ASSIGNMENT - Task 3 (Personalized Cancer Diagnosis)

September 25, 2018

Personalized cancer diagnosis

1 OBJECTIVE :- Apply Logistic Regression with CountVectorizer Features , including both unigrams and bigrams

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

3. Exploratory Data Analysis

```
In [2]: import pandas as pd
        import matplotlib.pyplot as plt
        import re
        import time
        import warnings
        warnings.filterwarnings("ignore")
        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.cross_validation 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


        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

```
In [3]: data = pd.read_csv('training/training_variants')
        print('Number of data points : ', data.shape[0])
        print('Number of features : ', data.shape[1])
        print('Features : ', data.columns.values)
        data.head()
```

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

```
Out[3]:    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
<ul>
    <li><b>ID : </b>the id of the row used to link the mutation to the clinical evidence</li>
    <li><b>Gene : </b>the gene where this genetic mutation is located </li>
    <li><b>Variation : </b>the aminoacid change for this mutations </li>
    <li><b>Class :</b> 1-9 the class this genetic mutation has been classified on</li>
</ul>
```

3.1.2. Reading Text Data

```
In [4]: # note the seprator in this file
        data_text =pd.read_csv("training/training_text",sep="\|\|",engine="python",names=["ID"
        print('Number of data points : ', data_text.shape[0])
        print('Number of features : ', data_text.shape[1])
        print('Features : ', data_text.columns.values)
        data_text.head()
```

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

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

3.1.3. Preprocessing of text

```
In [5]: # loading stop words from nltk library
        stop_words = set(stopwords.words('english'))


        def nlp_preprocessing(total_text, index, column):
            if type(total_text) is not int:
                string = ""
                # replace every special char with space
                total_text = re.sub('[^a-zA-Z0-9\n]', ' ', total_text)
                # replace multiple spaces with single space
                total_text = re.sub('\s+',' ', total_text)
                # converting all the chars into lower-case.
                total_text = total_text.lower()

                for word in total_text.split():
                # if the word is a not a stop word then retain that word from the data
                    if not word in stop_words:
                        string += word + " "

                data_text[column][index] = string
```

```
In [6]: #text processing stage.
        start_time = time.clock()
        for index, row in data_text.iterrows():
            if type(row['TEXT']) is str:
                nlp_preprocessing(row['TEXT'], index, 'TEXT')
            else:
                print("there is no text description for id:",index)
        print('Time took for preprocessing the text :',time.clock() - start_time, "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 : 188.61710515944048 seconds
```

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

Out[7]:    ID    Gene             Variation  Class  \
        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

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

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

Out[8]:         ID    Gene             Variation  Class TEXT
        1109  1109   FANCA                S1088F      1  NaN
        1277  1277  ARID5B  Truncating Mutations      1  NaN
        1407  1407   FGFR3                 K508M      6  NaN
        1639  1639    FLT1         Amplification      6  NaN
        2755  2755    BRAF                 G596C      7  NaN

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

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

Out[10]:         ID   Gene Variation  Class          TEXT
         1109  1109  FANCA    S1088F      1  FANCA S1088F
```

3.1.4. Test, Train and Cross Validation Split
3.1.4.1. Splitting data into train, test and cross validation (64:20:16)

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

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

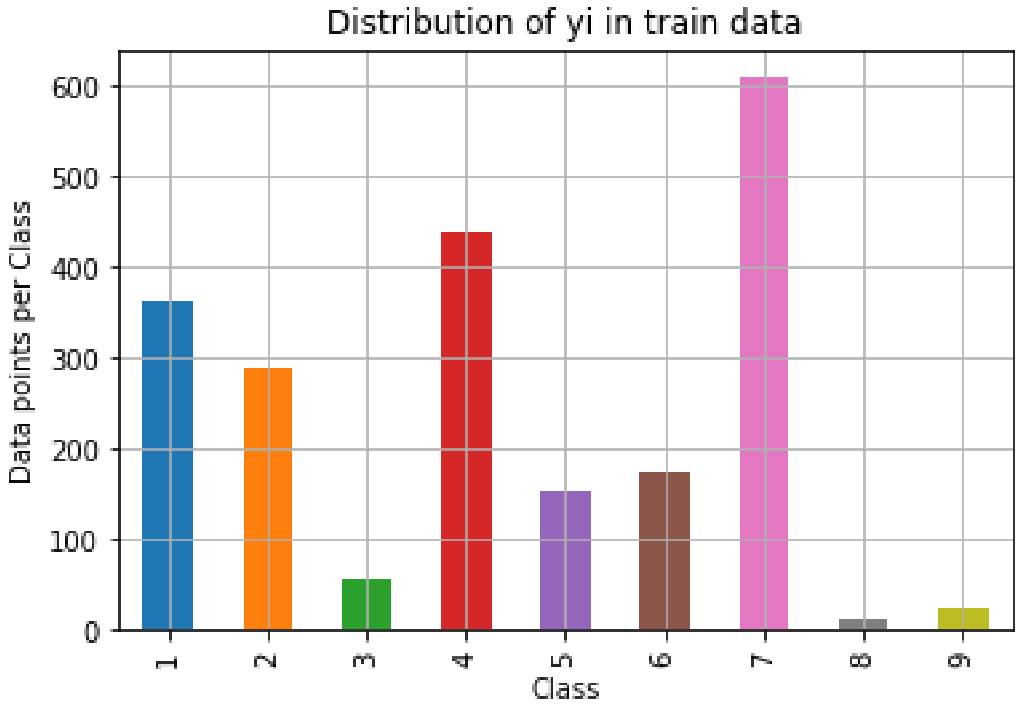
We split the data into train, test and cross validation data sets, preserving the ratio of class distribution in the original data set

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

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

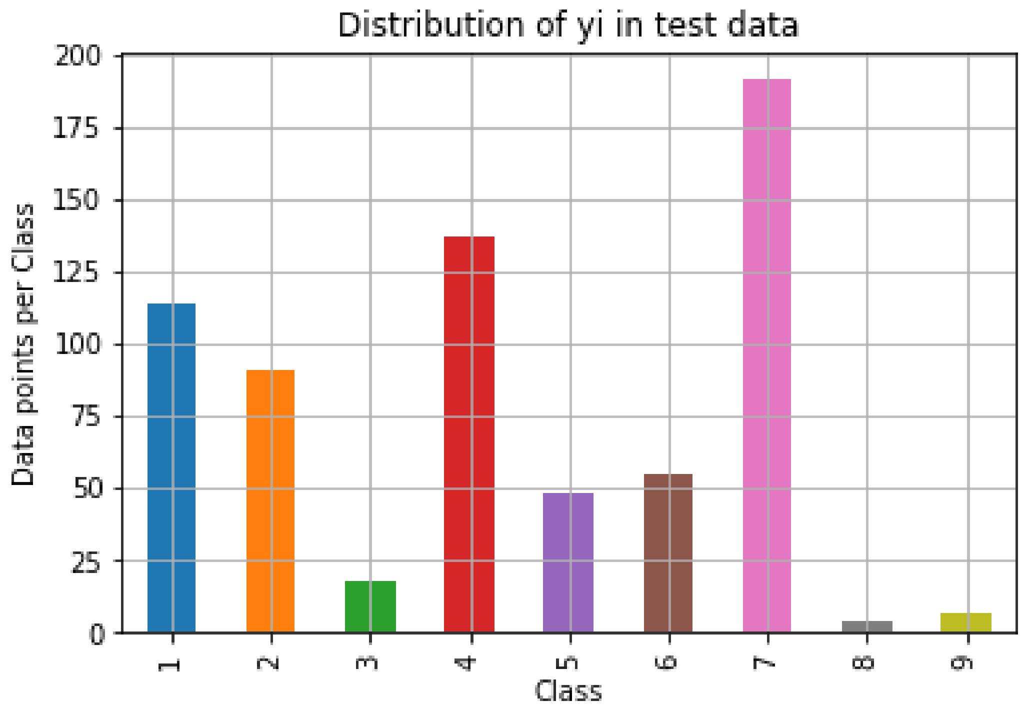
3.1.4.2. Distribution of y_i's in Train, Test and Cross Validation datasets

```
In [13]: # it returns a dict, keys as class labels and values as the number of data points in
         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.htm
         # -(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[


         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.htm
         # -(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.htm
         # -(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],
```

