Personalized cancer diagnosis

1. Business Problem

```
from google.colab import drive
drive.mount('/content/drive')
%cd ./drive/My Drive
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.m
[Errno 2] No such file or directory: './drive/My Drive'
/content/drive/My Drive
```

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 literatu

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-w 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 ot human experts/pathologists use to classify the genetic mutations.
- Both these data files are have a common column called ID
- Data file's information:
    - training_variants (ID , Gene, Variations, Class)
    - training_text (ID, Text)

2.1.2. Example Data Point

training_variants

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

training_text

ID,Text
0||Cyclin-dependent kinases (CDKs) regulate a variety of fundamental cellular processes. CDK10 stands out as c
cyclin has been identified and no kinase activity revealed. Previous work has shown that CDK10 silencing increa
homolog 2)-driven activation of the MAPK pathway, which confers tamoxifen resistance to breast cancer cells. T
ETS2 activity, and more generally the functions of CDK10, remain elusive. Here we demonstrate that CDK10 is a
an activating cyclin. Cyclin M, an orphan cyclin, is the product of FAM58A, whose mutations cause STAR syndror
features include toe syndactyly, telecanthus, and anogenital and renal malformations. We show that STAR syndr
interact with CDK10. Cyclin M silencing phenocopies CDK10 silencing in increasing c-Raf and in conferring tamo
CDK10/cyclin M phosphorylates ETS2 in vitro, and in cells it positively controls ETS2 degradation by the proteas
derived from a STAR patient, and this increase is attributable to decreased cyclin M levels. Altogether, our result
ETS2, which plays key roles in cancer and development. They also shed light on the molecular mechanisms und
(CDKs) play a pivotal role in the control of a number of fundamental cellular processes (1). The human genome
considered as members of the CDK family owing to their sequence similarity with bona fide CDKs, those known
almost 20 y ago (3, 4), CDK10 remains one of the two CDKs without an identified cyclin partner. This knowledge

biological functions. CDK10 can act as a positive cell cycle regulator in some cells (5, 6) or as a tumor suppress
ets erythroblastosis virus E26 oncogene homolog 2) transcription factor and inhibits its transcriptional activity t
knockdown derepresses ETS2, which increases the expression of the c-Raf protein kinase, activates the MAPK p
tamoxifen (6). ...

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

2.2.1. Type of Machine Learning Problem

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

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

2.3. Train, CV and Test Datasets

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

3. Exploratory Data Analysis

```
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.decomposition import TruncatedSVD
from sklearn.preprocessing import normalize
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.manifold import TSNE
import seaborn as sns
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics.classification import accuracy_score, log_loss
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.linear_model import SGDClassifier
from imblearn.over_sampling import SMOTE
from collections import Counter
from scipy.sparse import hstack
from sklearn.multiclass import OneVsRestClassifier
from sklearn.svm import SVC
from sklearn.model_selection import StratifiedKFold
from collections import Counter, defaultdict
from sklearn.calibration import CalibratedClassifierCV
from sklearn.naive_bayes import MultinomialNB
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import train_test_split
from sklearn.model_selection import GridSearchCV
import math
from sklearn.metrics import normalized_mutual_info_score
from sklearn.ensemble import RandomForestClassifier
warnings.filterwarnings("ignore")

from mlxtend.classifier import StackingClassifier

from sklearn import model_selection
from sklearn.linear_model import LogisticRegression
```

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

```
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 muta
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"],skip
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

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

```
# 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
```

```
[nltk_data] Downloading package stopwords to /root/nltk_data...
[nltk_data]   Package stopwords is already up-to-date!
```

```
#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 : 26.205351000000007 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	Variation	Class	TEXT
0	0	FAM58A	Truncating Mutations	1	cyclin dependent kinases cdks regulate variety...
1	1	CBL	W802*	2	abstract background non small cell lung cancer...
2	2	CBL	Q249E	2	abstract background non small cell lung cancer...
3	3	CBL	N454D	3	recent evidence demonstrated acquired uniparen...
4	4	CBL	L399V	4	oncogenic mutations monomeric casitas b lineag...

```
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 '
X_train, test_df, y_train, y_test = train_test_split(result, y_true, stratify=y_true, test_
# split the train data into train and cross validation by maintaining same distribution of
train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train, stratify=y_train, test_
```

We split the data into train, test and cross validation data sets, preserving the ratio of class distrib

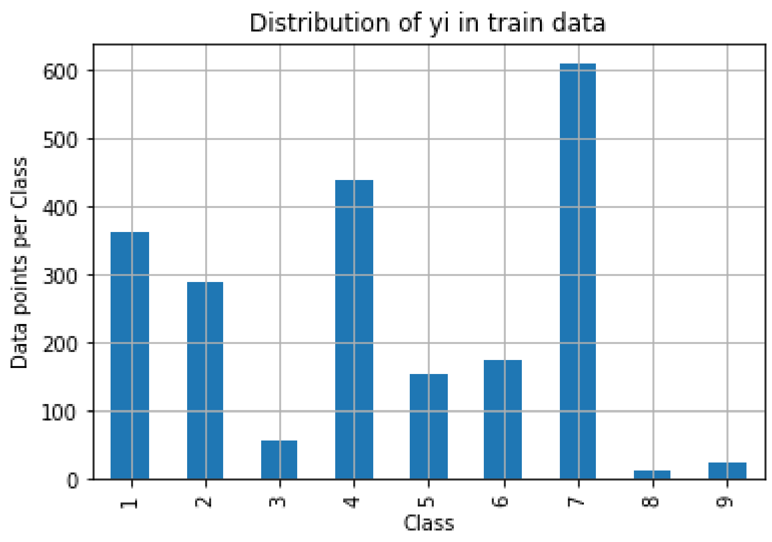
```
print('Number of data points in train data:', train_df.shape[0])
print('Number of data points in test data:', test_df.shape[0])
print('Number of data points in cross validation data:', cv_df.shape[0])
```

```
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
```

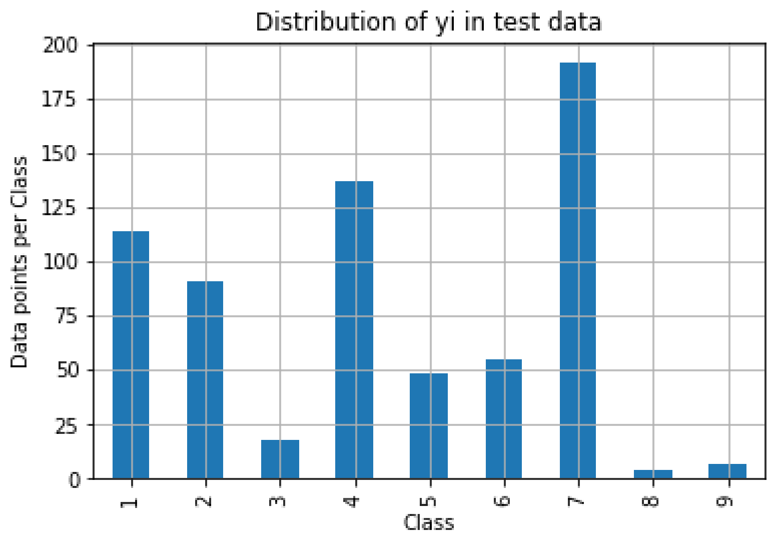
3.1.4.2. Distribution of y_i's in Train, Test and Cross Validation datasets

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

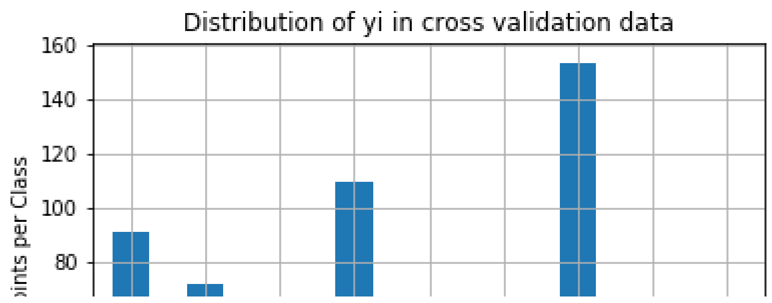
```
cv_class_distribution = cv_df['Class'].value_counts().sort_index()

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], '


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], '(

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], '(',
```

