PCD_BOW_ngram_LR

July 21, 2020

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

1. 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
3. https://www.youtube.com/watch?v=qxXRKVompI8

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:

```
<li>
training_variants (ID , Gene, Variations, Class)
</li>
<li>
training_text (ID, Text)
</li>
```

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 cla
```

2.2.2. Performance Metric
Source: 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

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

```
Go to this URL in a browser: https://accounts.google.com/o/oauth2/auth?client_id
=947318989803-6bn6qk8qdgf4n4g3pfee6491hc0brc4i.apps.googleusercontent.com&redire
ct_uri=urn%3aietf%3awg%3aoauth%3a2.0%3aoob&response_type=code&scope=email%20http
s%3a%2f%2fwww.googleapis.com%2fauth%2fdocs.test%20https%3a%2f%2fwww.googleapis.c
om%2fauth%2fdrive%20https%3a%2f%2fwww.googleapis.com%2fauth%2fdrive.photos.reado
nly%20https%3a%2f%2fwww.googleapis.com%2fauth%2fpeopleapi.readonly

Enter your authorization code:
ůůůůůůůůůů
Mounted at /content/drive
```

[ ]:
```
import os
os.chdir("/content/drive/My Drive/PCD")
!ls -l
```

```
total 207220
-rw------- 1 root root 212125752 Jun 20  2018 training_text
-rw------- 1 root root     66688 Jun 23  2017 training_variants
```

3. Exploratory Data Analysis

[ ]:
```
import pandas as pd
import matplotlib.pyplot as plt
import re
import time
import nltk
nltk.download("stopwords")
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
```

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

3.1. Reading Data

3.1.1. Reading Gene and Variation 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)
data.head()
```

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

[ ]:

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

training/training_variants is a comma separated file containing the description of the genetic
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

[ ]:
```
# note the seprator in this file
data_text =pd.
 ↪read_csv("training_text",sep="\|\|",engine="python",names=["ID","TEXT"],skiprows=1)
print('Number of data points : ', data_text.shape[0])
print('Number of features : ', data_text.shape[1])
print('Features : ', data_text.columns.values)
data_text.head()
```

Number of data points : 3321
Number of features : 2
Features : ['ID' 'TEXT']

[ ]:

	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

[ ]:
```
# 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.
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 : 28.683154000000002 seconds
```

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

[ ]:

	ID	Gene	...	Class	TEXT
0	0	FAM58A	...	1	cyclin dependent kinases cdks regulate variety...
1	1	CBL	...	2	abstract background non small cell lung cancer...
2	2	CBL	...	2	abstract background non small cell lung cancer...
3	3	CBL	...	3	recent evidence demonstrated acquired uniparen...
4	4	CBL	...	4	oncogenic mutations monomeric casitas b lineag...

[5 rows x 5 columns]

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

[ ]:

	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

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

[ ]:
```
result[result['ID']==1109]
```

[ ]:
```
        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)

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

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

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

[ ]:
```
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

[ ]:
```
# it returns a dict, keys as class labels and values as the number of data␣
↪points in that class
train_class_distribution = train_df['Class'].value_counts().sortlevel()
test_class_distribution = test_df['Class'].value_counts().sortlevel()
cv_class_distribution = cv_df['Class'].value_counts().sortlevel()

my_colors = '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]/train_df.
 ↪shape[0]*100), 3), '%)')

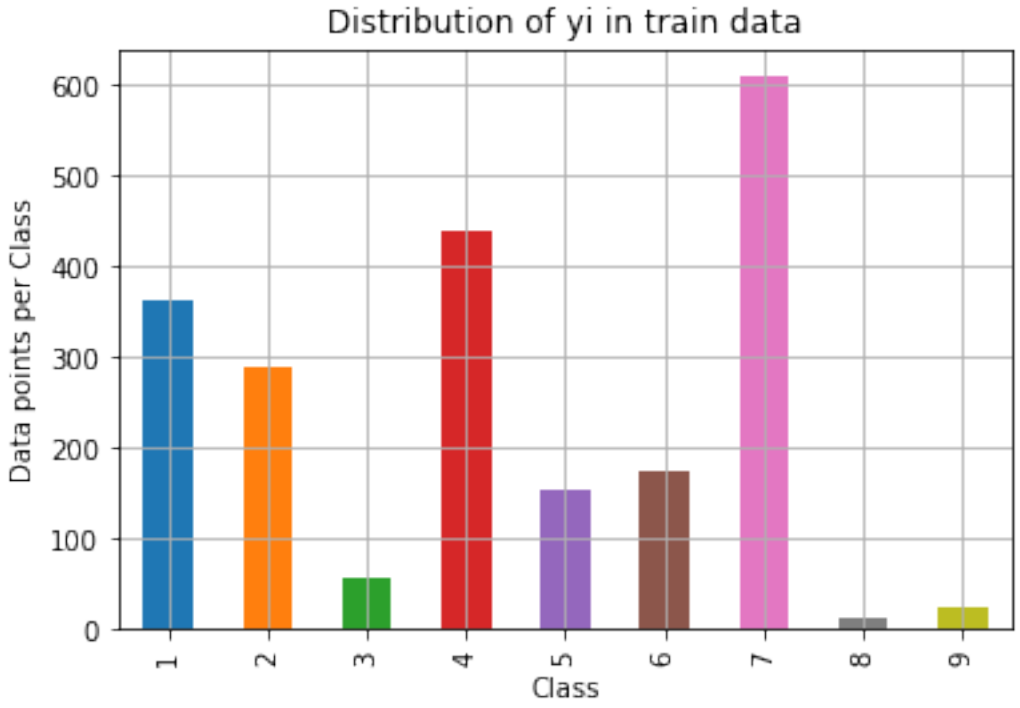

print('-'*80)
my_colors = 'rgbkymc'
test_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in test data')
plt.grid()
plt.show()

# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.
 ↪argsort.html
# -(train_class_distribution.values): the minus sign will give us in decreasing␣
 ↪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.
 ↪values[i], '(', np.round((test_class_distribution.values[i]/test_df.
 ↪shape[0]*100), 3), '%)')

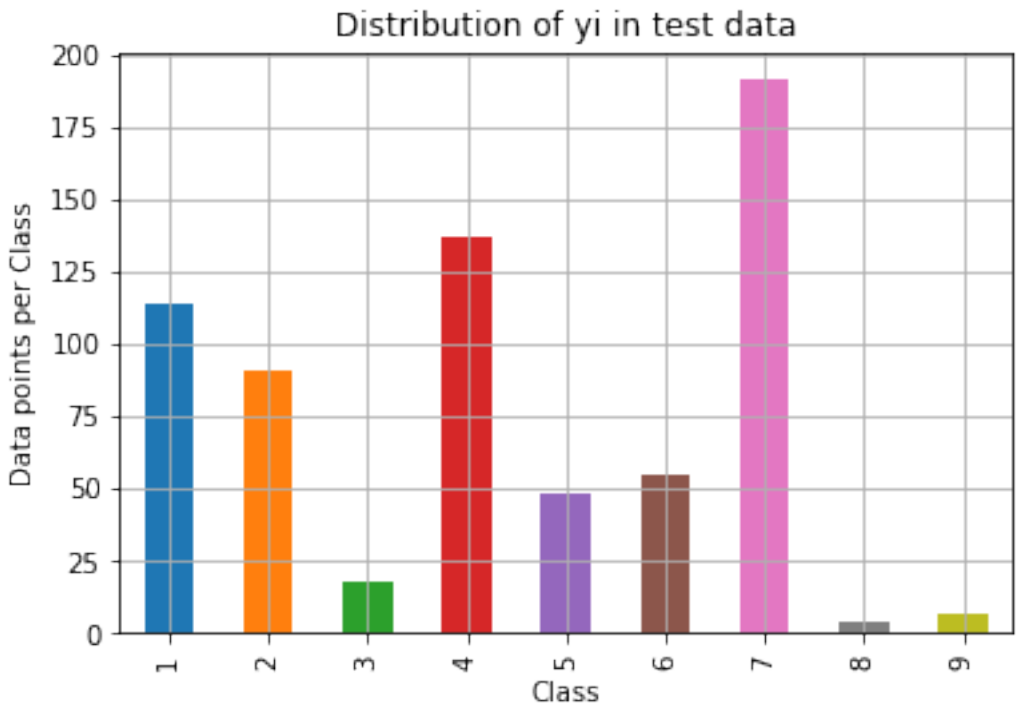
print('-'*80)
my_colors = 'rgbkymc'
cv_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in cross validation data')
plt.grid()
plt.show()

# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.
 ↪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:
```