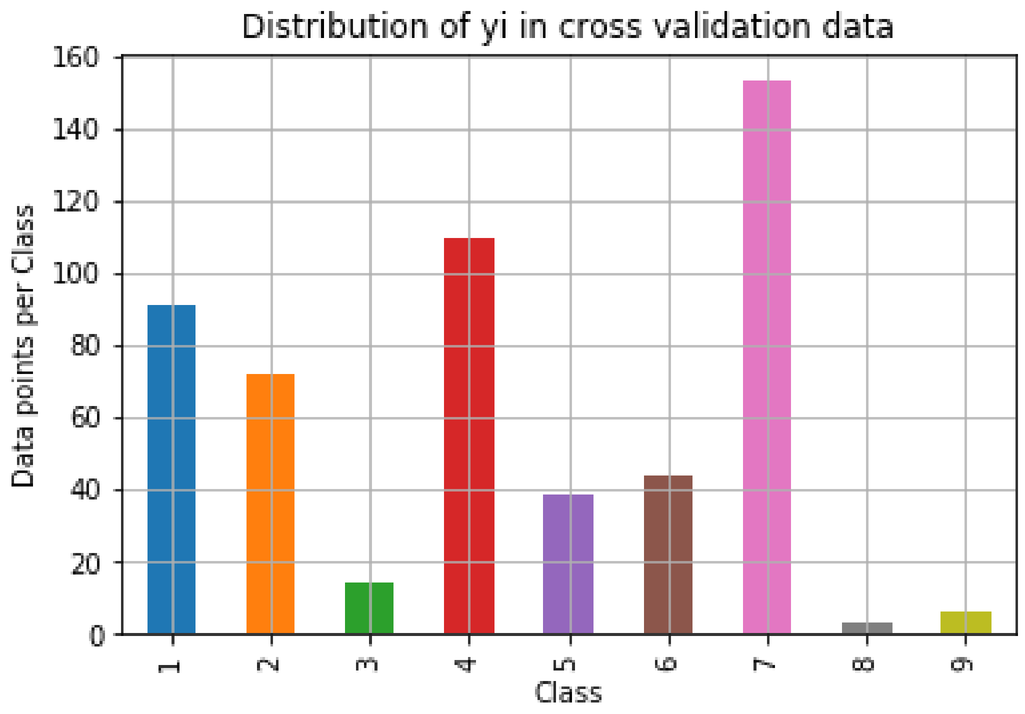


```
Number of data points in class 7 : 609 ( 28.672 %)
Number of data points in class 4 : 439 ( 20.669 %)
Number of data points in class 1 : 363 ( 17.09 %)
Number of data points in class 2 : 289 ( 13.606 %)
Number of data points in class 6 : 176 ( 8.286 %)
Number of data points in class 5 : 155 ( 7.298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

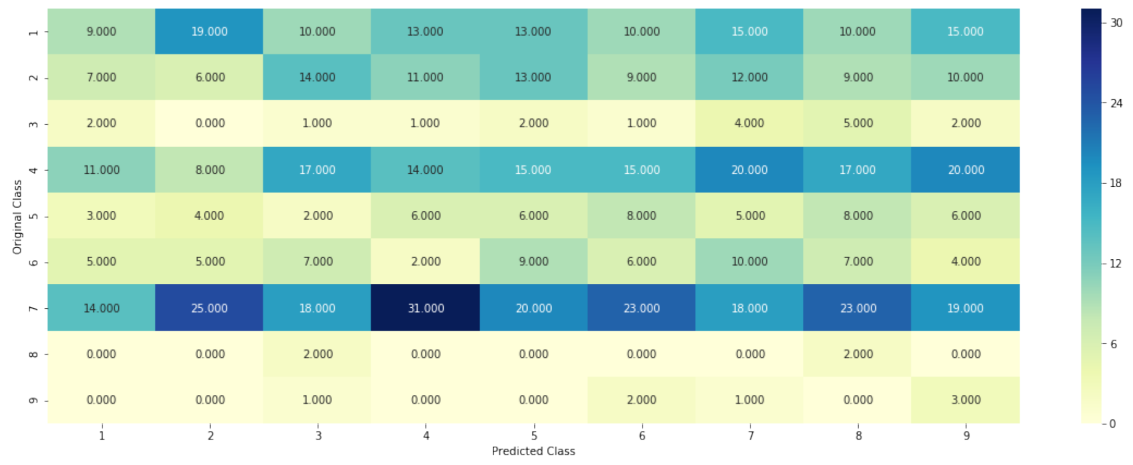
In a 'Random' Model, we generate the NINE class probabilites randomly such that they sum to 1.

```
In [14]: # This function plots the confusion matrices given y_i, y_i_hat.
         def plot_confusion_matrix(test_y, predict_y):
             C = confusion_matrix(test_y, predict_y)
             # C = 9,9 matrix, each cell (i,j) represents number of points of class i are pred

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

             # 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
             # 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
             # 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, yticklabe
             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, yticklabe
             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, yticklabe
             plt.xlabel('Predicted Class')
             plt.ylabel('Original Class')
             plt.show()
```

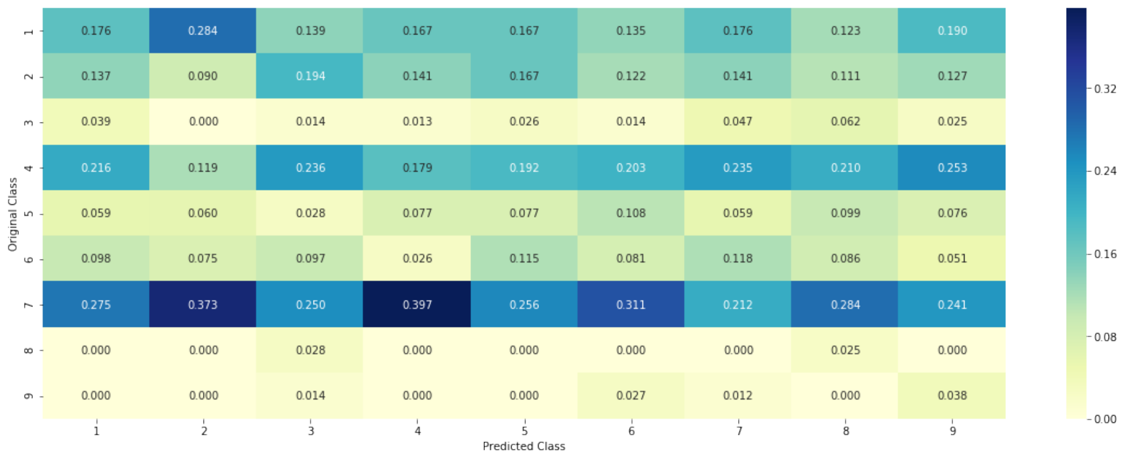
```
In [15]: # we need to generate 9 numbers and the sum of numbers should be 1
         # one solution is to genarate 9 numbers and divide each of the numbers by their sum
         # ref: https://stackoverflow.com/a/18662466/4084039
```

```
        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_predict


        # 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

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

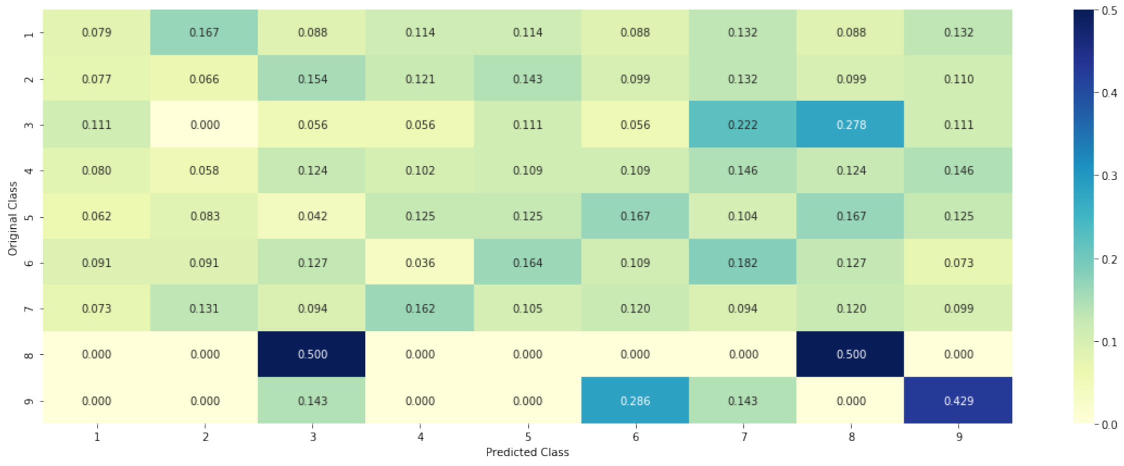
```
Log loss on Cross Validation Data using Random Model 2.452099167740608
Log loss on Test Data using Random Model 2.461602110997661
-------------------- Confusion matrix --------------------
```