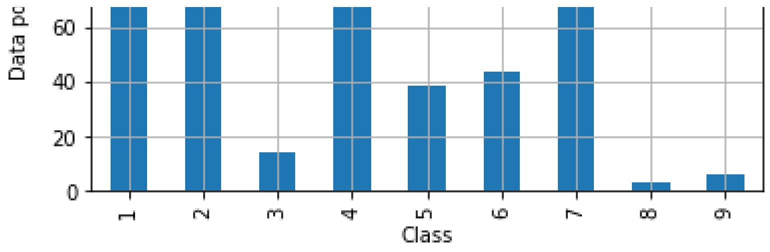


```
Number of data points in class 7 : 609 ( 28.672 %)
Number of data points in class 4 : 439 ( 20.669 %)
Number of data points in class 1 : 363 ( 17.09 %)
Number of data points in class 2 : 289 ( 13.606 %)
Number of data points in class 6 : 176 ( 8.286 %)
Number of data points in class 5 : 155 ( 7.298 %)
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 %)
--------------------------------------------------------------------------------
```





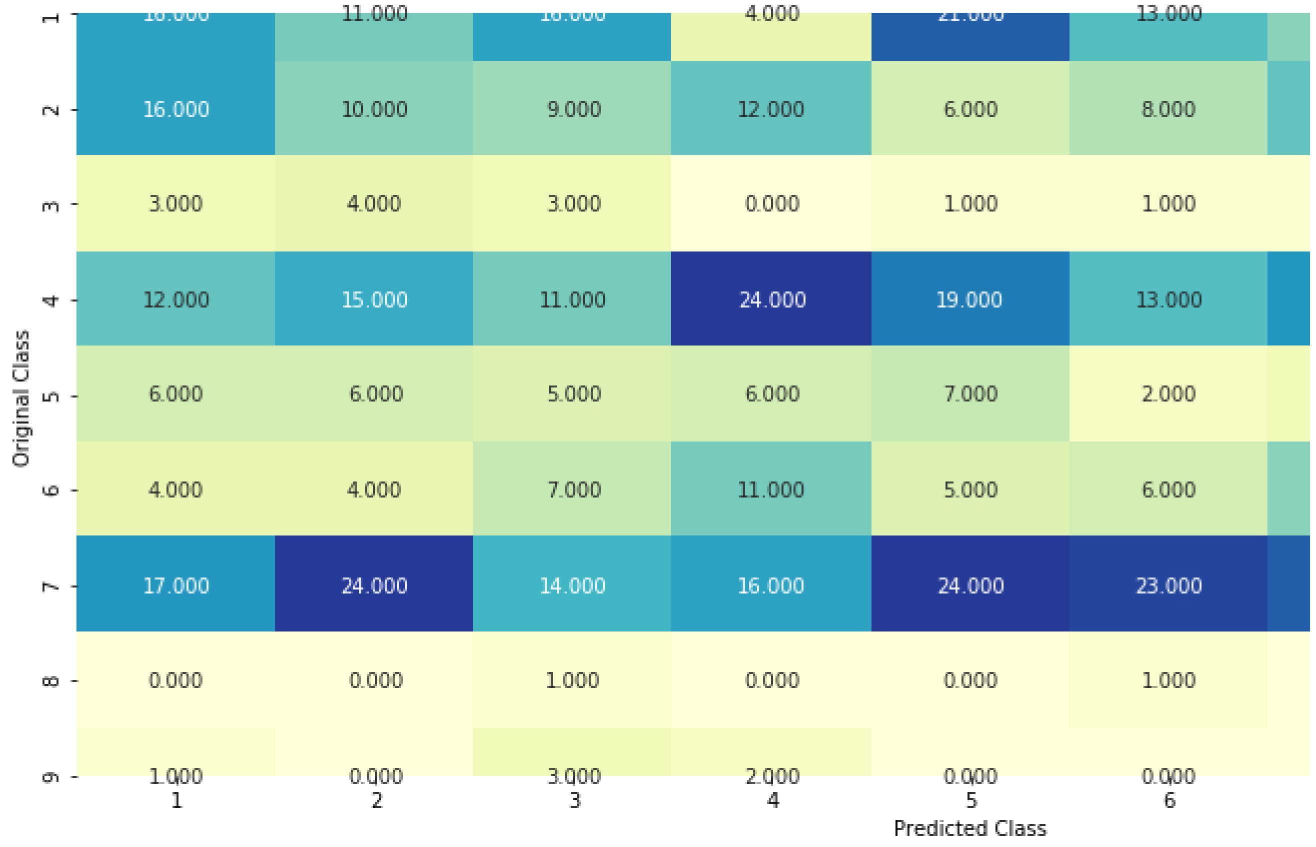
```
Number of data points in class 7 : 153 ( 28.759 %)
Number of data points in class 4 : 110 ( 20.677 %)
Number of data points in class 1 : 91 ( 17.105 %)
Number of data points in class 2 : 72 ( 13.534 %)
Number of data points in class 6 : 44 ( 8.271 %)
Number of data points in class 5 : 39 ( 7.331 %)
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

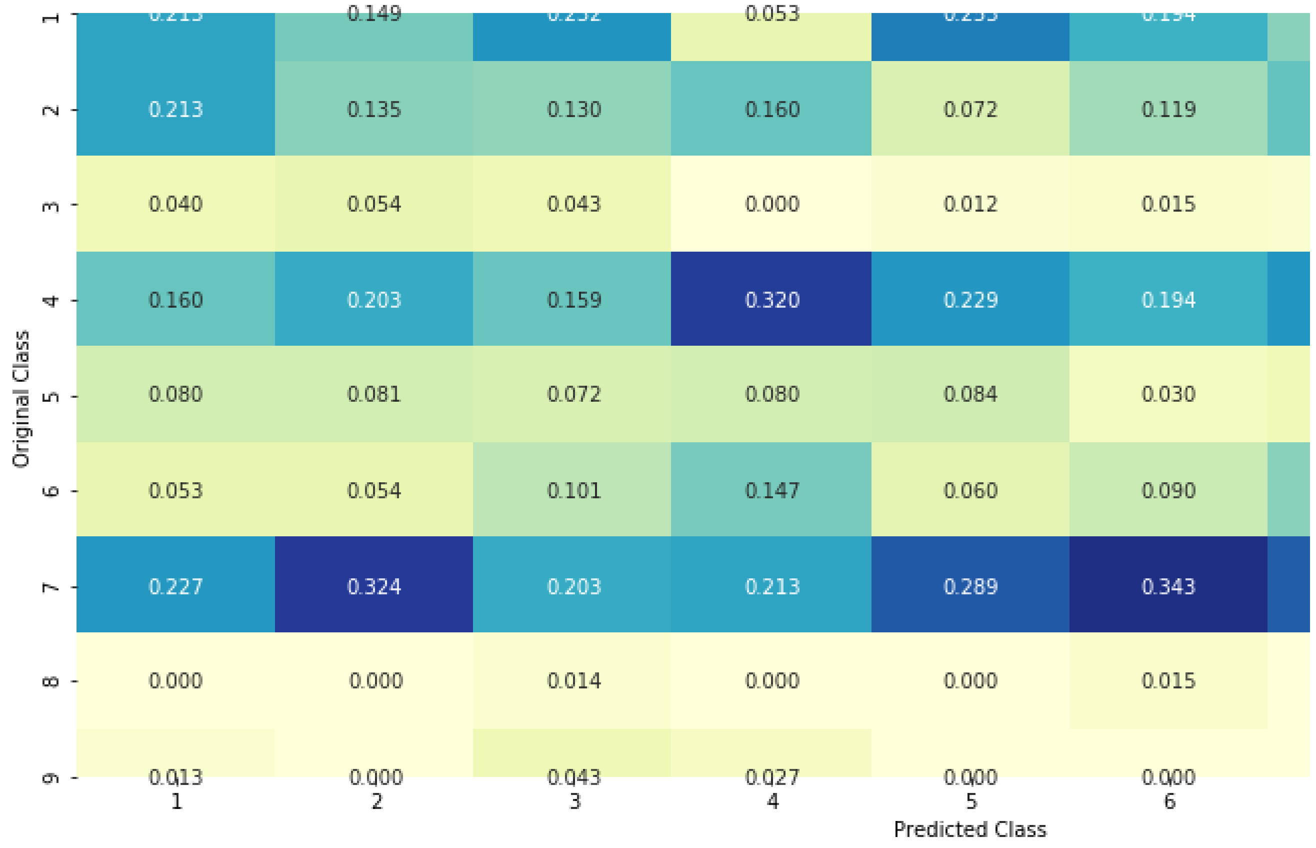
In a 'Random' Model, we generate the NINE class probabilites randomly such that they sum to 1.

