Personalized cancer diagnosis

Task 2

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 (https://www.youtube.com/watch?v=UwbuW7oK8rk (https://www.youtube.com/watch?v=UwbuW7oK8rk)
- 3. https://www.youtube.com/watch?v=qxXRKVompl8 (https://www.youtube.com/watch?v=qxXRKVompl8)

1.3. Real-world/Business objectives and constraints.

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

2. Machine Learning Problem Formulation

2.1. Data

2.1.1. Data Overview

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

2.1.2. Example Data Point

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

• • •

training text

ID,Text

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

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

2.2.1. Type of Machine Learning Problem

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

2.2.2. Performance Metric

Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation (<a href="https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluatio

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 probabilities => Metric is Log-loss. * No Latency constraints.

2.3. Train, CV and Test Datasets

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

3. Exploratory Data Analysis

```
In [1]: import pandas as pd
        import matplotlib.pyplot as plt
        import re
        import time
        import warnings
        import numpy as np
        from nltk.corpus import stopwords
        from sklearn.decomposition import TruncatedSVD
        from sklearn.preprocessing import normalize
        from sklearn.feature extraction.text import CountVectorizer
        from sklearn.manifold import TSNE
        import seaborn as sns
        from sklearn.neighbors import KNeighborsClassifier
        from sklearn.metrics import confusion matrix
        from sklearn.metrics.classification import accuracy score, log loss
        from sklearn.feature extraction.text import TfidfVectorizer
        from sklearn.linear model import SGDClassifier
        from imblearn.over sampling import SMOTE
        from collections import Counter
        from scipy.sparse import hstack
        from sklearn.multiclass import OneVsRestClassifier
        from sklearn.svm import SVC
        from sklearn.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
        warnings.filterwarnings("ignore")
        from mlxtend.classifier import StackingClassifier
        from sklearn import model selection
        from sklearn.linear model import LogisticRegression
```

precated in version 0.18 in favor of the model_selection module into which all the refactored classes and functions are moved. Also note that the interface of the new CV iterators are different from that of this module. This module will be removed in 0.20.

"This module will be removed in 0.20.", DeprecationWarning)

C:\Users\Himanshu Pc\Anaconda3\lib\site-packages\sklearn\ensemble\weight_boosting.py:29: DeprecationWarning: numpy.cor
e.umath_tests is an internal NumPy module and should not be imported. It will be removed in a future NumPy release.
from numpy.core.umath_tests import inner1d

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

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

Number of data points : 3321

Number of features : 4

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

Out[2]:

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

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

- **ID**: the id of the row used to link the mutation to the clinical evidence
- Gene: the gene where this genetic mutation is located

- Variation : the aminoacid change for this mutations
- Class: 1-9 the class this genetic mutation has been classified on

3.1.2. Reading Text Data

```
In [3]: # note the seprator in this file
         data text =pd.read csv("training text.csv",sep="\|\|",engine="python",names=["ID","TEXT"],skiprows=1)
         print('Number of data points : ', data text.shape[0])
         print('Number of features : ', data text.shape[1])
         print('Features : ', data text.columns.values)
         data text.head()
         Number of data points : 3321
         Number of features : 2
         Features : ['ID' 'TEXT']
Out[3]:
            ID
                                                  TEXT
                 Cyclin-dependent kinases (CDKs) regulate a var...
          1
                  Abstract Background Non-small cell lung canc...
                  Abstract Background Non-small cell lung canc...
                Recent evidence has demonstrated that acquired...
             4 Oncogenic mutations in the monomeric Casitas B...
In [4]: import nltk
         nltk.download('stopwords')
         [nltk data] Downloading package stopwords to C:\Users\Himanshu
         [nltk data]
                          Pc\AppData\Roaming\nltk data...
                        Package stopwords is already up-to-date!
         [nltk data]
Out[4]: True
```

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: 124.60713170000001 seconds
```

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

Out[7]:

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

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

Out[8]:

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

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

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])

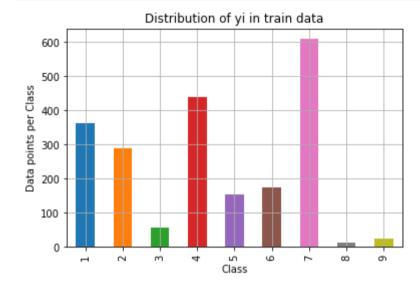
Number of data points in train data: 2124
    Number of data points in test data: 665
    Number of data points in cross validation data: 532
```

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

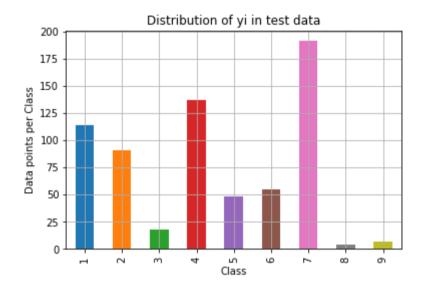
```
In [13]: # it returns a dict, keys as class labels and values as the number of data points in that class
         train class distribution = train df['Class'].value counts().sortlevel()
         test class distribution = test df['Class'].value counts().sortlevel()
         cv class distribution = cv df['Class'].value counts().sortlevel()
         my colors = 'rgbkymc'
         train class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.vlabel('Data points per Class')
         plt.title('Distribution of vi 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 vi:
             print('Number of data points in class', i+1, ':', train class distribution.values[i], '(', np.round((train class dist
         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 vi:
             print('Number of data points in class', i+1, ':',test class distribution.values[i], '(', np.round((test class distribution)))
         print('-'*80)
          mv colors = 'rgbkvmc'
         cv class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in cross validation data')
```

```
plt.grid()
plt.show()

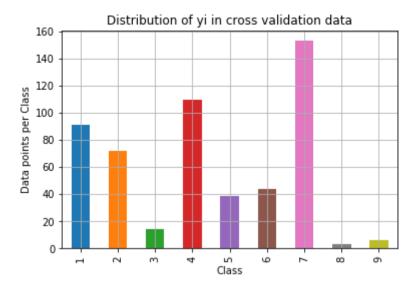
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',cv_class_distribution.values[i],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



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 predicted class j
             A = (((C.T)/(C.sum(axis=1))).T)
             #divid each element of the confusion matrix with the sum of elements in that column
             \# C = [[1, 2],
             # [3, 4]]
             # C.T = [[1, 3],
                      [2, 4]]
             # C.sum(axis = 1) axis=0 corresponds to columns and axis=1 corresponds to rows in two diamensional array
             # C.sum(axix = 1) = [[3, 7]]
             \# ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
                                         [2/3, 4/7]]
             # ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]]
                                        [3/7, 4/7]]
             # sum of row elements = 1
             B = (C/C.sum(axis=0))
             #divid each element of the confusion matrix with the sum of elements in that row
             \# C = [[1, 2],
                   [3, 4]]
             # C.sum(axis = 0) axis=0 corresonds to columns and axis=1 corresponds to rows in two diamensional array
             # C.sum(axix = 0) = [[4, 6]]
             \# (C/C.sum(axis=0)) = [[1/4, 2/6],
                                    [3/4, 4/6]]
             labels = [1,2,3,4,5,6,7,8,9]
             # representing A in heatmap format
             print("-"*20, "Confusion matrix", "-"*20)
             plt.figure(figsize=(20,7))
             sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
             plt.xlabel('Predicted Class')
             plt.ylabel('Original Class')
             plt.show()
             print("-"*20, "Precision matrix (Column Sum=1)", "-"*20)
             plt.figure(figsize=(20,7))
```

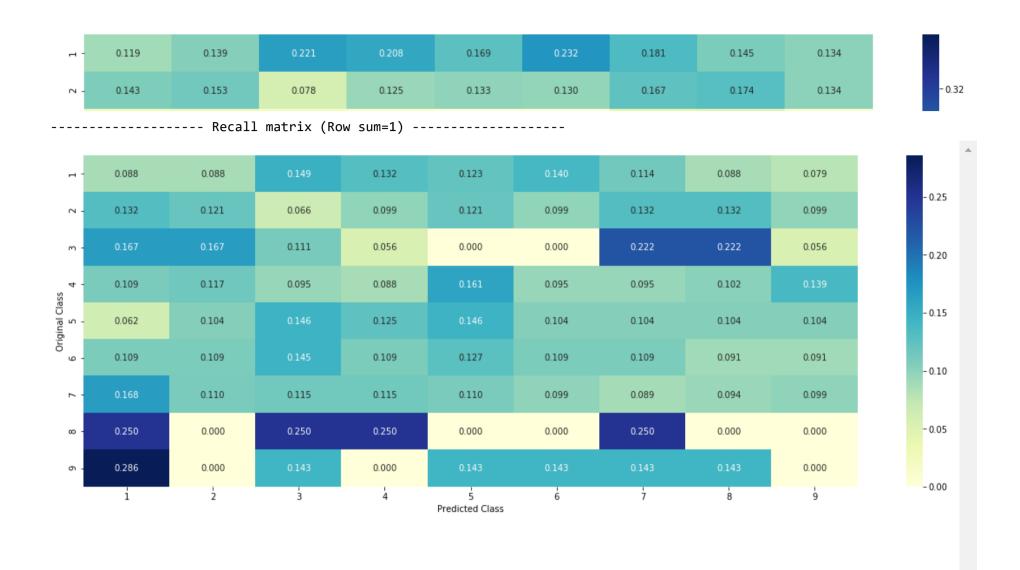
```
sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
plt.xlabel('Predicted Class')
plt.ylabel('Original Class')
plt.show()

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

```
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 v[i] = ((rand probs/sum(sum(rand probs)))[0])
         print("Log loss on Cross Validation Data using Random Model",log loss(y cv,cv predicted y, eps=1e-15))
         # Test-Set error.
         #we create a output array that has exactly same as the test data
         test predicted y = np.zeros((test data len,9))
         for i in range(test data len):
             rand probs = np.random.rand(1,9)
             test predicted y[i] = ((rand probs/sum(sum(rand probs)))[0])
         print("Log loss on Test Data using Random Model",log loss(y test,test predicted y, eps=1e-15))
         predicted y =np.argmax(test predicted y, axis=1)
         plot confusion matrix(y test, predicted y+1)
         Log loss on Cross Validation Data using Random Model 2.5033153426703136
```

r -	10.000	10.000	17.000	15.000	14.000	16.000	13.000	10.000	9.000
- 5	12.000	11.000	6.000	9.000	11.000	9.000	12.000	12.000	9.000
m -	3.000	3.000	2.000	1.000	0.000	0.000	4.000	4.000	1.000
ss 4	15.000	16.000	13.000	12.000	22.000	13.000	13.000	14.000	19.000
Original Class 5	3.000	5.000	7.000	6.000	7.000	5.000	5.000	5.000	5.000
Ori	6.000	6.000	8.000	6.000	7.000	6.000	6.000	5.000	5.000
۲.	32.000	21.000	22.000	22.000	21.000	19.000	17.000	18.000	19.000
ω -	1.000	0.000	1.000	1.000	0.000	0.000	1.000	0.000	0.000
ი -	2.000	0.000	1.000	0.000	1.000	1.000	1.000	1.000	0.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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



3.3 Univariate Analysis

```
In [16]: # code for response coding with Laplace smoothing.
         # alpha : used for laplace smoothing
         # feature: ['gene', 'variation']
         # df: ['train df', 'test df', 'cv df']
         # algorithm
         # -----
         # Consider all unique values and the number of occurances of given feature in train data dataframe
         # build a vector (1*9), the first element = (number of times it occured in class1 + 10*alpha / number of time it occurr
         # qv 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] to 'qv fea'
         # return 'qv fea'
         # -----
         # get av 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
                                                        3
             # E17K
```