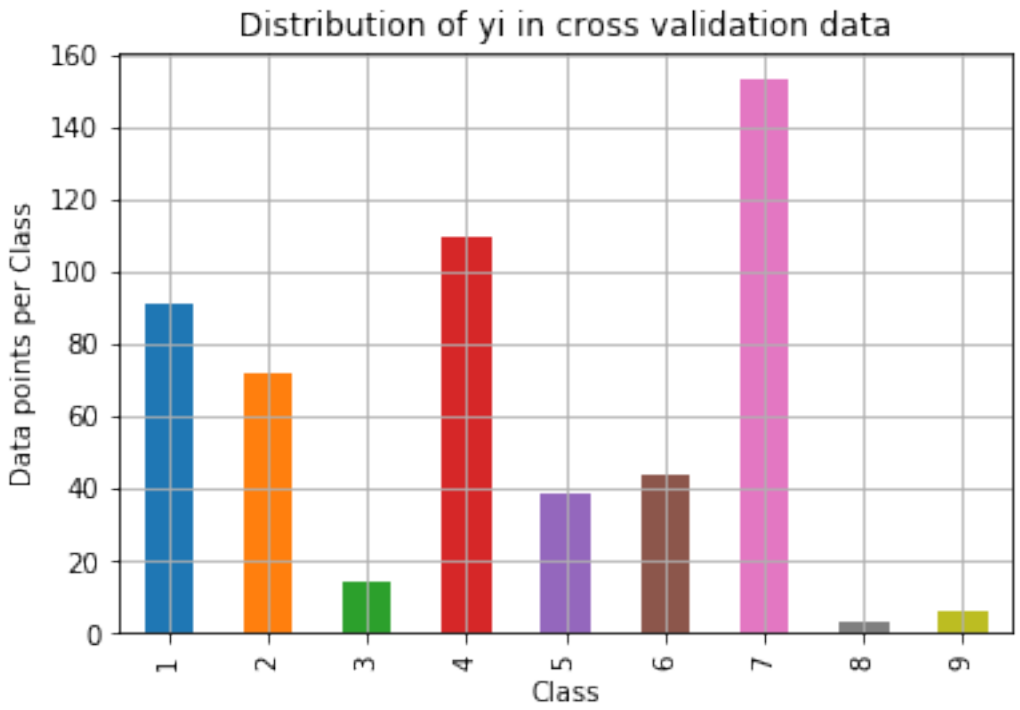
```
    print('Number of data points in class', i+1, ':',cv_class_distribution.
↪values[i], '(', np.round((cv_class_distribution.values[i]/cv_df.
↪shape[0]*100), 3), '%)')
```




```
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.

[ ]:
```
# This function plots the confusion matrices given y_i, y_i_hat.
def plot_confusion_matrix(test_y, predict_y):
    C = confusion_matrix(test_y, predict_y)
    # C = 9,9 matrix, each cell (i,j) represents number of points of class i␣
 ↪are predicted class j

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

    # C = [[1, 2],
```

```
    #     [3, 4]]
    # C.T = [[1, 3],
    #        [2, 4]]
    # C.sum(axis = 1)  axis=0 corresonds to columns and axis=1 corresponds to rows in two diamensional array
    # C.sum(axix =1) = [[3, 7]]
    # ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
    #                            [2/3, 4/7]]

    # ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]
    #                              [3/7, 4/7]]
    # sum of row elements = 1

    B =(C/C.sum(axis=0))
    #divid each element of the confusion matrix with the sum of elements in that row
    # C = [[1, 2],
    #     [3, 4]]
    # C.sum(axis = 0)  axis=0 corresonds to columns and axis=1 corresponds to rows in two diamensional array
    # C.sum(axix =0) = [[4, 6]]
    # (C/C.sum(axis=0)) = [[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, 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()
```

[ ]:
```
# 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]

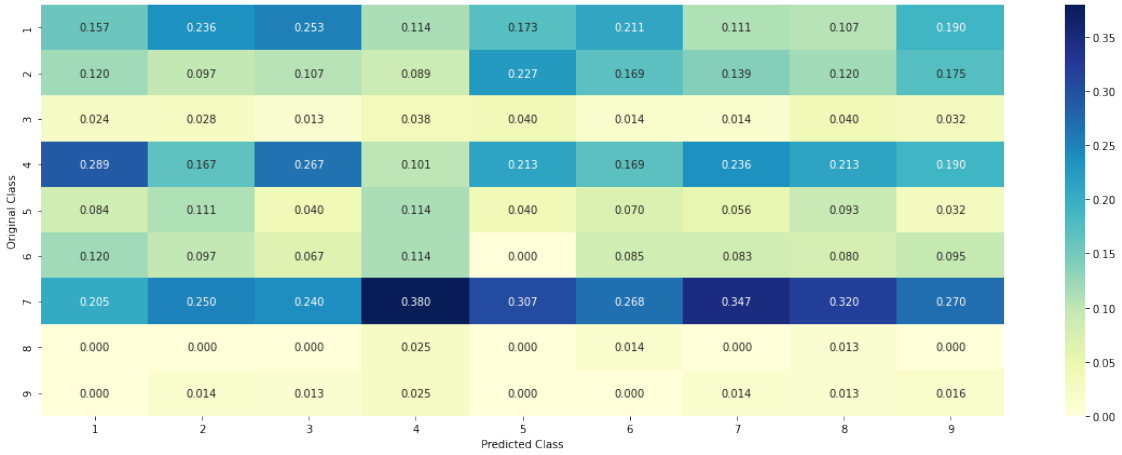
# we create a output array that has exactly same size as the CV data
cv_predicted_y = np.zeros((cv_data_len,9))
for i in range(cv_data_len):
    rand_probs = np.random.rand(1,9)
    cv_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Cross Validation Data using Random␣
 ↪Model",log_loss(y_cv,cv_predicted_y, 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_predicted_y, eps=1e-15))

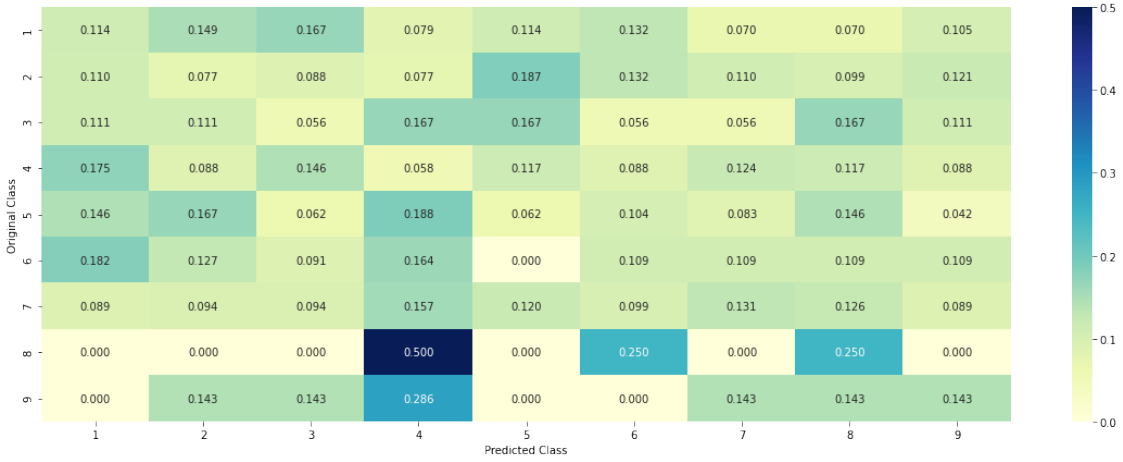
predicted_y =np.argmax(test_predicted_y, axis=1)
plot_confusion_matrix(y_test, predicted_y+1)
```

```
Log loss on Cross Validation Data using Random Model 2.5088038472695926
Log loss on Test Data using Random Model 2.487897745132674
-------------------- Confusion matrix --------------------
```

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



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



3.3 Univariate Analysis

[ ]:
```
# code for response coding with Laplace smoothing.
# alpha : used for laplace smoothing
# feature: ['gene', 'variation']
# df: ['train_df', 'test_df', 'cv_df']
# algorithm
# ----------
# Consider all unique values and the number of occurances of given feature in␣
 ↪train data dataframe
# build a vector (1*9) , the first element = (number of times it occured in␣
 ↪class1 + 10*alpha / number of time it occurred in total data+90*alpha)
# gv_dict is like a look up table, for every gene it store a (1*9)␣
 ↪representation of it
# for a value of feature in df:
# if it is in train data:
# we add the vector that was stored in 'gv_dict' look up table to 'gv_fea'
# if it is not there is train:
# we add [1/9, 1/9, 1/9, 1/9,1/9, 1/9, 1/9, 1/9, 1/9] to 'gv_fea'
# return 'gv_fea'
# ----------------------

# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
    # value_count: it contains a dict like
    # print(train_df['Gene'].value_counts())
    # output:
    #        {BRCA1      174
    #         TP53       106
    #         EGFR        86
    #         BRCA2       75
    #         PTEN        69
```

