Personalized cancer diagnosis

1. Business Problem

1.1 Description

Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training_variants.zip and training_text.zip from Kaggle.

Context:

Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/discussion/35336#198462

Problem statement:

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

1.2 Sources and some Useful Links

- 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)
- $3. \ \underline{https://www.youtube.com/watch?v=qxXRKVompl8\ (\underline{https://www.youtube.com/watch?v=qxXRKVompl8})}$

1.3. Real-world/Business objectives and constraints.

- 1. Its a task of classification of each data points into one of nine cancer classes correctly.
- 2. With the Prediction of label we also need probability of each data point belonging to any of the 9 classes.
- 3. Errors can be very costly.
- 4. Interpretability is also important.
- 5. Make the CV log-Loss and Test Log-Loss < 1.0

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:/
- 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

training_variants

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

training_text

ID.Text

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

2.2 Mapping the real world problem to an ML problem

2.2.1 Type of Problem

There are 9 different Classes a Genetic Mutation can be classified into i.e Multiclass Classification Problem.

2.2.2 Performance Metric

Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation (https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation (https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation (https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation (https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation)

Metric(s):

- · Multi class log-loss
- Confusion matrix

2.2.3. Machine Learing Objectives and Constraints

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

Constraints:

- Interpretability
- · Class probabilities are needed.
- Penalize the errors in class probabilites => Metric is Log-loss.
- · No Latency constraints.

2.3. Train, CV and Test Datasets

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

3. Exploratory Data Analysis

```
In [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.model_selection import StratifiedKFold
        from collections import Counter, defaultdict
        from sklearn.calibration import CalibratedClassifierCV
        from sklearn.naive_bayes import MultinomialNB
        from sklearn.naive_bayes import GaussianNB
        from sklearn.model_selection import train_test_split
        from sklearn.model_selection import GridSearchCV
        import math
        from sklearn.metrics import normalized mutual info score
        from sklearn.ensemble import RandomForestClassifier
        warnings.filterwarnings("ignore")
        from mlxtend.classifier import StackingClassifier
        from sklearn import model_selection
        from sklearn.linear_model import LogisticRegression
```

3.1 Reading Data

3.1.1. Reading Gene and Variation Data

```
In [2]: data = pd.read_csv('training variants')
        print('Number of data points : ', data.shape[0])
        print('Number of features : ', data.shape[1])
        print('Features : ', data.columns.values)
        data.head()
        Number of data points : 3321
        Number of features: 4
```

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

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 [194]: # note the seprator in this file
            data_text =pd.read_csv("training_text",sep="\|\|",engine="python",names=["ID","TEXT"],skiprows=1)
            print('Number of data points : ', data_text.shape[0])
print('Number of features : ', data_text.shape[1])
            print('Features : ', data_text.columns.values)
            data_text.head()
            Number of data points : 3321
            Number of features : 2
            Features : ['ID' 'TEXT']
```

Out[194]:

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

3.1.3. Preprocessing of text

```
In [176]: # 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 [177]: #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")
```

Time took for preprocessing the text : 1965.2896444840062 seconds

result['Feature_3'] = result['Feature_2'] / result['Feature_1']

merging both gene_variations and text data based on ID

```
In [178]: result = pd.merge(data, data_text,on='ID', how='left')
    result.head()
```

Out[178]:

	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 [179]: result["text_variation"]=result["TEXT"]+result["Variation"]
In [195]: result['text_backup']=data_text["TEXT"]
In [181]: result["gene_variation"]=result["Gene"]+" "+result["Variation"]
In [182]: #feature 1 is Number of Words in Text column
    result['Feature_1']= result["text_backup"].apply(lambda x: len(str(x).split()))
In [183]: #Feature 2 - Count of characters in a statement
    result['Feature_2'] = result["text_backup"].apply(lambda x: len(str(x)))
In [184]: #Feature 3-Diversity_score i.e. Average length of words used in statement
```

```
In [197]: result['Variation Share'] = result.apply(lambda r: sum([1 for w in r['Variation'].split(' ') if w
           in r['text_backup'].split(' ')]), axis=1)
          result["Variation_Share"].value_counts()
Out[197]: 1
               1672
               1577
          0
          2
                 58
          3
                 10
          5
                  2
          4
                  2
          Name: Variation_Share, dtype: int64
In [198]: result.drop("text_backup",axis=1,inplace=True)
```