```
# 061L
                                               3
                                               2
    # S222D
    # P130S
    # ...
    # }
    value count = train df[feature].value counts()
   # qv dict : Gene Variation Dict, which contains the probability array for each gene/variation
   gv dict = dict()
   # denominator will contain the number of time that particular feature occured in whole data
   for i, denominator in value count.items():
       # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticular class
       # vec is 9 diamensional vector
       vec = []
       for k in range(1,10):
            # print(train df.loc[(train df['Class']==1) & (train df['Gene']=='BRCA1')])
                                          Variation Class
                     ID Gene
            # 2470 2470 BRCA1
                                              S1715C
            # 2486 2486 BRCA1
                                              S1841R
                                                          1
            # 2614 2614 BRCA1
                                                 M1R
                                                         1
            # 2432 2432 BRCA1
                                             L1657P
                                                         1
            # 2567 2567 BRCA1
                                              T1685A
                                                         1
            # 2583 2583 BRCA1
                                              E1660G
                                                          1
            # 2634 2634 BRCA1
                                              W1718L
                                                          1
           # cls cnt.shape[0] will return the number of rows
            cls cnt = train df.loc[(train df['Class']==k) & (train df[feature]==i)]
           # cls cnt.shape[0](numerator) will contain the number of time that particular feature occured in whole data
            vec.append((cls cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
        # we are adding the gene/variation to the dict as key and vec as value
        gv dict[i]=vec
   return gv_dict
# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
   # print(gv_dict)
       {'BRCA1': [0.20075757575757575, 0.03787878787878788, 0.068181818181818177, 0.13636363636363635, 0.25, 0.193181
           'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 0.27040816326530615, 0.061224489795
           'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.068181818181818177, 0.0681818181818177, 0.062
```

```
'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.0606060606060608, 0.078787878787878782, 0.1393939393
       'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 0.46540880503144655, 0.07547169811
       'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.072847682119205295, 0.066225165562
       'BRAF': [0.066666666666666666. 0.179999999999999. 0.073333333333334. 0.07333333333334. 0.09333333333
gv dict = get gv fea dict(alpha, feature, df)
# value count is similar in get av fea dict
value count = train df[feature].value counts()
# qv fea: Gene variation feature, it will contain the feature for each feature value in the data
gv fea = []
# for every feature values in the given data frame we will check if it is there in the train data then we will add t
# if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to gv fea
for index, row in df.iterrows():
   if row[feature] in dict(value count).keys():
        gv fea.append(gv dict[row[feature]])
   else:
        gv fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
         qv fea.append([-1,-1,-1,-1,-1,-1,-1,-1])
return gv fea
```

when we caculate the probability of a feature belongs to any particular class, we apply laplace smoothing

(numerator + 10*alpha) / (denominator + 90*alpha)

3.2.1 Univariate Analysis on Gene Feature

Q1. Gene, What type of feature it is?

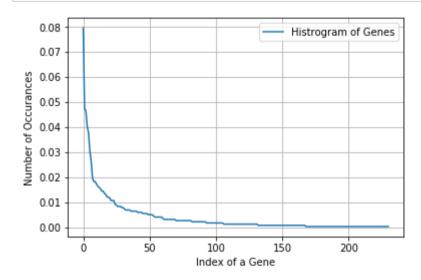
Ans. Gene is a categorical variable

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

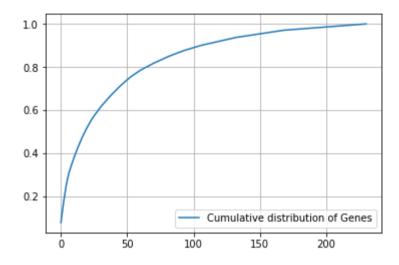
```
In [17]: unique_genes = train_df['Gene'].value_counts()
         print('Number of Unique Genes :', unique_genes.shape[0])
         # the top 10 genes that occured most
         print(unique_genes.head(10))
         Number of Unique Genes : 231
         BRCA1
                  169
         EGFR
                  101
         TP53
                   99
         PTEN
                   86
         BRCA2
                   80
         KIT
                   65
         BRAF
                   56
         ALK
                   42
         ERBB2
                   39
         FGFR2
                   39
         Name: Gene, dtype: int64
In [18]: print("Ans: There are", unique_genes.shape[0], "different categories of genes in the train data, and they are distibuted
```

Ans: There are 231 different categories of genes in the train data, and they are distibuted as follows

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



```
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-aicourse-online/lessons/handling-categorical-and-numerical-features/

- 1. One hot Encoding
- 2. Response coding

We will choose the appropriate featurization based on the ML model we use. For this problem of multi-class classification with categorical features, one-hot encoding is better for Logistic regression while response coding is better for Random Forests.

```
In [21]: #response-coding of the Gene feature
         # alpha is used for laplace smoothing
         alpha = 1
         # train gene feature
         train gene feature responseCoding = np.array(get gv feature(alpha, "Gene", train df))
         # test gene feature
         test gene feature responseCoding = np.array(get_gv_feature(alpha, "Gene", test_df))
         # cross validation gene feature
         cv gene feature responseCoding = np.array(get_gv_feature(alpha, "Gene", cv_df))
In [22]: print("train gene feature responseCoding is converted feature using respone coding method. The shape of gene feature:",
         train gene feature responseCoding is converted feature using respone coding method. The shape of gene feature: (2124,
         9)
In [23]: # one-hot encoding of Gene feature.
         from sklearn.feature extraction.text import TfidfVectorizer
         gene vectorizer = TfidfVectorizer()
         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]: 205
                   EGFR
         908
                 PDGFRA
         3069
                 NOTCH1
         694
                 CDKN2B
                   TP53
         502
         Name: Gene, dtype: object
```

```
gene vectorizer.get feature names()
In [25]:
Out[25]: ['abl1',
           'acvr1',
           'ago2',
           'akt1',
           'akt2',
           'akt3',
           'alk',
           'apc',
           'ar',
           'araf',
           'arid1b',
           'arid2',
           'arid5b',
           'asxl1',
           'atm',
           'atrx',
           'aurka',
           'axl',
           'b2m',
          print("train gene feature onehotCoding is converted feature using one-hot encoding method. The shape of gene feature:",
In [26]:
```

train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature: (2124, 2 31)

Q4. How good is this gene feature in predicting y i?

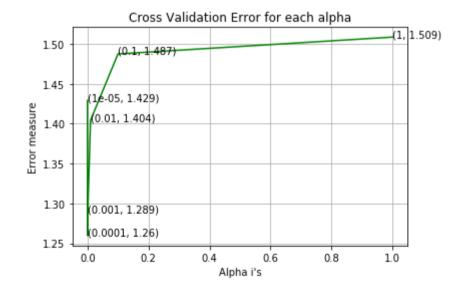
There are many ways to estimate how good a feature is, in predicting y_i. One of the good methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y_i.

```
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/sklearn.linear model.SGDClassifier
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         # predict(X) Predict class labels for samples in X.
         #-----
         # video Link:
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train gene feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train gene feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv gene feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error array[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
         plt.show()
         best_alpha = np.argmin(cv_log_error_array)
         clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
```

```
clf.fit(train_gene_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_gene_feature_onehotCoding, y_train)

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

For values of alpha = 1e-05 The log loss is: 1.429228899186377
For values of alpha = 0.0001 The log loss is: 1.2597402994982916
For values of alpha = 0.001 The log loss is: 1.2885303197883522
For values of alpha = 0.01 The log loss is: 1.404154679357312
For values of alpha = 0.1 The log loss is: 1.487374202847152
For values of alpha = 1 The log loss is: 1.5085111816306274



```
For values of best alpha = 0.0001 The train log loss is: 1.0444280458539423

For values of best alpha = 0.0001 The cross validation log loss is: 1.2597402994982916

For values of best alpha = 0.0001 The test log loss is: 1.195465777441181
```

Q5. Is the Gene feature stable across all the data sets (Test, Train, Cross validation)?

Ans. Yes, it is. Otherwise, the CV and Test errors would be significantly more than train error.

```
In [28]: print("Q6. How many data points in Test and CV datasets are covered by the ", unique_genes.shape[0], " genes in train da
    test_coverage=test_df[test_df['Gene'].isin(list(set(train_df['Gene'])))].shape[0]
    cv_coverage=cv_df[cv_df['Gene'].isin(list(set(train_df['Gene'])))].shape[0]

print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_coverage/test_df.shape[0])*100)

print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_coverage/cv_df.shape[0])*100)

Q6. How many data points in Test and CV datasets are covered by the 231 genes in train dataset?
Ans
1. In test data 645 out of 665 : 96.99248120300751
2. In cross validation data 515 out of 532 : 96.80451127819549
```

3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it?

Ans. Variation is a categorical variable

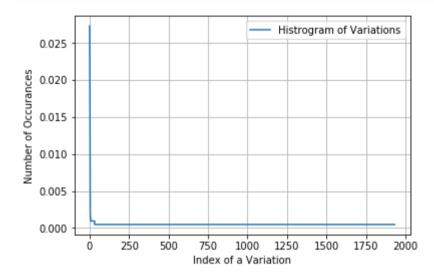
Q8. How many categories are there?

```
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 : 1933
         Truncating Mutations
                                 58
         Deletion
                                 48
         Amplification
                                 39
         Fusions
                                 17
         Overexpression
                                  5
         Q61H
         G12V
         A146T
                                  2
         G12S
                                  2
         Y64A
         Name: Variation, dtype: int64
```

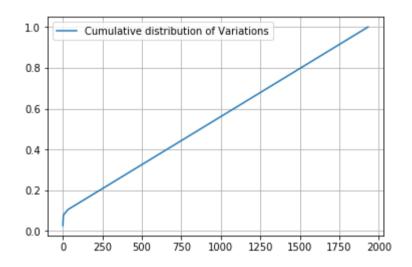
```
In [30]: print("Ans: There are", unique_variations.shape[0] ,"different categories of variations in the train data, and they are
```

Ans: There are 1933 different categories of variations in the train data, and they are distibuted as follows

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



[0.02730697 0.04990584 0.06826742 ... 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-aicourse-online/lessons/handling-categorical-and-numerical-features/

- 1. One hot Encoding
- 2. Response coding

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

```
In [33]: # alpha is used for laplace smoothing
         alpha = 1
         # train gene feature
         train variation feature responseCoding = np.array(get gv feature(alpha, "Variation", train df))
         # test gene feature
         test variation feature responseCoding = np.array(get gv feature(alpha, "Variation", test df))
         # cross validation gene feature
         cv variation feature responseCoding = np.array(get gv feature(alpha, "Variation", cv df))
In [34]: print("train variation feature responseCoding is a converted feature using the response coding method. The shape of Vari
         train variation feature responseCoding is a converted feature using the response coding method. The shape of Variation
         feature: (2124, 9)
In [35]: # one-hot encoding of variation feature.
         variation vectorizer = CountVectorizer()
         train variation feature onehotCoding = variation_vectorizer.fit_transform(train_df['Variation'])
         test variation feature onehotCoding = variation vectorizer.transform(test df['Variation'])
         cv variation feature onehotCoding = variation vectorizer.transform(cv df['Variation'])
In [36]: print("train variation feature onehotEncoded is converted feature using the onne-hot encoding method. The shape of Varia
         train variation feature onehotEncoded is converted feature using the onne-hot encoding method. The shape of Variation f
         eature: (2124, 1964)
         Q10. How good is this Variation feature in predicting v i?
```

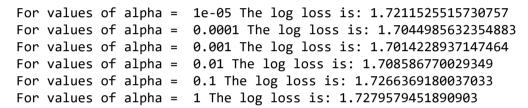
Q10. How good is this variation leature in predicting

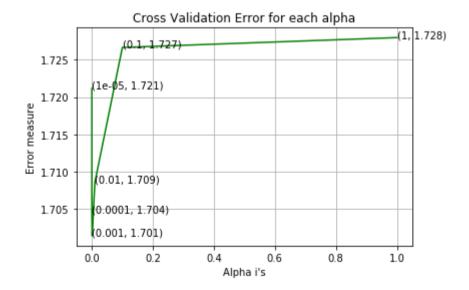
Let's build a model just like the earlier!