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



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



3.3 Univariate Analysis

```
In [16]: # code for response coding with Laplace smoothing.
         # alpha : used for laplace smoothing
         # feature: ['gene', 'variation']
         # df: ['train_df', 'test_df', 'cv_df']
         # algorithm
         # ----------
         # Consider all unique values and the number of occurances of given feature in train d
         # build a vector (1*9) , the first element = (number of times it occured in class1 + 
         # gv_dict is like a look up table, for every gene it store a (1*9) representation of
         # 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 ge
    gv_dict = dict()

    # denominator will contain the number of time that particular feature occured in t
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to pert
        # 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 partic
                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, 
        #      'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 
        #      'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.06818181818181
        #      'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.060606060606060608, 
        #      'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 
        #      'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0
        #      'BRAF': [0.066666666666666666, 0.17999999999999999, 0.073333333333333334, 
        #      ...
        #     }
        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 va
        gv_fea = []
        # for every feature values in the given data frame we will check if it is there i
        # 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?

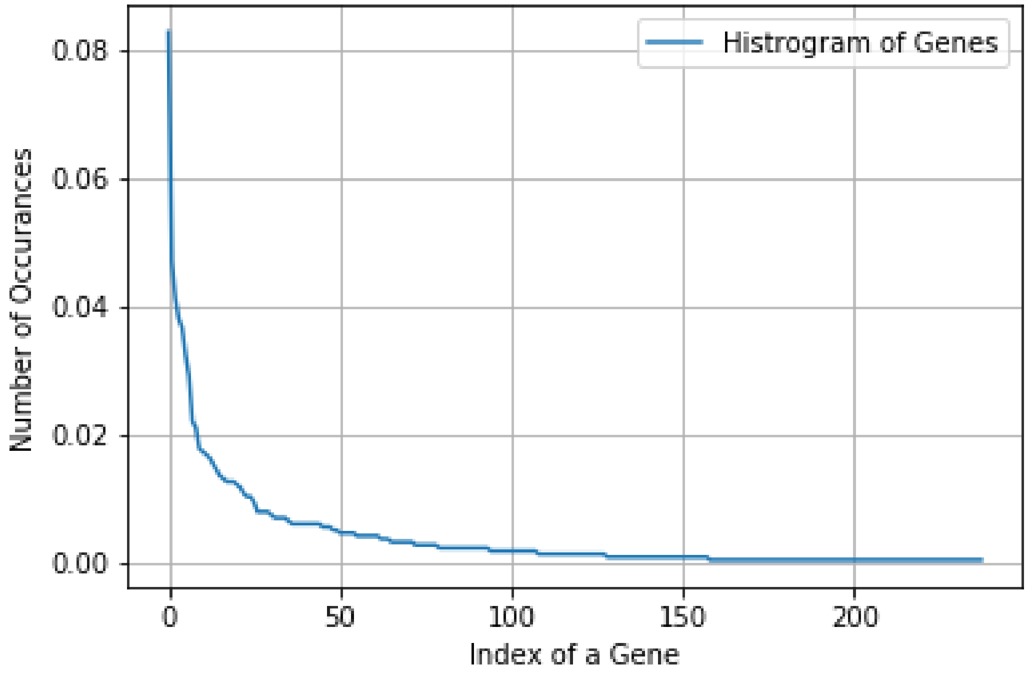
```
In [17]: unique_genes = train_df['Gene'].value_counts()
         print('Number of Unique Genes :', unique_genes.shape[0])
         # the top 10 genes that occured most
         print(unique_genes.head(10))
```

```
Number of Unique Genes : 238
BRCA1     176
TP53      100
EGFR       88
BRCA2      81
PTEN       78
KIT        69
BRAF       62
ALK        47
ERBB2      45
PIK3CA     38
Name: Gene, dtype: int64
```

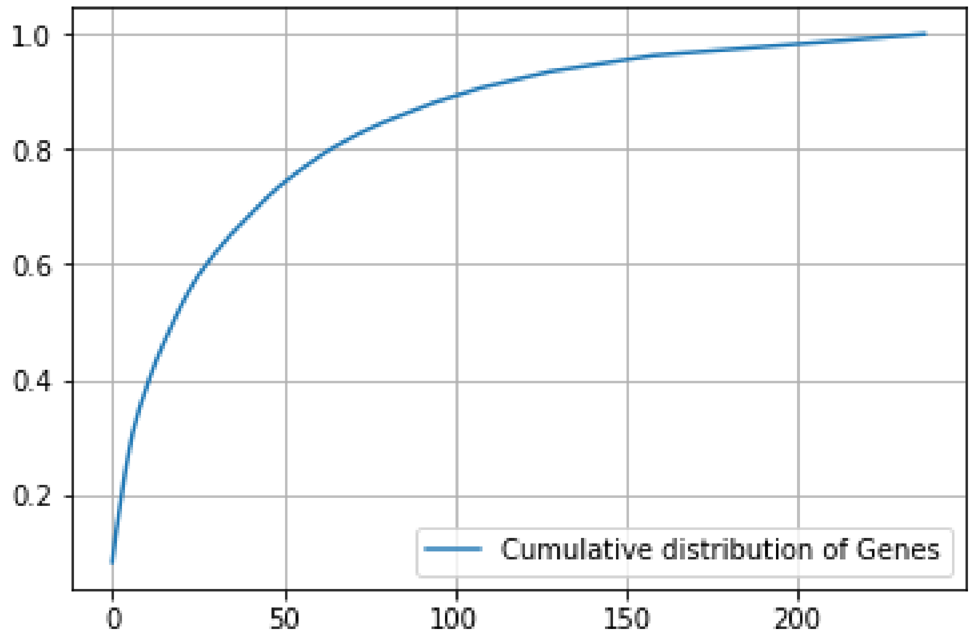
```
In [18]: print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in the
```

```
Ans: There are 238 different categories of genes in the train data, and they are distibuted as
```

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



```
In [20]: 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.

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

```
In [22]: print("train_gene_feature_responseCoding is converted feature using respone coding me
```

```
train_gene_feature_responseCoding is converted feature using respone coding method. The shape
```

```
In [23]: # one-hot encoding of Gene feature.
         gene_vectorizer = CountVectorizer(ngram_range=(1,2))
         train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gene'])
         test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gene'])
         cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
```

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

```
Out[24]: 2540    BRCA1
         2135    KEAP1
         432      TP53
         227      EGFR
         2662    BRCA1
         Name: Gene, dtype: object
```

```
In [25]: gene_vectorizer.get_feature_names()
```

```
Out[25]: ['abl1',
          'acvr1',
          'ago2',
          'akt1',
          'akt2',
'akt3',
'alk',
'apc',
'ar',
'araf',
'arid1a',
'arid5b',
'asxl1',
'asxl2',
'atm',
'atr',
'atrx',
'aurka',
'aurkb',
'b2m',
'bap1',
'bard1',
'bcl10',
'bcl2',
'bcl2l11',
'bcor',
'braf',
'brca1',
'brca2',
'brd4',
'brip1',
'btk',
'card11',
'carm1',
'casp8',
'cbl',
'ccnd1',
'ccnd2',
'ccnd3',
'ccne1',
'cdh1',
'cdk12',
'cdk4',
'cdk6',
'cdkn1a',
'cdkn1b',
'cdkn2a',
'cdkn2b',
'chek2',
'cic',
'crebbp',
'ctcf',
'ctla4',
'ctnnb1',
'ddr2',
'dicer1',
'dnmt3a',
'dnmt3b',
'dusp4',
'egfr',
'eif1ax',
'elf3',
'ep300',
'epas1',
'epcam',
'erbb2',
'erbb3',
'erbb4',
'ercc2',
'ercc3',
'ercc4',
'erg',
'esr1',
'etv1',
'etv6',
'ewsr1',
'ezh2',
'fam58a',
'fanca',
'fancc',
'fat1',
'fbxw7',
'fgf3',
'fgfr1',
'fgfr2',
'fgfr3',
'fgfr4',
'flt1',
'flt3',
'foxa1',
'foxl2',
'fubp1',
'gata3',
'gli1',
'gnaq',
'gnas',
'h3f3a',
'hist1h1c',
'hla',
'hnf1a',
'hras',
'idh1',
'idh2',
'igf1r',
'ikzf1',
'inpp4b',
'jak1',
'jak2',
'jun',
'kdm5a',
'kdm5c',
'kdm6a',
'kdr',
'keap1',
'kit',
'kmt2a',
'kmt2b',
'kmt2c',
'kmt2d',
'knstrn',
'kras',
'lats1',
'lats2',
'map2k1',
'map2k2',
'map2k4',
'map3k1',
'mapk1',
'mdm2',
'med12',
'mef2b',
'men1',
'met',
'mga',
'mlh1',
'mpl',
'msh2',
'msh6',
'mtor',
'myc',
'mycn',
'myd88',
'myod1',
'nf1',
'nf2',
'nfe2l2',
'nfkbia',
'nkx2',
'notch1',
'notch2',
'npm1',
'nras',
'ntrk1',
'ntrk2',
'ntrk3',
'nup93',
'pak1',
'pax8',
'pbrm1',
'pdgfra',
'pdgfrb',
'pik3ca',
'pik3cb',
'pik3cd',
'pik3r1',
'pik3r2',
'pik3r3',
'pim1',
'pms1',
'pms2',
'pole',
'ppm1d',
'ppp2r1a',
'ppp6c',
'prdm1',
'ptch1',
'pten',
'ptpn11',
'ptprd',
'ptprt',
'rab35',
'rac1',
'rad21',
'rad50',
'rad51b',
'rad54l',
'raf1',
'rasa1',
'rb1',
'rbm10',
'ret',
'rheb',
'rhoa',
'rictor',
'rit1',
'rnf43',
'ros1',
         'rras2',
         'runx1',
         'rxra',
         'sdhb',
         'setd2',
         'sf3b1',
         'shoc2',
         'shq1',
         'smad2',
         'smad3',
         'smad4',
         'smarca4',
         'smarcb1',
         'smo',
         'sos1',
         'sox9',
         'spop',
         'src',
         'stag2',
         'stat3',
         'stk11',
         'tcf3',
         'tcf7l2',
         'tert',
         'tet1',
         'tet2',
         'tgfbr1',
         'tgfbr2',
         'tmprss2',
         'tp53',
         'tp53bp1',
         'tsc1',
         'tsc2',
         'u2af1',
         'vegfa',
         'vhl',
         'whsc1',
         'xpo1',
         'xrcc2',
         'yap1']
```

```
In [26]: print("train_gene_feature_onehotCoding is converted feature using one-hot encoding me
```

```
train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape c
```