In [198]: result.urop(text_backup ,axis=1,inplace=irue

In [200]: result.head()

Out[200]:

	ID	Gene	Variation	Class	TEXT	gene_variation	Feature_1	Feature_2	Feature_3	Gene_Share	٧
0	0	FAM58A	Truncating Mutations	1	cyclin dependent kinases cdks regulate variety	FAM58A Truncating Mutations	4370	30836	7.056293	1	1
1	1	CBL	W802*	2	abstract background non small cell lung cancer	CBL W802*	4139	27844	6.727229	1	1
2	2	CBL	Q249E	2	abstract background non small cell lung cancer	CBL Q249E	4139	27844	6.727229	1	1
3	3	CBL	N454D	3	recent evidence demonstrated acquired uniparen	CBL N454D	3841	28093	7.313981	1	1
4	4	CBL	L399V	4	oncogenic mutations monomeric casitas b lineag	CBL L399V	4254	31649	7.439821	1	1

3.1.4. Test, Train and Cross Validation Split

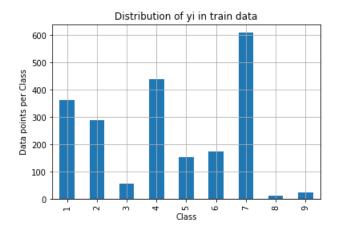
3.1.4.1. Splitting data into train, test and cross validation (64:20:16)

In [202]: 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])

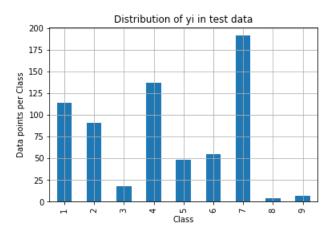
Number of data points in train data: 2124 Number of data points in test data: 665

Number of data points in cross validation data: 532

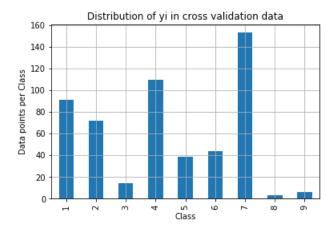
```
In [203]: # it returns a dict, keys as class labels and values as the number of data points in that class
          train_class_distribution = train_df['Class'].value_counts().sortlevel()
          test_class_distribution = test_df['Class'].value_counts().sortlevel()
          cv_class_distribution = cv_df['Class'].value_counts().sortlevel()
          my_colors = 'rgbkymc'
          train_class_distribution.plot(kind='bar')
          plt.xlabel('Class')
          plt.ylabel('Data points per Class')
          plt.title('Distribution of yi in train data')
          plt.grid()
          plt.show()
          # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
          # -(train_class_distribution.values): the minus sign will give us in decreasing order
          sorted_yi = np.argsort(-train_class_distribution.values)
          for i in sorted_yi:
              print('Number of data points in class', i+1, ':',train_class_distribution.values[i], '(', np.r
          ound((train_class_distribution.values[i]/train_df.shape[0]*100), 3), '%)')
          print('-'*80)
          my_colors = 'rgbkymc'
          test_class_distribution.plot(kind='bar')
          plt.xlabel('Class')
          plt.ylabel('Data points per Class')
          plt.title('Distribution of yi in test data')
          plt.grid()
          plt.show()
          # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
          # -(train_class_distribution.values): the minus sign will give us in decreasing order
          sorted_yi = np.argsort(-test_class_distribution.values)
          for i in sorted_yi:
              print('Number of data points in class', i+1, ':',test_class_distribution.values[i], '(', np.ro
          und((test_class_distribution.values[i]/test_df.shape[0]*100), 3), '%)')
          print('-'*80)
          my_colors = 'rgbkymc'
          cv_class_distribution.plot(kind='bar')
          plt.xlabel('Class')
          plt.ylabel('Data points per Class')
          plt.title('Distribution of yi in cross validation data')
          plt.grid()
          plt.show()
          # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
          # -(train_class_distribution.values): the minus sign will give us in decreasing order
          sorted_yi = np.argsort(-train_class_distribution.values)
          for i in sorted_yi:
              print('Number of data points in class', i+1, ':',cv_class_distribution.values[i], '(', np.roun
          d((cv_class_distribution.values[i]/cv_df.shape[0]*100), 3), '%)')
```



