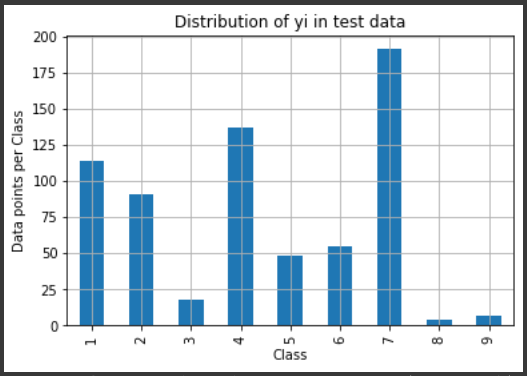
```
train data pts: 2124
test data pts: 665
CV data pts: 532
```

```
# through value counts and plotting histogram will know the sense of DISTRIBUTION.

# it returns a dict, keys as class labels and values as the number of data points in that class
#checking disb. of class (target) column in all(tr, cv, te)
train_class_distribution = train_df['Class'].value_counts().sort_index()
test_class_distribution = test_df['Class'].value_counts().sort_index()
cv_class_distribution = cv_df['Class'].value_counts().sort_index()

my_colors = 'rgbkymc'
train_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in train data')
plt.grid()
plt.show()

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

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()

sorted_yi = np.argsort(-test_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',test_class_distribution.values[i], '(', np.round((test_class_distribution.values[i]/test_

print('-'*80)
my_colors = 'rgbkymc'
cv_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in cross validation data')
plt.grid()
plt.show()
```

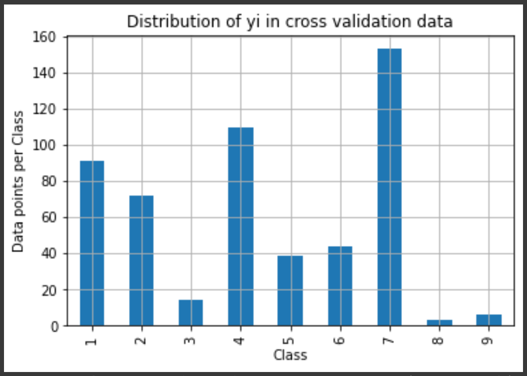
```
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',cv_class_distribution.values[i], '(', np.round((cv_class_distribution.values[i]/cv_df.sh
```



```
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 %)
```

This shows that we are maintaining distribution of each class in all form of data like same disb for train, test and cv dataset.

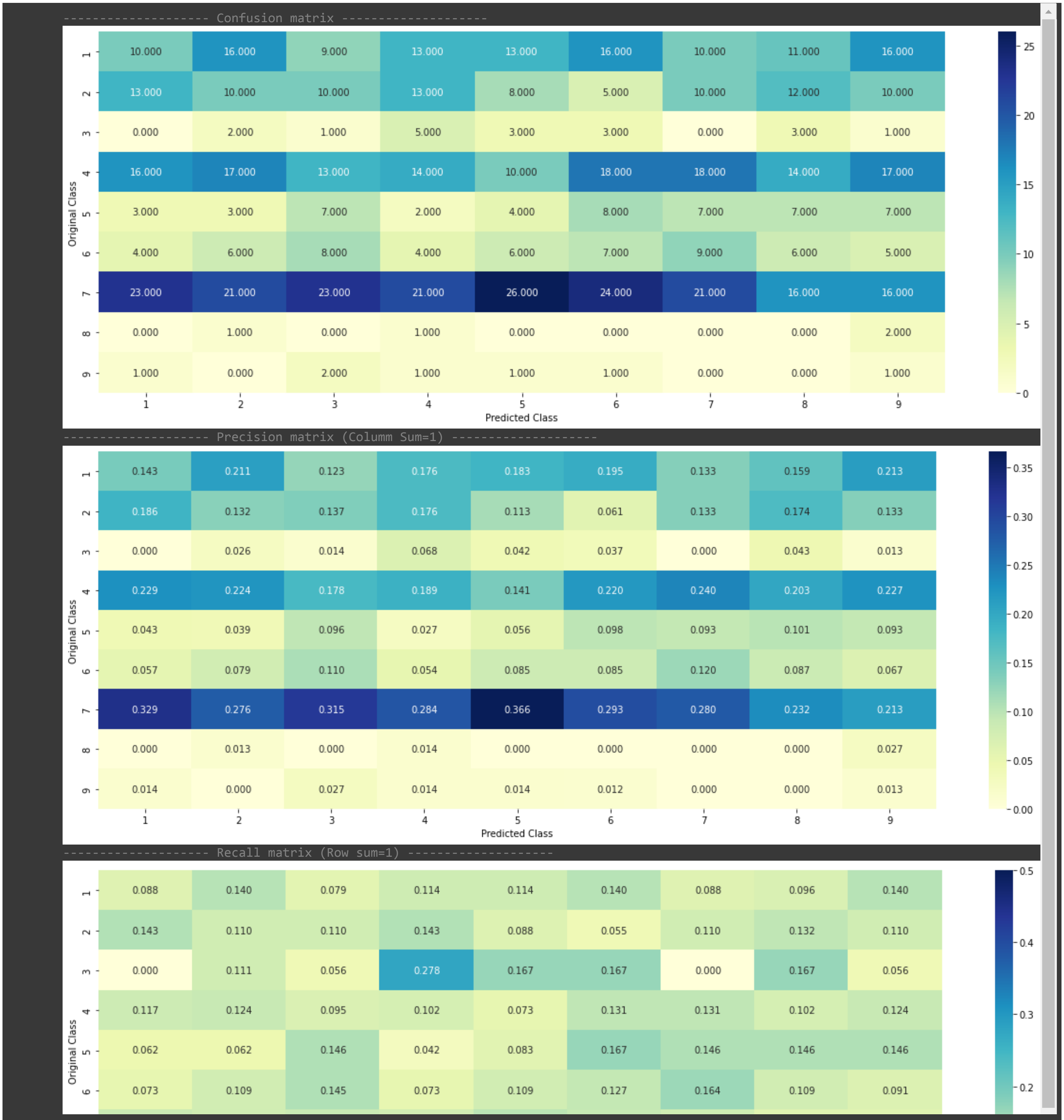
```
#Making base model
#Random Model (dumb model):- Randomly picks one of the nine classes
'''?????'''
# we need to generate 9 numbers and the sum of numbers should be 1
# one solution is to genarate 9 numbers and divide each of the numbers by their sum
# ref: https://stackoverflow.com/a/18662466/4084039
test_data_len = test_df.shape[0]
cv_data_len = cv_df.shape[0]

# we create a output array that has exactly same size as the CV data
cv_predicted_y = np.zeros((cv_data_len,9))
for i in range(cv_data_len):
    rand_probs = np.random.rand(1,9)     ###randomly choosing class
    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))

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

predicted_y =np.argmax(test_predicted_y, axis=1)
```

```
Log loss on Cross Validation Data using Random Model 2.4016161118578716
Log loss on Test Data using Random Model 2.44478600958592
```

We need log loss of our model to be lesser than random model.