```
    #         KIT         61
    #         BRAF        60
    #         ERBB2       47
    #         PDGFRA      46
    #         ...}
    # print(train_df['Variation'].value_counts())
    # output:
    # {
    # Truncating_Mutations                     63
    # Deletion                                 43
    # Amplification                            43
    # Fusions                                  22
    # Overexpression                            3
    # E17K                                      3
    # Q61L                                      3
    # S222D                                     2
    # P130S                                     2
    # ...
    # }
    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):
    # print(gv_dict)
    #     {'BRCA1': [0.200757575757575, 0.037878787878788, 0.
↪068181818181818177, 0.13636363636363635, 0.25, 0.1931818181818181, 0.
↪037878787878788, 0.037878787878788, 0.037878787878788],
    #      'TP53': [0.32142857142857145, 0.061224489795918366, 0.
↪061224489795918366, 0.27040816326530615, 0.061224489795918366, 0.
↪066326530612244902, 0.051020408163265307, 0.051020408163265307, 0.
↪056122448979591837],
    #      'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.
↪068181818181818177, 0.068181818181818177, 0.0625, 0.34659090909090912, 0.
↪0625, 0.056818181818181816],
    #      'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.
↪060606060606060608, 0.078787878787878782, 0.1393939393939394, 0.
↪34545454545454546, 0.060606060606060608, 0.060606060606060608, 0.
↪060606060606060608],
    #      'PTEN': [0.069182389937106917, 0.062893081761006289, 0.
↪069182389937106917, 0.46540880503144655, 0.07547169811320754, 0.
↪062893081761006289, 0.069182389937106917, 0.062893081761006289, 0.
↪062893081761006289],
    #      'KIT': [0.066225165562913912, 0.25165562913907286, 0.
↪072847682119205295, 0.072847682119205295, 0.066225165562913912, 0.
↪066225165562913912, 0.27152317880794702, 0.066225165562913912, 0.
↪066225165562913912],
    #      'BRAF': [0.066666666666666666, 0.17999999999999999, 0.
↪073333333333333334, 0.073333333333333334, 0.093333333333333338, 0.
↪080000000000000002, 0.29999999999999999, 0.066666666666666666, 0.
↪066666666666666666],
    #      ...
    #     }
    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)

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?

[ ]:
```
unique_genes = train_df['Gene'].value_counts()
print('Number of Unique Genes :', unique_genes.shape[0])
# the top 10 genes that occured most
print(unique_genes.head(10))
```

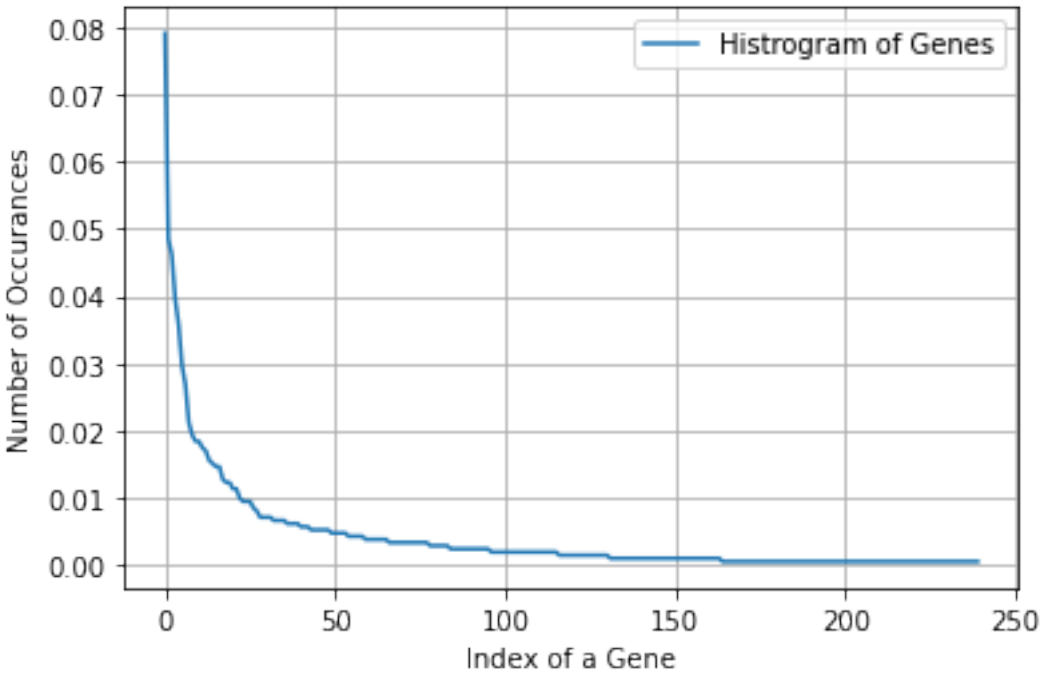
```
Number of Unique Genes : 240
BRCA1     168
TP53      103
EGFR       98
BRCA2      84
PTEN       76
BRAF       63
KIT        57
ALK        45
PIK3CA     41
ERBB2      39
Name: Gene, dtype: int64
```

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

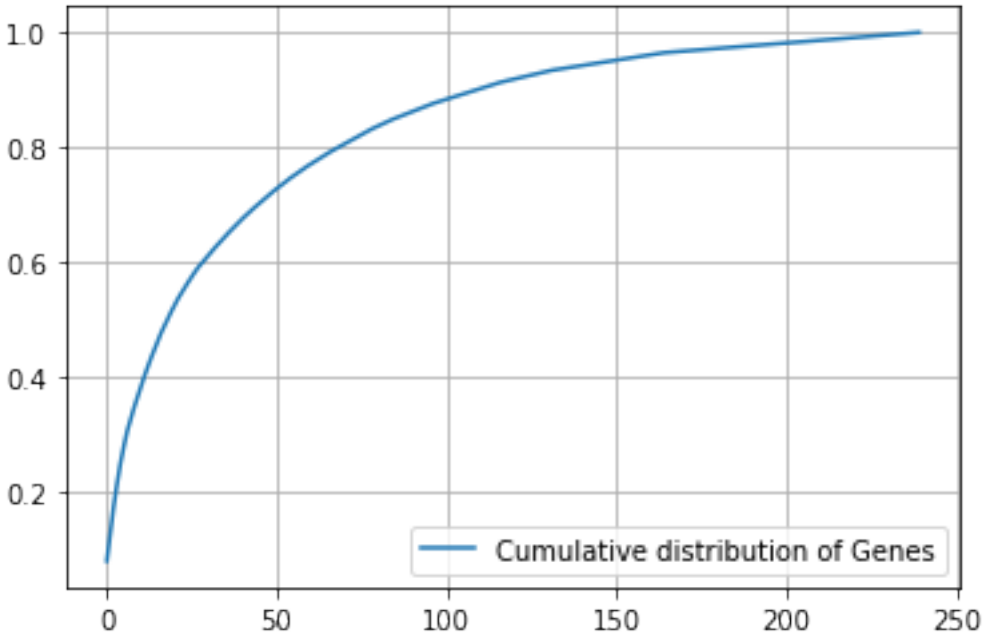
```
Ans: There are 240 different categories of genes in the train data, and they are
distibuted as follows
```

[ ]:
```
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()
```



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



Q3. How to featurize this Gene feature ?

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

One hot Encoding

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.

[ ]:
```
#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))
```

[ ]:
```
print("train_gene_feature_responseCoding is converted feature using respone␣
 ↪coding method. The shape of gene feature:",␣
 ↪train_gene_feature_responseCoding.shape)
```

```
train_gene_feature_responseCoding is converted feature using respone coding
method. The shape of gene feature: (2124, 9)
```

[ ]:
```
# one-hot encoding of Gene feature.
gene_vectorizer = CountVectorizer(ngram_range=(1,3))
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_df['Gene'].head()
```

[ ]:
```
2537    BRCA1
2449    BRCA1
2846    BRCA2
1755     IDH1
991      TSC1
Name: Gene, dtype: object
```