Number of data points in class 7 : 609 (28.672 %) Number of data points in class 4 : 439 (20.669 %) Number of data points in class 1 : 363 (17.09 %) Number of data points in class 2 : 289 (13.606 %) Number of data points in class 6 : 176 (8.286 %) Number of data points in class 5 : 155 (7.298 %) Number of data points in class 3 : 57 (2.684 %) Number of data points in class 9 : 24 (1.13 %) Number of data points in class 8 : 12 (0.565 %)



Number of data points in class 7 : 191 (28.722%) Number of data points in class 4 : 137 (20.602%) Number of data points in class 1 : 114 (17.143%) Number of data points in class 2 : 91 (13.684%) Number of data points in class 6 : 55 (8.271%) Number of data points in class 5 : 48 (7.218%) Number of data points in class 3 : 18 (2.707%) Number of data points in class 9 : 7 (1.053%) Number of data points in class 8 : 4 (0.602%)



```
Number of data points in class 7 : 153 ( 28.759 \%) Number of data points in class 4 : 110 ( 20.677 \%) Number of data points in class 1 : 91 ( 17.105 \%) Number of data points in class 2 : 72 ( 13.534 \%) Number of data points in class 6 : 44 ( 8.271 \%) Number of data points in class 5 : 39 ( 7.331 \%) Number of data points in class 3 : 14 ( 2.632 \%) Number of data points in class 9 : 6 ( 1.128 \%) Number of data points in class 8 : 3 ( 0.564 \%)
```

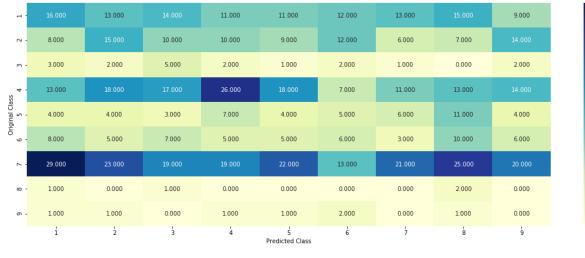
3.2 Prediction using a 'Random' Model

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

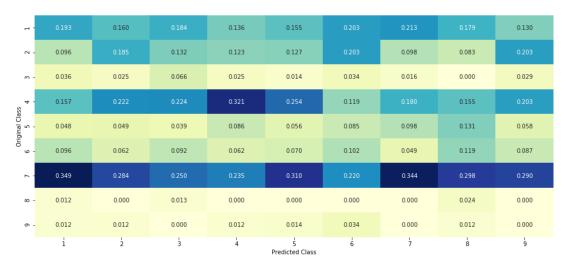
```
In [204]: # This function plots the confusion matrices given y_i, y_i_hat.
          def plot_confusion_matrix(test_y, predict_y):
              C = confusion_matrix(test_y, predict_y)
              # C = 9.9 matrix, each cell (i,j) represents number of points of class i are predicted class j
              A = (((C.T)/(C.sum(axis=1))).T)
              #divid each element of the confusion matrix with the sum of elements in that column
              \# C = [[1, 2],
                    [3, 4]]
              # C.T = [[1, 3],
                       [2, 4]]
              # C.sum(axis = 1) axis=0 corresonds to columns and axis=1 corresponds to rows in two diamensi
          onal 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 diamensi
          onal arrav
              # C.sum(axix = 0) = [[4, 6]]
              \# (C/C.sum(axis=0)) = [[1/4, 2/6],
                                      [3/4, 4/6]]
              labels = [1,2,3,4,5,6,7,8,9]
              # representing A in heatmap format
              print("-"*20, "Confusion matrix", "-"*20)
              plt.figure(figsize=(20,7))
              sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
              plt.xlabel('Predicted Class')
              plt.ylabel('Original Class')
              plt.show()
              print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
              plt.figure(figsize=(20,7))
              sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
              plt.xlabel('Predicted Class')
              plt.ylabel('Original Class')
              plt.show()
              # representing B in heatmap format
              print("-"*20, "Recall matrix (Row sum=1)", "-"*20)
              plt.figure(figsize=(20,7))
              sns.heatmap(A, annot=True, cmap="Y1GnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
              plt.xlabel('Predicted Class')
              plt.ylabel('Original Class')
              plt.show()
```

```
In [205]: # we need to generate 9 numbers and the sum of numbers should be 1
          # one solution is to genarate 9 numbers and divide each of the numbers by their sum
          # ref: https://stackoverflow.com/a/18662466/4084039
          test_data_len = test_df.shape[0]
          cv_data_len = cv_df.shape[0]
          # we create a output array that has exactly same size as the CV data
          cv_predicted_y = np.zeros((cv_data_len,9))
          for i in range(cv_data_len):
              rand_probs = np.random.rand(1,9)
              cv_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
          print("Log loss on Cross Validation Data using Random Model",log_loss(y_cv,cv_predicted_y, eps=1e-
          15))
          # Test-Set error.
          #we create a output array that has exactly same as the test data
          test_predicted_y = np.zeros((test_data_len,9))
          for i in range(test_data_len):
              rand_probs = np.random.rand(1,9)
              test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
          print("Log loss on Test Data using Random Model",log_loss(y_test,test_predicted_y, eps=1e-15))
          predicted_y =np.argmax(test_predicted_y, axis=1)
          plot_confusion_matrix(y_test, predicted_y+1)
```