```
In [37]: | alpha = [10 ** x for x in range(-5, 1)] |
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, v[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         # predict(X) Predict class labels for samples in X.
         #-----
         # video Link:
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train variation feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train variation feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv variation feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error array[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
         plt.show()
```

```
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
clf.fit(train_variation_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_variation_feature_onehotCoding, y_train)

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





```
For values of best alpha = 0.001 The train log loss is: 1.0714262196625013

For values of best alpha = 0.001 The cross validation log loss is: 1.7014228937147464

For values of best alpha = 0.001 The test log loss is: 1.6934979089250732
```

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.

Q12. How many data points are covered by total 1933 genes in test and cross validation data sets? Ans

- 1. In test data 70 out of 665 : 10.526315789473683
- 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?

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

```
In [41]: # building a CountVectorizer with all the words that occured minimum 3 times in train data
# Reference - https://buhrmann.github.io/tfidf-analysis.html
text_vectorizer = TfidfVectorizer(min_df=3)
train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()

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

final_fts = train_text_feature_onehotCoding.toarray().sum(axis=0)
top_lk_fts = np.argsort(final_fts)[::-1][0:1000]

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

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

Total number of unique words in train data : 52855

```
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 i 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
```

train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train_text_feature_responseCoding.sum(axis=1)).
test text feature responseCoding = (test text feature responseCoding.T/test text feature responseCoding.sum(axis=1)).T

cv text feature responseCoding = (cv text feature responseCoding.T/cv text feature responseCoding.sum(axis=1)).T

we convert each row values such that they sum to 1

```
In [45]: # don't forget to normalize every feature
         train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding[:,top_1k_fts], 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[:,top_1k_fts], 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[:,top 1k fts], axis=0)
In [46]: print( train text feature onehotCoding.shape)
         print(test text feature onehotCoding.shape)
         print(cv text feature onehotCoding.shape)
         (2124, 1000)
         (665, 1000)
         (532, 1000)
In [47]: #https://stackoverflow.com/a/2258273/4084039
         sorted text fea dict = dict(sorted(text fea dict.items(), key=lambda x: x[1] , reverse=True))
         sorted text occur = np.array(list(sorted text fea dict.values()))
```

In [48]: # Number of words for a given frequency.
print(Counter(sorted_text_occur))

Counter({0.017934441704394233: 313, 0.03431923769297222: 236, 0.011277558733376377: 231, 0.021309456155699007: 223, 0.0841860290653762: 205, 0.3330221744812404: 154, 0.21510343232332796: 130, 0.014686548022060701: 127, 0.064152006164 95627: 124, 0.017812897527400954: 116, 0.041400945757954326: 115, 0.06128211560731485: 110, 0.04418970107945162: 108, 0.10509540770516547: 105, 0.06274877899729857: 102, 0.024487265016113324: 99, 0.032221395984043125: 98, 0.03483613619 1600996: 93, 0.12950399536473373: 88, 0.025804193053244665: 88, 0.024117879426990736: 85, 0.015961806558021575: 85, 0.03381623805999512: 82, 0.03215890625802947: 79, 0.02036686040588048: 78, 0.01115145943432505: 77, 0.043573153047941 245: 76, 0.016359378755454686: 73, 0.026152865605715482: 68, 0.05720855812992253: 67, 0.04469764785297529: 64, 0.0435 74115196151765: 64, 0.022990101662539: 64, 0.021949053656975435: 63, 0.15160712160314466: 62, 0.06614444729389045: 6 0, 0.023910720062271067: 58, 0.01552513137008564: 58, 0.05401913450010369: 57, 0.02780203761708643: 56, 0.01399416217 5609483: 56, 0.052601197650032995: 55, 0.04481499037704162: 55, 0.03171720644353171: 55, 0.027340599777748106: 55, 0. 024550098058064664: 54, 0.022555117466752754: 54, 0.021265368078569647: 54, 0.014629839776652552: 54, 0.2077386615768 0368: 52, 0.01870657143726904: 52, 0.015052592829190923: 52, 0.08446940365284634: 50, 0.027010650099231974: 50, 0.018 165035483886347: 50, 0.01644586509562593: 50, 0.08603103451105196: 49, 0.01261264032088736: 49, 0.028692883835239793: 48, 0.026748627077242824: 48, 0.022349781372801136: 48, 0.0089618106233534: 48, 0.07497441518051895: 47, 0.0328358359 4839404: 47, 0.020512952104763258: 47, 0.14949390809041957: 46, 0.04850833632982919: 46, 0.03450100540935392: 46, 0.0 1882456254654479: 46, 0.06288839907932976: 45, 0.04446368688952694: 45, 0.020867228858467087: 45, 0.05033884348217182 4: 43, 0.04930146185047533: 43, 0.03235191530506621: 43, 0.05537090061264073: 41, 0.04690428725963047: 41, 0.01963306 102242494: 41, 0.00993121284994268: 41, 0.030123166780268818: 40, 0.0265432290929526: 40, 0.015523038963677195: 39, 0.19574012359113718: 38, 0.054113779635093846: 38, 0.04731678568050374: 38, 0.034058318109026944: 38, 0.0326976726845

```
In [49]: # Train a Logistic regression+Calibration model using text features whicha re on-hot encoded
         alpha = [10 ** x for x in range(-5, 1)]
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         #-----
         # video Link:
         #_____
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train text feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train text feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv text feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error array[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
         plt.show()
```

```
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
clf.fit(train_text_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_onehotCoding, y_train)

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

```
For values of alpha = 1e-05 The log loss is: 1.2312050568184227

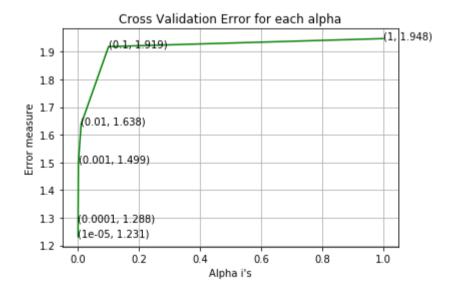
For values of alpha = 0.0001 The log loss is: 1.287891737144318

For values of alpha = 0.001 The log loss is: 1.4986687471426732

For values of alpha = 0.01 The log loss is: 1.637970223360734

For values of alpha = 0.1 The log loss is: 1.9189685168583874

For values of alpha = 1 The log loss is: 1.9478998340502305
```



```
For values of best alpha = 1e-05 The train log loss is: 0.8052349094757469

For values of best alpha = 1e-05 The cross validation log loss is: 1.2312050568184227

For values of best alpha = 1e-05 The test log loss is: 1.0905987111534998
```

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

Ans. Yes, it seems like!

```
In [50]: def get_intersec_text(df):
    df_text_vec = CountVectorizer(min_df=3)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_fea = 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 [51]: 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")

96.545 % of word of test data appeared in train data
98.08 % of word of Cross Validation appeared in train data
```

4. Machine Learning Models

```
In [52]: #Data preparation for ML models.
         #Misc. functionns for ML models
         def predict and plot confusion matrix(train x, train y,test x, test y, clf):
             clf.fit(train x, train y)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train x, train y)
             pred y = sig clf.predict(test x)
             # for calculating log loss we will provide the array of probabilities belongs to each class
             print("Log loss:",log loss(test y, sig clf.predict proba(test x)))
             # calculating the number of data points that are misclassified
             print("Number of mis-classified points :", np.count nonzero((pred y- test y))/test y.shape[0])
             plot confusion matrix(test y, pred y)
In [53]: 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 [54]: # this function will be used just for naive bayes
         # for the given indices, we will print the name of the features
         # and we will check whether the feature present in the test point text or not
         def get_impfeature_names(indices, text, gene, var, no_features):
              gene count vec = CountVectorizer()
              var count vec = CountVectorizer()
              text count vec = CountVectorizer(min df=3)
              gene vec = gene count vec.fit(train df['Gene'])
             var vec = var count vec.fit(train df['Variation'])
             text vec = text count vec.fit(train df['TEXT'])
             fea1_len = len(gene_vec.get_feature_names())
             fea2_len = len(var_count_vec.get_feature_names())
              word present = 0
              for i,v in enumerate(indices):
                  if (v < fea1 len):</pre>
                      word = gene vec.get feature names()[v]
                      yes no = True if word == gene else False
                      if yes no:
                          word present += 1
                          print(i, "Gene feature [{}] present in test data point [{}]".format(word,yes no))
                  elif (v < fea1 len+fea2 len):</pre>
                      word = var vec.get feature names()[v-(fea1 len)]
                      yes no = True if word == var else False
                      if yes_no:
                          word present += 1
                          print(i, "variation feature [{}] present in test data point [{}]".format(word,yes no))
                  else:
                      word = text vec.get feature names()[v-(fea1 len+fea2 len)]
                      yes no = True if word in text.split() else False
                      if yes_no:
                          word present += 1
                          print(i, "Text feature [{}] present in test data point [{}]".format(word,yes no))
             print("Out of the top ",no_features," features ", word_present, "are present in query point")
```

```
In [55]: # merging gene, variance and text features
         # building train, test and cross validation data sets
         # a = [[1, 2]]
               [3, 411
         # b = [[4, 5]].
               [6, 711]
         \# hstack(a, b) = [[1, 2, 4, 5],
                          Γ 3. 4. 6. 711
         train gene var onehotCoding = hstack((train gene feature onehotCoding, train variation feature onehotCoding))
         test gene var onehotCoding = hstack((test gene feature onehotCoding,test variation feature onehotCoding))
         cv gene var onehotCoding = hstack((cv gene feature onehotCoding,cv variation feature onehotCoding))
         train x onehotCoding = hstack((train gene var onehotCoding, train text feature onehotCoding)).tocsr()
         train y = np.array(list(train df['Class']))
         test x onehotCoding = hstack((test gene var onehotCoding, test text feature onehotCoding)).tocsr()
         test y = np.array(list(test df['Class']))
         cv x onehotCoding = hstack((cv gene var onehotCoding, cv text feature onehotCoding)).tocsr()
         cv y = np.array(list(cv df['Class']))
         train gene var responseCoding = np.hstack((train gene feature responseCoding,train variation feature responseCoding))
         test gene var responseCoding = np.hstack((test gene feature responseCoding,test variation feature responseCoding))
         cv gene var responseCoding = np.hstack((cv gene feature responseCoding,cv variation feature responseCoding))
         train x responseCoding = np.hstack((train gene var responseCoding, train text feature responseCoding))
         test x responseCoding = np.hstack((test gene var responseCoding, test text feature responseCoding))
         cv x responseCoding = np.hstack((cv gene var responseCoding, cv text feature responseCoding))
```

```
In [56]: print("One hot encoding features :")
         print("(number of data points * number of features) in train data = ", train x onehotCoding.shape)
         print("(number of data points * number of features) in test data = ", test x onehotCoding.shape)
         print("(number of data points * number of features) in cross validation data =", cv x onehotCoding.shape)
         One hot encoding features :
         (number of data points * number of features) in train data = (2124, 3195)
         (number of data points * number of features) in test data = (665, 3195)
         (number of data points * number of features) in cross validation data = (532, 3195)
In [57]: print(" Response encoding features :")
         print("(number of data points * number of features) in train data = ", train x responseCoding.shape)
         print("(number of data points * number of features) in test data = ", test x responseCoding.shape)
         print("(number of data points * number of features) in cross validation data =", cv x responseCoding.shape)
          Response encoding features :
         (number of data points * number of features) in train data = (2124, 27)
         (number of data points * number of features) in test data = (665, 27)
         (number of data points * number of features) in cross validation data = (532, 27)
```