```
# 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

    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
    # 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
    # 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=l
    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=l
    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=l
    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,


# 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-

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

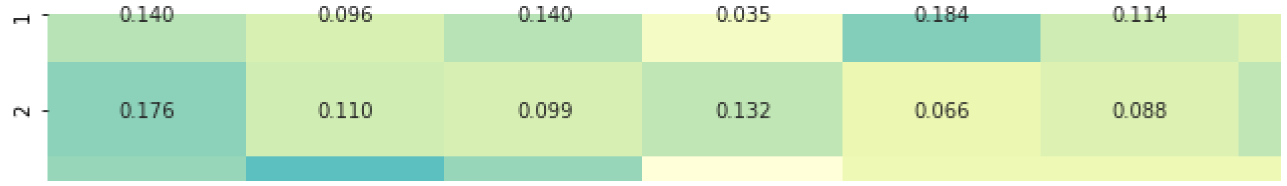
```
Log loss on Cross Validation Data using Random Model 2.521407936893321
Log loss on Test Data using Random Model 2.476820657807575
-------------------- Confusion matrix --------------------
```

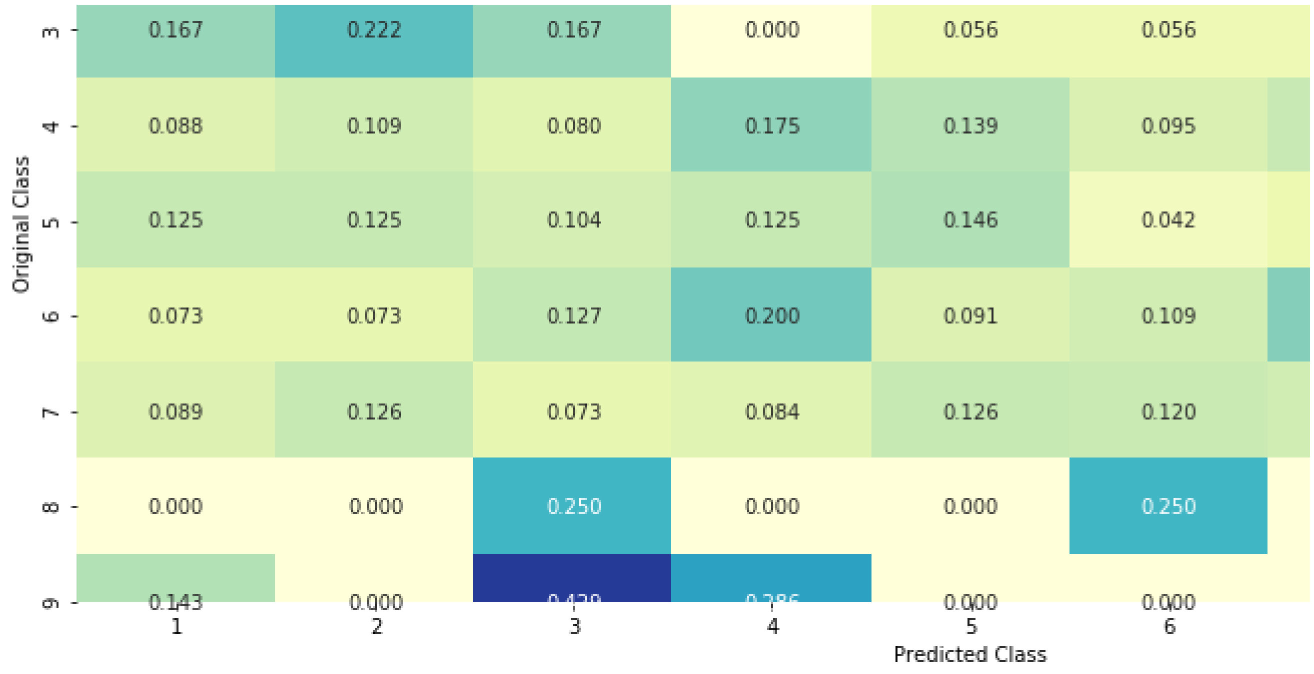


```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



```
-------------------- 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 d
# build a vector (1*9) , the first element = (number of times it occured in class1 + 10*al
# 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/va
    gv_dict = dict()

    # denominator will contain the number of time that particular feature occured in whole
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticula
        # 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
            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': [0.20075757575757575, 0.03787878787878788, 0.068181818181818177, 0.136
    #      'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 0.270
    #      'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.0681818181818181817
    #      'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.060606060606060608, 0.07
    #      'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 0.46
    #      'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.0728
    #      'BRAF': [0.066666666666666666, 0.17999999999999999, 0.073333333333333334, 0.073
    #      ...
    #     }
    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 i
    gv_fea = []
    # for every feature values in the given data frame we will check if it is there in the
    # 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 sm

- (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))
```

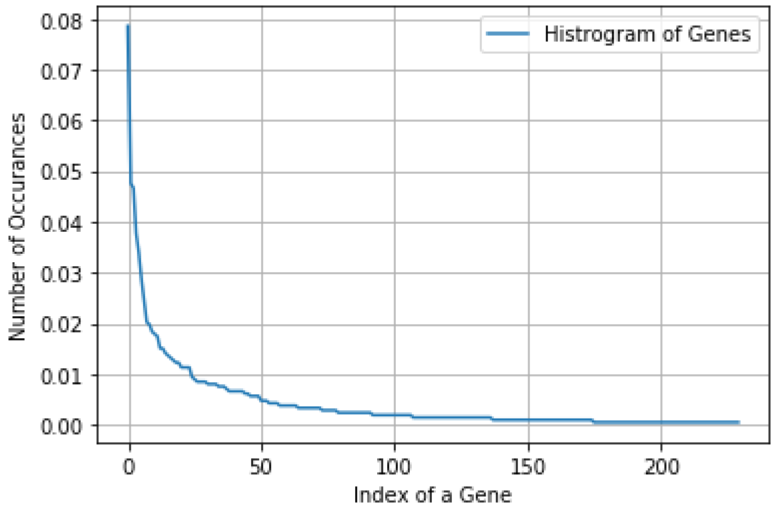
```
Number of Unique Genes : 230
BRCA1     167
EGFR      101
TP53       99
BRCA2      80
PTEN       72
KIT        61
BRAF       52
ERBB2      43
ALK        42
PDGFRA     39
Name: Gene, dtype: int64
```