----- Confusion matrix -----



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



0.30

0.24

- 0.18

-0.12

- 0.06

0.3

- 0.2

-0.1

-00

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



```
In [206]: # 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 / nu
          mber of time it occurred in total data+90*alpha)
          # gv_dict is like a look up table, for every gene it store a (1*9) representation of it
          # for a value of feature in df:
          # if it is in train data:
          # we add the vector that was stored in 'gv_dict' look up table to 'gv_fea'
          # if it is not there is train:
          # we add [1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9] to 'gv_fea'
          # return 'gv_fea'
          # get_gv_fea_dict: Get Gene varaition Feature Dict
          def get_gv_fea_dict(alpha, feature, df):
              # value_count: it contains a dict like
              # print(train_df['Gene'].value_counts())
              # output:
                        {BRCA1
              #
                                    174
                        TP53
                                    106
                        EGFR
                                     86
                        BRCA2
                                     75
              #
                        PTEN
              #
                        KIT
                                     61
              #
                        BRAF
                                     60
              #
                        ERBB2
                                     47
              #
                        PDGFRA
                                     46
                         ...}
              # print(train_df['Variation'].value_counts())
              # output:
              # {
              # Truncating_Mutations
                                                          63
                                                          43
              # Deletion
                                                          43
              # Amplification
              # Fusions
                                                          22
              # Overexpression
                                                           3
              # E17K
                                                           3
                                                           3
              # Q61L
              # S222D
              # P130S
              # ...
              value_count = train_df[feature].value_counts()
              # gv_dict : Gene Variation Dict, which contains the probability array for each gene/variation
              gv_dict = dict()
              # denominator will contain the number of time that particular feature occured in whole data
              for i, denominator in value_count.items():
                  # vec will contain (p(yi==1/Gi)) probability of gene/variation belongs to perticular class
                  # vec is 9 diamensional vector
                  vec = []
                   for k in range(1,10):
                       # print(train_df.loc[(train_df['Class']==1) & (train_df['Gene']=='BRCA1')])
                                                       Variation Class
                                ID Gene
                       # 2470 2470 BRCA1
                                                          S1715C
                                                          S1841R
                       # 2486 2486 BRCA1
                                                                      1
                       # 2614 2614 BRCA1
                                                             M1R
                                                                      1
                       # 2432 2432 BRCA1
                                                          L1657P
                                                                      1
                       # 2567 2567 BRCA1
                                                          T1685A
                                                                      1
                       # 2583 2583 BRCA1
                                                          E1660G
                       # 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, 0.037878787878788, 0.068181818181818177, 0.13636363636
363635, 0.25, 0.19318181818181818, 0.037878787878788, 0.0378787878787878787878787878787878],
           'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 0.27040816326
530615, 0.061224489795918366, 0.066326530612244902, 0.051020408163265307, 0.051020408163265307, 0.
056122448979591837],
          'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.068181818181818177, 0.068
1818181818177, 0.0625, 0.34659090909090912, 0.0625, 0.056818181818181816],
          'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.06060606060606060, 0.0787878787
87878782, 0.13939393939394, 0.34545454545454546, 0.06060606060606060, 0.0606060606060606, 0.0
60606060606060608],
          'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 0.4654088050
3144655, 0.075471698113207544, 0.062893081761006289, 0.069182389937106917, 0.062893081761006289,
0.062893081761006289],
           'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.072847682119
205295, 0.066225165562913912, 0.066225165562913912, 0.27152317880794702, 0.066225165562913912, 0.0
66225165562913912],
           'BRAF': [0.066666666666666666, 0.17999999999999, 0.0733333333333334, 0.07333333333
3333334, 0.093333333333333338, 0.080000000000000002, 0.2999999999999, 0.066666666666666666, 0.
#
         }
    gv_dict = get_gv_fea_dict(alpha, feature, df)
    # value_count is similar in get_gv_fea_dict
    value count = train df[feature].value_counts()
    # gv_fea: Gene_variation feature, it will contain the feature for each feature value in the da
ta
    gv_fea = []
    # for every feature values in the given data frame we will check if it is there in the train d
ata then we will add the feature to gv_fea
    # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to gv_fea
    for index, row in df.iterrows():
       if row[feature] in dict(value_count).keys():
           gv_fea.append(gv_dict[row[feature]])
            gv_fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
             gv_fea.append([-1,-1,-1,-1,-1,-1,-1,-1])
    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

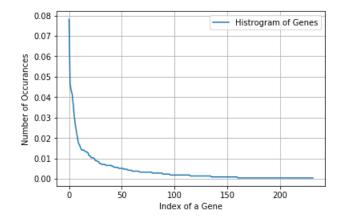
Q2. How many categories are there and How they are distributed?

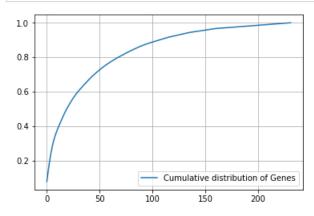
```
In [207]: unique genes = train_df['Gene'].value_counts()
           print('Number of Unique Genes :', unique_genes.shape[0])
           # the top 10 genes that occured most
          print(unique_genes.head(10))
          Number of Unique Genes : 232
          BRCA1
                     166
          TP53
                      99
          EGFR
                      92
          PTFN
                      88
          BRCA2
                      77
          KIT
                      65
          BRAF
                      56
          ERBB2
                      49
          ALK
                      43
          PDGFRA
                      37
          Name: Gene, dtype: int64
```

In [208]: print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in the train data, a
nd they are distibuted as follows",)

Ans: There are 232 different categories of genes in the train data, and they are distibuted as fol lows