4.1. Base Line Model

4.1.1. Naive Bayes

4.1.1.1. Hyper parameter tuning

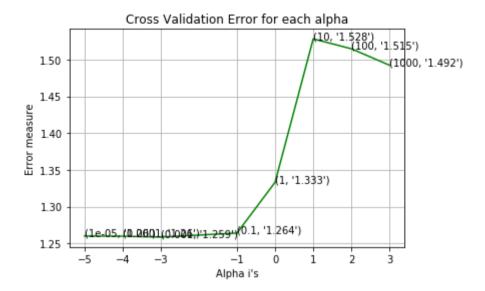
```
In [58]: # find more about Multinomial Naive base function here http://scikit-learn.org/stable/modules/generated/sklearn.naive ba
         # -----
         # default paramters
         # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=None)
         # some of methods of MultinomialNB()
         # fit(X, v[, sample weight]) Fit Naive Bayes classifier according to X, v
         # predict(X) Perform classification on an array of test vectors X.
         # predict log proba(X) Return log-probability estimates for the test vector X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-algorithm-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.Ca
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='siamoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, v[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-algorithm-1/
         # -----
         alpha = [0.00001, 0.0001, 0.001, 0.1, 1, 10, 100,1000]
         cv log error array = []
         for i in alpha:
             print("for alpha =", i)
             clf = MultinomialNB(alpha=i)
             clf.fit(train x onehotCoding, train y)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train x onehotCoding, train y)
             sig clf probs = sig clf.predict proba(cv x onehotCoding)
             cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
             # to avoid rounding error while multiplying probabilites we use log-probability estimates
             print("Log Loss :",log loss(cv y, sig clf probs))
```

```
fig, ax = plt.subplots()
ax.plot(np.log10(alpha), cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv log error array[i]))
plt.grid()
plt.xticks(np.log10(alpha))
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = MultinomialNB(alpha=alpha[best alpha])
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train v)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y, labels=clf
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, predict y, la
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y, labels=clf.c
for alpha = 1e-05
Log Loss: 1.2602538209854242
for alpha = 0.0001
Log Loss: 1.259920383687711
for alpha = 0.001
Log Loss: 1.2587969584012375
for alpha = 0.1
Log Loss: 1.2641875870596706
for alpha = 1
Log Loss: 1.333203286285047
for alpha = 10
Log Loss: 1.5279693911229684
for alpha = 100
```

Log Loss: 1.5145462970878025

for alpha = 1000

Log Loss: 1.4922075790521818



For values of best alpha = 0.001 The train log loss is: 0.535997354839793

For values of best alpha = 0.001 The cross validation log loss is: 1.2587969584012375

For values of best alpha = 0.001 The test log loss is: 1.146580618792004

4.1.1.2. Testing the model with best hyper paramters

```
In [59]: # find more about Multinomial Naive base function here http://scikit-learn.org/stable/modules/generated/sklearn.naive_ba
         # -----
         # default paramters
         # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=None)
         # some of methods of MultinomialNB()
         # fit(X, v[, sample weight]) Fit Naive Bayes classifier according to X, v
         # predict(X) Perform classification on an array of test vectors X.
         # predict log proba(X) Return log-probability estimates for the test vector X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-algorithm-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.Ca
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='siamoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, v[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         clf = MultinomialNB(alpha=alpha[best alpha])
         clf.fit(train x onehotCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x onehotCoding, train y)
         sig clf probs = sig clf.predict proba(cv x onehotCoding)
         # to avoid rounding error while multiplying probabilites we use log-probability estimates
         print("Log Loss :",log loss(cv y, sig clf probs))
         print("Number of missclassified point :", np.count nonzero((sig clf.predict(cv x onehotCoding) - cv y))/cv y.shape[0])
         plot confusion matrix(cv y, sig clf.predict(cv x onehotCoding.toarray()))
```

H -	56.000	4.000	0.000	14.000	11.000	5.000	1.000	0.000	0.000
2 -	2.000	25.000	0.000	2.000	0.000	0.000	43.000	0.000	0.000
m -	2.000	0.000	0.000	3.000	1.000	0.000	8.000	0.000	0.000
4 -	19.000	2.000	1.000	72.000	7.000	2.000	7.000	0.000	0.000
Original Class	4.000	1.000	1.000	3.000	17.000	4.000	9.000	0.000	0.000
Original P	5.000	1.000	2.000	0.000	6.000	15.000	15.000	0.000	0.000
7 -	1.000	29.000	1.000	0.000	0.000	0.000	122.000	0.000	0.000
∞ -	1.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000
o -	0.000	0.000	0.000	1.000	0.000	0.000	1.000	1.000	3.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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



- 0.8

- 0.6

- 0.4

- 0.2

-0.0

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

г.	0.615	0.044	0.000	0.154	0.121	0.055	0.011	0.000	0.000
2 -	0.028	0.347	0.000	0.028	0.000	0.000	0.597	0.000	0.000
14 -	0.020	0.547	0.000	0.020	0.000	0.000	0.357	0.000	0.000
m -	0.143	0.000	0.000	0.214	0.071	0.000	0.571	0.000	0.000
4 4	0.173	0.018	0.009	0.655	0.064	0.018	0.064	0.000	0.000
Original Class 5	0.103	0.026	0.026	0.077	0.436	0.103	0.231	0.000	0.000
9 -	0.114	0.023	0.045	0.000	0.136	0.341	0.341	0.000	0.000
۲ -	0.007	0.190	0.007	0.000	0.000	0.000	0.797	0.000	0.000
ω -	0.333	0.000	0.000	0.000	0.000	0.000	0.333	0.000	0.333

4.1.1.3. Feature Importance, Correctly classified point

```
In [60]: test point index = 1
         no feature = 100
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices=np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test df['
         Predicted Class: 6
         Predicted Class Probabilities: [[0.0559 0.0392 0.0101 0.0625 0.031 0.7082 0.0868 0.0029 0.0033]]
         Actual Class: 6
         37 Text feature [08] present in test data point [True]
         56 Text feature [013] present in test data point [True]
         62 Text feature [000] present in test data point [True]
         93 Text feature [104brca2] present in test data point [True]
         94 Text feature [111] present in test data point [True]
         Out of the top 100 features 5 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

4.2. K Nearest Neighbour Classification

4.2.1. Hyper parameter tuning

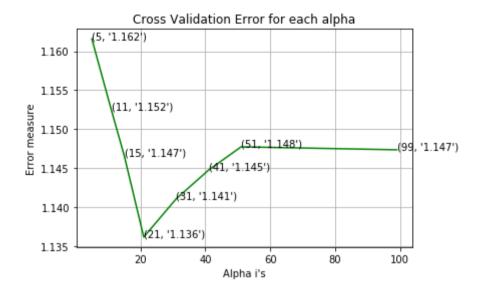
```
In [62]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KNeighb
         # -----
         # default parameter
         # KNeighborsClassifier(n neighbors=5, weights='uniform', algorithm='auto', leaf size=30, p=2,
         # metric='minkowski', metric params=None, n jobs=1, **kwarqs)
         # methods of
         # fit(X, v): Fit the model using X as training data and v as target values
         # predict(X):Predict the class labels for the provided data
         # predict proba(X):Return probability estimates for the test data X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/k-nearest-neighbors-geometric-intu
         #-----
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.Ca
         # 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 = [5, 11, 15, 21, 31, 41, 51, 99]
         cv log error array = []
         for i in alpha:
             print("for alpha =", i)
             clf = KNeighborsClassifier(n neighbors=i)
             clf.fit(train x responseCoding, train y)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train x responseCoding, train y)
             sig clf probs = sig clf.predict proba(cv x responseCoding)
             cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
             # to avoid rounding error while multiplying probabilites we use log-probability estimates
```

```
print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x responseCoding, train y)
predict y = sig clf.predict proba(train x responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_y, labels=clf
predict v = sig clf.predict proba(cv x responseCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, predict y, la
predict y = sig clf.predict proba(test x responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y, labels=clf.c
for alpha = 5
Log Loss: 1.1615810560746531
for alpha = 11
Log Loss: 1.1524895332763279
for alpha = 15
Log Loss: 1.1465831664444128
for alpha = 21
Log Loss: 1.1361695729523122
for alpha = 31
Log Loss: 1.14107467847058
for alpha = 41
Log Loss: 1.1447647885569086
for alpha = 51
```

Log Loss: 1.1477360662180307

for alpha = 99

Log Loss: 1.1473573847031386



For values of best alpha = 21 The train log loss is: 0.7495357428161341

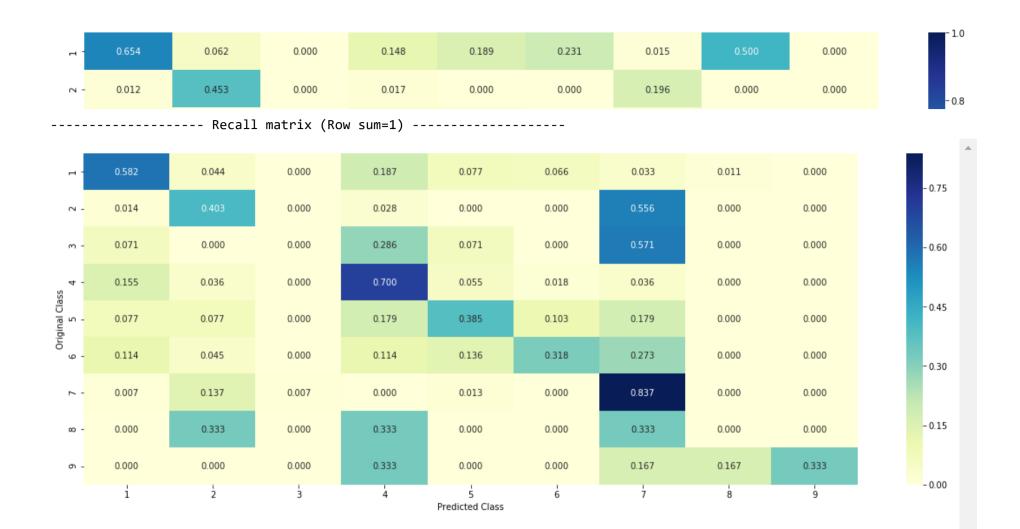
For values of best alpha = 21 The cross validation log loss is: 1.1361695729523122

For values of best alpha = 21 The test log loss is: 1.028719811612548

4.2.2. Testing the model with best hyper paramters

r -	53.000	4.000	0.000	17.000	7.000	6.000	3.000	1.000	0.000
- 2	1.000	29.000	0.000	2.000	0.000	0.000	40.000	0.000	0.000
m -	1.000	0.000	0.000	4.000	1.000	0.000	8.000	0.000	0.000
ss 4 -	17.000	4.000	0.000	77.000	6.000	2.000	4.000	0.000	0.000
Original Class 5	3.000	3.000	0.000	7.000	15.000	4.000	7.000	0.000	0.000
Original Property	5.000	2.000	0.000	5.000	6.000	14.000	12.000	0.000	0.000
۲ -	1.000	21.000	1.000	0.000	2.000	0.000	128.000	0.000	0.000
œ -	0.000	1.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000
6 -	0.000	0.000	0.000	2.000	0.000	0.000	1.000	1.000	2.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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



4.2.3. Sample Query point -1

4.2.4. Sample Query Point-2