logloss lies b/w 0 to infinity, 0 logloss is the best case. Minizing the err of our model.

```
# This function plots the confusion matrices given y_i, y_i_hat.
#defining the fn for matrix
def plot_confusion_matrix(test_y, predict_y):
    C = confusion_matrix(test_y, predict_y)

    A =(((C.T)/(C.sum(axis=1))).T)
    #divid each element of the confusion matrix with the sum of elements in that column

    B =(C/C.sum(axis=0))

    labels = [1,2,3,4,5,6,7,8,9]
    # representing A in heatmap format
    print("-"*20, "Confusion matrix", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()

    print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()

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

plot_confusion_matrix(y_test, predicted_y+1)
```



```
-------------------- Confusion matrix --------------------
```

Original Class	1	2	3	4	5	6	7	8	9
1	10.000	16.000	9.000	13.000	13.000	16.000	10.000	11.000	16.000
2	13.000	10.000	10.000	13.000	8.000	5.000	10.000	12.000	10.000
3	0.000	2.000	1.000	5.000	3.000	3.000	0.000	3.000	1.000
4	16.000	17.000	13.000	14.000	10.000	18.000	18.000	14.000	17.000
5	3.000	3.000	7.000	2.000	4.000	8.000	7.000	7.000	7.000
6	4.000	6.000	8.000	4.000	6.000	7.000	9.000	6.000	5.000
7	23.000	21.000	23.000	21.000	26.000	24.000	21.000	16.000	16.000
8	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000	2.000
9	1.000	0.000	2.000	1.000	1.000	1.000	0.000	0.000	1.000

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

Original Class	1	2	3	4	5	6	7	8	9
1	0.143	0.211	0.123	0.176	0.183	0.195	0.133	0.159	0.213
2	0.186	0.132	0.137	0.176	0.113	0.061	0.133	0.174	0.133
3	0.000	0.026	0.014	0.068	0.042	0.037	0.000	0.043	0.013
4	0.229	0.224	0.178	0.189	0.141	0.220	0.240	0.203	0.227
5	0.043	0.039	0.096	0.027	0.056	0.098	0.093	0.101	0.093
6	0.057	0.079	0.110	0.054	0.085	0.085	0.120	0.087	0.067
7	0.329	0.276	0.315	0.284	0.366	0.293	0.280	0.232	0.213
8	0.000	0.013	0.000	0.014	0.000	0.000	0.000	0.000	0.027
9	0.014	0.000	0.027	0.014	0.014	0.012	0.000	0.000	0.013

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

Original Class									
1	0.088	0.140	0.079	0.114	0.114	0.140	0.088	0.096	0.140
2	0.143	0.110	0.110	0.143	0.088	0.055	0.110	0.132	0.110
3	0.000	0.111	0.056	0.278	0.167	0.167	0.000	0.167	0.056
4	0.117	0.124	0.095	0.102	0.073	0.131	0.131	0.102	0.124
5	0.062	0.062	0.146	0.042	0.083	0.167	0.146	0.146	0.146
6	0.073	0.109	0.145	0.073	0.109	0.127	0.164	0.109	0.091

Ideally we want all of these diagonal element should be very large(it shows that actual values are same as model preicted values , so the model is perfect).

confusion matrix represents no of points in a cell.

Pre & Re represents % in a cell

Diagonal elments tells what precision is of each class, off-diagonal tells the sense of err that our model makes.

Ideally pre & re should be 1, but in random_M diag ele.s are very low tells about performance of model prediction.

EDA

Gene Feature Analysis

Q1. Gene, What type of feature it is ?

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

Q3. How to featurize this Gene feature ? Encoding

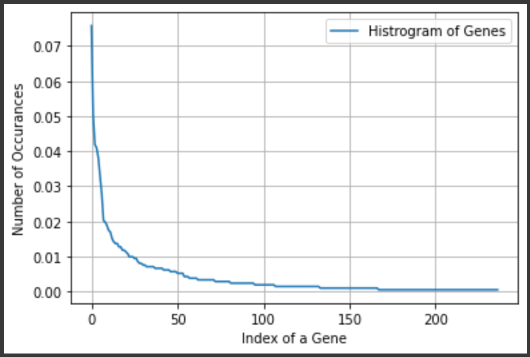
Q4. How good is this gene feature in predicting y_i? Feature Importance? Build lr model on this one feature only

Laplace smoothing is a way to avoid overfitting

```
#Gene feature: ctegorical data, so we need to check no of categories it is divided in this feature.

unique_genes= train_df.value_counts('Gene')
#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 : 237
Gene
BRCA1     161
TP53      107
EGFR       89
BRCA2      87
PTEN       81
KIT        70
BRAF       59
ALK        43
ERBB2      42
PDGFRA     40
dtype: int64
```

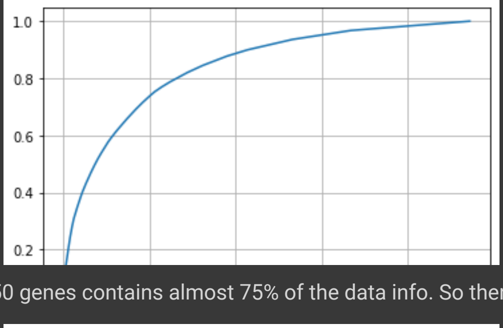
```
#Histogram
s = sum(unique_genes.values);
h = unique_genes.values/s;
plt.plot(h, label="Histrogram of Genes")
plt.xlabel('Index of a Gene')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



Skewed disb.

very few gene has large no. of occurrence

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



top 50 genes contains almost 75% of the data info. So there are lot of genes that occurs very few time.

```
#Categorical to numerical
#One hot Encoding: one is one and rest is zero
#Response coding: Mean-
value replacement
```

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 Knn (assumption).

In high Dim. LR, lr-svm works well. In low dim. knn, NB, DT works well.

```
###### we are applying response coding to convert categorical data to numerical
# code for response coding with Laplace smoothing.
# alpha : used for laplace smoothing

# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):

    value_count = train_df[feature].value_counts()
    # gv_dict : Gene Variation Dict, which contains the probability array for each gene/variation
    gv_dict = dict()

    # denominator will contain the number of time that particular feature occured in whole data
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticular class
        # vec is 9 diamensional vector
        vec = []
        for k in range(1,10):
            # print(train_df.loc[(train_df['Class']==1) & (train_df['Gene']=='BRCA1')])
            #         ID   Gene             Variation  Class
            # 2470  2470  BRCA1                S1715C      1
            # 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):

    gv_dict = get_gv_fea_dict(alpha, feature, df)
    # value_count is similar in get_gv_fea_dict
    value_count = train_df[feature].value_counts()

    # gv_fea: Gene_variation feature, it will contain the feature for each feature value in the data
    gv_fea = []
    # for every feature values in the given data frame we will check if it is there in the train data then we will add the feature to gv_fea
    # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to gv_fea
    for index, row in df.iterrows():
        if row[feature] in dict(value_count).keys():
            gv_fea.append(gv_dict[row[feature]])
        else:
            gv_fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
#             gv_fea.append([-1,-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)