```
In [209]: 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()
```





Q3. How to featurize this Gene feature?

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

- 1. One hot Encoding
- 2. Response coding

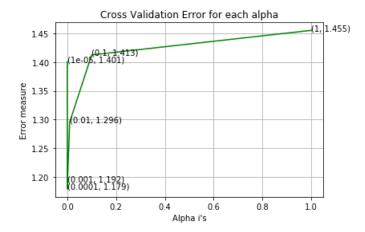
We will choose the One hot Encoding featurization based here for now. For this problem of multi-class classification with categorical features, one-hot encoding is better for Logistic regression while response coding is better for Random Forests.

```
In [211]: # one-hot encoding of Gene feature.
          gene_vectorizer = CountVectorizer()
          train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gene'])
          test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gene'])
          cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
In [212]: cv_gene_feature_onehotCoding.shape
Out[212]: (532, 231)
In [213]: print("train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The sha
          pe of gene feature:", train gene feature onehotCoding.shape)
          train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of g
          ene feature: (2124, 231)
In [214]: # creating a dataframe of the vectorized features
          df_gene_train = pd.DataFrame(train_gene_feature_onehotCoding.toarray(), columns=gene_vectorizer.ge
          t_feature_names())
          df_gene_test = pd.DataFrame(test_gene_feature_onehotCoding.toarray(), columns=gene_vectorizer.get_
          feature names())
          df_gene_cv = pd.DataFrame(cv_gene_feature_onehotCoding.toarray(), columns=gene_vectorizer.get_feat
          ure_names())
```

How Good is gene feature in predicting y_i