```
In [75]: clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
         clf.fit(train x responseCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x responseCoding, train y)
         test point index = 100
         predicted cls = sig clf.predict(test x responseCoding[test point index].reshape(1,-1))
         print("Predicted Class :", predicted cls[0])
         print("Actual Class :", test y[test point index])
         neighbors = clf.kneighbors(test x responseCoding[test point index].reshape(1, -1), alpha[best alpha])
         print("the k value for knn is",alpha[best alpha], "and the nearest neighbours of the test points belongs to classes",trai
         print("Fequency of nearest points :",Counter(train y[neighbors[1][0]]))
         Predicted Class: 1
         Actual Class: 4
         the k value for knn is 21 and the nearest neighbours of the test points belongs to classes [1 4 1 1 1 4 1 1 1 1 1 1 4 1
         1 1 1 1 1 4 4]
         Feguency of nearest points : Counter({1: 16, 4: 5})
```

4.3. Logistic Regression

4.3.1. With Class balancing

4.3.1.1. Hyper paramter tuning

```
In [76]:
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.SGDClassifier
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.Ca
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='siamoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, v[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         # video Link:
         alpha = [10 ** x for x in range(-6, 3)]
         cv log error array = []
         for i in alpha:
             print("for alpha =", i)
             clf = SGDClassifier(class weight='balanced', alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train x onehotCoding, train y)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train x onehotCoding, train y)
             sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
             cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
```

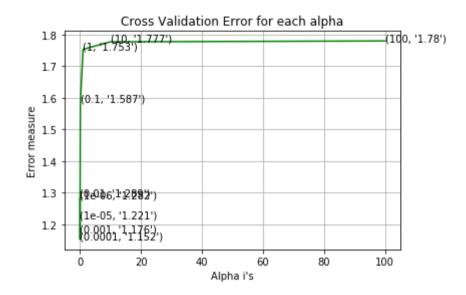
```
# to avoid rounding error while multiplying probabilites we use log-probability estimates
    print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.vlabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y, labels=clf
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, predict y, la
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y, labels=clf.c
for alpha = 1e-06
Log Loss: 1.2820795654430093
for alpha = 1e-05
Log Loss: 1.2207100064099214
for alpha = 0.0001
Log Loss: 1.1520352125506361
for alpha = 0.001
Log Loss: 1.1756087391832577
for alpha = 0.01
Log Loss: 1.2886861334650623
for alpha = 0.1
Log Loss: 1.5866921789363262
for alpha = 1
Log Loss: 1.7534743668053976
```

for alpha = 10

Log Loss : 1.777078295217653

for alpha = 100

Log Loss: 1.7798465959611116



For values of best alpha = 0.0001 The train log loss is: 0.4379416661335392

For values of best alpha = 0.0001 The cross validation log loss is: 1.1520352125506361

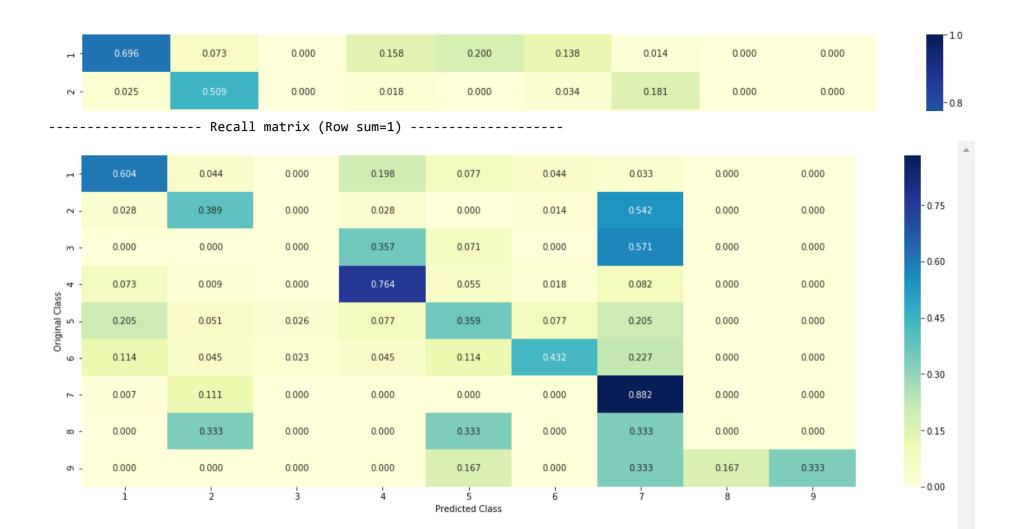
For values of best alpha = 0.0001 The test log loss is: 0.9954243573188598

4.3.1.2. Testing the model with best hyper paramters

- 1	55.000	4.000	0.000	18.000	7.000	4.000	3.000	0.000	0.000
- 2	2.000	28.000	0.000	2.000	0.000	1.000	39.000	0.000	0.000
m -	0.000	0.000	0.000	5.000	1.000	0.000	8.000	0.000	0.000
ss 4	8.000	1.000	0.000	84.000	6.000	2.000	9.000	0.000	0.000
Original Class 5	8.000	2.000	1.000	3.000	14.000	3.000	8.000	0.000	0.000
Orig	5.000	2.000	1.000	2.000	5.000	19.000	10.000	0.000	0.000
۲-	1.000	17.000	0.000	0.000	0.000	0.000	135.000	0.000	0.000
ω -	0.000	1.000	0.000	0.000	1.000	0.000	1.000	0.000	0.000
ი -	0.000	0.000	0.000	0.000	1.000	0.000	2.000	1.000	2.000
	i	2	3	4	5 Predicted Class	6	7	8	9

- 25

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



```
In [78]: def get imp feature names(text, indices, removed ind = []):
             word present = 0
             tabulte_list = []
             incresingorder ind = 0
             for i in indices:
                 if i < train gene feature onehotCoding.shape[1]:</pre>
                      tabulte list.append([incresingorder ind, "Gene", "Yes"])
                 elif i< 18:
                     tabulte list.append([incresingorder ind, "Variation", "Yes"])
                 if ((i > 17) & (i not in removed ind)):
                      word = train text features[i]
                     yes no = True if word in text.split() else False
                      if yes no:
                          word present += 1
                     tabulte list.append([incresingorder ind,train text features[i], yes no])
                 incresingorder ind += 1
             print(word present, "most importent features are present in our query point")
             print("-"*50)
             print("The features that are most importent of the ",predicted cls[0]," class:")
             print (tabulate(tabulte list, headers=["Index", 'Feature name', 'Present or Not']))
```

4.3.1.3.1. Correctly Classified point

```
In [79]: # from tabulate import tabulate
         clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test df['
         Predicted Class: 6
         Predicted Class Probabilities: [[9.000e-03 5.600e-03 2.000e-04 3.400e-03 3.770e-02 9.432e-01 4.000e-04
           4.000e-04 1.000e-04]]
         Actual Class: 6
         11 Text feature [049] present in test data point [True]
         418 Text feature [001] present in test data point [True]
         Out of the top 500 features 2 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

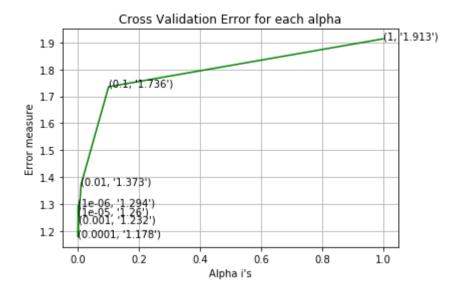
```
In [80]: test point index = 100
         no feature = 500
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test df['
         Predicted Class: 1
         Predicted Class Probabilities: [[5.812e-01 7.220e-02 5.000e-04 3.369e-01 2.300e-03 3.800e-03 1.400e-03
           1.500e-03 2.000e-04]]
         Actual Class: 4
         19 Text feature [117] present in test data point [True]
         153 Text feature [1087] present in test data point [True]
         Out of the top 500 features 2 are present in query point
```

4.3.2. Without Class balancing

4.3.2.1. Hyper paramter tuning

```
In [81]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
         #_____
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.Ca
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='siamoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, v[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         # video Link:
         alpha = [10 ** x for x in range(-6, 1)]
         cv log error array = []
         for i in alpha:
             print("for alpha =", i)
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train x onehotCoding, 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='12', loss='log', random state=42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y, labels=clf
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, predict y, la
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y, labels=clf.c
for alpha = 1e-06
Log Loss: 1.293690472637134
for alpha = 1e-05
Log Loss: 1.260347713730887
for alpha = 0.0001
Log Loss: 1.1779713526755606
for alpha = 0.001
Log Loss: 1.2322725633450609
for alpha = 0.01
Log Loss: 1.3731366566674625
for alpha = 0.1
Log Loss: 1.7356180965445045
for alpha = 1
Log Loss: 1.9134224113398473
```



```
For values of best alpha = 0.0001 The train log loss is: 0.4295583799747194

For values of best alpha = 0.0001 The cross validation log loss is: 1.1779713526755606

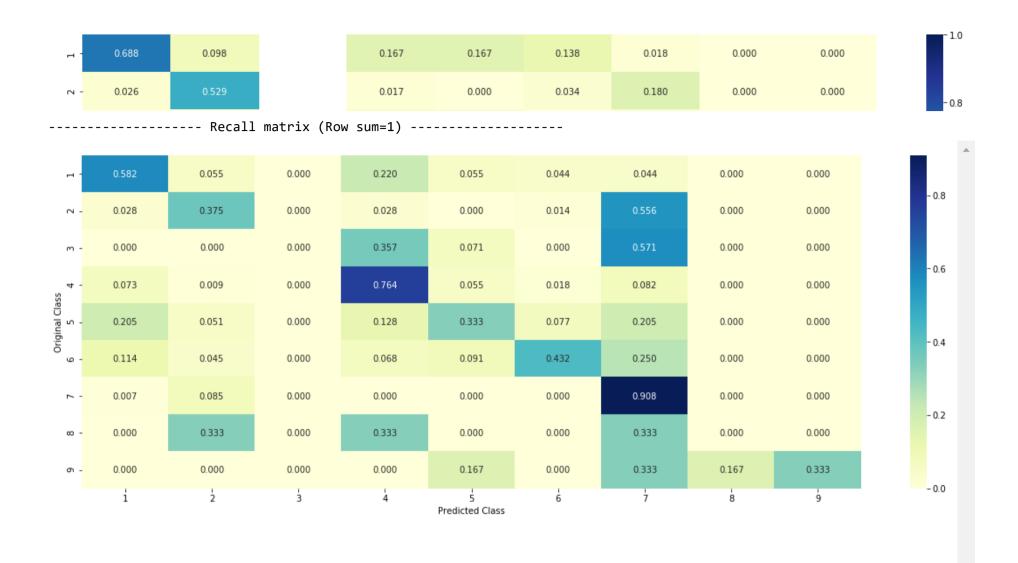
For values of best alpha = 0.0001 The test log loss is: 1.016897811677835
```