```
print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in the train
```

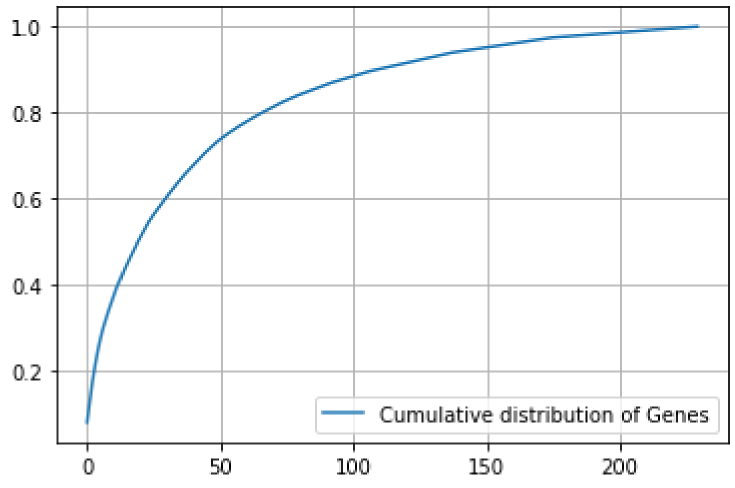
```
Ans: There are 230 different categories of genes in the train data, and they are dist
```

```
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.appliedaic online/lessons/handling-categorical-and-numerical-features/

1. One hot Encoding
2. Response coding

We will choose the appropriate featurization based on the ML model we use. For this problem of n

```
#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.
```

```
train_gene_feature_responseCoding is converted feature using respone coding method. T
```

```
# one-hot encoding of Gene feature.
from sklearn.feature_extraction.text import CountVectorizer
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_df['Gene'].head()
```

```
1567     ALK
193     EGFR
3033     KIT
995     TSC1
972     ESR1
Name: Gene, dtype: object
```

```
gene_vectorizer.get_feature_names()
```

```
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
 'akt3',
 'alk',
 'apc',
 'ar',
 'araf',
 'arid1a',
 'arid2',
 'arid5b',
 'asxl2',
 'atm',
 'atr',
 'atrx',
 'aurka',
 'aurkb',
 'axin1',
 'axl',
 'b2m',
 'bap1',
 'bcl2',
 'bcl2l11',
 'bcor',
 'braf',
 'brca1',
 'brca2',
 'brd4',
 'brip1',
 'btk',
 'card11',
 'carm1',
 'casp8',
 'cbl',
 'ccnd1',
 'ccnd3',
 'ccne1',
 'cdh1',
 'cdk12',
 'cdk4',
 'cdk6',
 'cdkn1a',
 'cdkn1b',
 'cdkn2a',
 'cdkn2b',
 'cdkn2c',
 'cebpa',
 'chek2',
 'cic',
 'crebbp',
 'ctcf',
 'ctnnb1',
 'ddr2',
 'dicer1',
 'dnmt3a',
 'dnmt3b',
 'dusp4',
 'egfr',
 'elf3',
 'ep300',
 'epas1',
 'erbb2',
 'erbb3',
 'erbb4',
 'ercc2',
 'ercc3',
 'ercc4',
 'erg',
 'errfi1',
 'esr1',
 'etv1',
 'etv6',
 'ewsr1',
 'ezh2',
 'fanca',
 'fat1',
 'fbxw7',
 'fgf3',
 'fgfr1',
 'fgfr2',
 'fgfr3',
 'fgfr4',
 'flt1',
 'flt3',
 'foxa1',
 'foxl2',
 'foxo1',
 'fubp1',
 'gata3',
 'gli1',
 'gna11',
 'gnaq',
 'gnas',
 'h3f3a',
 'hist1h1c',
 'hla',
 'hnf1a',
 'hras',
 'idh1',
 'idh2',
 'igf1r',
 'ikbke',
 'il7r',
 'inpp4b',
 'jak1',
 'jak2',
 'jun',
 'kdm5a',
 'kdm5c',
 'kdm6a',
 'kdr',
 'keap1',
 'kit',
 'kmt2a',
 'kmt2b',
 'kmt2c',
 'kmt2d',
 'knstrn',
 'kras',
 'map2k1',
 'map2k2',
 'map2k4',
 'map3k1',
 'mapk1',
 'med12',
 'mef2b',
 'met',
 'mga',
 'mlh1',
 'mpl',
 'msh2',
 'msh6',
 'mtor',
 'myc',
 'mycn',
 'myd88',
 'nf1',
 'nf2',
 'nfe2l2',
 'nfkbia',
 'nkx2',
 'notch1',
 'notch2',
 'npm1',
 'nras',
 'nsd1',
 'ntrk1',
 'ntrk2',
 'ntrk3',
 'nup93',
 'pax8',
 'pbrm1',
 'pdgfra',
 'pdgfrb',
 'pik3ca',
 'pik3cb',
 'pik3r1',
 'pik3r2',
 'pim1',
 'pms1',
 'pms2',
 'pole',
 'ppm1d',
 'ppp2r1a',
 'ppp6c',
 'prdm1',
 'ptch1',
 'pten',
 'ptpn11',
 'ptprd',
 'ptprt',
 'rab35',
 'rac1',
 'rad21',
 'rad50',
 'rad51b',
 'rad51c',
 'rad51d',
 'raf1',
 'rara',
 'rasa1',
 'rb1',
 'rbm10',
 'ret',
 'rheb',
 'rhoa',
 'rictor',
 'rit1',
 'ros1',
 'rras2',
 'runx1',
 'rxra',
 'rybp',
 'sdhb',
 'sdhc',
 'setd2',
 'sf3b1',
 'shoc2',
 'smad2',
 'smad3',
 'smad4',
 'smarca4',
 'smarcb1',
 'smo',
 'sos1',
 'sox9',
 'spop',
 'src',
 'srsf2',
 'stat3',
 'stk11',
 'tcf7l2',
 'tert',
 'tet1',
 'tet2',
 'tgfbr1',
 'tgfbr2',
 'tmprss2',
 'tp53',
 'tsc1',
 'tsc2',
 'u2af1',
 'vhl',
 'whsc1',
 'xpo1',
 'xrcc2',
 'yap1']
```

```
print("train_gene_feature_onehotCoding is converted feature using one-hot encoding method.
```

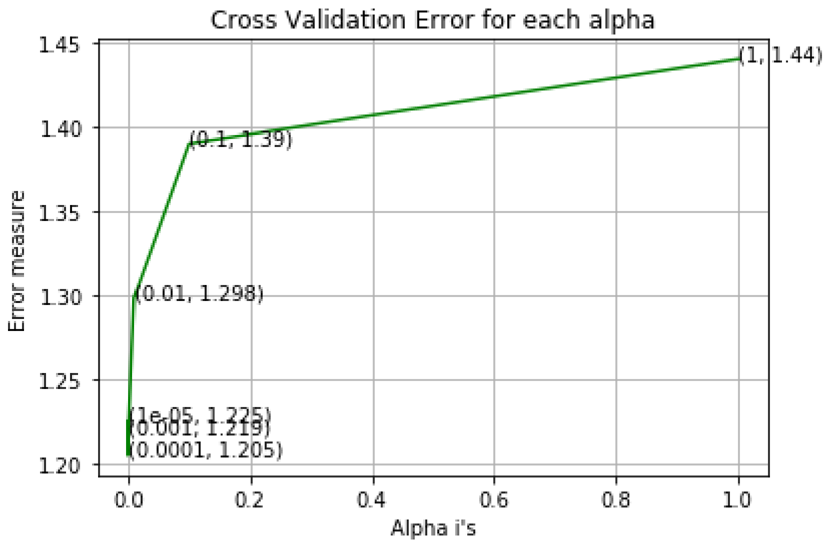
```
train_gene_feature_onehotCoding is converted feature using one-hot encoding method. T
```

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 method
feature. In this case, we will build a logistic regression model using only Gene feature (one hot enc

```
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/skle
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=Tru
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optima
# 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 Desc
# 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

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(
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:
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
     For values of alpha =  1e-05 The log loss is: 1.2254869720931472
     For values of alpha =  0.0001 The log loss is: 1.2054278064762987
     For values of alpha =  0.001 The log loss is: 1.219062625666711
     For values of alpha =  0.01 The log loss is: 1.2984614214098167
     For values of alpha =  0.1 The log loss is: 1.3899199693065867
     For values of alpha =  1 The log loss is: 1.4399401483834313
```



```
For values of best alpha =  0.0001 The train log loss is: 0.9971548697412427
For values of best alpha =  0.0001 The cross validation log loss is: 1.20542780647629
For values of best alpha =  0.0001 The test log loss is: 1.2083363109766747
```