```
In [215]: 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.line
          ar_model.SGDClassifier.html
          # -----
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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 class labels for samples in X.
          # predict(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.cla
          sses_, 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.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_gene_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
```

For values of alpha = 1e-05 The log loss is: 1.4005555527470852
For values of alpha = 0.0001 The log loss is: 1.179340161820206
For values of alpha = 0.001 The log loss is: 1.1920606034079948
For values of alpha = 0.01 The log loss is: 1.2955107368017145
For values of alpha = 0.1 The log loss is: 1.412544823106519
For values of alpha = 1 The log loss is: 1.4552582366725741



For values of best alpha = 0.0001 The train log loss is: 1.0415595201966887
For values of best alpha = 0.0001 The cross validation log loss is: 1.179340161820206
For values of best alpha = 0.0001 The test log loss is: 1.2086527043791122

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?

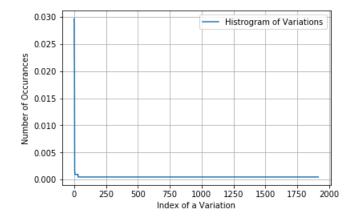
```
In [216]: unique_variations = train_df['Variation'].value_counts()
    print('Number of Unique Variations :', unique_variations.shape[0])
    # the top 10 variations that occured most
    print(unique_variations.head(10))
```

```
Number of Unique Variations : 1916
Truncating_Mutations
Deletion
                         48
Amplification
                         46
Fusions
                         26
E17K
                          3
Overexpression
                          3
S308A
                          2
V321M
                          2
Q61R
Q61K
Name: Variation, dtype: int64
```

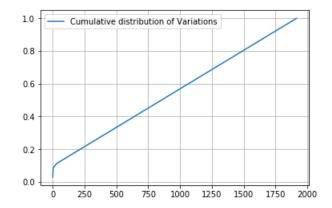
In [217]: print("Ans: There are", unique_variations.shape[0] ,"different categories of variations in the tra
in data, and they are distibuted as follows",)

Ans: There are 1916 different categories of variations in the train data, and they are distibuted as follows

```
In [218]: 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()
```



[0.02966102 0.05225989 0.07391714 ... 0.99905838 0.99952919 1.



Q9. How to featurize this Variation feature?

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

- 1. One hot Encoding
- 2. Response coding

We will be using One hot Encoding method to featurize the Variation Feature

```
In [220]: # 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'])
```

Q11. Is the Variation feature stable across all the data sets (Test, Train, Cross validation)?

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

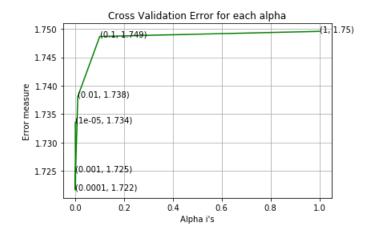
In [221]: print("Q12. How many data points are covered by total ", unique_variations.shape[0], " genes in te
 st and cross validation data sets?")
 test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
 cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
 print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_coverage/test_df.shape[0])*100)
 print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(cv_coverage/cv_df.shape[0])*100)

Q12. How many data points are covered by total $\,$ 1916 $\,$ genes in test and cross validation data set s? Ans

- 1. In test data 59 out of 665 : 8.87218045112782
- 2. In cross validation data 49 out of 532 : 9.210526315789473

```
In [223]: alpha = [10 ** x for x in range(-5, 1)]
          # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.line
          ar_model.SGDClassifier.html
          # -----
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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 class labels for samples in X.
          # predict(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.cla
          sses_, 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.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_variation_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
```

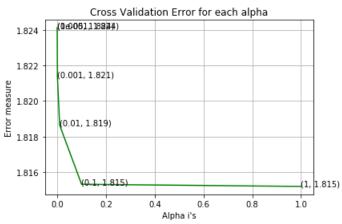
```
For values of alpha = 1e-05 The log loss is: 1.7335721680090286
For values of alpha = 0.0001 The log loss is: 1.72166551571151
For values of alpha = 0.001 The log loss is: 1.7249727158308956
For values of alpha = 0.01 The log loss is: 1.7380948794689282
For values of alpha = 0.1 The log loss is: 1.748669375869514
For values of alpha = 1 The log loss is: 1.7495674317353667
```



For values of best alpha = 0.0001 The train log loss is: 0.7456583822237609
For values of best alpha = 0.0001 The cross validation log loss is: 1.72166551571151
For values of best alpha = 0.0001 The test log loss is: 1.7242034752511008

3.2.3 Univariate analysis on number of words feature