Laplace is used to avoid overfitting problem. In case of probabilities, it adds additive to avoid very low prob.answers as well to avoid 0/0 problem.

```
#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))
```

```
train_gene_feature_responseCoding.shape
```

```
(2124, 9)
```

```
# one-hot encoding of Gene feature.
gene_vectorizer = CountVectorizer()
train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gene'])
test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gene'])
cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
```

```
train_gene_feature_onehotCoding.shape
#now the cols(features) increase due to one hot encoding
```

```
(2124, 236)
```

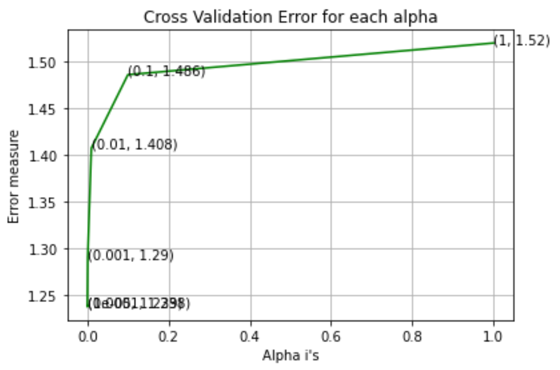
Q4. How good is this gene feature in predicting y_i?

There are many ways to know 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.

```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
#Finding best alpha (Lambda from course, i.e regularization)

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.SGDClassifier.html
cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)       #SGDClassifier, penalty='l2'
    clf.fit(train_gene_feature_onehotCoding, y_train)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")                       #CalibratedClassifierCV
    sig_clf.fit(train_gene_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))

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='l2', loss='log', random_state=42)
clf.fit(train_gene_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
```

```
sig_clf.fit(train_gene_feature_onehotCoding, y_train)

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

```
For values of alpha =  1e-05 The log loss is: 1.2390385028897883
For values of alpha =  0.0001 The log loss is: 1.2379856641709304
For values of alpha =  0.001 The log loss is: 1.2902658189028375
For values of alpha =  0.01 The log loss is: 1.4075194364112533
For values of alpha =  0.1 The log loss is: 1.4858798368525592
For values of alpha =  1 The log loss is: 1.5196969757814573
```



```
For values of best alpha =  0.0001 The train log loss is: 0.980569851846758
For values of best alpha =  0.0001 The cross validation log loss is: 1.2379856641709304
For values of best alpha =  0.0001 The test log loss is: 1.1857653338315801
```

So logloss of gene featr is better than random model. so we will use this as feature to build our final model.

Train, test, cv loss is almost same, so its not overfit. If they have major difference then model called over fit.

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.

```
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)
```

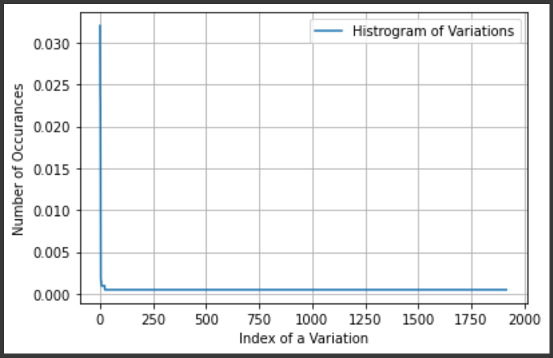
```
Q6. How many data points in Test and CV datasets are covered by the  237  genes in train dataset?
Ans
1. In test data 649 out of 665 : 97.59398496240601
2. In cross validation data 513 out of  532 : 96.42857142857143
```

Variation Feature Analysis

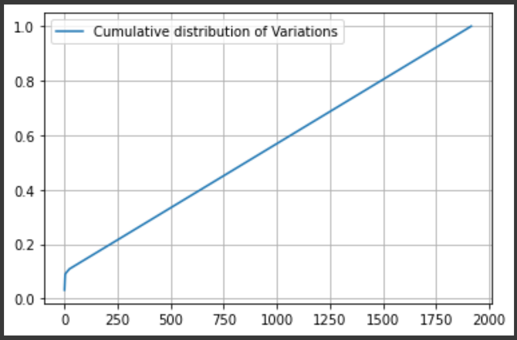
```
unique_variations= train_df.value_counts('Variation')
print('No of unique/different variations', unique_variations.shape[0])
unique_variations.head(10)
```

```
No of unique/different variations 1916
Variation
Truncating_Mutations    68
Deletion                51
Amplification           48
Fusions                 22
Overexpression           4
Q61H                     3
Q61L                     3
P130S                    2
G67R                     2
E17K                     2
dtype: int64
```

```
#histogram
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()
```



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



shows only top 5 has more data points, after that its plateau

When see line on 45 degree, understand most vars occurs only once or twice.

```
#convert categorical
#We will be using both these methods to featurize the Variation Feature(encodings)

# 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))
```

Response coding takes 1m 15s to execute the above code

```
print("The shape of Variation feature:", train_variation_feature_responseCoding.shape)
```

```
The shape of Variation feature: (2124, 9)
```

```
# one-hot encoding of variation feature.
variation_vectorizer = CountVectorizer()
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'])
```

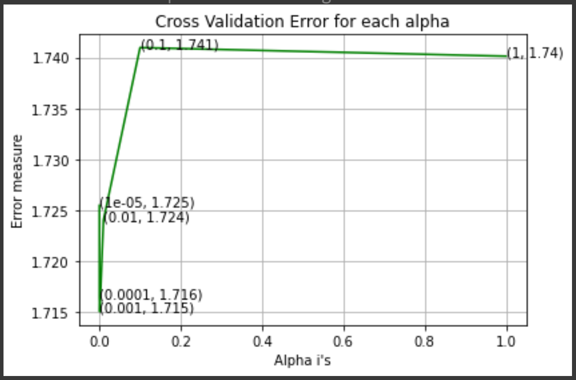
It takes 0s to execute

```
print("The shape of Variation feature:", train_variation_feature_onehotCoding.shape)
```

```
The shape of Variation feature: (2124, 1951)
```

```
#Build model to check feature importance with LR model

alpha = [10 ** x for x in range(-5, 1)]

cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
    clf.fit(train_variation_feature_onehotCoding, y_train)

    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_variation_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)

    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, labels=clf.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='l2', loss='log', random_state=42)
clf.fit(train_variation_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_variation_feature_onehotCoding, y_train)

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

```
For values of alpha =  1e-05 The log loss is: 1.725492277662838
For values of alpha =  0.0001 The log loss is: 1.7164664214553957
For values of alpha =  0.001 The log loss is: 1.71506692047849
For values of alpha =  0.01 The log loss is: 1.7240354348870013
For values of alpha =  0.1 The log loss is: 1.740966589353858
For values of alpha =  1 The log loss is: 1.7401237569076347
```



```
For values of best alpha =  0.001 The train log loss is: 1.1141204260336752
For values of best alpha =  0.001 The cross validation log loss is: 1.71506692047849
For values of best alpha =  0.001 The test log loss is: 1.6932100486871344
```

logloss less than random model, so feature is useful

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

Not sure! But lets be very sure using the below analysis.

```
print("Q12. How many data points are covered by total ", unique_variations.shape[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'])))].shape[0]
print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_coverage/test_df.shape[0])*100)
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_coverage/cv_df.shape[0])*100)
```

```
Q12. How many data points are covered by total  1916  genes in test and cross validation data sets?
Ans
1. In test data 54 out of 665 : 8.1203007518797
2. In cross validation data 58 out of  532 : 10.902255639097744
```

Shows instability in this feature, but loss is < 2.5, let's go with this.