4.3.2.2. Testing model with best hyper parameters

	53.000	5.000	0.000	20.000	5.000	4.000	4.000	0.000	0.000
- 2	2.000	27.000	0.000	2.000	0.000	1.000	40.000	0.000	0.000
m -	0.000	0.000	0.000	5.000	1.000	0.000	8.000	0.000	0.000
. 4 -	8.000	1.000	0.000	84.000	6.000	2.000	9.000	0.000	0.000
Original Class 5	8.000	2.000	0.000	5.000	13.000	3.000	8.000	0.000	0.000
0 -	5.000	2.000	0.000	3.000	4.000	19.000	11.000	0.000	0.000
۲ -	1.000	13.000	0.000	0.000	0.000	0.000	139.000	0.000	0.000
ω -	0.000	1.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000
ი -	0.000	0.000	0.000	0.000	1.000	0.000	2.000	1.000	2.000
	i	2	3	4	5 Predicted Class	6	7	8	9

- 25

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



```
In [83]: clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
         print("Actual Class :", test v[test point index])
         indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test df['
         Predicted Class: 6
         Predicted Class Probabilities: [[9.900e-03 6.100e-03 1.000e-04 4.200e-03 3.730e-02 9.415e-01 7.000e-04
           0.000e+00 0.000e+0011
         Actual Class: 6
         20 Text feature [001] present in test data point [True]
         117 Text feature [049] present in test data point [True]
         352 Text feature [08] present in test data point [True]
         Out of the top 500 features 3 are present in guery point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

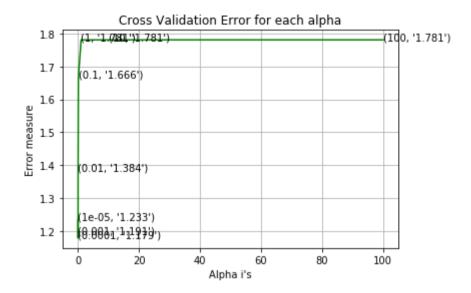
```
In [84]: test point index = 100
         no feature = 500
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test df['
         Predicted Class: 1
         Predicted Class Probabilities: [[5.849e-01 6.770e-02 2.000e-04 3.394e-01 2.100e-03 3.100e-03 2.500e-03
           1.000e-04 0.000e+00]]
         Actual Class: 4
         11 Text feature [117] present in test data point [True]
         427 Text feature [1087] present in test data point [True]
         Out of the top 500 features 2 are present in query point
```

4.4. Linear Support Vector Machines

4.4.1. Hyper paramter tuning

```
In [85]: # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/generated/skle
         # -----
         # default parameters
         # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001,
         # cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', random state=None)
         # Some of methods of SVM()
         # fit(X, v, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathematical-derivation-copy-8/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.Ca
         # 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(-5, 3)]
         cv log error array = []
         for i in alpha:
             print("for C =", i)
            clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced')
             clf = SGDClassifier( class weight='balanced', alpha=i, penalty='12', loss='hinge', random state=42)
             clf.fit(train x onehotCoding, train y)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train x onehotCoding, train y)
             sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
             cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
```

```
print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
# clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced')
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='hinge', random state=42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y, labels=clf
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, predict y, la
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y, labels=clf.c
for C = 1e-05
Log Loss: 1.2332430422408749
for C = 0.0001
Log Loss: 1.178949205535011
for C = 0.001
Log Loss: 1.1907205174128939
for C = 0.01
Log Loss: 1.38372327382502
for C = 0.1
Log Loss: 1.66649482119244
for C = 1
Log Loss: 1.7805139670746548
for C = 10
Log Loss: 1.7806004756908558
```



```
For values of best alpha = 0.0001 The train log loss is: 0.4843472074024008

For values of best alpha = 0.0001 The cross validation log loss is: 1.178949205535011

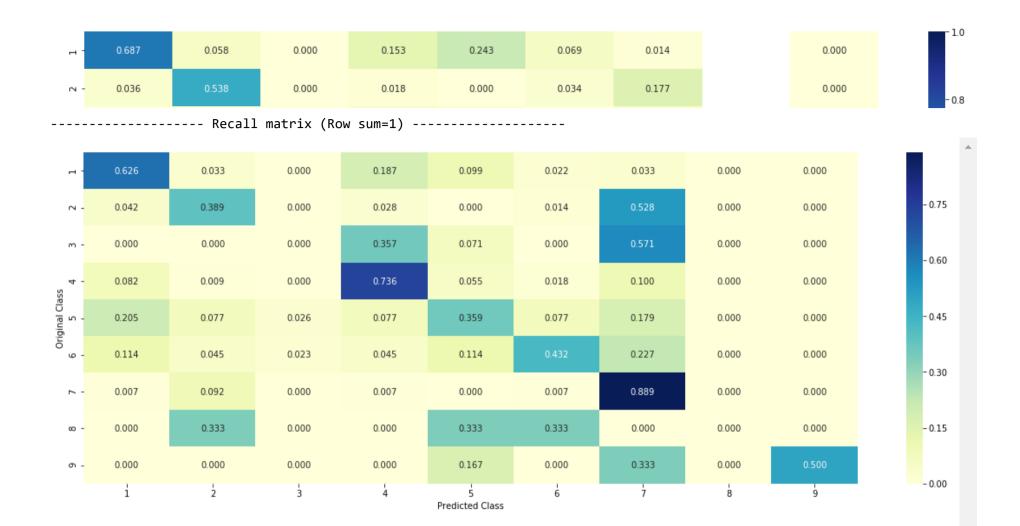
For values of best alpha = 0.0001 The test log loss is: 1.053816098758451
```

4.4.2. Testing model with best hyper parameters

- 1	57.000	3.000	0.000	17.000	9.000	2.000	3.000	0.000	0.000
- 2	3.000	28.000	0.000	2.000	0.000	1.000	38.000	0.000	0.000
m -	0.000	0.000	0.000	5.000	1.000	0.000	8.000	0.000	0.000
ss 4	9.000	1.000	0.000	81.000	6.000	2.000	11.000	0.000	0.000
Original Class 5	8.000	3.000	1.000	3.000	14.000	3.000	7.000	0.000	0.000
Oriç	5.000	2.000	1.000	2.000	5.000	19.000	10.000	0.000	0.000
۲-	1.000	14.000	0.000	1.000	0.000	1.000	136.000	0.000	0.000
ω -	0.000	1.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000
ი -	0.000	0.000	0.000	0.000	1.000	0.000	2.000	0.000	3.000
	i	2	3	4	5 Predicted Class	6	7	8	9

- 25

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



4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

```
In [87]: | clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', random state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         # test point index = 100
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(abs(-clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index],test df['
         Predicted Class: 6
         Predicted Class Probabilities: [[2.390e-02 5.540e-02 2.100e-03 4.420e-02 6.660e-02 7.986e-01 8.600e-03
           5.000e-04 1.000e-04]]
         Actual Class : 6
         Out of the top 500 features 0 are present in query point
```

4.3.3.2. For Incorrectly classified point

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

```
In [89]: # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, v, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         # predict proba (X) Perform classification on samples in X.
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their-constructi
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.Ca
         # 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 = [100,200,500,1000,2000]
         \max depth = [5, 10]
         cv log error array = []
         for i in alpha:
             for j in max depth:
                 print("for n estimators =", i,"and max depth = ", j)
```

```
clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, random state=42, n jobs=-1)
        clf.fit(train x onehotCoding, train y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig clf.fit(train x onehotCoding, train y)
        sig clf probs = sig clf.predict proba(cv x onehotCoding)
        cv log error array.append(log loss(cv v, sig clf probs, labels=clf.classes , eps=1e-15))
        print("Log Loss :",log loss(cv y, sig clf probs))
'''fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[int(i/2)],max depth[int(i%2)],str(txt)), (features[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', max depth=max depth[int(best alpha/2)]
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best estimator = ', alpha[int(best alpha/2)], "The train log loss is:",log loss(y train, predict y,
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best estimator = ', alpha[int(best alpha/2)], "The cross validation log loss is:",log loss(y cv, pr
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss is:",log_loss(y_test, predict_y, l
for n estimators = 100 and max depth = 5
Log Loss: 1.2550943058706716
for n estimators = 100 and max depth = 10
Log Loss: 1.2652870179708249
for n estimators = 200 and max depth = 5
Log Loss: 1.249200406837101
for n_estimators = 200 and max depth = 10
Log Loss: 1.2592712924638831
```

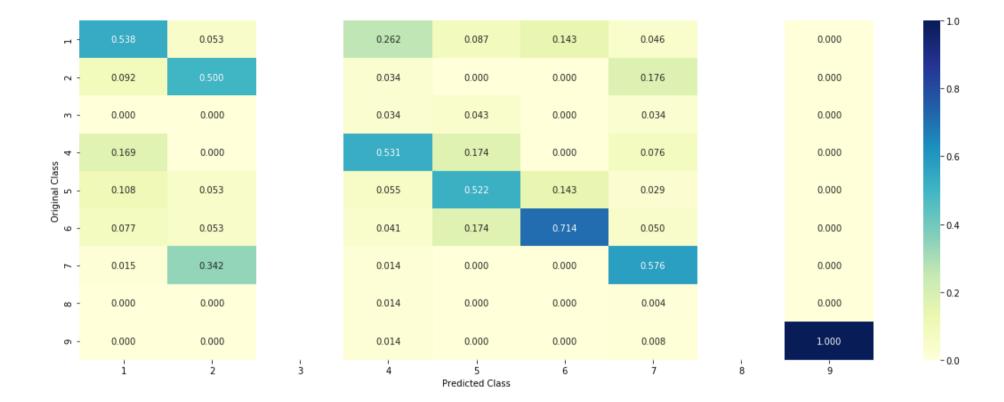
```
for n_estimators = 500 and max depth = 5
Log Loss : 1.2482148129895727
for n_estimators = 500 and max depth = 10
Log Loss : 1.2553227549412975
for n_estimators = 1000 and max depth = 5
Log Loss : 1.248393302898599
for n_estimators = 1000 and max depth = 10
Log Loss : 1.2524934816011564
for n_estimators = 2000 and max depth = 5
Log Loss : 1.2491871099410945
for n_estimators = 2000 and max depth = 10
Log Loss : 1.2520829537059068
For values of best estimator = 500 The train log loss is: 0.8764422331679262
For values of best estimator = 500 The cross validation log loss is: 1.2482148129895727
For values of best estimator = 500 The test log loss is: 1.1677440324629056
```

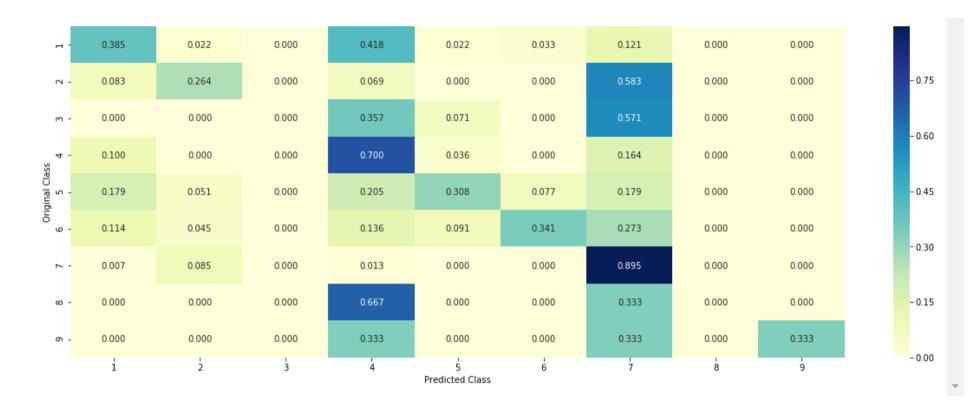
4.5.2. Testing model with best hyper parameters (One Hot Encoding)