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

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

```
Q6. How many data points in Test and CV datasets are covered by the  230  genes in tr
Ans
1. In test data 645 out of 665 : 96.99248120300751
2. In cross validation data 512 out of  532 : 96.2406015037594
```

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
```

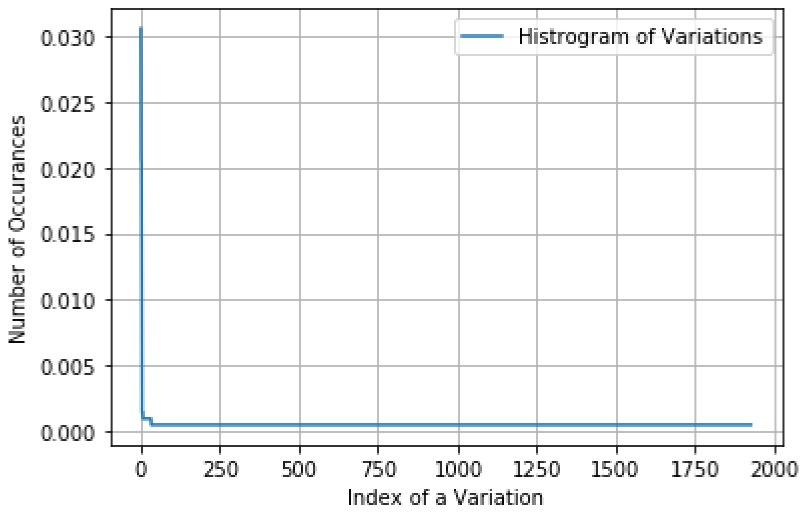
```
print(unique_variations.head(10))
```

```
Number of Unique Variations : 1927
Truncating_Mutations         65
Amplification                44
Deletion                     43
Fusions                      17
Q61R                          3
E17K                          3
G12V                          3
F28L                          2
T286A                         2
Promoter_Hypermethylation     2
Name: Variation, dtype: int64
```

```
print("Ans: There are", unique_variations.shape[0] ,"different categories of variations in
```

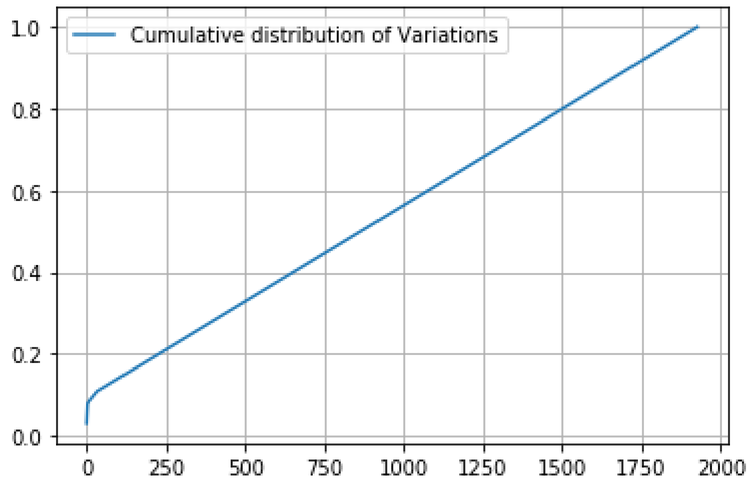
```
Ans: There are 1927 different categories of variations in the train data, and they ar
```

```
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()
```

```
[0.03060264 0.05131827 0.07156309 ... 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.appliedai online/lessons/handling-categorical-and-numerical-features/

1. One hot Encoding
2. Response coding

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

```
# alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train
# test gene feature
test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", test_d
# 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 co
```

```
train_variation_feature_responseCoding is a converted feature using the response codi
```

```
# one-hot encoding of variation feature.
variation_vectorizer = CountVectorizer()
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variat
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 encod
```

```
train_variation_feature_onehotEncoded is converted feature using the onne-hot encodin
```

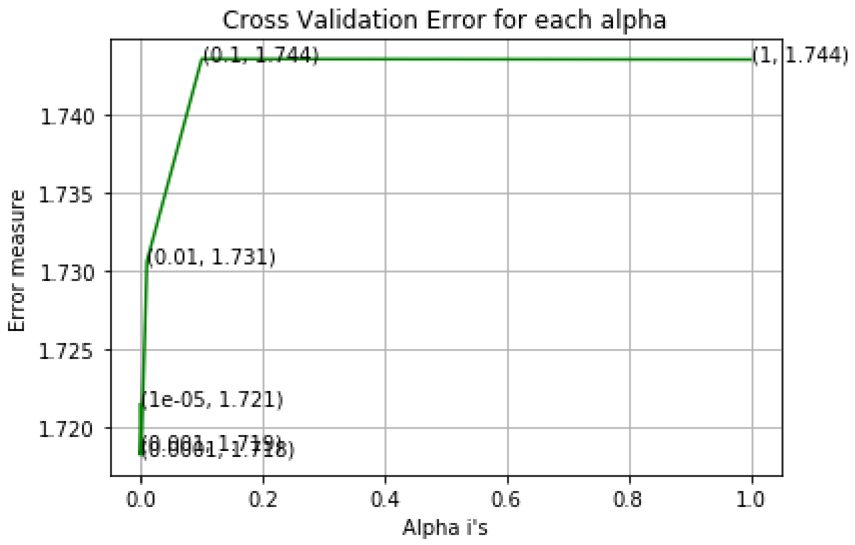
Q10. How good is this Variation feature in predicting y_i?

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/skle
# ------------------------------
# default parameters
# SGDClassifier(loss=’hinge’, penalty=’l2’, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tru
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=’optima
# 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 Desc
# 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

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(
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:
```

```
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
```

```
For values of alpha =  1e-05 The log loss is: 1.7214583885649164
For values of alpha =  0.0001 The log loss is: 1.7182236237363129
For values of alpha =  0.001 The log loss is: 1.7186182904318406
For values of alpha =  0.01 The log loss is: 1.7305969702954247
For values of alpha =  0.1 The log loss is: 1.7435719730145527
For values of alpha =  1 The log loss is: 1.7435378092187095
```



```
For values of best alpha =  0.0001 The train log loss is: 0.7745004388198726
For values of best alpha =  0.0001 The cross validation log loss is: 1.71822362373631
For values of best alpha =  0.0001 The test log loss is: 1.6927740737501427
```

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], " gen
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/
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_coverag
```

```
Q12. How many data points are covered by total  1927  genes in test and cross validat
Ans
1. In test data 69 out of 665 : 10.37593984962406
2. In cross validation data 55 out of  532 : 10.338345864661653
```

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
# cls_text is a data frame
# for every row in data fram 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,
            text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TEXT'].
            row_index += 1
    return text_feature_responseCoding


text_vectorizer = CountVectorizer(ngram_range=(1, 4),max_features=3000)
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
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 occ
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))
```

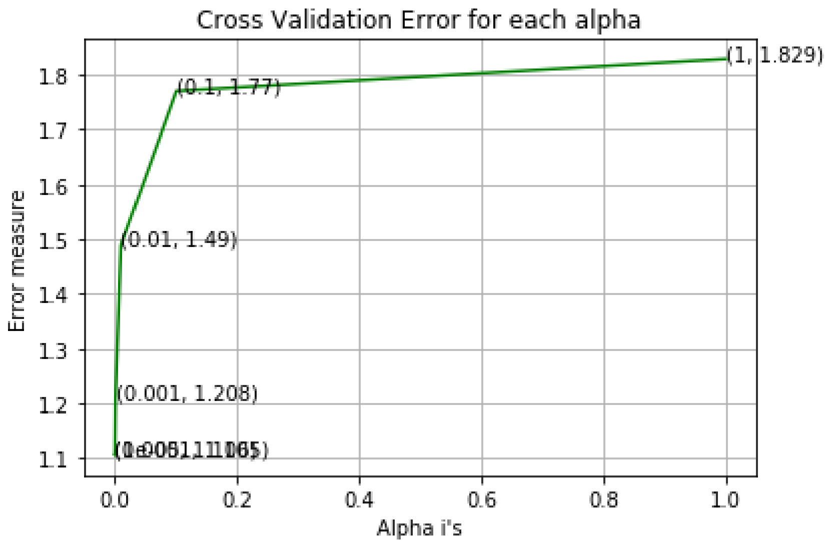
```
Total number of unique words in train data : 3000
```