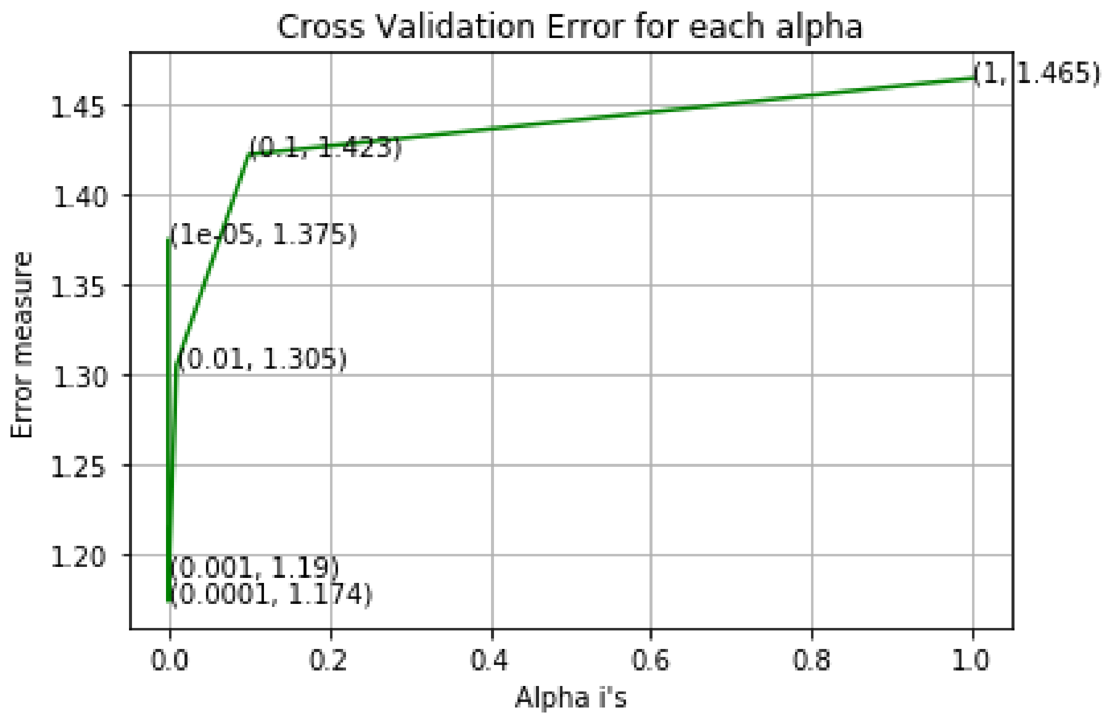
Q4. How good is this gene feature in predicting y_i?
There are many ways to estimate how good a feature is, in predicting y_i. One of the good

methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y_i.

```
In [27]: alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.

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

         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_l
        predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
        print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
        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_lo
```

```
For values of alpha =  1e-05 The log loss is: 1.375063722726775
For values of alpha =  0.0001 The log loss is: 1.1744000920873736
For values of alpha =  0.001 The log loss is: 1.189841816884131
For values of alpha =  0.01 The log loss is: 1.3053228123952432
For values of alpha =  0.1 The log loss is: 1.4226124194894003
For values of alpha =  1 The log loss is: 1.4648444750842369
```



```
For values of best alpha =  0.0001 The train log loss is: 1.0657497275989964
For values of best alpha =  0.0001 The cross validation log loss is: 1.1744000920873736
For values of best alpha =  0.0001 The test log loss is: 1.231969241885972
```

Q5. Is the Gene feature stable across all the data sets (Test, Train, Cross validation)?
Ans. Yes, it is. Otherwise, the CV and Test errors would be significantly more than train error.

```
In [28]: print("Q6. How many data points in Test and CV datasets are covered by the ", unique_g
         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_cove
         print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_co
```

```
Q6. How many data points in Test and CV datasets are covered by the  238  genes in train datas
Ans
1. In test data 648 out of 665 : 97.44360902255639
2. In cross validation data 518 out of  532 : 97.36842105263158
```

3.2.2 Univariate Analysis on Variation Feature
Q7. Variation, What type of feature is it ?
Ans. Variation is a categorical variable
Q8. How many categories are there?

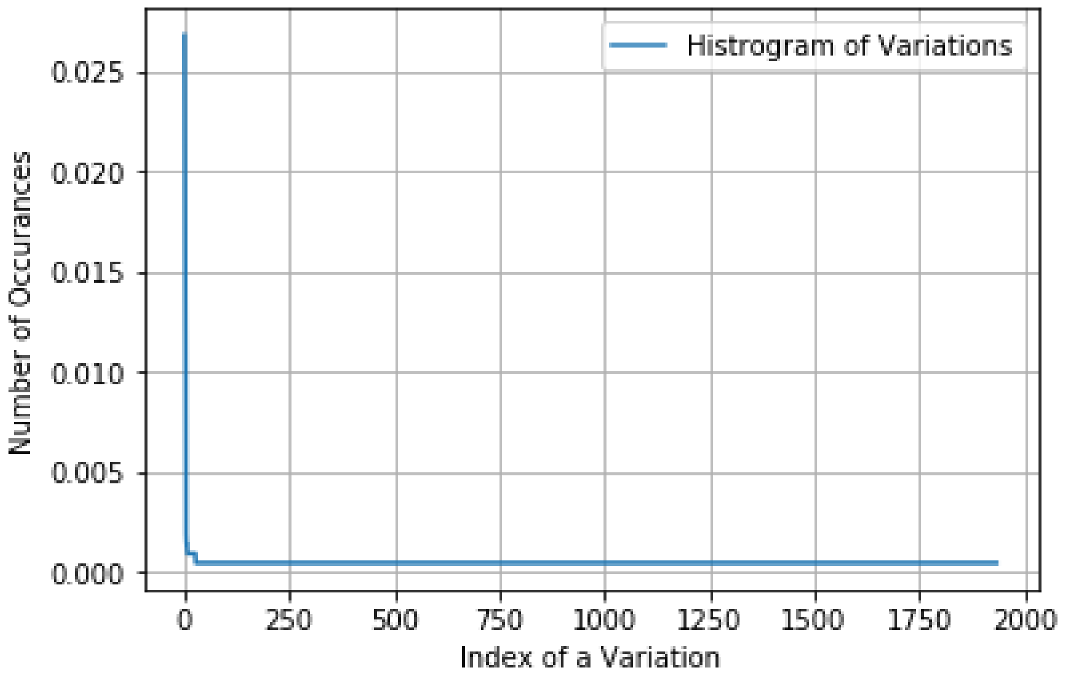
```
In [29]: unique_variations = train_df['Variation'].value_counts()
         print('Number of Unique Variations :', unique_variations.shape[0])
         # the top 10 variations that occured most
         print(unique_variations.head(10))
```

```
Number of Unique Variations : 1936
Truncating_Mutations    57
Deletion                46
Amplification           41
Fusions                 21
Overexpression           4
Q61R                     3
G12V                     3
G13D                     2
Y64A                     2
Q61H                     2
Name: Variation, dtype: int64
```

```
In [30]: print("Ans: There are", unique_variations.shape[0] ,"different categories of variatio
```