```
In [90]: # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, v, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         # predict proba (X) Perform classification on samples in X.
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their-constructi
         clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', max depth=max depth[int(best alpha
         predict and plot confusion matrix(train x onehotCoding, train y,cv x onehotCoding,cv y, clf)
```

H -	35.000	2.000	0.000	38.000	2.000	3.000	11.000	0.000	0.000
- 2	6.000	19.000	0.000	5.000	0.000	0.000	42.000	0.000	0.000
m -	0.000	0.000	0.000	5.000	1.000	0.000	8.000	0.000	0.000
5S 4 -	11.000	0.000	0.000	77.000	4.000	0.000	18.000	0.000	0.000
Original Class 5	7.000	2.000	0.000	8.000	12.000	3.000	7.000	0.000	0.000
Ori	5.000	2.000	0.000	6.000	4.000	15.000	12.000	0.000	0.000
۲ -	1.000	13.000	0.000	2.000	0.000	0.000	137.000	0.000	0.000
ω -	0.000	0.000	0.000	2.000	0.000	0.000	1.000	0.000	0.000
o -	0.000	0.000	0.000	2.000	0.000	0.000	2.000	0.000	2.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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





4.5.3. Feature Importance

4.5.3.1. Correctly Classified point

```
In [91]: # test point index = 10
         clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', max depth=max depth[int(best alpha
         clf.fit(train x onehotCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x onehotCoding, train y)
         test point index = 1
         no feature = 100
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         get impfeature names(indices[:no feature], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_point_index]
         Predicted Class: 6
         Predicted Class Probabilities: [[7.200e-03 4.100e-03 6.400e-03 5.700e-03 2.051e-01 7.632e-01 7.400e-03
           7.000e-04 2.000e-0411
         Actual Class: 6
         0 Text feature [0001] present in test data point [True]
         1 Text feature [01] present in test data point [True]
         12 Text feature [13] present in test data point [True]
         30 Text feature [000] present in test data point [True]
         66 Text feature [045] present in test data point [True]
         95 Text feature [013] present in test data point [True]
         Out of the top 100 features 6 are present in query point
```

4.5.3.2. Inorrectly Classified point

```
In [92]: test point index = 100
         no feature = 100
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index]),4))
         print("Actuall Class :", test y[test point index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index]
         Predicted Class: 1
         Predicted Class Probabilities: [[0.3821 0.0905 0.0196 0.2457 0.0902 0.0929 0.0635 0.0085 0.0068]]
         Actuall Class: 4
         0 Text feature [0001] present in test data point [True]
         1 Text feature [01] present in test data point [True]
         12 Text feature [13] present in test data point [True]
         30 Text feature [000] present in test data point [True]
         Out of the top 100 features 4 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

```
In [93]: # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, v, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         # predict proba (X) Perform classification on samples in X.
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their-constructi
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.calibration.Ca
         # 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 = [10,50,100,200,500,1000]
         max depth = [2,3,5,10]
         cv log error array = []
         for i in alpha:
             for j in max depth:
                 print("for n estimators =", i,"and max depth = ", j)
```

```
clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, random state=42, n jobs=-1)
        clf.fit(train x responseCoding, train y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig clf.fit(train x responseCoding, train y)
        sig clf probs = sig clf.predict proba(cv x responseCoding)
        cv log error array.append(log loss(cv v, sig clf probs, labels=clf.classes , eps=1e-15))
        print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[int(i/4)],max depth[int(i%4)],str(txt)), (features[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='gini', max depth=max depth[int(best alpha/4)]
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x responseCoding, train y)
predict y = sig clf.predict proba(train x responseCoding)
print('For values of best alpha = ', alpha[int(best alpha/4)], "The train log loss is:",log loss(y train, predict y, lab
predict y = sig clf.predict proba(cv x responseCoding)
print('For values of best alpha = ', alpha[int(best alpha/4)], "The cross validation log loss is:",log loss(y cv, predic
predict y = sig clf.predict proba(test x responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The test log loss is:",log_loss(y_test, predict_y, label
for n estimators = 10 and max depth = 2
Log Loss: 2.1396158620410772
for n estimators = 10 and max depth = 3
Log Loss: 1.8253984221775816
for n_estimators = 10 and max depth = 5
Log Loss: 1.5932937108315584
for n estimators = 10 and max depth = 10
```

```
Log Loss : 2.032961196490442
for n estimators = 50 and max depth = 2
Log Loss: 1.8302465804253756
for n_{estimators} = 50 and max depth = 3
Log Loss: 1.5203722322484539
for n estimators = 50 and max depth = 5
Log Loss: 1.3724465559765668
for n estimators = 50 and max depth = 10
Log Loss: 1.7741076862080802
for n_{estimators} = 100 and max depth = 2
Log Loss: 1.6955573829864947
for n_estimators = 100 and max depth = 3
Log Loss: 1.5217293921762525
for n estimators = 100 and max depth = 5
Log Loss: 1.3402852840550363
for n estimators = 100 and max depth = 10
Log Loss: 1.7182186018638175
for n estimators = 200 and max depth = 2
Log Loss: 1.6927941073979533
for n estimators = 200 and max depth = 3
Log Loss: 1.5384308692905582
for n estimators = 200 and max depth = 5
Log Loss: 1.4051315958754826
for n estimators = 200 and max depth = 10
Log Loss: 1.6980856739016488
for n estimators = 500 and max depth = 2
Log Loss: 1.747196585304519
for n estimators = 500 and max depth = 3
Log Loss: 1.6116286845091206
for n estimators = 500 and max depth = 5
Log Loss: 1.4188527723369866
for n estimators = 500 and max depth = 10
Log Loss: 1.692914155032921
for n estimators = 1000 and max depth = 2
Log Loss: 1.734259102836383
for n estimators = 1000 and max depth = 3
Log Loss: 1.606952961052826
for n_estimators = 1000 and max depth = 5
Log Loss: 1.4315171523662278
for n_estimators = 1000 and max depth = 10
Log Loss: 1.6424980650145842
For values of best alpha = 100 The train log loss is: 0.056154254021325845
```

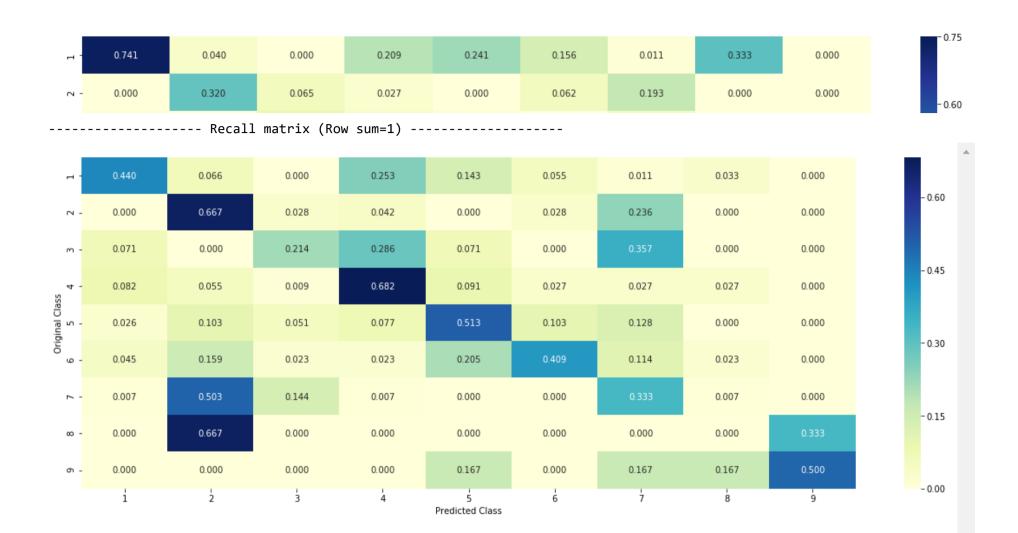
For values of best alpha = 100 The cross validation log loss is: 1.3402852840550366 For values of best alpha = 100 The test log loss is: 1.2483371340759994

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

```
In [94]: # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, v, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         # predict proba (X) Perform classification on samples in X.
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their-constructi
         clf = RandomForestClassifier(max depth=max depth[int(best alpha%4)], n estimators=alpha[int(best alpha/4)], criterion='g
         predict and plot confusion matrix(train x responseCoding, train y,cv x responseCoding,cv y, clf)
```

_									
	40.000	6.000	0.000	23.000	13.000	5.000	1.000	3.000	0.000
2 -	0.000	48.000	2.000	3.000	0.000	2.000	17.000	0.000	0.000
m -	1.000	0.000	3.000	4.000	1.000	0.000	5.000	0.000	0.000
SS 4 -	9.000	6.000	1.000	75.000	10.000	3.000	3.000	3.000	0.000
Original Class 5	1.000	4.000	2.000	3.000	20.000	4.000	5.000	0.000	0.000
oric 6	2.000	7.000	1.000	1.000	9.000	18.000	5.000	1.000	0.000
۲ -	1.000	77.000	22.000	1.000	0.000	0.000	51.000	1.000	0.000
ω -	0.000	2.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000
თ -	0.000	0.000	0.000	0.000	1.000	0.000	1.000	1.000	3.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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



4.5.5. Feature Importance

4.5.5.1. Correctly Classified point

```
In [95]: clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='gini', max depth=max depth[int(best alpha
         clf.fit(train x responseCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x responseCoding, train y)
         test point index = 1
         no feature = 27
         predicted cls = sig clf.predict(test x responseCoding[test point index].reshape(1,-1))
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x responseCoding[test point index].reshape(1
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         for i in indices:
             if i<9:
                 print("Gene is important feature")
             elif i<18:
                 print("Variation is important feature")
             else:
                 print("Text is important feature")
         Predicted Class: 6
         Predicted Class Probabilities: [[0.0102 0.0031 0.0129 0.0079 0.135 0.8169 0.0027 0.0053 0.006 ]]
         Actual Class: 6
         Variation is important feature
         Variation is important feature
         Variation is important feature
         Variation is important feature
         Gene is important feature
         Variation is important feature
         Variation is important feature
         Text is important feature
         Text is important feature
         Gene is important feature
         Text is important feature
         Text is important feature
         Text is important feature
         Gene is important feature
```

Variation is important feature
Gene is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Gene is important feature