[ ]:
```
gene_vectorizer.get_feature_names()
```

[ ]:
```
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
 'akt3',
 'alk',
 'apc',
 'ar',
 'araf',
 'arid1b',
 'arid2',
 'arid5b',
 'asxl1',
 'asxl2',
 'atm',
 'atrx',
 'aurkb',
 'axin1',
 'axl',
 'b2m',
 'bap1',
 'bard1',
 'bcl10',
 'bcl2',
 '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',
'cebpa',
'chek2',
'cic',
'crebbp',
'ctcf',
'ctla4',
'ctnnb1',
'ddr2',
'dicer1',
'dnmt3a',
'dnmt3b',
'egfr',
'elf3',
'ep300',
'epas1',
'epcam',
'erbb2',
'erbb3',
'erbb4',
'ercc2',
'ercc4',
'erg',
'errfi1',
'esr1',
'etv1',
'etv6',
'ewsr1',
'ezh2',
```

```
'fam58a',
'fanca',
'fat1',
'fbxw7',
'fgf19',
'fgf3',
'fgfr1',
'fgfr2',
'fgfr3',
'fgfr4',
'flt1',
'flt3',
'foxa1',
'foxl2',
'foxp1',
'fubp1',
'gata3',
'gli1',
'gna11',
'gnaq',
'gnas',
'h3f3a',
'hist1h1c',
'hla',
'hnf1a',
'hras',
'idh1',
'idh2',
'igf1r',
'ikzf1',
'il7r',
'jak1',
'jak2',
'jun',
'kdm5a',
'kdm5c',
'kdm6a',
'kdr',
'keap1',
'kit',
'klf4',
'kmt2a',
'kmt2b',
'kmt2c',
'kmt2d',
'knstrn',
'kras',
```

```
'lats2',
'map2k1',
'map2k2',
'map2k4',
'map3k1',
'mapk1',
'mdm2',
'med12',
'mef2b',
'men1',
'met',
'mlh1',
'mpl',
'msh2',
'msh6',
'mtor',
'myc',
'mycn',
'myd88',
'myod1',
'ncor1',
'nf1',
'nf2',
'nfe2l2',
'nfkbia',
'nkx2',
'notch1',
'notch2',
'npm1',
'nras',
'nsd1',
'ntrk1',
'ntrk2',
'ntrk3',
'nup93',
'pax8',
'pbrm1',
'pdgfra',
'pdgfrb',
'pik3ca',
'pik3cb',
'pik3cd',
'pik3r1',
'pik3r2',
'pim1',
'pms2',
'pole',
```

```
'ppm1d',
'ppp2r1a',
'ppp6c',
'prdm1',
'pten',
'ptpn11',
'ptprd',
'ptprt',
'rab35',
'rac1',
'rad21',
'rad50',
'rad51b',
'rad51c',
'rad54l',
'raf1',
'rara',
'rasa1',
'rb1',
'rbm10',
'ret',
'rheb',
'rhoa',
'rictor',
'rit1',
'rnf43',
'ros1',
'runx1',
'rxra',
'rybp',
'setd2',
'sf3b1',
'shq1',
'smad2',
'smad3',
'smad4',
'smarca4',
'smarcb1',
'smo',
'sos1',
'sox9',
'spop',
'src',
'srsf2',
'stag2',
'stat3',
'stk11',
```

```
 'tcf3',
 'tcf7l2',
 'tert',
 'tet1',
 'tet2',
 'tgfbr1',
 'tgfbr2',
 'tmprss2',
 'tp53',
 'tp53bp1',
 'tsc1',
 'tsc2',
 'u2af1',
 'vegfa',
 'vhl',
 'whsc1',
 'whsc1l1',
 'xpo1',
 'xrcc2',
 'yap1']
```

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

```
train_gene_feature_onehotCoding is converted feature using one-hot encoding
method. The shape of gene feature: (2124, 239)
```

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.

[ ]:
```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/
 ↪generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15,␣
 ↪fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,␣
 ↪learning_rate=optimal, eta0=0.0, power_t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with␣
 ↪Stochastic Gradient Descent.
```

```
# predict(X)        Predict class labels for samples in X.

#------------------------------
# video link:
#------------------------------

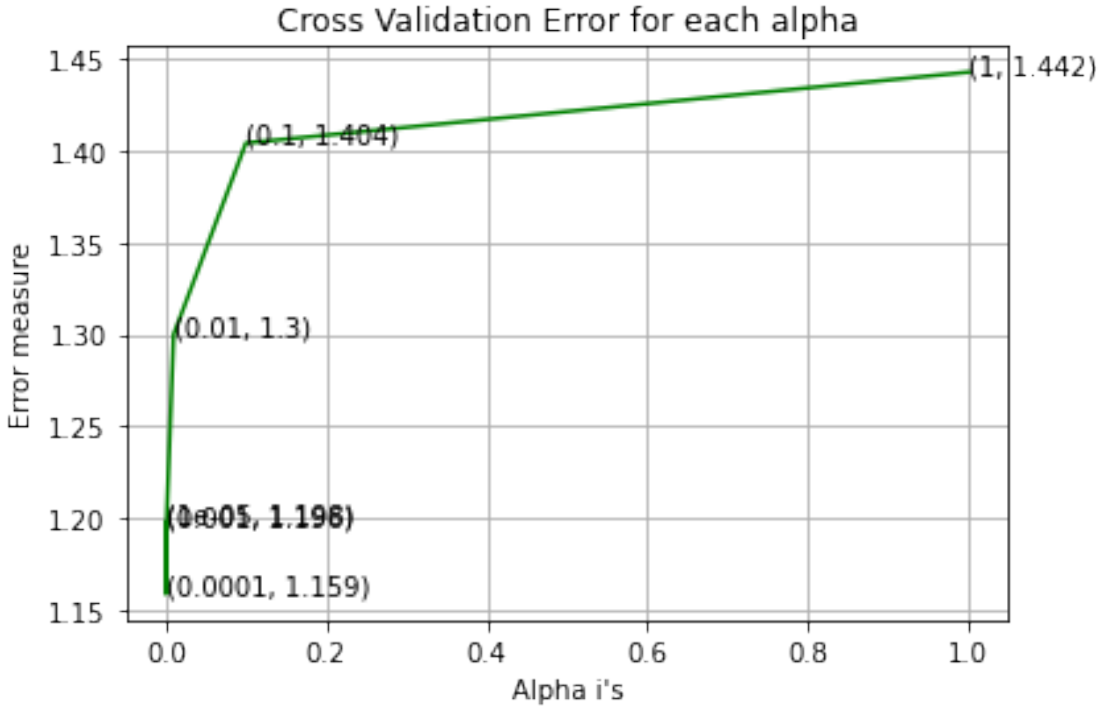

cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
    clf.fit(train_gene_feature_onehotCoding, y_train)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_gene_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(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_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:
 ↪",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha =  1e-05 The log loss is: 1.1975800795058558
For values of alpha =  0.0001 The log loss is: 1.1590426179417324
For values of alpha =  0.001 The log loss is: 1.1959898640450148
For values of alpha =  0.01 The log loss is: 1.2999352042715278
For values of alpha =  0.1 The log loss is: 1.4038858401096033
For values of alpha =  1 The log loss is: 1.4423897723525352
```




```
For values of best alpha =  0.0001 The train log loss is: 1.0061824975433085
For values of best alpha =  0.0001 The cross validation log loss is:
1.1590426179417324
For values of best alpha =  0.0001 The test log loss is: 1.1500749249331368
```

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  240  genes
in train dataset?
Ans
1. In test data 653 out of 665 : 98.19548872180451
2. In cross validation data 514 out of  532 : 96.61654135338345
```

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?

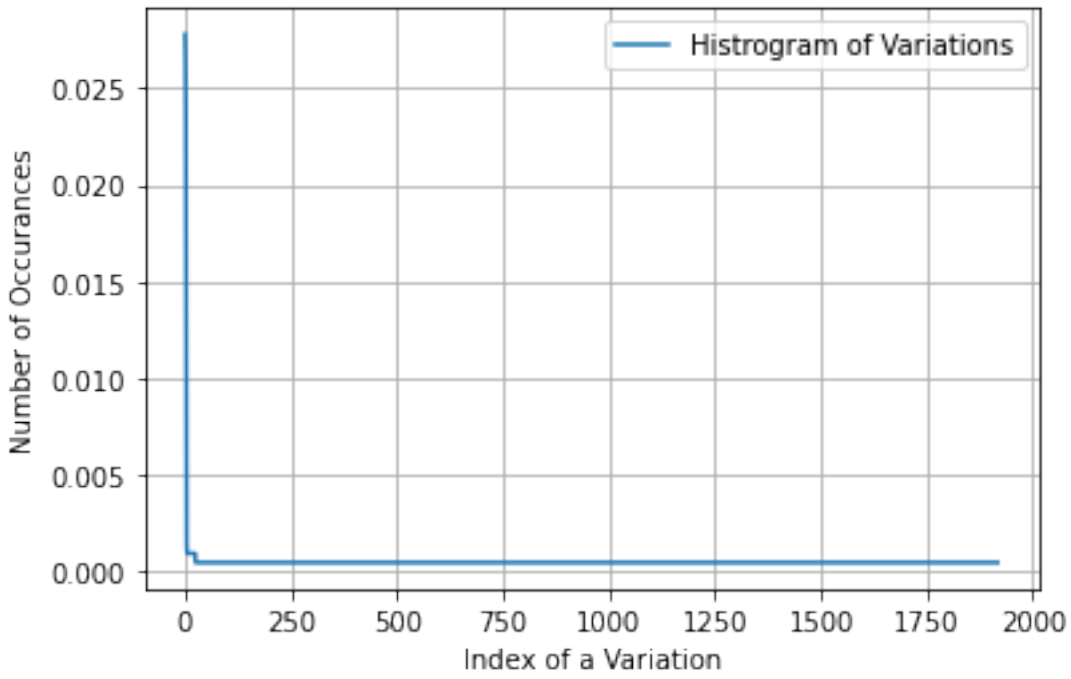
[ ]:
```
unique_variations = train_df['Variation'].value_counts()
print('Number of Unique Variations :', unique_variations.shape[0])
# the top 10 variations that occured most
print(unique_variations.head(10))
```