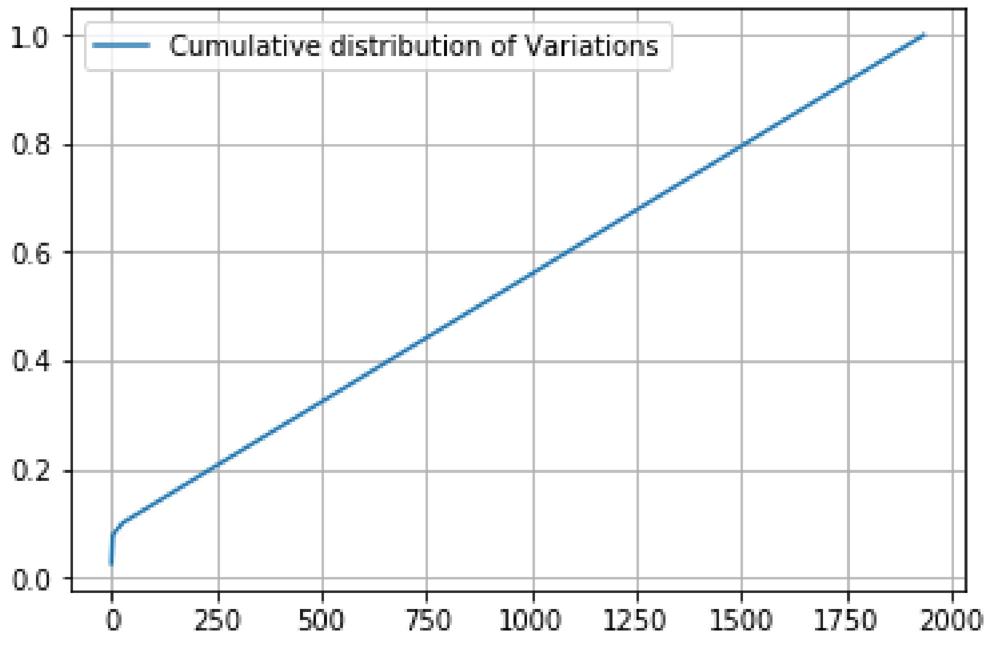
```
Ans: There are 1936 different categories of variations in the train data, and they are distibu
```

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



```
In [32]: c = np.cumsum(h)
         print(c)
         plt.plot(c,label='Cumulative distribution of Variations')
         plt.grid()
         plt.legend()
         plt.show()
```

```
[0.02683616 0.04849341 0.06779661 ... 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

```
In [33]: # alpha is used for laplace smoothing
         alpha = 1
         # train gene feature
         train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", t
         # test gene feature
         test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", te
         # cross validation gene feature
         cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", cv_c
```

```
In [34]: print("train_variation_feature_responseCoding is a converted feature using the respons
```

```
train_variation_feature_responseCoding is a converted feature using the response coding method
```

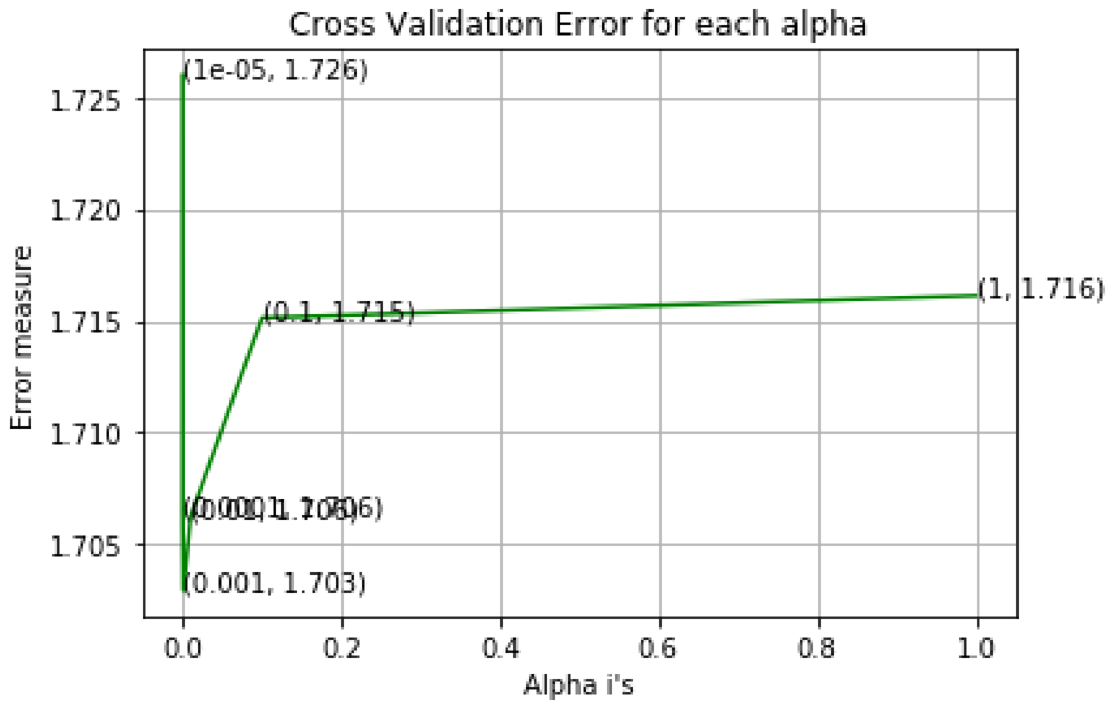
```
In [35]: # one-hot encoding of variation feature.
         variation_vectorizer = CountVectorizer(ngram_range=(1,2))
         train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Va
         test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variatio
         cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation']]
In [36]: print("train_variation_feature_onehotEncoded is converted feature using the onne-hot e

train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method.
```

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

```
In [37]: alpha = [10 ** x for x in range(-5, 1)]

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

         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=4
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_
predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log los
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_l
```

```
For values of alpha =  1e-05 The log loss is: 1.7259804819131999
For values of alpha =  0.0001 The log loss is: 1.7063050092322196
For values of alpha =  0.001 The log loss is: 1.7029545445641736
For values of alpha =  0.01 The log loss is: 1.7062266665449326
For values of alpha =  0.1 The log loss is: 1.7151296672130445
For values of alpha =  1 The log loss is: 1.7161238737907758
```



```
For values of best alpha =  0.001 The train log loss is: 1.131530373948977
For values of best alpha =  0.001 The cross validation log loss is: 1.7029545445641736
For values of best alpha =  0.001 The test log loss is: 1.6911020720303618
```

Q11. Is the Variation feature stable across all the data sets (Test, Train, Cross validation)?
Ans. Not sure! But lets be very sure using the below analysis.

```
In [38]: print("Q12. How many data points are covered by total ", unique_variations.shape[0], '
         test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))].sha
         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_cove
         print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_co
```

```
Q12. How many data points are covered by total  1936  genes in test and cross validation data s
Ans
1. In test data 73 out of 665 : 10.977443609022556
2. In cross validation data 59 out of  532 : 11.090225563909774
```

3.2.3 Univariate Analysis on Text Feature

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

```
In [39]: # 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
```

```
In [40]: import math
         #https://stackoverflow.com/a/1602964
         def get_text_responsecoding(df):
             text_feature_responseCoding = np.zeros((df.shape[0],9))
             for i in range(0,9):
                 row_index = 0
                 for index, row in df.iterrows():
                     sum_prob = 0
                     for word in row['TEXT'].split():
                         sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(total_dict.get(w
                     text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TE
                     row_index += 1
             return text_feature_responseCoding
```

```
In [41]: # building a CountVectorizer with all the words that occured minimum 3 times in train
         text_vectorizer = CountVectorizer(ngram_range=(1,2))
         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*nu
         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 i
         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 : 2361939
```

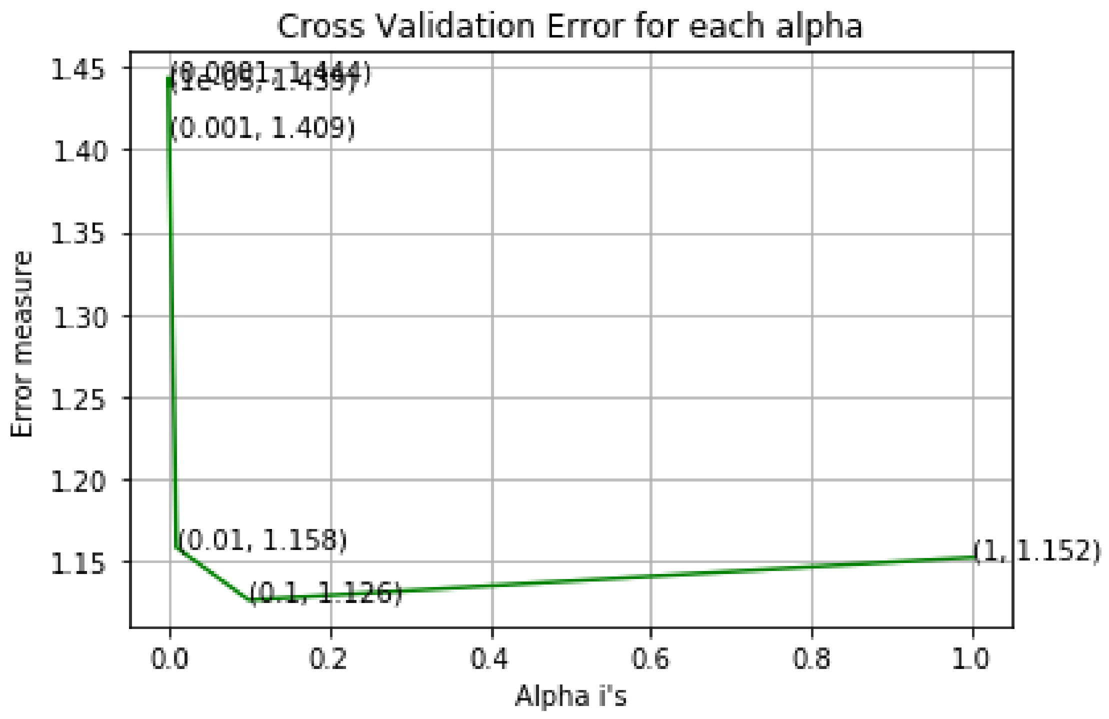
```
In [42]: dict_list = []
         # dict_list =[] contains 9 dictoinaries each corresponds to a class
         for i in range(1,10):
             cls_text = train_df[train_df['Class']==i]
             # build a word dict based on the words in that class
             dict_list.append(extract_dictionary_paddle(cls_text))
             # append it to dict_list