4.5.5.2. Incorrectly Classified point

```
In [96]: test point index = 100
         predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x responseCoding[test point index].reshape(1
         print("Actual Class :", test v[test point index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         for i in indices:
             if i<9:
                 print("Gene is important feature")
             elif i<18:
                 print("Variation is important feature")
             else:
                 print("Text is important feature")
         Predicted Class: 1
         Predicted Class Probabilities: [[0.6685 0.002 0.0017 0.3165 0.001 0.0026 0.0019 0.0033 0.0025]]
         Actual Class: 4
         Variation is important feature
         Variation is important feature
         Variation is important feature
         Variation is important feature
         Gene is important feature
         Variation is important feature
         Variation is important feature
         Text is important feature
         Text is important feature
         Gene is important feature
         Text is important feature
         Text is important feature
         Text is important feature
         Gene is important feature
         Variation is important feature
         Gene is important feature
         Text is important feature
         Gene is important feature
         Gene is important feature
         Variation is important feature
         Variation is important feature
```

```
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Gene is important feature
```

4.7 Stack the models

4.7.1 testing with hyper parameter tuning

```
In [97]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, tol=None,
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power t=0.5,
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
         # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/generated/skle
         # default parameters
         # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001,
         # cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', random state=None)
         # Some of methods of SVM()
         # fit(X, v, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathematical-derivation-copy-8/
         # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/generated/skle
         # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples split=2,
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity decrease=0.0,
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm start=False,
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
```

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

Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.970

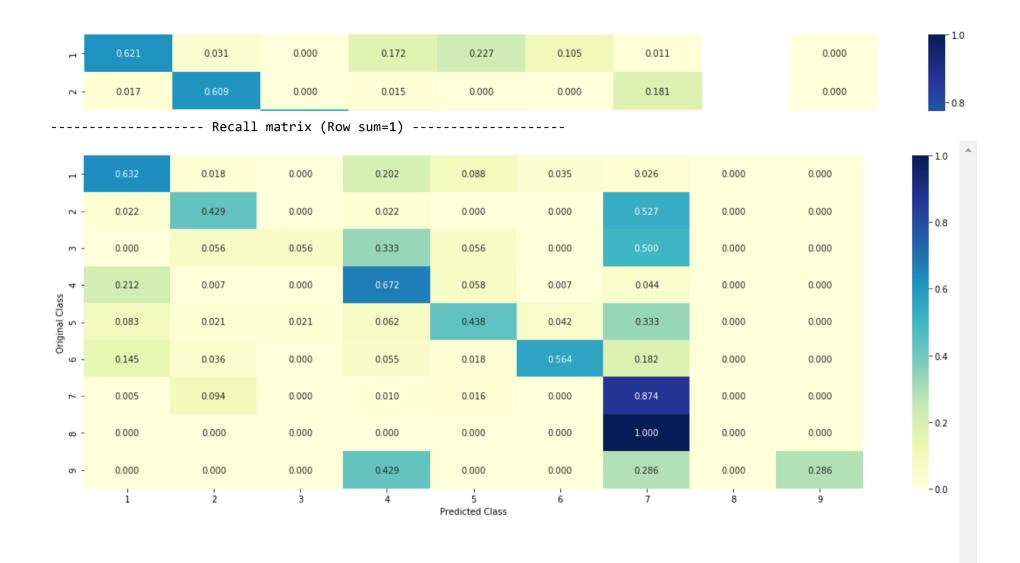
4.7.2 testing the model with the best hyper parameters

```
In [98]: lr = LogisticRegression(C=0.1)
         sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=lr, use_probas=True)
         sclf.fit(train x onehotCoding, train y)
         log error = log loss(train v, sclf.predict proba(train x onehotCoding))
         print("Log loss (train) on the stacking classifier :",log error)
         log error = log loss(cv v, sclf.predict proba(cv x onehotCoding))
         print("Log loss (CV) on the stacking classifier :",log error)
         log error = log loss(test v, sclf.predict proba(test x onehotCoding))
         print("Log loss (test) on the stacking classifier :",log error)
         print("Number of missclassified point :", np.count nonzero((sclf.predict(test x onehotCoding)- test y))/test y.shape[0])
         plot confusion matrix(test y=test y, predict y=sclf.predict(test x onehotCoding))
         Log loss (train) on the stacking classifier: 0.5446597903382286
         Log loss (CV) on the stacking classifier: 1.2262893401386683
         Log loss (test) on the stacking classifier: 1.1351665562235762
         Number of missclassified point: 0.3609022556390977
         ----- Confusion matrix -----
```

- 1	72.000	2.000	0.000	23.000	10.000	4.000	3.000	0.000	0.000
- 5	2.000	39.000	0.000	2.000	0.000	0.000	48.000	0.000	0.000
m -	0.000	1.000	1.000	6.000	1.000	0.000	9.000	0.000	0.000
5S 4	29.000	1.000	0.000	92.000	8.000	1.000	6.000	0.000	0.000
Original Class 5	4.000	1.000	1.000	3.000	21.000	2.000	16.000	0.000	0.000
oric 6	8.000	2.000	0.000	3.000	1.000	31.000	10.000	0.000	0.000
۲-	1.000	18.000	0.000	2.000	3.000	0.000	167.000	0.000	0.000
ω -	0.000	0.000	0.000	0.000	0.000	0.000	4.000	0.000	0.000
თ -	0.000	0.000	0.000	3.000	0.000	0.000	2.000	0.000	2.000
	i	2	3	4	5 Predicted Class	6	7	8	9

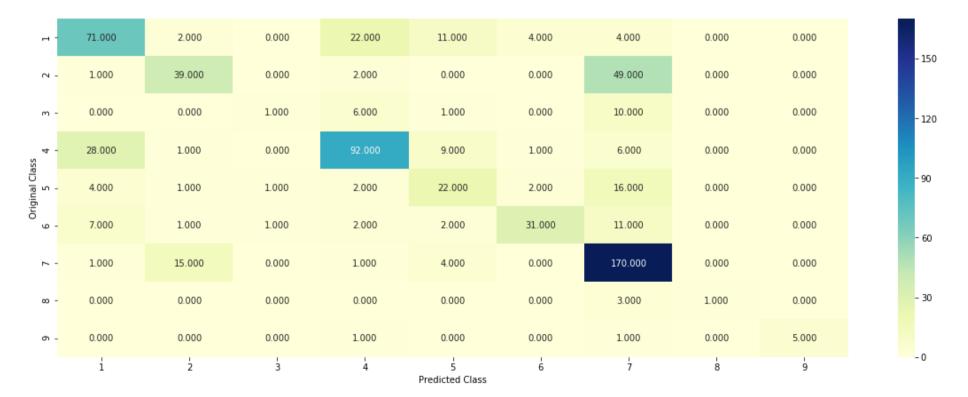
- 30

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



4.7.3 Maximum Voting classifier

In [99]: #Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassifier.html
 from sklearn.ensemble import VotingClassifier
 vclf = VotingClassifier(estimators=[('lr', sig_clf1), ('svc', sig_clf2), ('rf', sig_clf3)], voting='soft')
 vclf.fit(train_x_onehotCoding, train_y)
 print("Log loss (train) on the VotingClassifier :", log_loss(train_y, vclf.predict_proba(train_x_onehotCoding)))
 print("Log loss (CV) on the VotingClassifier :", log_loss(cv_y, vclf.predict_proba(cv_x_onehotCoding)))
 print("Log loss (test) on the VotingClassifier :", log_loss(test_y, vclf.predict_proba(test_x_onehotCoding)))
 print("Number of missclassified point :", np.count_nonzero((vclf.predict(test_x_onehotCoding) - test_y))/test_y.shape[0])
 plot_confusion_matrix(test_y=test_y, predict_y=vclf.predict(test_x_onehotCoding))





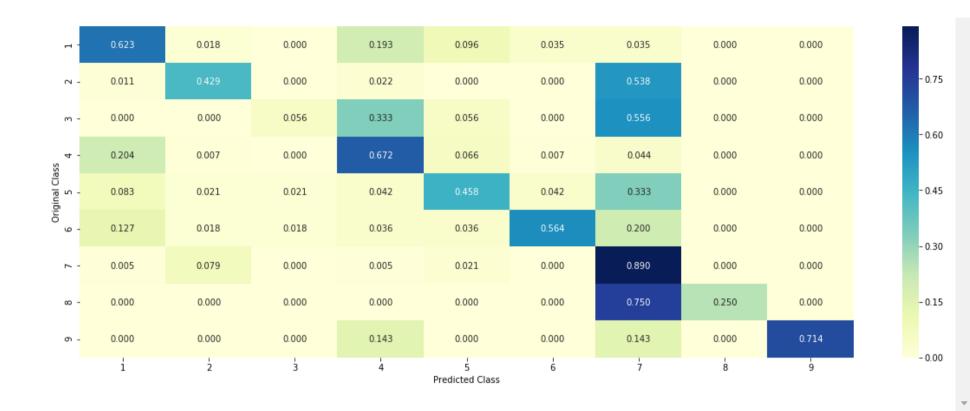
- 0.6

- 0.4

- 0.2

-0.0

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



Comparing the scores from all the above models

Performance of various model with TFIDF Vectorizer & Top 1000 features

```
In [102]: # http://zetcode.com/python/prettytable/
from prettytable import PrettyTable
#If you get a ModuleNotFoundError error , install prettytable using: pip3 install prettytable
x = PrettyTable()
x.field_names = ["Model-Name", "Train loss", "CV loss", "Test Loss", "% Misclassified"]
x.add_row(["Naive Bayes", "0.535", "1.258", "1.146", "41.72"])
x.add_row(["KNN", "0.749", "1.136", "1.028", "40.22"])
x.add_row(["LR with class Balancing", "0.437", "1.152", "0.995", "36.65"])
x.add_row(["LR without class Balancing", "0.429", "1.117", "1.016", "36.65"])
x.add_row(["Linear SVM", "0.484", "1.178", "1.053", "36.46"])
x.add_row(["RF(One Hot Encoding)", "0.896", "1.248", "1.167", "44.17"])
x.add_row(["RF(Response coding)", "0.05", "1.340", "1.248", "51.50"])
x.add_row(["Stacking Classifier", "0.544", "1.226", "1.135", "36.09"])
x.add_row(["Max voting classifier", "0.822", "1.241", "1.141", "35.03"])
print(x)
```

Model-Name	Train loss	CV loss	Test Loss	 % Misclassified
Horse Hayes Naive Bayes KNN LR with class Balancing LR without class Balancing Linear SVM RF(One Hot Encoding)	0.535	1.258	1.146	41.72
	0.749	1.136	1.028	40.22
	0.437	1.152	0.995	36.65
	0.429	1.117	1.016	36.65
	0.484	1.178	1.053	36.46
	0.896	1.248	1.167	44.17
RF(Response coding) Stacking Classifier Max voting classifier	0.05	1.340	1.248	51.50
	0.544	1.226	1.135	36.09
	0.822	1.241	1.141	35.03

Conclusion / Observations:-

- 1. We got the minimum test loss with Logistic Regression(with class balancing) which is 1.078 but the percentage of misclassified points are on the higher side being 36.65%.
- 2. We got the minimum misclassified points with Maximum voting classifier with 35.03% with test log loss of 1.14.

- 3. Random Forest with Response coding gave the maximum misclassified points with 51.50% of misclassified points. Also there is severe over-fitting with this model where the train loss is 0.05 while the test loss is 1.248 which is highest amongst all.
- 4. So for Task-2 where we used TFIDF vectorizer with top 1000 words we got minimum mis-classified points with Max voting classifier but this model is not very interpretable.