Not good as gene feature.

Text feature Analysis

```
#Dict consists of word and count, occurrence of words
# cls_text is a data frame, 'TEXT' split the words by space, make a dict with those words
# increment its count whenever we see that word

def extract_dictionary_paddle(cls_text):
    dictionary = defaultdict(int)
    for index, row in cls_text.iterrows():
        for word in row['TEXT'].split():
            dictionary[word] +=1
    return dictionary
```

```
#one hot encoding of text is bow, and response coding is like assumption of NB(naive bayes)

#Resoponse coding for text
import math
#https://stackoverflow.com/a/1602964
def get_text_responsecoding(df):
    text_feature_responseCoding = np.zeros((df.shape[0],9))
    for i in range(0,9):
        row_index = 0
        for index, row in df.iterrows():
            sum_prob = 0
            for word in row['TEXT'].split():
                sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(total_dict.get(word,0)+90)))
            text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TEXT'].split()))
            row_index += 1
    return text_feature_responseCoding
```

```
#one hot encoding of text

# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer = CountVectorizer(min_df=3)
train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()

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

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


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

```
Total number of unique words in train data : 54166
```

```
dict_list = []
# dict_list =[] contains 9 dictoinaries each corresponds to a class
for i in range(1,10):
    cls_text = train_df[train_df['Class']==i]
    # build a word dict based on the words in that class
    dict_list.append(extract_dictionary_paddle(cls_text))
    # append it to dict_list

# dict_list[i] is build on i'th  class text data
# total_dict is buid on whole training text data
total_dict = extract_dictionary_paddle(train_df)


confuse_array = []
for i in train_text_features:
    ratios = []
    max_val = -1
    for j in range(0,9):
        ratios.append((dict_list[j][i]+10 )/(total_dict[i]+90))
    confuse_array.append(ratios)
confuse_array = np.array(confuse_array)
```

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

```
#Normalizing each row
# 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
```

```
#on train, normalizing
# we use the same vectorizer that was trained on train data
train_text_feature_onehotCoding = text_vectorizer.transform(train_df['TEXT'])
# don't forget to normalize every feature in one hot encoding as well
train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding, axis=0)

#on test
test_text_feature_onehotCoding = text_vectorizer.transform(test_df['TEXT'])
test_text_feature_onehotCoding = normalize(test_text_feature_onehotCoding, axis=0)

#on CV
cv_text_feature_onehotCoding = text_vectorizer.transform(cv_df['TEXT'])
cv_text_feature_onehotCoding = normalize(cv_text_feature_onehotCoding, axis=0)
```

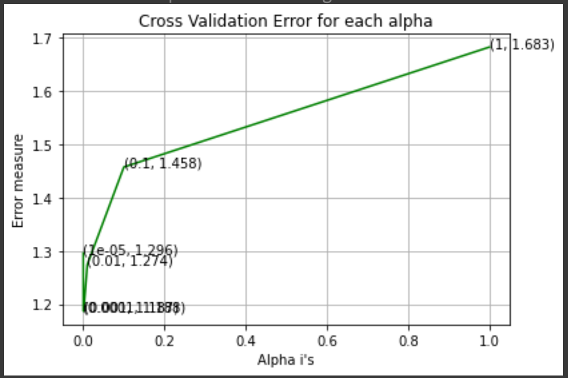
```
#https://stackoverflow.com/a/2258273/4084039
sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambda x: x[1] , reverse=True))
sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))
```

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

```
Counter({3: 5665, 4: 3696, 5: 2849, 6: 2558, 7: 1895, 9: 1834, 8: 1761, 11: 1624, 10: 1300, 12: 1289, 14: 1069, 15: 889, 13: 878, 17: 80
```

```
#To check feature importance, use lr + calibrated classifier with one hot encoding

alpha = [10 ** x for x in range(-5, 1)]

cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
    clf.fit(train_text_feature_onehotCoding, y_train)

    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_text_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))

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

best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
clf.fit(train_text_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_onehotCoding, y_train)

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

```
For values of alpha =  1e-05 The log loss is: 1.2958901991481013
For values of alpha =  0.0001 The log loss is: 1.187519130417096
For values of alpha =  0.001 The log loss is: 1.186753552871852
For values of alpha =  0.01 The log loss is: 1.2743500625995643
For values of alpha =  0.1 The log loss is: 1.4576168428528846
For values of alpha =  1 The log loss is: 1.6829086010991874
```



```
For values of best alpha =  0.001 The train log loss is: 0.6638738351470486
For values of best alpha =  0.001 The cross validation log loss is: 1.186753552871852
For values of best alpha =  0.001 The test log loss is: 1.0788532086184717
```

Takes 1m 44s to compute, loss is lesser.

```
def get_intersec_text(df):
    df_text_vec = CountVectorizer(min_df=3)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

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

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

```
97.0 % of word of test data appeared in train data
97.902 % of word of Cross Validation appeared in train data
```

Text feature is stable & it is useful fetr.

ML Models

```
#) For high dimensions(typically): LR, Linear svm works well, (random forest may also perform well
#) For low dimensions(typically): Knn, Decision tree, Random forest
```

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

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)
```

```
#Stacking the three types of features

# merging gene, variance and text features
# building train, test and cross validation data sets
# a = [[1, 2],
#      [3, 4]]
# b = [[4, 5],
#      [6, 7]]
# hstack(a, b) = [[1, 2, 4, 5],
#                [ 3, 4, 6, 7]]

train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,train_variation_feature_onehotCoding))
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_onehotCoding))
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehotCoding))

train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text_feature_onehotCoding)).tocsr()
train_y = np.array(list(train_df['Class']))

test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_feature_onehotCoding)).tocsr()
test_y = np.array(list(test_df['Class']))

cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text_feature_onehotCoding)).tocsr()
cv_y = np.array(list(cv_df['Class']))
```

```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCoding.shape)
print("(number of data points * number of features) in test data = ", test_x_onehotCoding.shape)
print("(number of data points * number of features) in cross validation data =", cv_x_onehotCoding.shape)
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 56357)
(number of data points * number of features) in test data =  (665, 56357)
(number of data points * number of features) in cross validation data = (532, 56357)
```

```
#Stacking with response coding
train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,train_variation_feature_responseCoding))
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_feature_responseCoding))
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_feature_responseCoding))

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_responseCoding))
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_responseCoding))
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCoding))
```