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


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

```
In [43]: #response coding of text features
         train_text_feature_responseCoding  = get_text_responsecoding(train_df)
         test_text_feature_responseCoding  = get_text_responsecoding(test_df)
         cv_text_feature_responseCoding  = get_text_responsecoding(cv_df)
```

```
In [44]: # https://stackoverflow.com/a/16202486
         # we convert each row values such that they sum to 1
         train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train_text_fe
         test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_featu
         cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_res

In [45]: # 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)

In [46]: #https://stackoverflow.com/a/2258273/4084039
         sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambda x: x[1] , reverse
         sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))

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

Counter({1: 1120890, 2: 384208, 3: 178200, 4: 134864, 5: 76182, 6: 60389, 8: 45067, 7: 41800, 9


In [48]: # Train a Logistic regression+Calibration model using text features whicha re on-hot
         alpha = [10 ** x for x in range(-5, 1)]

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

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_l
predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
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_lo
```

```
For values of alpha =  1e-05 The log loss is: 1.438891539589418
For values of alpha =  0.0001 The log loss is: 1.4436719382209038
For values of alpha =  0.001 The log loss is: 1.408816731922225
For values of alpha =  0.01 The log loss is: 1.1580957747958407
For values of alpha =  0.1 The log loss is: 1.1260683549592077
For values of alpha =  1 The log loss is: 1.1520146812098149
```



```
For values of best alpha =  0.1 The train log loss is: 0.6838124689208502
For values of best alpha =  0.1 The cross validation log loss is: 1.1260683549592077
For values of best alpha =  0.1 The test log loss is: 1.2796363534082154
```

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

```
In [49]: def get_intersec_text(df):
             df_text_vec = CountVectorizer(ngram_range=(1,2))
             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
```

```
In [50]: 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
70.18 % of word of test data appeared in train data
76.673 % of word of Cross Validation appeared in train data
```

4. Machine Learning Models

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

         #Misc. functionns for ML models


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

             # for calculating log_loss we willl provide the array of probabilities belongs to
             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))/tes
             plot_confusion_matrix(test_y, pred_y)

In [52]: def report_log_loss(train_x, train_y, test_x, test_y,  clf):
             clf.fit(train_x, train_y)
             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_x, train_y)
             sig_clf_probs = sig_clf.predict_proba(test_x)
             return log_loss(test_y, sig_clf_probs, eps=1e-15)

In [53]: # this function will be used just for naive bayes
         # for the given indices, we will print the name of the features
         # and we will check whether the feature present in the test point text or not
         def get_impfeature_names(indices, text, gene, var, no_features):
             gene_count_vec = CountVectorizer(ngram_range=(1,2))
             var_count_vec = CountVectorizer(ngram_range=(1,2))
             text_count_vec = CountVectorizer(ngram_range=(1,2))

             gene_vec = gene_count_vec.fit(train_df['Gene'])
             var_vec  = var_count_vec.fit(train_df['Variation'])
             text_vec = text_count_vec.fit(train_df['TEXT'])

             fea1_len = len(gene_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(w
            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 [{}]".form
            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(w

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

Stacking the three types of features

```
In [54]: # merging gene, variance and text features

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

         train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,train_variation
         test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_fe
         cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_

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

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

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


         train_gene_var_responseCoding = np.hstack((train_gene_feature_responseCoding,train_va
         test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCoding,test_varia
         cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variation_f
        train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_feature_
        test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature_res
        cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_response(

In [55]: print("One hot encoding features :")
         print("(number of data points * number of features) in train data = ", train_x_onehot(
         print("(number of data points * number of features) in test data = ", test_x_onehotCod
         print("(number of data points * number of features) in cross validation data =", cv_x_
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (2124, 2364253)
(number of data points * number of features) in test data =  (665, 2364253)
(number of data points * number of features) in cross validation data = (532, 2364253)
```

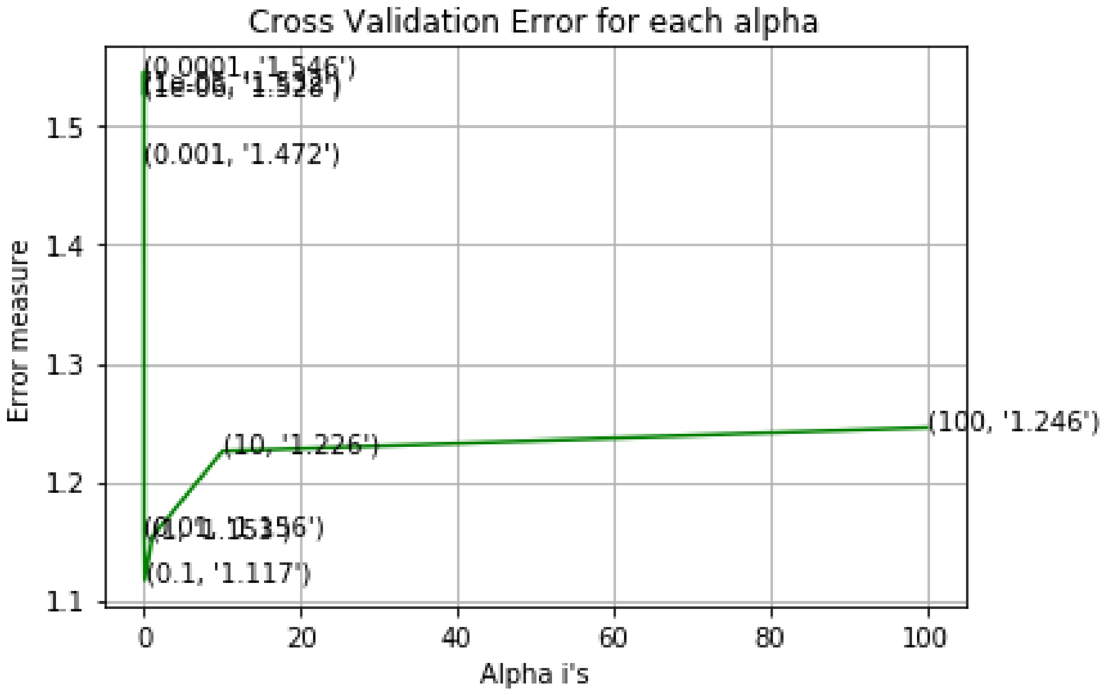
```
In [56]: print(" Response encoding features :")
         print("(number of data points * number of features) in train data = ", train_x_respons
         print("(number of data points * number of features) in test data = ", test_x_response(
         print("(number of data points * number of features) in cross validation data =", cv_x_
```

```
 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. Logistic Regression
4.1.1. With Class balancing
4.1.1.1. Hyper paramter tuning

```
In [57]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # 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 Gr
         # predict(X)        Predict class labels for samples in X.

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


         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
         # ----------------------------
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
         #
         # 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', ra
             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=
             # to avoid rounding error while multiplying probabilites we use log-probability e
             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', lo
         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_l
         predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
         print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
         predict_y = sig_clf.predict_proba(test_x_onehotCoding)
         print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_lo
         # Variables that will be used in the end to make comparison table of all models
         lr_balance_train = log_loss(y_train, sig_clf.predict_proba(train_x_onehotCoding), labe
         lr_balance_cv = log_loss(y_cv, sig_clf.predict_proba(cv_x_onehotCoding), labels=clf.cl
         lr_balance_test = log_loss(y_test, sig_clf.predict_proba(test_x_onehotCoding), labels=
```