```
Number of Unique Variations : 1918
Truncating_Mutations    59
Deletion                57
Amplification           50
Fusions                 22
Overexpression           3
T58I                     2
G67R                     2
S308A                    2
E17K                     2
E542K                    2
Name: Variation, dtype: int64
```

[ ]:
```
print("Ans: There are", unique_variations.shape[0] ,"different categories of␣
 ↪variations in the train data, and they are distibuted as follows",)
```

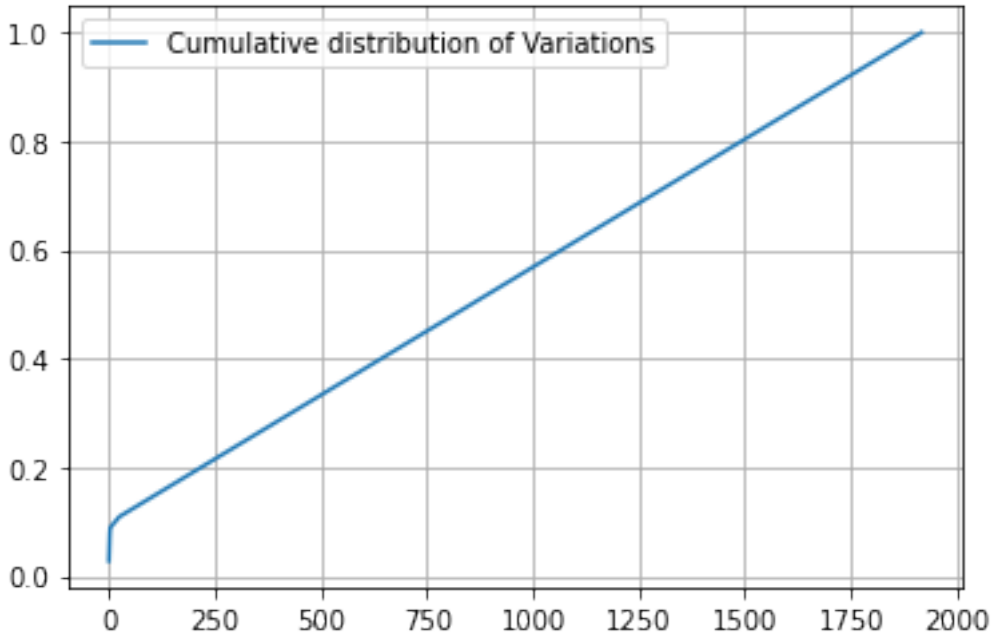
```
Ans: There are 1918 different categories of variations in the train data, and
they are distibuted as follows
```

[ ]:
```
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()
```



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

```
[0.02777778 0.05461394 0.07815443 ... 0.99905838 0.99952919 1.        ]
```



Q9. How to featurize this Variation feature ?

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

One hot Encoding

Response coding

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

[ ]:
```
# 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))
```

[ ]:
```
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)
```

[ ]:
```
# one-hot encoding of variation feature.
variation_vectorizer = CountVectorizer(ngram_range=(1,3))
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'])
```

[ ]:
```
print("train_variation_feature_onehotEncoded is converted feature using the␣
 ↪onne-hot encoding method. The shape of Variation feature:",␣
 ↪train_variation_feature_onehotCoding.shape)
```

```
train_variation_feature_onehotEncoded is converted feature using the onne-hot
encoding method. The shape of Variation feature: (2124, 2053)
```

Q10. How good is this Variation feature in predicting y_i?
Let's build a model just like the earlier!

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

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/
 ↪generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15,␣
 ↪fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,␣
 ↪learning_rate=optimal, eta0=0.0, power_t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with␣
 ↪Stochastic Gradient Descent.
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link:
#-------------------------------


cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='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)

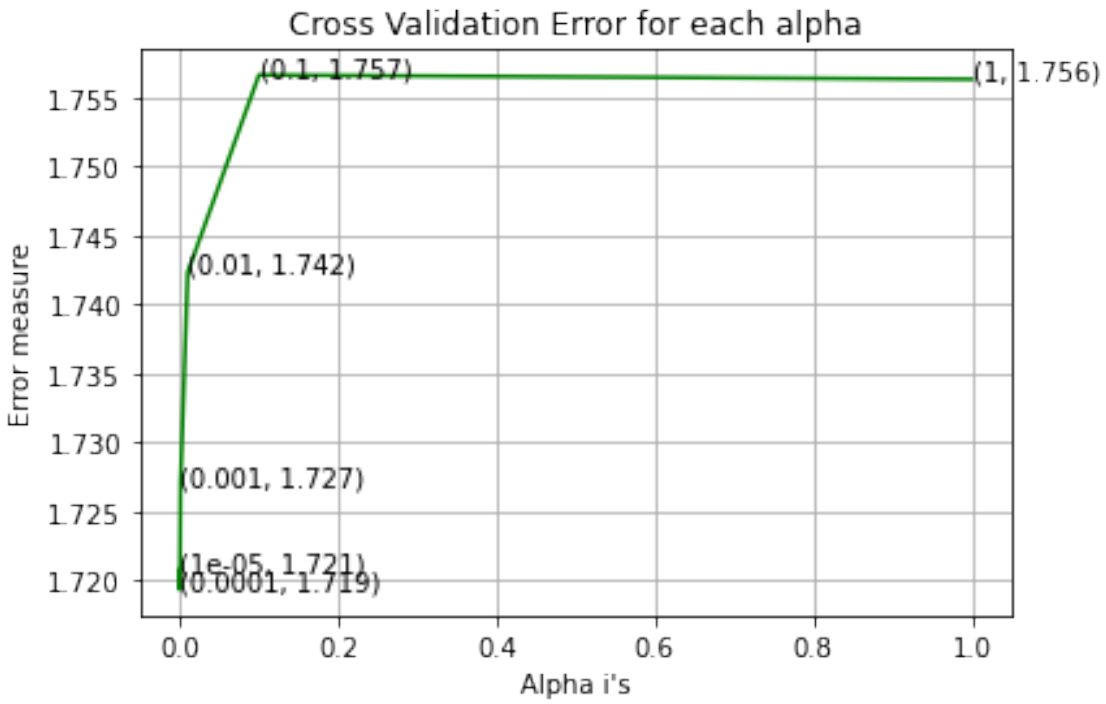
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_,␣
 ↪eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv,␣
 ↪predict_y, labels=clf.classes_, eps=1e-15))

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

```
For values of alpha =  1e-05 The log loss is: 1.7207476487572677
For values of alpha =  0.0001 The log loss is: 1.7193230273243498
For values of alpha =  0.001 The log loss is: 1.726995530183674
For values of alpha =  0.01 The log loss is: 1.742324818179992
For values of alpha =  0.1 The log loss is: 1.7566376272022663
For values of alpha =  1 The log loss is: 1.7563276745470453
```




```
For values of best alpha =  0.0001 The train log loss is: 0.710578246017075
For values of best alpha =  0.0001 The cross validation log loss is:
1.7193230273243498
For values of best alpha =  0.0001 The test log loss is: 1.7099233127881008
```

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.

[ ]:
```
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  1918  genes in test and cross
validation data sets?
Ans
1. In test data 57 out of 665 : 8.571428571428571
2. In cross validation data 58 out of  532 : 10.902255639097744
```

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?

[ ]:
```
# cls_text is a data frame
# for every row in data frame consider the '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
```

[ ]:
```
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
```

[ ]:
```
# building a CountVectorizer with all the words that occured minimum 3 times in␣
 ↪train data
text_vectorizer = CountVectorizer(min_df=3,ngram_range=(1,3))
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 : 1861236
```

[ ]:
```
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)
```

[ ]:
```
# 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
```

[ ]:
```
# don't forget to normalize every feature
train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding,␣
 ↪axis=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,␣
 ↪axis=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)
```

[ ]:
```
#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: 445398, 4: 280222, 5: 193407, 6: 173703, 7: 106059, 10: 84860, 8:
79705, 9: 76345, 12: 37095, 13: 36233, 14: 35178, 11: 29310, 16: 24627, 15:
21830, 20: 16947, 21: 15285, 17: 12165, 18: 11922, 24: 11196, 23: 8827, 41:
7981, 19: 7459, 25: 7433, 31: 7244, 22: 6353, 36: 6278, 45: 5986, 26: 5365, 28:
4766, 27: 4344, 66: 3968, 30: 3850, 29: 3359, 32: 3343, 58: 2775, 33: 2619, 42:
2395, 34: 2372, 37: 2347, 40: 2267, 35: 2267, 39: 1914, 38: 1901, 46: 1680, 48:
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```
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944: 1, 927: 1, 912: 1, 908: 1, 900: 1, 897: 1, 895: 1, 893: 1, 890: 1, 877: 1,
875: 1, 872: 1, 868: 1, 866: 1, 864: 1, 860: 1, 855: 1, 849: 1, 820: 1, 812: 1,
782: 1, 748: 1, 736: 1, 732: 1, 705: 1, 698: 1, 690: 1, 661: 1})
```

[ ]:
```
# Train a Logistic regression+Calibration model using text features whicha re␣
 ↪on-hot encoded
alpha = [10 ** x for x in range(-5, 1)]