```
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_featur
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_r
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_respons


# 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=Tru
sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))


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

```
Counter({1076: 25, 1058: 7, 2034: 6, 1417: 6, 1356: 6, 970: 6, 949: 6, 944: 6, 1865:
```

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

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skle
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=Tru
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optima
# 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 Desc
# 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

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(
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:
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
     For values of alpha =  1e-05 The log loss is: 1.1062609997184072
     For values of alpha =  0.0001 The log loss is: 1.1050212115355451
     For values of alpha =  0.001 The log loss is: 1.2076101657356986
     For values of alpha =  0.01 The log loss is: 1.489547424365572
     For values of alpha =  0.1 The log loss is: 1.7704202281882038
     For values of alpha =  1 The log loss is: 1.8290237929154367
```



```
For values of best alpha =  0.0001 The train log loss is: 0.775172935681742
For values of best alpha =  0.0001 The cross validation log loss is: 1.10502121153554
For values of best alpha =  0.0001 The test log loss is: 1.117808344414387
```

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"
```

```
8.122 % of word of test data appeared in train data
9.558 % 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
    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.s
    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()
    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,y
        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(w
        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,y

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

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_feat
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_oneho

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

test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_feature_onehotCoding))
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_variati
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_variation_
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_featur

train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_resp
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_respons
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_responseCodin
```

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

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 5195)
(number of data points * number of features) in test data =  (665, 5195)
(number of data points * number of features) in cross validation data = (532, 5195)
```

```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train_x_responseCod
print("(number of data points * number of features) in test data = ", test_x_responseCodin
print("(number of data points * number of features) in cross validation data =", cv_x_resp
```

```
 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)
```

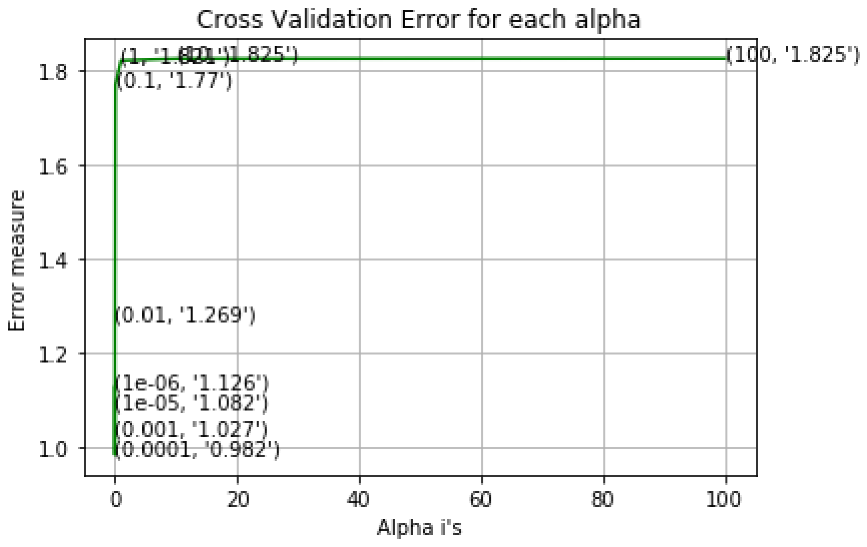
4.3. Logistic Regression

4.3.1. With Class balancing

4.3.1.1. Hyper paramter tuning

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skle
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=Tru
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optima
# 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 Desc
# predict(X)  Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geom
#------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/ge
# ----------------------------
# 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
    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 estima
        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='
    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(
    predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
    print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:
    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
         for alpha = 1e-06
         Log Loss : 1.1256514221873013
         for alpha = 1e-05
         Log Loss : 1.0815758044811028
         for alpha = 0.0001
         Log Loss : 0.9822877914127222
         for alpha = 0.001
         Log Loss : 1.0269150913611906
         for alpha = 0.01
         Log Loss : 1.2692840859116858
         for alpha = 0.1
         Log Loss : 1.7697258164084642
         for alpha = 1
         Log Loss : 1.821035382711037
         for alpha = 10
         Log Loss : 1.824834748637531
         for alpha = 100
         Log Loss : 1.8252308745911767
```

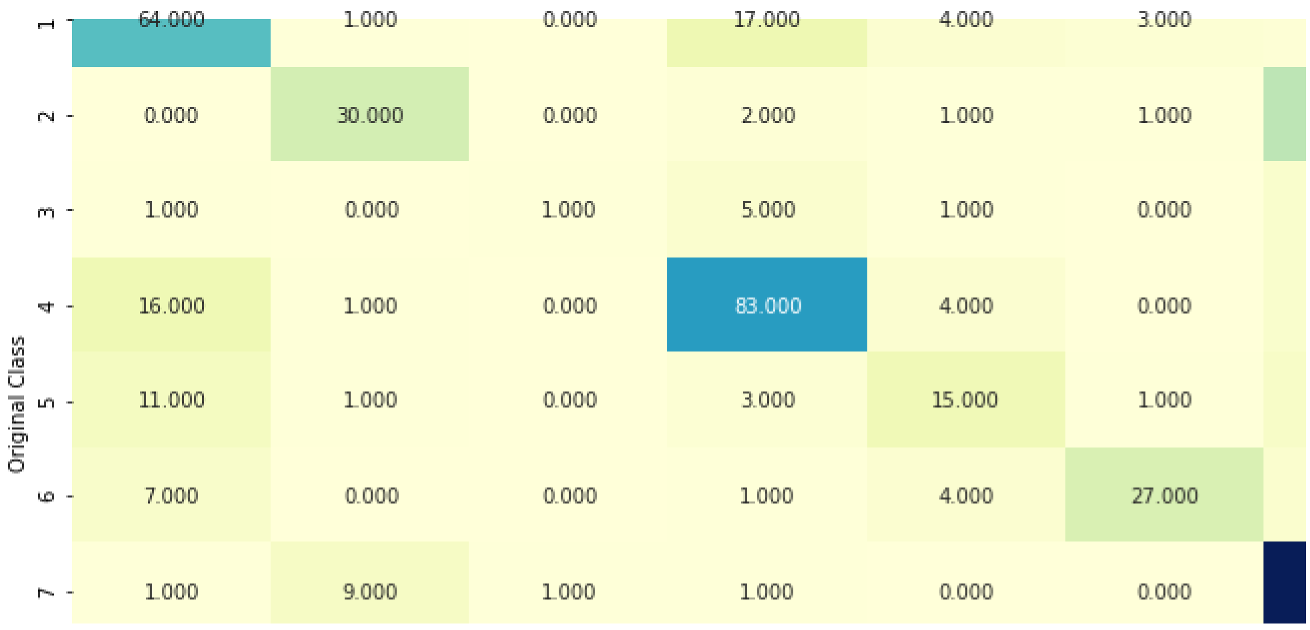


```
For values of best alpha =  0.0001 The train log loss is: 0.41910881649958365
For values of best alpha =  0.0001 The cross validation log loss is: 0.98228779141272
For values of best alpha =  0.0001 The test log loss is: 1.0007562269974497
```

4.3.1.2. Testing the model with best hyper paramters

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skle
# ------------------------------
# default parameters
# SGDClassifier(loss=’hinge’, penalty=’l2’, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tru
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=’optima
# 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 Desc
# predict(X)  Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geom
#------------------------------
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y,
```