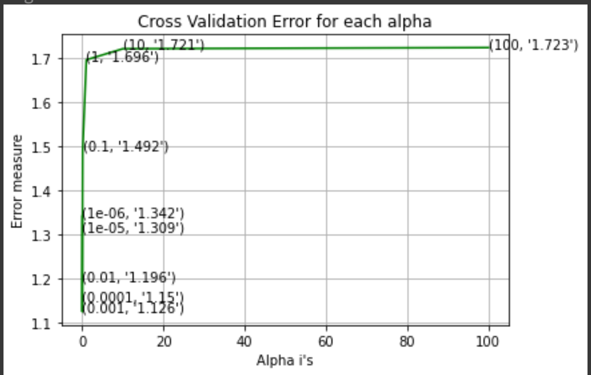
```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_responseCoding.shape)
print("(number of data points * number of features) in test data = ", test_x_responseCoding.shape)
print("(number of data points * number of features) in cross validation data =", cv_x_responseCoding.shape)
```

```
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 27)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data = (532, 27)
```

Logistic Regression with class balancing + one hot using sgd classifier and on top of that will use clibrated classifier to get results in probabilities(bcoz of log loss as well)

```
# LR with class balancing + one hot

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='l2', loss='log', random_state=42)
    #balanced, l2, loss is log, using sgd
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")     #using calibrated
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

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


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

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

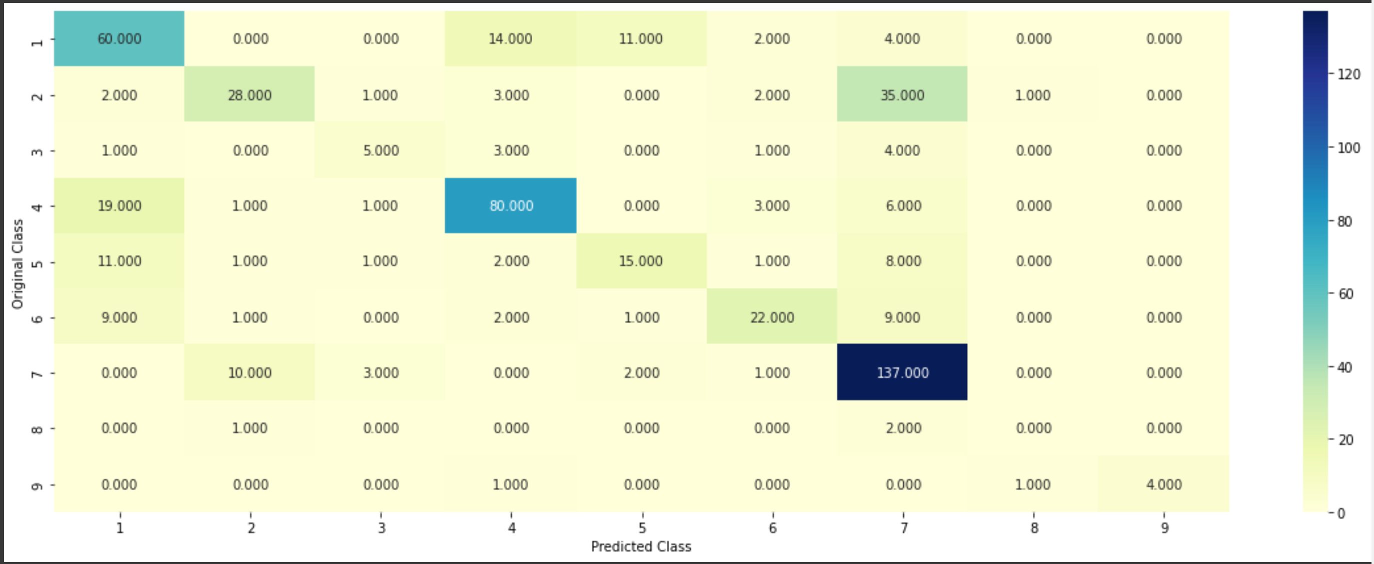
```
for alpha = 1e-06
Log Loss : 1.3417861986674617
for alpha = 1e-05
Log Loss : 1.3088095931795636
for alpha = 0.0001
Log Loss : 1.150017783616169
for alpha = 0.001
Log Loss : 1.125595940181861
for alpha = 0.01
Log Loss : 1.1960059857816896
for alpha = 0.1
Log Loss : 1.491864806636216
for alpha = 1
Log Loss : 1.6955358408516246
for alpha = 10
Log Loss : 1.7205539395989482
for alpha = 100
Log Loss : 1.723183811484437
```



```
For values of best alpha =  0.001 The train log loss is: 0.5299347835832008
For values of best alpha =  0.001 The cross validation log loss is: 1.125595940181861
For values of best alpha =  0.001 The test log loss is: 1.0227420906357843
```

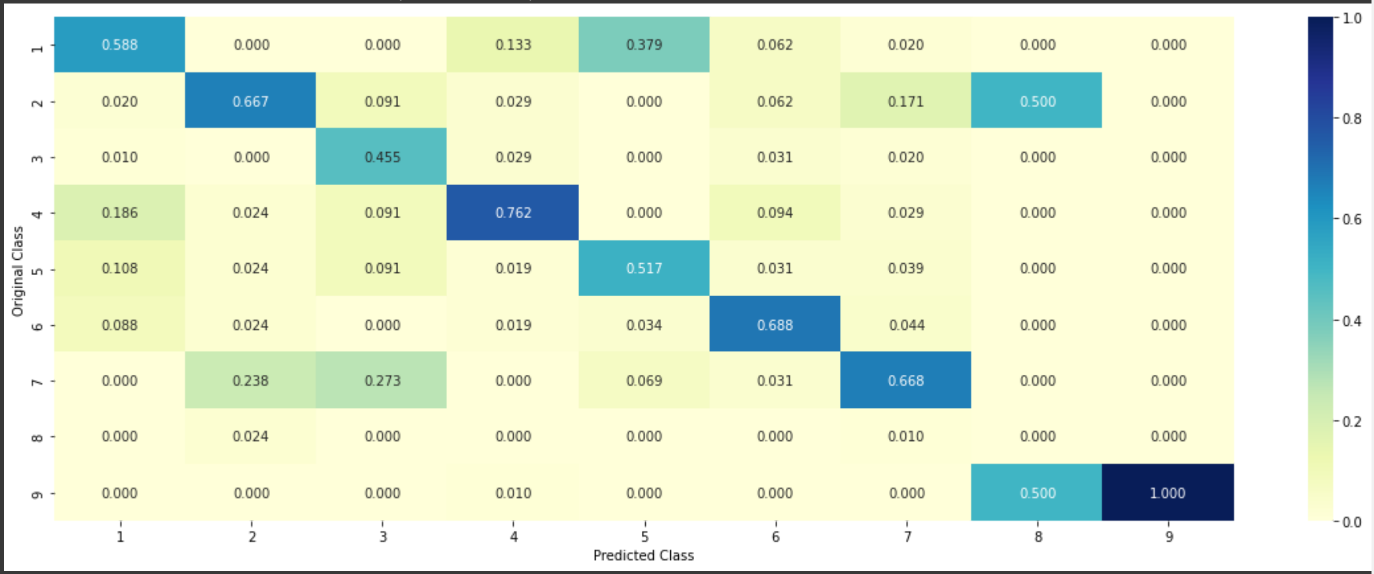
```
#Testing the model with best hyper paramters

clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, clf)
```

```
Log loss : 1.125595940181861
Number of mis-classified points : 0.34022556390977443
-------------------- Confusion matrix --------------------
```



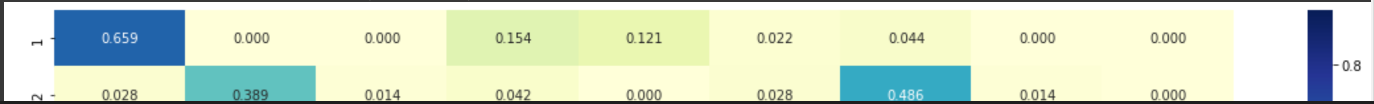
	1	2	3	4	5	6	7	8	9
1	60.000	0.000	0.000	14.000	11.000	2.000	4.000	0.000	0.000
2	2.000	28.000	1.000	3.000	0.000	2.000	35.000	1.000	0.000
3	1.000	0.000	5.000	3.000	0.000	1.000	4.000	0.000	0.000
4	19.000	1.000	1.000	80.000	0.000	3.000	6.000	0.000	0.000
5	11.000	1.000	1.000	2.000	15.000	1.000	8.000	0.000	0.000
6	9.000	1.000	0.000	2.000	1.000	22.000	9.000	0.000	0.000
7	0.000	10.000	3.000	0.000	2.000	1.000	137.000	0.000	0.000
8	0.000	1.000	0.000	0.000	0.000	0.000	2.000	0.000	0.000
9	0.000	0.000	0.000	1.000	0.000	0.000	0.000	1.000	4.000

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



	1	2	3	4	5	6	7	8	9
1	0.588	0.000	0.000	0.133	0.379	0.062	0.020	0.000	0.000
2	0.020	0.667	0.091	0.029	0.000	0.062	0.171	0.500	0.000
3	0.010	0.000	0.455	0.029	0.000	0.031	0.020	0.000	0.000
4	0.186	0.024	0.091	0.762	0.000	0.094	0.029	0.000	0.000
5	0.108	0.024	0.091	0.019	0.517	0.031	0.039	0.000	0.000
6	0.088	0.024	0.000	0.019	0.034	0.688	0.044	0.000	0.000
7	0.000	0.238	0.273	0.000	0.069	0.031	0.668	0.000	0.000
8	0.000	0.024	0.000	0.000	0.000	0.000	0.010	0.000	0.000
9	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.500	1.000

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



1	0.659	0.000	0.000	0.154	0.121	0.022	0.044	0.000	0.000
2	0.028	0.389	0.014	0.042	0.000	0.028	0.486	0.014	0.000

```
#Feature importance

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]:
            tabulte_list.append([incresingorder_ind, "Gene", "Yes"])
        elif i< 18:
            tabulte_list.append([incresingorder_ind,"Variation", "Yes"])
        if ((i > 17) & (i not in removed_ind)) :
            word = train_text_features[i]
            yes_no = True if word in text.split() else False
            if yes_no:
                word_present += 1
            tabulte_list.append([incresingorder_ind,train_text_features[i], yes_no])
        incresingorder_ind += 1
    print(word_present, "most importent features are present in our query point")
    print("-"*50)
    print("The features that are most importent of the ",predicted_cls[0]," class:")
    print (tabulate(tabulte_list, headers=["Index",'Feature name', 'Present or Not']))
```

```
# 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):
            word = gene_vec.get_feature_names()[v]
            yes_no = True if word == gene else False
            if yes_no:
                word_present += 1
                print(i, "Gene feature [{}] present in test data point [{}]".format(word,yes_no))
        elif (v < fea1_len+fea2_len):
            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 [{}]".format(word,yes_no))

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

```
#Correctly Classified point

# from tabulate import tabulate
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', 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(-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
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0283 0.4293 0.0058 0.024  0.0138 0.016  0.4721 0.0066 0.0041]]
Actual Class : 2
--------------------------------------------------
222 Text feature [loss] present in test data point [True]
345 Text feature [transform] present in test data point [True]
431 Text feature [receptor] present in test data point [True]
472 Text feature [specimen] present in test data point [True]
Out of the top  500  features  4 are present in query point
```

```
# In correctly classify

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_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
```

```
Predicted Class : 5
Predicted Class Probabilities: [[4.710e-02 1.214e-01 1.300e-03 1.700e-02 6.070e-01 2.400e-03 1.959e-01
  7.200e-03 6.000e-04]]
Actual Class : 5
--------------------------------------------------
Out of the top  500  features  0 are present in query point
```

LR without class balancing

```
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='l2', loss='log', random_state=42)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

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

best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

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

```
for alpha = 1e-06
Log Loss : 1.2958579172658222
for alpha = 1e-05
Log Loss : 1.2782485027184536
for alpha = 0.0001
```

```
#Testing model with best hyper parameters

clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, clf)
```

```
#Feature Importance, Correctly Classified point

clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', 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(-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
```

```
Predicted Class : 2
Predicted Class Probabilities: [[0.0294 0.4593 0.0059 0.0246 0.0142 0.0156 0.4416 0.0065 0.0029]]
Actual Class : 2
--------------------------------------------------
Out of the top  500  features  0 are present in query point
```

```
#Incorrectly Classified point

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_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
```

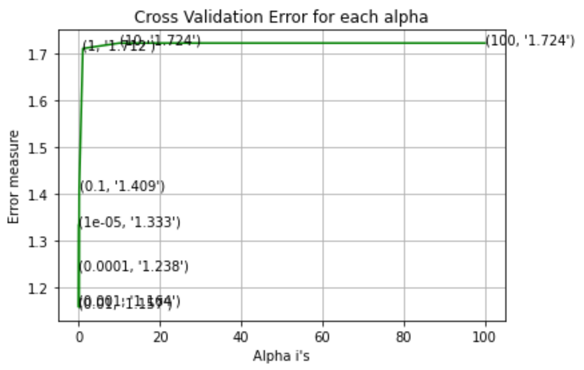
```
Predicted Class : 5
Predicted Class Probabilities: [[0.0518 0.1318 0.0011 0.0151 0.5301 0.0022 0.2609 0.0062 0.0008]]
Actual Class : 5
--------------------------------------------------
428 Text feature [encodes] present in test data point [True]
438 Text feature [identified] present in test data point [True]
Out of the top  500  features  2 are present in query point
```

Linear Support Vector Machines (Linear SVM)

```
#class balancing + one hot + balancing

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='l2', loss='hinge', random_state=42) # sgd, balanced, l2, loss is hinge
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")   #using calibrated
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