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/
 ↪generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15,␣
 ↪fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,␣
 ↪learning_rate=optimal, eta0=0.0, power_t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with␣
 ↪Stochastic Gradient Descent.
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link:
#------------------------------


cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='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)
```

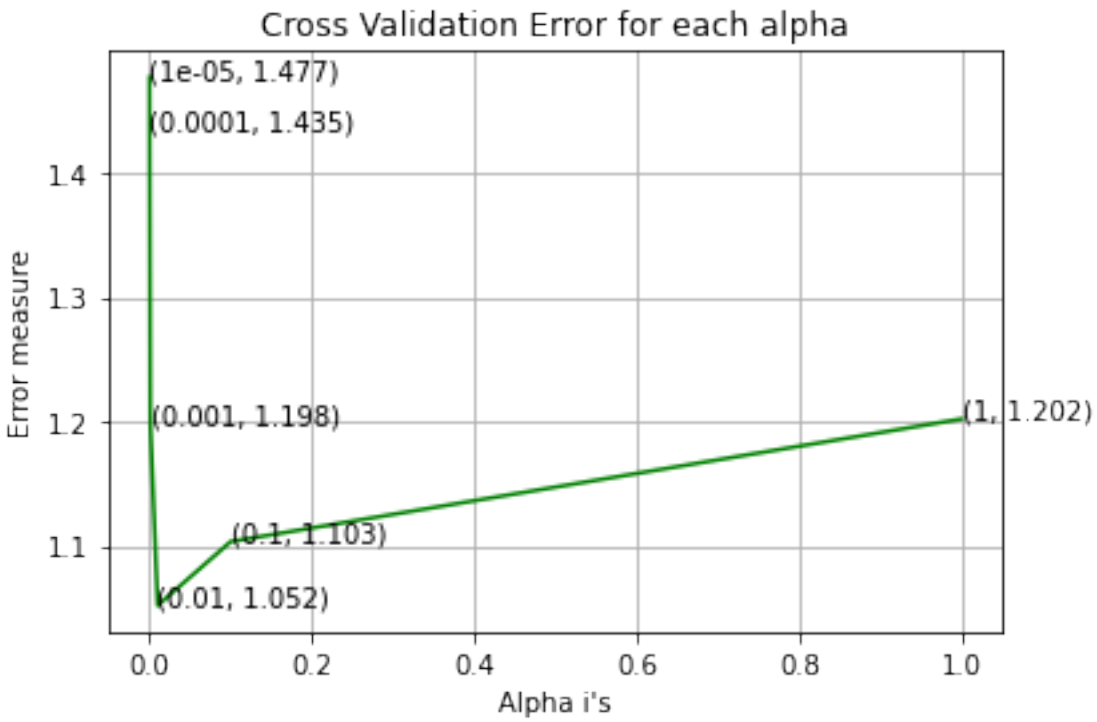
```
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_,␣
 ↪eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv,␣
 ↪predict_y, labels=clf.classes_, eps=1e-15))

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

```
For values of alpha =  1e-05 The log loss is: 1.4768185342682982
For values of alpha =  0.0001 The log loss is: 1.4346906310450065
For values of alpha =  0.001 The log loss is: 1.1978989975277825
For values of alpha =  0.01 The log loss is: 1.0520080204659137
For values of alpha =  0.1 The log loss is: 1.1033830631722568
For values of alpha =  1 The log loss is: 1.2020149247829088
```




```
For values of best alpha =  0.01 The train log loss is: 0.7513084613362182
For values of best alpha =  0.01 The cross validation log loss is:
1.0520080204659137
For values of best alpha =  0.01 The test log loss is: 1.0962167451622822
```

Q. Is the Text feature stable across all the data sets (Test, Train, Cross validation)?
Ans. Yes, it seems like!

[ ]:
```
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")
```

```
97.097 % of word of test data appeared in train data
97.421 % of word of Cross Validation appeared in train data
```

4. Machine Learning Models

[ ]:
```
#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 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)
```

[ ]:
```
# 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(ngram_range=(1,3))
    var_count_vec = CountVectorizer(ngram_range=(1,3))
    text_count_vec = CountVectorizer(min_df=3,ngram_range=(1,3))

    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")
```

Stacking the three types of BOW 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']))


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("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, 1863528)
(number of data points * number of features) in test data =  (665, 1863528)
(number of data points * number of features) in cross validation data = (532,
1863528)
```

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

```
 Response encoding features :
(number of data points * number of features) in train data =  (2124, 27)
```

```
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data = (532,
27)
```

4.1. Base Line Model

Logistic Regression with BOW ngram =(1,3) and Class balancing

[ ]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/
 ↪generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15,␣
 ↪fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,␣
 ↪learning_rate=optimal, eta0=0.0, power_t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with␣
 ↪Stochastic Gradient Descent.
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
 ↪lessons/geometric-intuition-1/
#-------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
 ↪modules/generated/sklearn.calibration.CalibratedClassifierCV.html
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None,␣
 ↪method=sigmoid, cv=3)
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
#-----------------------------------
# video link:
#-----------------------------------

alpha = [10 ** x for x in range(-6, 3)]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
```

```
    clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='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))
    # to avoid rounding error while multiplying probabilites we use␣
 ↪log-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

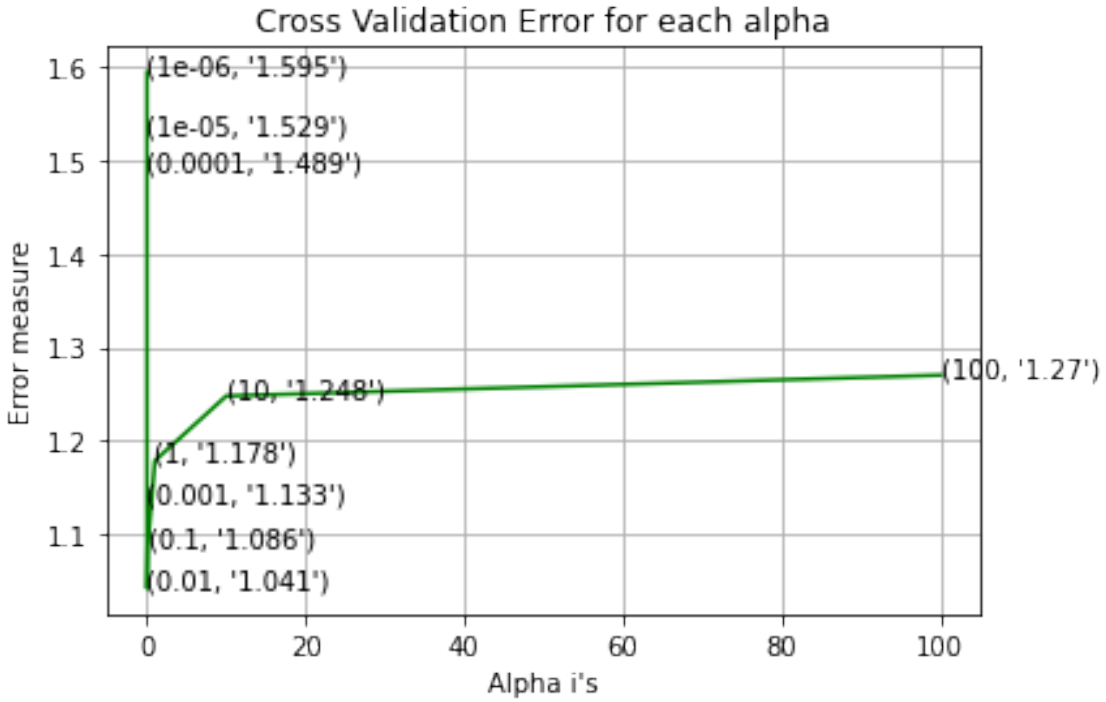
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
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_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:
 ↪",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.5950238895067985
for alpha = 1e-05
Log Loss : 1.528519025799228
for alpha = 0.0001
Log Loss : 1.4889089243498643
for alpha = 0.001
```

```
Log Loss : 1.133179264821804
for alpha = 0.01
Log Loss : 1.041066336881157
for alpha = 0.1
Log Loss : 1.085719611561209
for alpha = 1
Log Loss : 1.1781582970759825
for alpha = 10
Log Loss : 1.247630102990052
for alpha = 100
Log Loss : 1.269920522662356
```




```
For values of best alpha =  0.01 The train log loss is: 0.7335814397454019
For values of best alpha =  0.01 The cross validation log loss is:
1.041066336881157
For values of best alpha =  0.01 The test log loss is: 1.0984763733995617
```