```
In [224]: alpha = [10 ** x for x in range(-5, 1)]
           cv_log_error_array=[]
           for i in alpha:
               clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
               clf.fit(train_df["Feature_1"].reshape(-1,1), y_train)
               sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
               sig_clf.fit(train_df.Feature_1.reshape(-1,1), y_train)
               predict_y = sig_clf.predict_proba(cv_df.Feature_1.reshape(-1,1))
               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.cla
           sses , 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_df.Feature_1.reshape(-1,1), y_train)
           sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
           sig_clf.fit(train_df.Feature_1.reshape(-1,1), y_train)
          predict_y = sig_clf.predict_proba(train_df.Feature_1.reshape(-1,1))
          print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
           predict_y, labels=clf.classes_, eps=1e-15))
           predict_y = sig_clf.predict_proba(cv_df.Feature_1.reshape(-1,1))
           print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
           ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
           predict y = sig clf.predict proba(test_df.Feature 1.reshape(-1,1))
           print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
          For values of alpha = 1e-05 The log loss is: 1.8241096612789325
          For values of alpha = 0.0001 The log loss is: 1.8241096612794818
For values of alpha = 0.001 The log loss is: 1.8213303970404182
          For values of alpha = 0.01 The log loss is: 1.8186476370872977
          For values of alpha = 0.1 The log loss is: 1.8153239532039447
          For values of alpha = 1 The log loss is: 1.8152017039678854
```

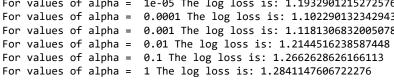


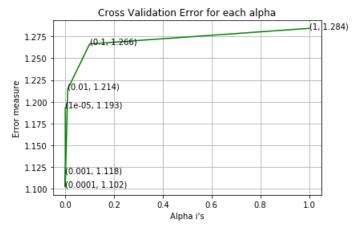
```
For values of best alpha = 1 The train log loss is: 1.8145762602898243

For values of best alpha = 1 The cross validation log loss is: 1.8152017039678854

For values of best alpha = 1 The test log loss is: 1.8027729211835348
```

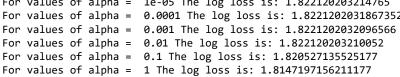
```
In [227]: alpha = [10 ** x for x in range(-5, 1)]
          cv_log_error_array=[]
          for i in alpha:
              clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
              clf.fit(df_geneandvar_train, y_train)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(df_geneandvar_train, y_train)
              predict_y = sig_clf.predict_proba(df_geneandvar_cv)
              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.cla
          sses_, 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(df_geneandvar_train, y_train)
          sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(df_geneandvar_train, y_train)
          predict_y = sig_clf.predict_proba(df_geneandvar_train)
          print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
           predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(df_geneandvar_cv)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(df_geneandvar_test)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
          For values of alpha = 1e-05 The log loss is: 1.1932901215272576
          For values of alpha = 0.0001 The log loss is: 1.102290132342943
          For values of alpha = 0.001 The log loss is: 1.1181306832005078
          For values of alpha = 0.01 The log loss is: 1.2144516238587448
```

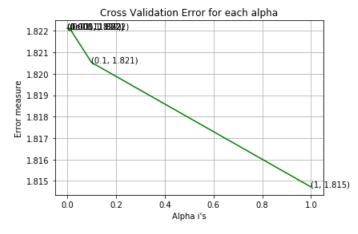




```
For values of best alpha = 0.0001 The train log loss is: 0.5215962530649423
For values of best alpha = 0.0001 The cross validation log loss is: 1.102290132342943
For values of best alpha = 0.0001 The test log loss is: 1.1352915779532327
```

```
In [228]: alpha = [10 ** x for x in range(-5, 1)]
          cv_log_error_array=[]
          for i in alpha:
              clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
              clf.fit(train_df["Feature_2"].reshape(-1,1), y_train)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(train_df.Feature_2.reshape(-1,1), y_train)
              predict_y = sig_clf.predict_proba(cv_df.Feature_2.reshape(-1,1))
              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.cla
          sses , 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_df.Feature_2.reshape(-1,1), y_train)
          sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(train_df.Feature_2.reshape(-1,1), y_train)
          predict_y = sig_clf.predict_proba(train_df.Feature_2.reshape(-1,1))
          print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
           predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_df.Feature_2.reshape(-1,1))
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_df.Feature_2.reshape(-1,1))
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
          For values of alpha = 1e-05 The log loss is: 1.822120203214765
          For values of alpha = 0.0001 The log loss is: 1.8221202031867352
          For values of alpha = 0.001 The log loss is: 1.8221202032096566
          For values of alpha = 0.01 The log loss is: 1.822120203210052
```





```
For values of best alpha = 1 The train log loss is: 1.8157875187232202
For values of best alpha = 1 The cross validation log loss is: 1.8147197156211177
For values of best alpha = 1 The test log loss is: 1.805133499817863
```

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