```
for alpha = 1e-06
Log Loss : 1.528100429339769
for alpha = 1e-05
Log Loss : 1.5317871743792535
for alpha = 0.0001
Log Loss : 1.5461164891705341
for alpha = 0.001
Log Loss : 1.4720074521434952
for alpha = 0.01
Log Loss : 1.1556838815265633
for alpha = 0.1
Log Loss : 1.116607671022237
for alpha = 1
Log Loss : 1.15323944264721
for alpha = 10
Log Loss : 1.2257097953657432
for alpha = 100
Log Loss : 1.2456776853766127
```

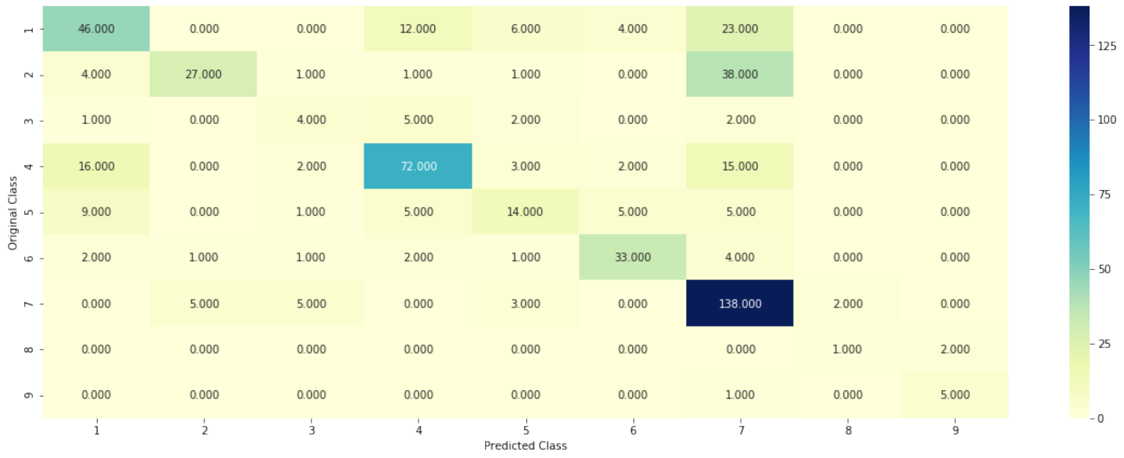


```
For values of best alpha =  0.1 The train log loss is: 0.6839246694590282
For values of best alpha =  0.1 The cross validation log loss is: 1.116607671022237
For values of best alpha =  0.1 The test log loss is: 1.2757087574173855
```

4.1.1.2. Testing the model with best hyper paramters

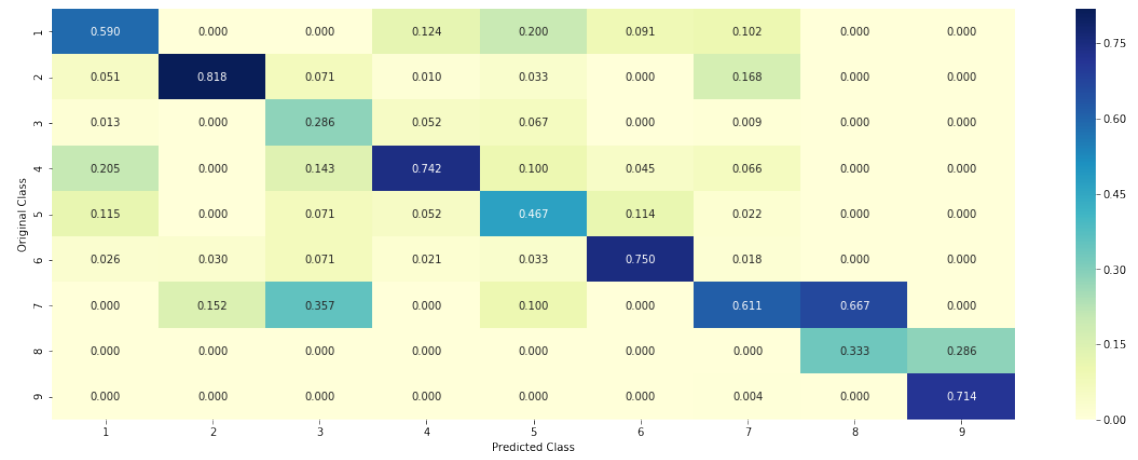
```
In [58]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # 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 Gr
         # predict(X)       Predict class labels for samples in X.

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

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

         # Variables that will be used in the end to make comparison table of models
         lr_balance_misclassified = (np.count_nonzero((sig_clf.predict(cv_x_onehotCoding)- cv_
```

```
Log loss : 1.116607671022237
Number of mis-classified points : 0.3609022556390977
-------------------- Confusion matrix --------------------
```

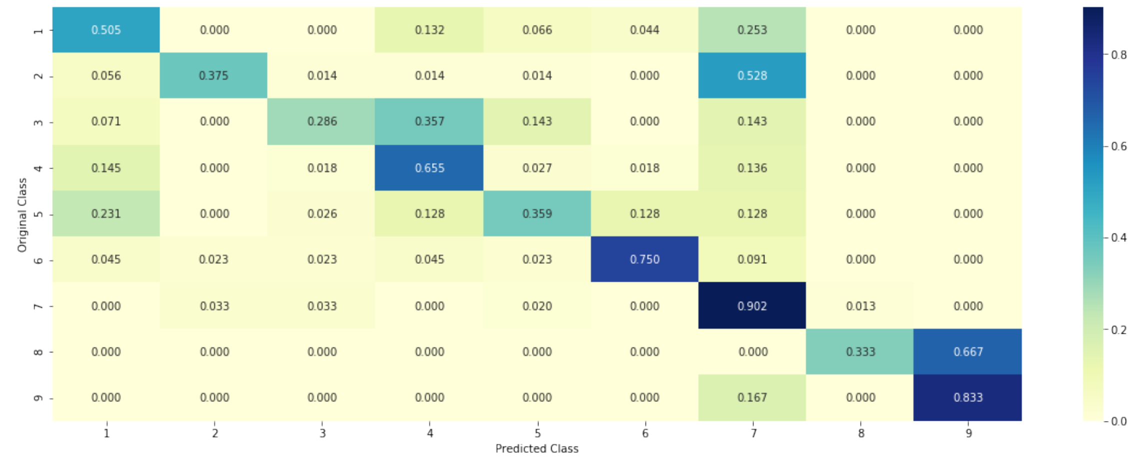


	1	2	3	4	5	6	7	8	9
1	46.000	0.000	0.000	12.000	6.000	4.000	23.000	0.000	0.000
2	4.000	27.000	1.000	1.000	1.000	0.000	38.000	0.000	0.000
3	1.000	0.000	4.000	5.000	2.000	0.000	2.000	0.000	0.000
4	16.000	0.000	2.000	72.000	3.000	2.000	15.000	0.000	0.000
5	9.000	0.000	1.000	5.000	14.000	5.000	5.000	0.000	0.000
6	2.000	1.000	1.000	2.000	1.000	33.000	4.000	0.000	0.000
7	0.000	5.000	5.000	0.000	3.000	0.000	138.000	2.000	0.000
8	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	2.000
9	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	5.000

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



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



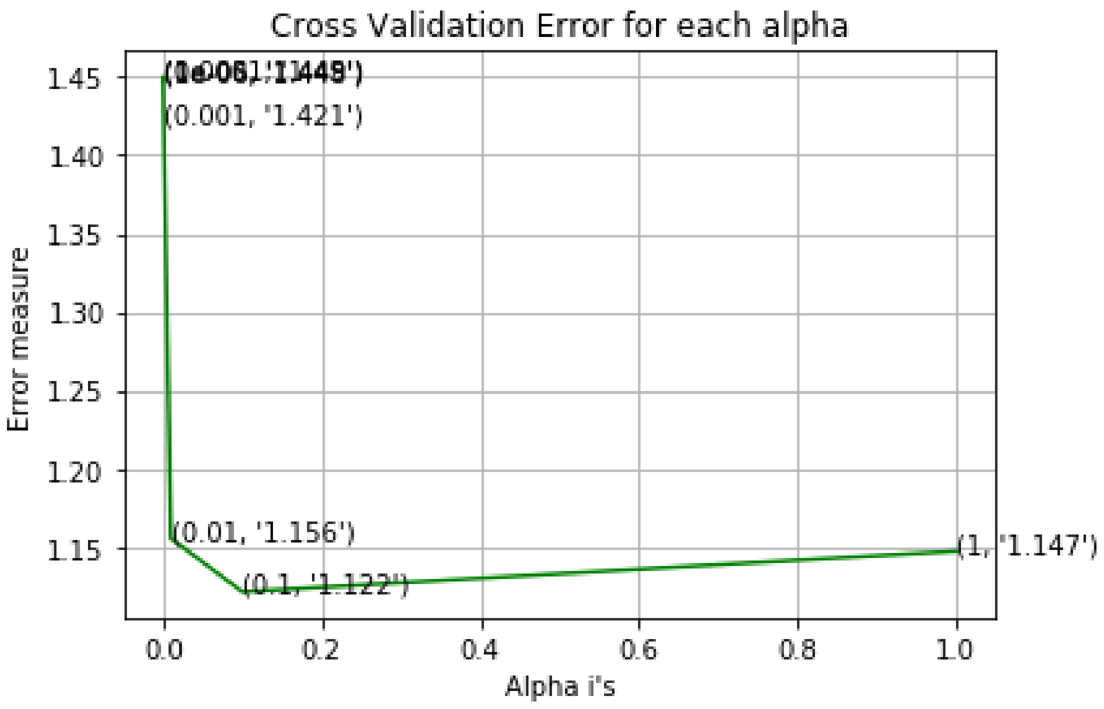
4.1.2. Without Class balancing

4.1.2.1. Hyper paramter tuning

```
In [59]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # 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 Gr
         # predict(X)        Predict class labels for samples in X.