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


best_alpha = np.argmin(cv_log_error_array)
# clf = SVC(C=i,kernel='linear',probability=True, class_weight='balanced')
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='hinge', random_state=42)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
```

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

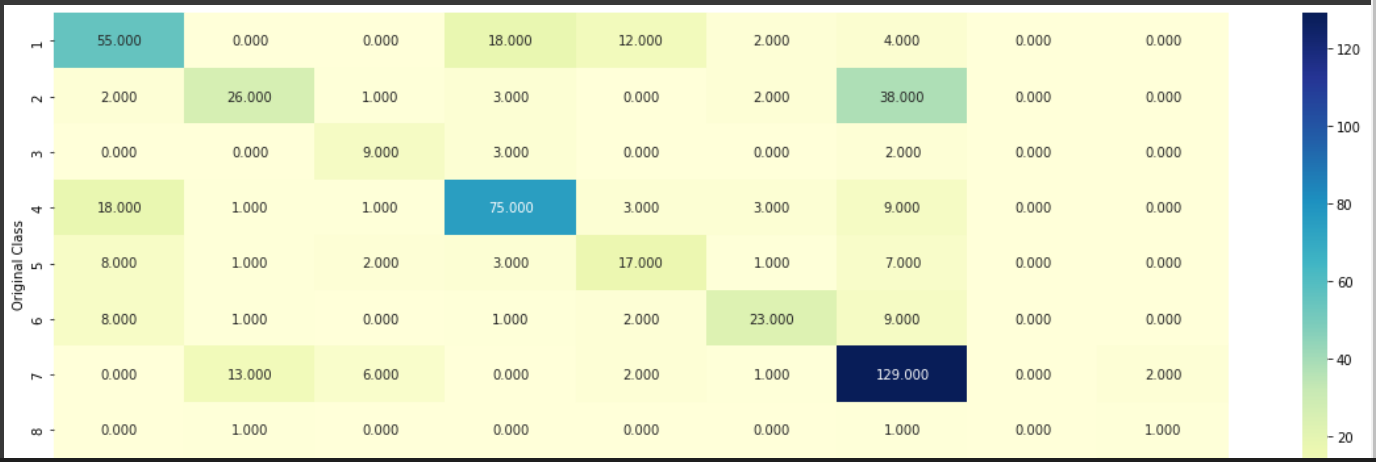
```
for C = 1e-05
Log Loss : 1.333471772271453
for C = 0.0001
Log Loss : 1.2375711605977042
for C = 0.001
Log Loss : 1.1639996923279505
for C = 0.01
Log Loss : 1.1572054630493918
for C = 0.1
Log Loss : 1.4089374758495252
for C = 1
Log Loss : 1.7120252875295436
for C = 10
Log Loss : 1.723619466558825
for C = 100
Log Loss : 1.7236216895626009
```



```
For values of best alpha =  0.01 The train log loss is: 0.7457370499744578
For values of best alpha =  0.01 The cross validation log loss is: 1.1572054630493918
For values of best alpha =  0.01 The test log loss is: 1.1231553127906733
```

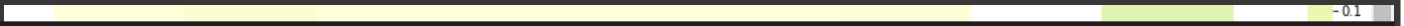
```
#Testing model with best hyper parameters

clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge', random_state=42,class_weight='balanced')
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf)
```

```
Log loss : 1.1572054630493918
Number of mis-classified points : 0.36278195488721804
-------------------- Confusion matrix --------------------
```



```
#Correctly classify

clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge', random_state=42)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
# test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-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
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0822 0.2712 0.0112 0.0656 0.0305 0.0348 0.4929 0.0071 0.0046]]
Actual Class : 2
--------------------------------------------------
314 Text feature [transform] present in test data point [True]
386 Text feature [activation] present in test data point [True]
Out of the top  500  features  2 are present in query point
```



```
#In-correctly classify

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_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
```

```
Predicted Class : 5
Predicted Class Probabilities: [[0.1353 0.0872 0.0217 0.1065 0.3935 0.0548 0.1784 0.0194 0.0032]]
Actual Class : 5
--------------------------------------------------
469 Text feature [segregated] present in test data point [True]
Out of the top  500  features  1 are present in query point
```

Random Forest Classifier , a powerful variation of decision tree.

Although DT is not good for high dimensions but RF is power ful so we will try with one hot.

RF with Response coding is useless bcoz it got overfit (train and cv,test result has much differnece)

```
#RF + one hot
alpha = [100,200,500,1000,2000]
max_depth = [5, 10]
cv_log_error_array = []
for i in alpha:
    for j in max_depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gini', max_depth=j, random_state=42, n_jobs=-1)
        clf.fit(train_x_onehotCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_onehotCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))

'''fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
ax.plot(features, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[int(i/2)],max_depth[int(i%2)],str(txt)), (features[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
'''

best_alpha = np.argmin(cv_log_error_array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max_depth[int(best_alpha%2)], random_state=42
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_,
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.c
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss is:",log_loss(y_test, predict_y, labels=clf.classes_, e
```

Taking more than 16 mins, so I'm dropping it.

```
#with best hyper para

clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max_depth[int(best_alpha%2)],
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf)
```

```
#Correctly classify

# 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
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

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

```
#In correctly classify

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

```
# RF With Response Coding

alpha = [10,50,100,200,500,1000]
```

```
max_depth = [2,3,5,10]
cv_log_error_array = []
for i in alpha:
    for j in max_depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gini', max_depth=j, random_state=42, n_jobs=-1)
        clf.fit(train_x_responseCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_responseCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))
'''
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
ax.plot(features, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[int(i/4)],max_depth[int(i%4)],str(txt)), (features[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
'''