```
Log loss : 0.9822877914127222
Number of mis-classified points : 0.3101503759398496
-------------------- Confusion matrix --------------------
```

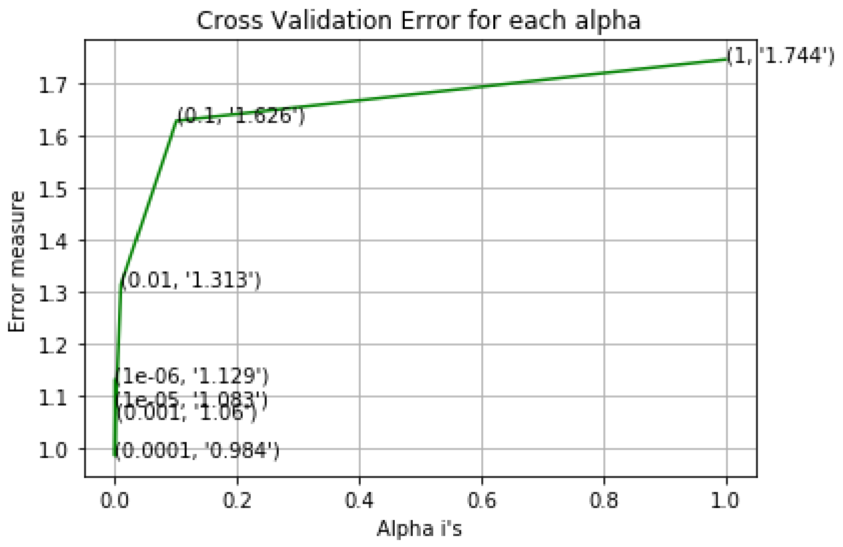


4.3.2. Without Class balancing

4.3.2.1. Hyper paramter tuning

```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skle
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=Tru
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optima
# 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 Desc
# predict(X)  Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geom
#------------------------------



# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/ge
# ----------------------------
# 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:
```

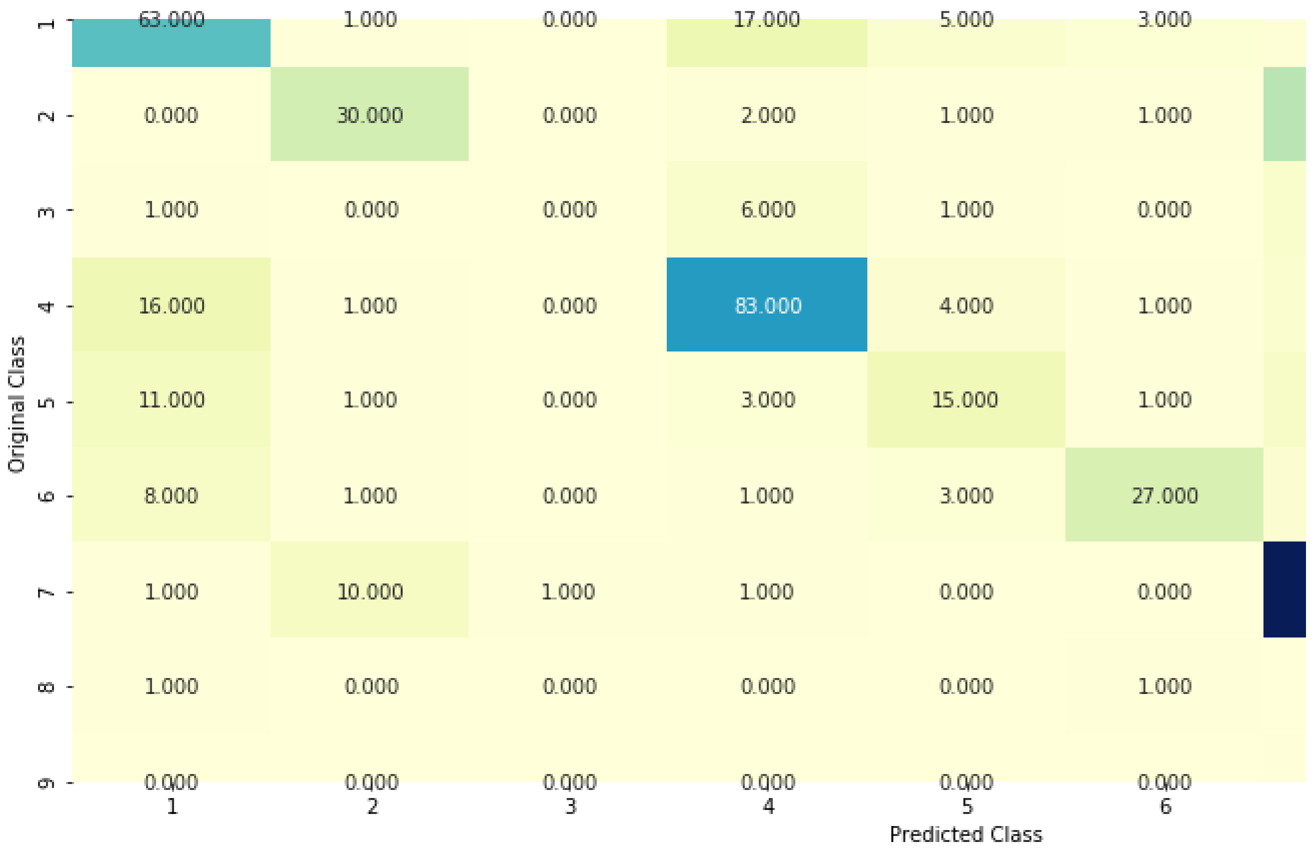
```
# video link:
#------------------------------------

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(
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:
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
     for alpha = 1e-06
     Log Loss : 1.1289478774289834
     for alpha = 1e-05
     Log Loss : 1.082966959630053
     for alpha = 0.0001
     Log Loss : 0.9841972790396977
     for alpha = 0.001
     Log Loss : 1.0595201291228797
     for alpha = 0.01
     Log Loss : 1.3130838347423228
     for alpha = 0.1
     Log Loss : 1.6264926408443185
     for alpha = 1
     Log Loss : 1.7444588751139316
```



```
For values of best alpha =  0.0001 The train log loss is: 0.41697344201024755
For values of best alpha =  0.0001 The cross validation log loss is: 0.98419727903969
For values of best alpha =  0.0001 The test log loss is: 1.0020670858233494
```

4.3.2.2. Testing model with best hyper parameters

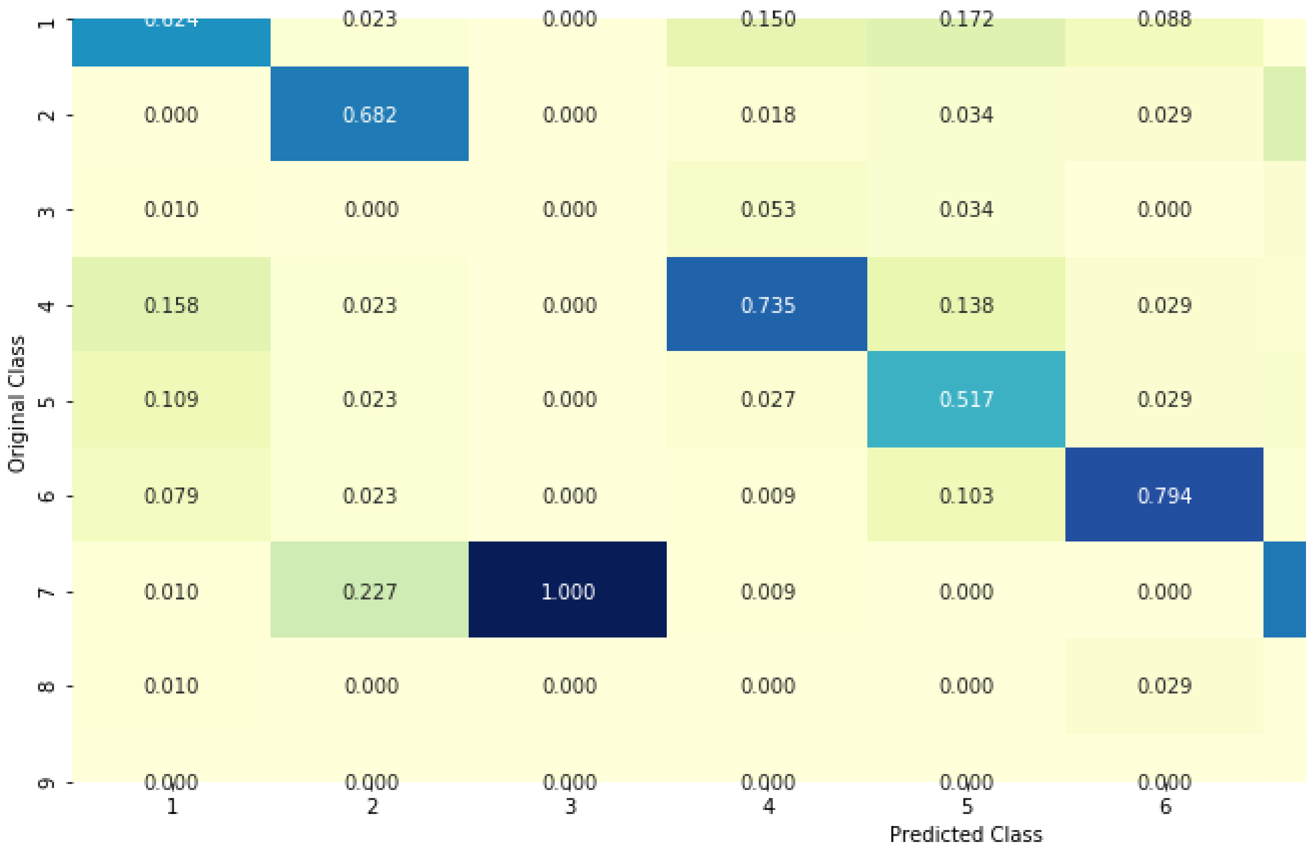
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/skle
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=Tru
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate='optima
# 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 Desc
# 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,
     Log loss : 0.9841972790396977
     Number of mis-classified points : 0.3176691729323308
     -------------------- Confusion matrix --------------------
```