Testing the model with best hyper paramters

[ ]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/
 ↪generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15,␣
 ↪fit_intercept=True, max_iter=None, tol=None,
```

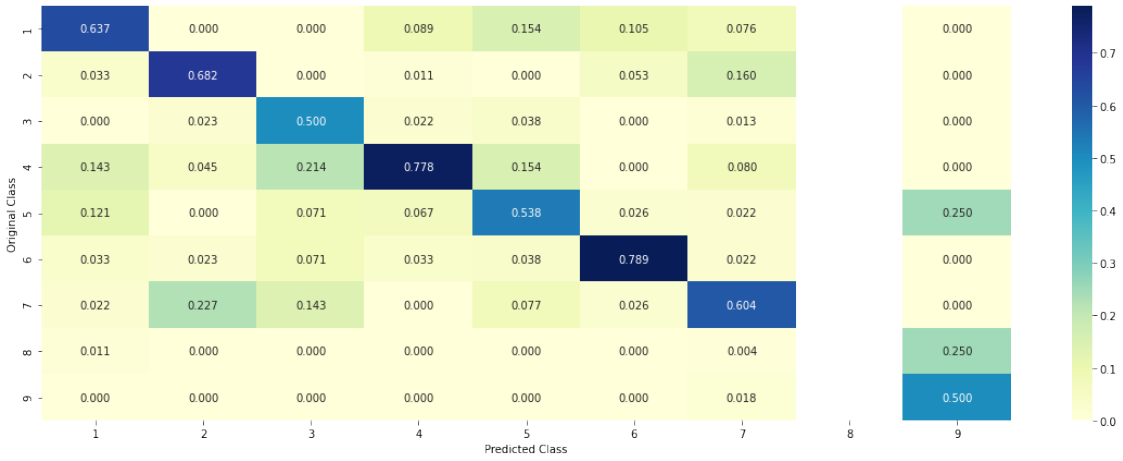
```
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,␣
 ↪learning_rate=optimal, eta0=0.0, power_t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with␣
 ↪Stochastic Gradient Descent.
# predict(X)        Predict class labels for samples in X.

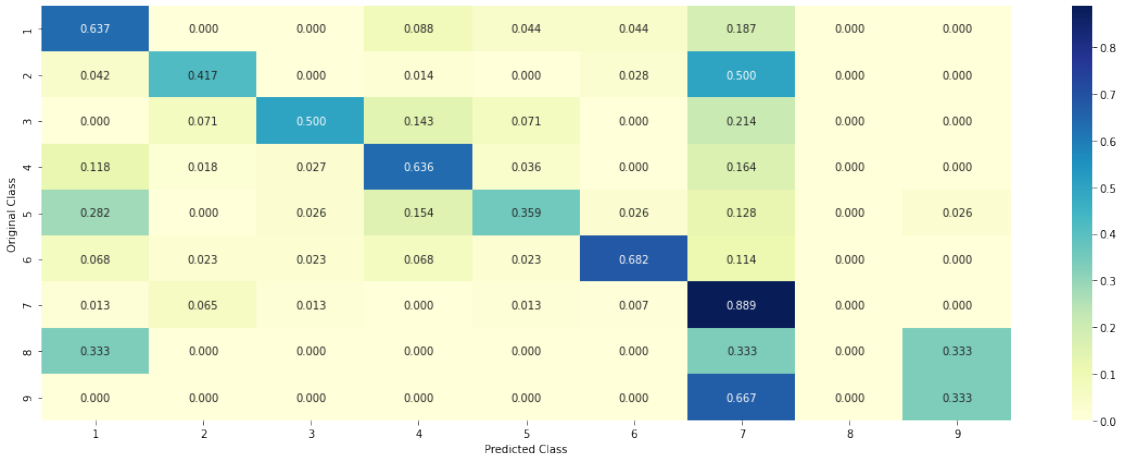
#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
 ↪lessons/geometric-intuition-1/
#-------------------------------
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha],␣
 ↪penalty='l2', loss='log', random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,␣
 ↪cv_x_onehotCoding, cv_y, clf)
```

```
Log loss : 1.041066336881157
Number of mis-classified points : 0.34774436090225563
-------------------- Confusion matrix --------------------
```


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



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



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']))
```

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_point_index],␣
 ↪no_feature)
```

```
Predicted Class : 6
Predicted Class Probabilities: [[0.0064 0.0248 0.0037 0.0081 0.1144 0.8148
0.0186 0.0045 0.0047]]
Actual Class : 6
--------------------------------------------------
389 Text feature [previously] present in test data point [True]
397 Text feature [performed] present in test data point [True]
412 Text feature [found] present in test data point [True]
433 Text feature [presence] present in test data point [True]
435 Text feature [described] present in test data point [True]
498 Text feature [results] present in test data point [True]
Out of the top  500  features  6 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_point_index],␣
 ↪no_feature)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.1994 0.1386 0.0222 0.1884 0.0651 0.0585
0.3109 0.0062 0.0106]]
Actual Class : 7
--------------------------------------------------
151 Text feature [missense] present in test data point [True]
190 Text feature [loss] present in test data point [True]
223 Text feature [function] present in test data point [True]
224 Text feature [mim] present in test data point [True]
226 Text feature [individuals] present in test data point [True]
289 Text feature [suppressor] present in test data point [True]
321 Text feature [protein] present in test data point [True]
324 Text feature [dna] present in test data point [True]
325 Text feature [affected] present in test data point [True]
Out of the top  500  features  9 are present in query point
```

Without Class balancing

[ ]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/
 ↪generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15,␣
 ↪fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,␣
 ↪learning_rate=optimal, eta0=0.0, power_t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with␣
 ↪Stochastic Gradient Descent.
# predict(X)        Predict class labels for samples in X.

#------------------------------
```

```
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/
 ↪lessons/geometric-intuition-1/
#------------------------------



# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/
 ↪modules/generated/sklearn.calibration.CalibratedClassifierCV.html
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None,␣
 ↪method=sigmoid, cv=3)
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])        Fit the calibrated model
# get_params([deep])        Get parameters for this estimator.
# predict(X)        Predict the target of new samples.
# predict_proba(X)        Posterior probabilities of classification
#-------------------------------------
# video link:
#-------------------------------------

alpha = [10 ** x for x in range(-6, 1)]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = SGDClassifier(alpha=i, penalty='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))

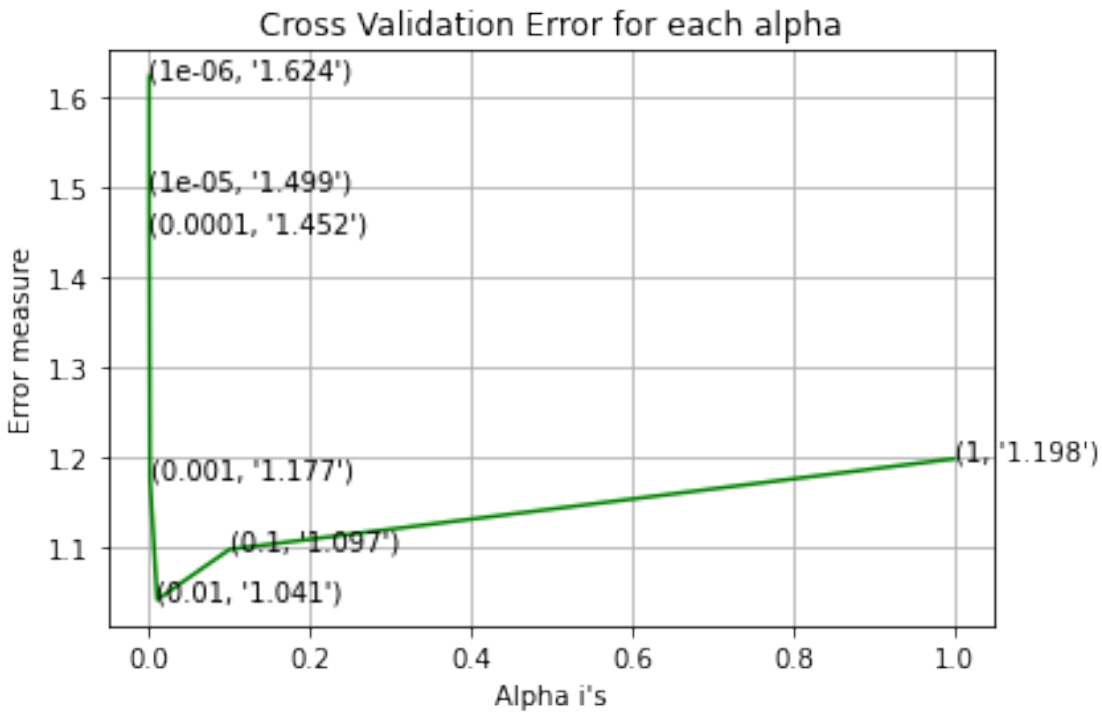
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
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_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:
 ↪",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.6238007160702748
for alpha = 1e-05
Log Loss : 1.4993642321529355
for alpha = 0.0001
Log Loss : 1.4516479814262566
for alpha = 0.001
Log Loss : 1.1767979507818411
for alpha = 0.01
Log Loss : 1.041276211781357
for alpha = 0.1
Log Loss : 1.0973385152220392
for alpha = 1
Log Loss : 1.1981450667217117
```




```
For values of best alpha =  0.01 The train log loss is: 0.7272041854788291
For values of best alpha =  0.01 The cross validation log loss is:
1.041276211781357
For values of best alpha =  0.01 The test log loss is: 1.0895054100865529
```