best_alpha = np.argmin(cv_log_error_array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gini', max_depth=max_depth[int(best_alpha%4)], random_state=42
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
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The cross validation log loss is:",log_loss(y_cv, predict_y, labels=clf.class
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The test log loss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1
```

I'm dropping RF with respone coding bcoz it got overfit

Stacking (combining the models), suffer interpretability

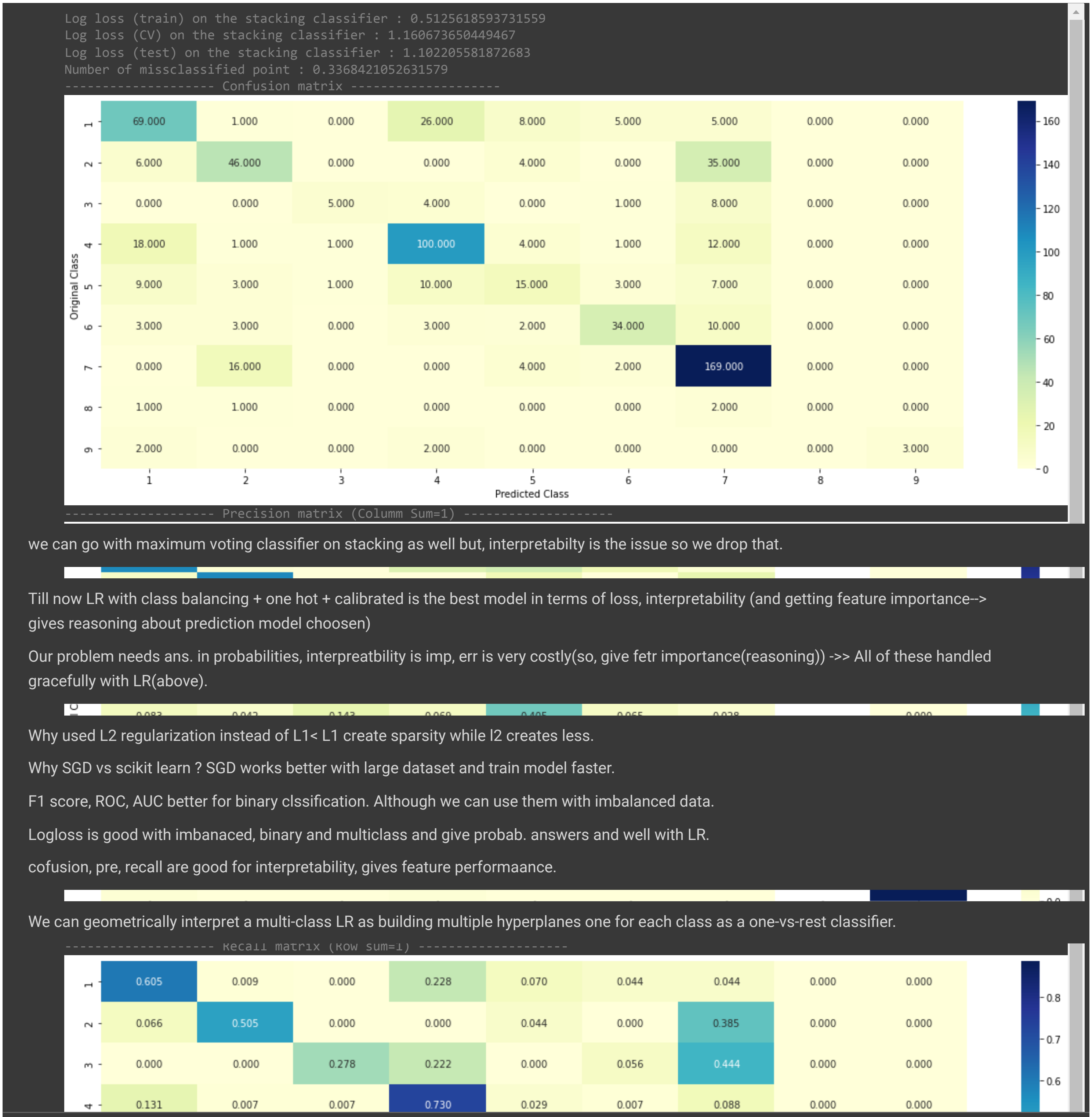
```
#stacking= merging (combine models to perform better)
# Stacking with stacking classifier
# LR + lr svm + NB with one hot encoding + balancing


clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class_weight='balanced', random_state=0)
clf1.fit(train_x_onehotCoding, train_y)
sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")

clf2 = SGDClassifier(alpha=1, penalty='l2', loss='hinge', class_weight='balanced', random_state=0)
clf2.fit(train_x_onehotCoding, train_y)
sig_clf2 = CalibratedClassifierCV(clf2, method="sigmoid")


clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train_x_onehotCoding, train_y)
sig_clf3 = CalibratedClassifierCV(clf3, method="sigmoid")

sig_clf1.fit(train_x_onehotCoding, train_y)
print("Logistic Regression :  Log Loss: %0.2f" % (log_loss(cv_y, sig_clf1.predict_proba(cv_x_onehotCoding))))
sig_clf2.fit(train_x_onehotCoding, train_y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf2.predict_proba(cv_x_onehotCoding))))
sig_clf3.fit(train_x_onehotCoding, train_y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba(cv_x_onehotCoding))))
print("-"*50)
alpha = [0.0001,0.001,0.01,0.1,1,10]
best_alpha = 999
for i in alpha:
    lr = LogisticRegression(C=i)
    sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=lr, use_probas=True)
    sclf.fit(train_x_onehotCoding, train_y)
    print("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" % (i, log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))))
    log_error =log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    if best_alpha > log_error:
        best_alpha = log_error
```

```
Logistic Regression :  Log Loss: 1.13
Support vector machines : Log Loss: 1.71
Naive Bayes : Log Loss: 1.30
--------------------------------------------------
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 1.819
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 1.725
Stacking Classifer : for the value of alpha: 0.010000 Log Loss: 1.331
Stacking Classifer : for the value of alpha: 0.100000 Log Loss: 1.161
Stacking Classifer : for the value of alpha: 1.000000 Log Loss: 1.417
Stacking Classifer : for the value of alpha: 10.000000 Log Loss: 1.788
```

NB log loss is 1.20

NB works well with text data. Although, here, LR is the best so far.

```
#with best hyper

lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=lr, use_probas=True)
sclf.fit(train_x_onehotCoding, train_y)

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

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

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

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



```
Log loss (train) on the stacking classifier : 0.5125618593731559
Log loss (CV) on the stacking classifier : 1.160673650449467
Log loss (test) on the stacking classifier : 1.102205581872683
Number of missclassified point : 0.3368421052631579
-------------------- Confusion matrix --------------------
```

Original Class \ Predicted Class	1	2	3	4	5	6	7	8	9
1	69.000	1.000	0.000	26.000	8.000	5.000	5.000	0.000	0.000
2	6.000	46.000	0.000	0.000	4.000	0.000	35.000	0.000	0.000
3	0.000	0.000	5.000	4.000	0.000	1.000	8.000	0.000	0.000
4	18.000	1.000	1.000	100.000	4.000	1.000	12.000	0.000	0.000
5	9.000	3.000	1.000	10.000	15.000	3.000	7.000	0.000	0.000
6	3.000	3.000	0.000	3.000	2.000	34.000	10.000	0.000	0.000
7	0.000	16.000	0.000	0.000	4.000	2.000	169.000	0.000	0.000
8	1.000	1.000	0.000	0.000	0.000	0.000	2.000	0.000	0.000
9	2.000	0.000	0.000	2.000	0.000	0.000	0.000	0.000	3.000

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

we can go with maximum voting classifier on stacking as well but, interpretabilty is the issue so we drop that.

Till now LR with class balancing + one hot + calibrated is the best model in terms of loss, interpretability (and getting feature importance--> gives reasoning about prediction model choosen)

Our problem needs ans. in probabilities, interpreatbility is imp, err is very costly(so, give fetr importance(reasoning)) ->> All of these handled gracefully with LR(above).

Why used L2 regularization instead of L1< L1 create sparsity while l2 creates less.

Why SGD vs scikit learn ? SGD works better with large dataset and train model faster.

F1 score, ROC, AUC better for binary clssification. Although we can use them with imbalanced data.

Logloss is good with imbanaced, binary and multiclass and give probab. answers and well with LR.

cofusion, pre, recall are good for interpretability, gives feature performaance.

We can geometrically interpret a multi-class LR as building multiple hyperplanes one for each class as a one-vs-rest classifier.

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

1	0.605	0.009	0.000	0.228	0.070	0.044	0.044	0.000	0.000
2	0.066	0.505	0.000	0.000	0.044	0.000	0.385	0.000	0.000
3	0.000	0.000	0.278	0.222	0.000	0.056	0.444	0.000	0.000
4	0.131	0.007	0.007	0.730	0.029	0.007	0.088	0.000	0.000