Original Class	1	2	3	4	5	6
1	63.000	1.000	0.000	17.000	5.000	3.000
2	0.000	30.000	0.000	2.000	1.000	1.000
3	1.000	0.000	0.000	6.000	1.000	0.000
4	16.000	1.000	0.000	83.000	4.000	1.000
5	11.000	1.000	0.000	3.000	15.000	1.000
6	8.000	1.000	0.000	1.000	3.000	27.000
7	1.000	10.000	1.000	1.000	0.000	0.000
8	1.000	0.000	0.000	0.000	0.000	1.000
9	0.000	0.000	0.000	0.000	0.000	0.000

Predicted Class

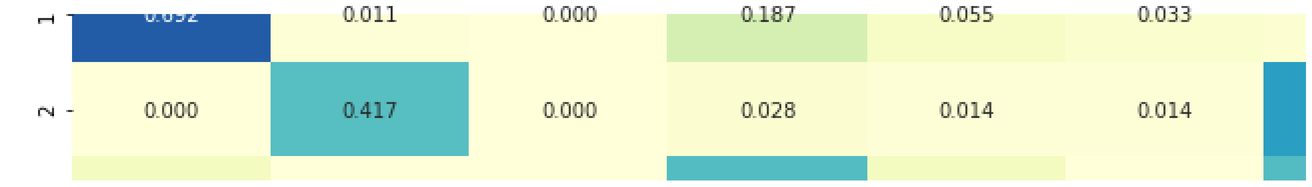
```
-------------------- Precision matrix (Columm Sum=1) --------------------
```



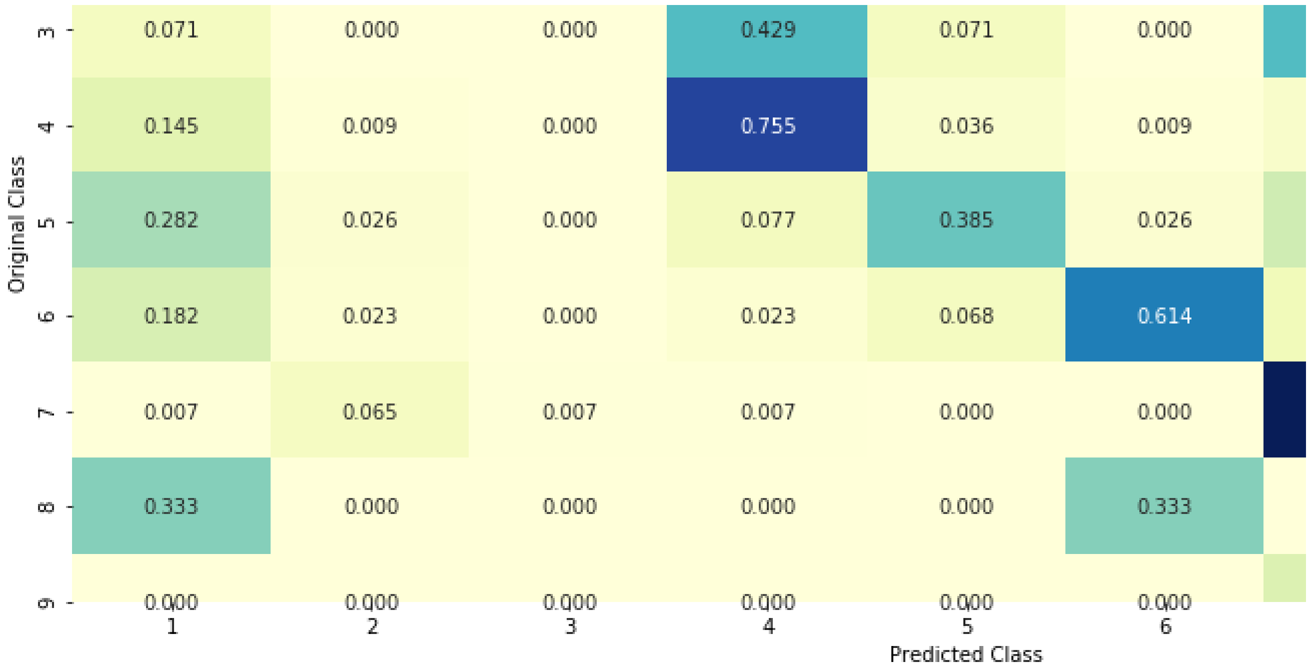
Original Class	1	2	3	4	5	6
1	0.624	0.023	0.000	0.150	0.172	0.088
2	0.000	0.682	0.000	0.018	0.034	0.029
3	0.010	0.000	0.000	0.053	0.034	0.000
4	0.158	0.023	0.000	0.735	0.138	0.029
5	0.109	0.023	0.000	0.027	0.517	0.029
6	0.079	0.023	0.000	0.009	0.103	0.794
7	0.010	0.227	1.000	0.009	0.000	0.000
8	0.010	0.000	0.000	0.000	0.000	0.029
9	0.000	0.000	0.000	0.000	0.000	0.000

Predicted Class

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



1	0.692	0.011	0.000	0.187	0.055	0.033
2	0.000	0.417	0.000	0.028	0.014	0.014



Conclusion

```
#Logistic Regression with countvectorizer features

from prettytable import PrettyTable

x = PrettyTable()

x.field_names = ["Class Balancing", "Train loss ", "CV Loss", "Test Loss","Misclassified p

x.add_row(["Yes", 0.41, 0.98, 1.00,0.31])
x.add_row(["No", 0.41, 0.98, 1.090,0.31])

print(x)
```

```
+-----------------+-------------+---------+-----------+----------------------+
| Class Balancing | Train loss  | CV Loss | Test Loss | Misclassified points |
+-----------------+-------------+---------+-----------+----------------------+
|       Yes       |     0.41    |   0.98  |    1.0    |         0.31         |
|        No       |     0.41    |   0.98  |    1.09   |         0.31         |
+-----------------+-------------+---------+-----------+----------------------+
```