Testing model with best hyper parameters

[ ]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/
 ↪generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15,␣
 ↪fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None,␣
 ↪learning_rate=optimal, eta0=0.0, power_t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)

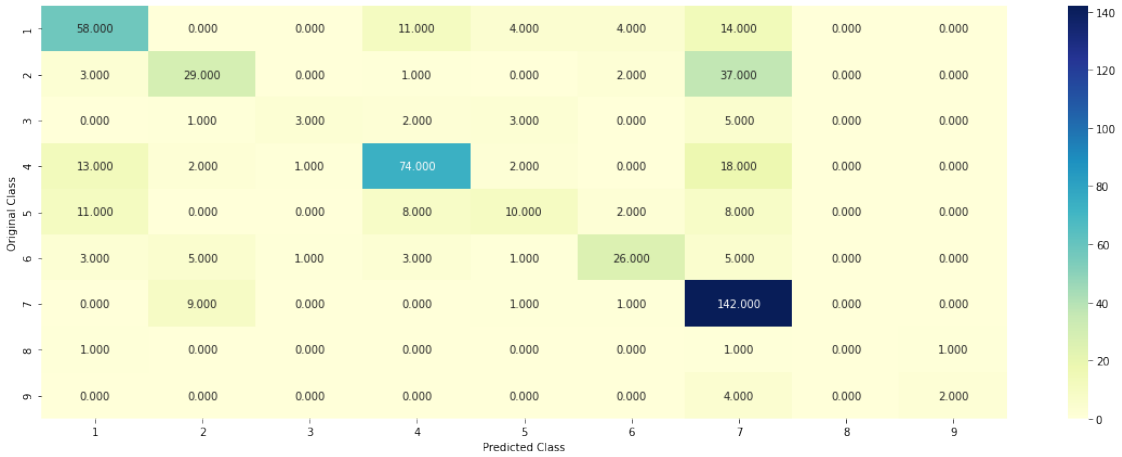
# some of methods
# fit(X, y[, coef_init, intercept_init, ])        Fit linear model with␣
 ↪Stochastic Gradient Descent.
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link:
```

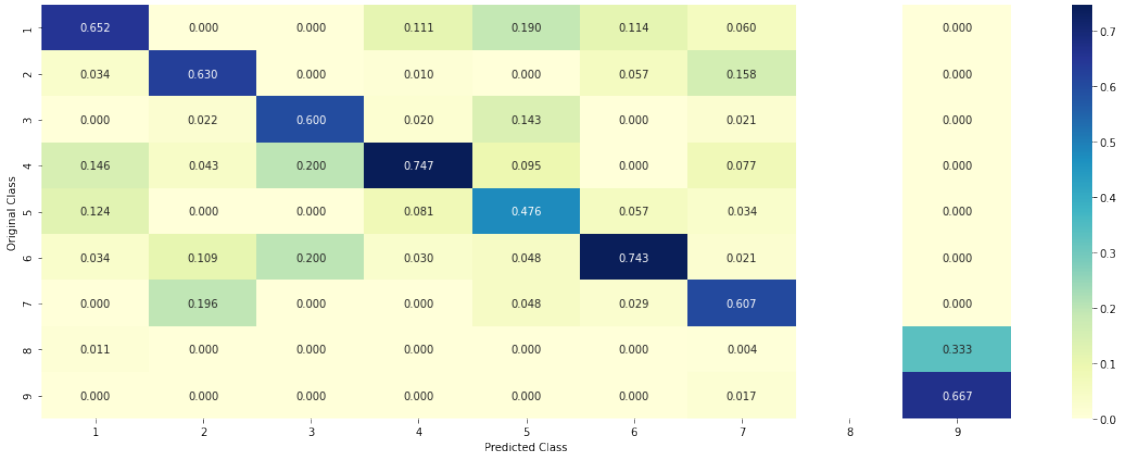
```
#------------------------------

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)
```

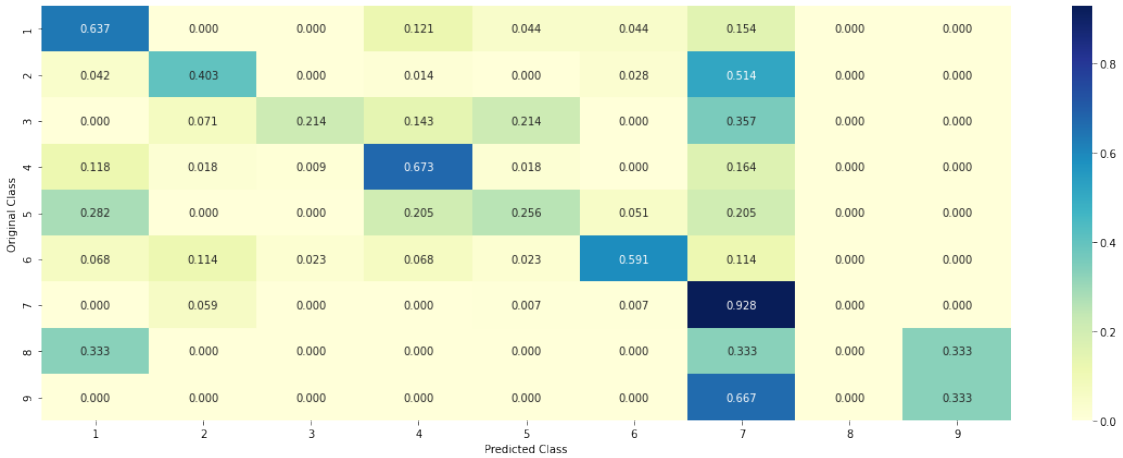
```
Log loss : 1.041276211781357
Number of mis-classified points : 0.3533834586466165
-------------------- Confusion matrix --------------------
```




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




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



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_point_index],␣
 ↪no_feature)
```

```
Predicted Class : 6
Predicted Class Probabilities: [[0.0066 0.0266 0.0039 0.0088 0.0949 0.8343 0.02
0.0034 0.0015]]
Actual Class : 6
--------------------------------------------------
302 Text feature [previously] present in test data point [True]
310 Text feature [performed] present in test data point [True]
315 Text feature [found] present in test data point [True]
332 Text feature [described] present in test data point [True]
333 Text feature [presence] present in test data point [True]
352 Text feature [additional] present in test data point [True]
353 Text feature [results] present in test data point [True]
360 Text feature [detected] present in test data point [True]
```

```
402 Text feature [resulting] present in test data point [True]
408 Text feature [two] present in test data point [True]
411 Text feature [cells] present in test data point [True]
414 Text feature [shown] present in test data point [True]
417 Text feature [identified] present in test data point [True]
426 Text feature [determine] present in test data point [True]
441 Text feature [pcr] present in test data point [True]
445 Text feature [protein] present in test data point [True]
453 Text feature [using] present in test data point [True]
456 Text feature [suggested] present in test data point [True]
462 Text feature [showed] present in test data point [True]
469 Text feature [mutation] present in test data point [True]
475 Text feature [show] present in test data point [True]
476 Text feature [addition] present in test data point [True]
484 Text feature [containing] present in test data point [True]
492 Text feature [mutations] present in test data point [True]
496 Text feature [type] present in test data point [True]
497 Text feature [sequenced] present in test data point [True]
498 Text feature [characterized] present in test data point [True]
Out of the top  500  features  27 are present in query point
```

[ ]:
```
test_point_index = 14
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_point_index],␣
 ↪no_feature)
```

```
Predicted Class : 2
Predicted Class Probabilities: [[0.0043 0.3969 0.0026 0.0021 0.2726 0.0007
0.3156 0.0043 0.0008]]
Actual Class : 7
--------------------------------------------------
316 Text feature [function] present in test data point [True]
330 Text feature [type] present in test data point [True]
454 Text feature [whether] present in test data point [True]
467 Text feature [dominant] present in test data point [True]
487 Text feature [indicated] present in test data point [True]
Out of the top  500  features  5 are present in query point
```

Apply Logistic regression with CountVectorizer Features, including both unigrams and bigra