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



         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modul
         # ----------------------------
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method=sigmoid, cv=
         #
         # 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=
             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=4
        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_
        predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
        print('For values of best alpha = ', alpha[best_alpha], "The cross validation log los
        predict_y = sig_clf.predict_proba(test_x_onehotCoding)
        print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l

        # Variables that will be used in the end to make comparison table of all models
        lr_train = log_loss(y_train, sig_clf.predict_proba(train_x_onehotCoding), labels=clf.
        lr_cv = log_loss(y_cv, sig_clf.predict_proba(cv_x_onehotCoding), labels=clf.classes_,
        lr_test = log_loss(y_test, sig_clf.predict_proba(test_x_onehotCoding), labels=clf.cla
```

```
for alpha = 1e-06
Log Loss : 1.4482170191030546
for alpha = 1e-05
Log Loss : 1.449367182497197
for alpha = 0.0001
Log Loss : 1.450163184095045
for alpha = 0.001
Log Loss : 1.4208468938915646
for alpha = 0.01
Log Loss : 1.155573501289515
for alpha = 0.1
Log Loss : 1.1215756276000022
for alpha = 1
Log Loss : 1.147370692220747
```

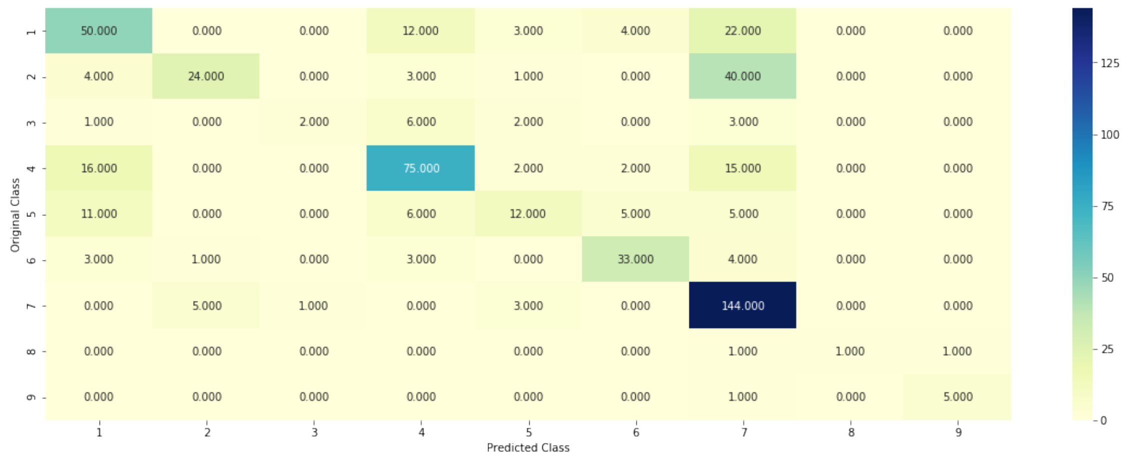


```
For values of best alpha =  0.1 The train log loss is: 0.6745181265032683
For values of best alpha =  0.1 The cross validation log loss is: 1.1215756276000022
For values of best alpha =  0.1 The test log loss is: 1.2728782499529145
```

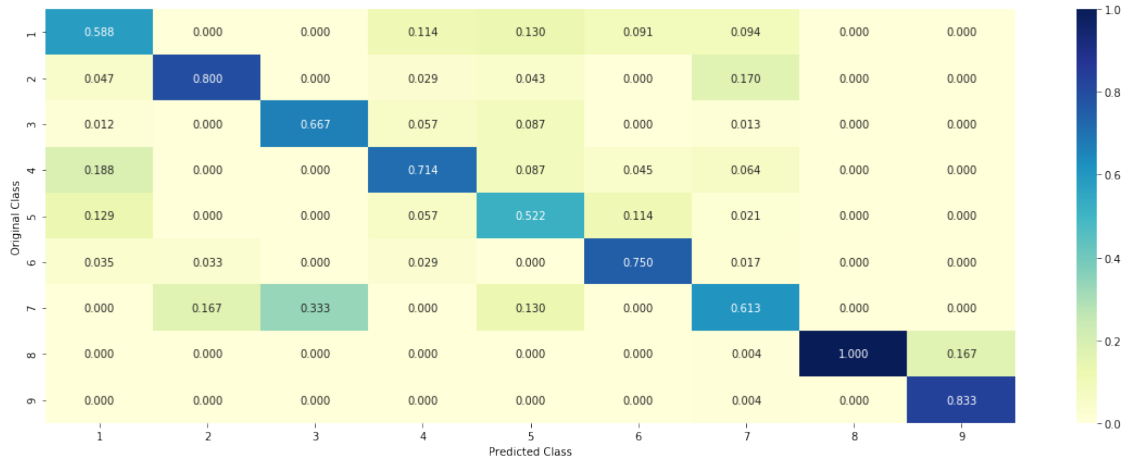
4.1.2.2. Testing model with best hyper parameters

```
In [60]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # 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 Gr
         # predict(X)        Predict class labels for samples in X.

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

         clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=4
         predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, c
         clf.fit(train_x_onehotCoding, train_y)
         sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig_clf.fit(train_x_onehotCoding, train_y)

         # Variables that will be used in the end to make comparison table of models
         lr_misclassified = (np.count_nonzero((sig_clf.predict(cv_x_onehotCoding)- cv_y))/cv_y
```

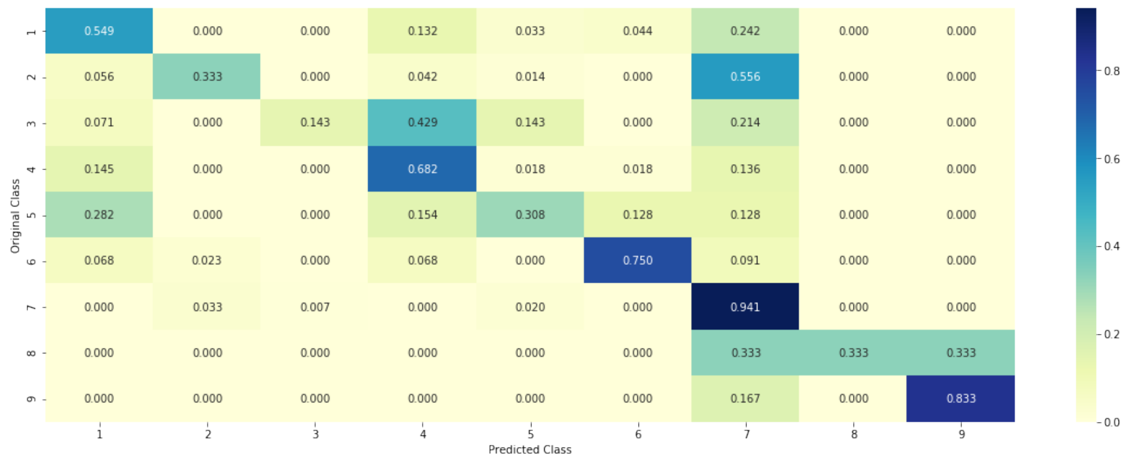
```
Log loss : 1.1215756276000022
Number of mis-classified points : 0.34962406015037595
-------------------- Confusion matrix --------------------
```



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



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



2 CONCLUSION

3 (a). Procedure Followed :-

STEP 1:- Replace CountVectorizer() by CountVectorizer(ngram_range=(1,2)) in all the one hot encoding section of gene , variation and text features to get unigrams and bigrams .

STEP 2:- Then Apply Logistic Regression

4 (b).Table (Model Performances):-

```
In [61]: # Creating table using PrettyTable library
         from prettytable import PrettyTable

         # Names of models
         names =['LR With Class Balancing','LR Without Class Balancing']

         # Training loss
         train_loss = [lr_balance_train,lr_train]

         # Cross Validation loss
         cv_loss = [lr_balance_cv,lr_cv]

         # Test loss
         test_loss = [lr_balance_test,lr_test]

         # Percentage Misclassified points
         misclassified = [lr_balance_misclassified,lr_misclassified]
```

```python
numbering = [1,2]

# Initializing prettytable
ptable = PrettyTable()

# Adding columns
ptable.add_column("S.NO.",numbering)
ptable.add_column("MODEL",names)
ptable.add_column("Train_loss",train_loss)
ptable.add_column("CV_loss",cv_loss)
ptable.add_column("Test_loss",test_loss)
ptable.add_column("Misclassified(%)",misclassified)

# Printing the Table
print(ptable)
```

```
+-------+----------------------------+--------------------+--------------------+---------------
| S.NO. |           MODEL            |     Train_loss     |      CV_loss       |     Test_loss
+-------+----------------------------+--------------------+--------------------+---------------
|   1   |  LR With Class Balancing   | 0.6839246694590282 | 1.116607671022237  | 1.27570875741
|   2   | LR Without Class Balancing | 0.6745181265032683 | 1.1215756276000022 | 1.27287824995
+-------+----------------------------+--------------------+--------------------+---------------
```