```
In [230]: 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 [267]: #building a CountVectorizer with all the words that occured minimum 3 times in train data

text_vectorizer = TfidfVectorizer(ngram_range=(1,4),max_features=2000)
    train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
    # getting all the feature names (words)
    train_text_features= text_vectorizer.get_feature_names()

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

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

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

Total number of unique words in train data : 2000

```
In [268]: train_text_fea_counts.shape
Out[268]: (2000,)
```

```
In [269]: dict_list = []
          # dict_list =[] contains 9 dictoinaries each corresponds to a class
          for i in range(1,10):
              cls_text = train_df[train_df['Class']==i]
              # build a word dict based on the words in that class
              dict_list.append(extract_dictionary_paddle(cls_text))
              # append it to dict_list
          # dict_list[i] is build on i'th class text data
          # total_dict is buid on whole training text data
          total_dict = extract_dictionary_paddle(train_df)
          confuse_array = []
          for i in train_text_features:
              ratios = []
              max_val = -1
              for j in range(0,9):
                  ratios.append((dict_list[j][i]+10 )/(total_dict[i]+90))
              confuse_array.append(ratios)
          confuse_array = np.array(confuse_array)
In [270]: # don't forget to normalize every feature
          train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding, axis=0)
          # we use the same vectorizer that was trained on train data
          test_text_feature_onehotCoding = text_vectorizer.transform(test_df['TEXT'])
          # don't forget to normalize every feature
          test_text_feature_onehotCoding = normalize(test_text_feature_onehotCoding, axis=0)
          # we use the same vectorizer that was trained on train data
          cv_text_feature_onehotCoding = text_vectorizer.transform(cv_df['TEXT'])
          # don't forget to normalize every feature
          cv_text_feature_onehotCoding = normalize(cv_text_feature_onehotCoding, axis=0)
In [271]: #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 [272]: print(train_text_feature_onehotCoding.shape)
          print(test_text_feature_onehotCoding.shape)
          print(cv_text_feature_onehotCoding.shape)
          (2124, 2000)
          (665, 2000)
          (532, 2000)
```

```
In [273]: # 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.line
          ar_model.SGDClassifier.html
          # -----
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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 class labels for samples in X.
          # predict(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.cla
          sses_, 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.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_text_feature_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.1105363411250055

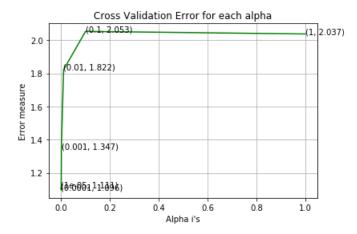
For values of alpha = 0.0001 The log loss is: 1.0964906815887412

For values of alpha = 0.001 The log loss is: 1.346817068493882

For values of alpha = 0.01 The log loss is: 1.8215906927561887

For values of alpha = 0.1 The log loss is: 2.0530451970564907

For values of alpha = 1 The log loss is: 2.0373670509665978
```



```
For values of best alpha = 0.0001 The train log loss is: 0.7467683268790596
For values of best alpha = 0.0001 The cross validation log loss is: 1.0964906815887412
For values of best alpha = 0.0001 The test log loss is: 1.1013255697297029
```

```
In [274]: df_text_train = pd.DataFrame(train_text_feature_onehotCoding.toarray(), columns=text_vectorizer.ge
t_feature_names())
df_text_test = pd.DataFrame(test_text_feature_onehotCoding.toarray(), columns=text_vectorizer.get_
feature_names())
df_text_cv = pd.DataFrame(cv_text_feature_onehotCoding.toarray(), columns=text_vectorizer.get_feature_names())
```

4. Machine Learning Models

```
In [275]: #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 [276]: 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 [277]: # 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")
```

Stacking all the features

```
In [278]: #target variables
          train_y = train_df['Class'].values
          test y = test_df['Class'].values
          cv_y = cv_df['Class'].values
          # concatenating all the vectorized dataframes
          df_gene_var_train = pd.concat([df_gene_train, df_var_train], axis=1)
          df_gene_var_test = pd.concat([df_gene_test, df_var_test], axis=1)
          df_gene_var_cv = pd.concat([df_gene_cv, df_var_cv], axis=1)
          df_gene_and_var_train = pd.concat([df_gene_var_train, df_geneandvar_train], axis=1)
          df_gene_and_var_test = pd.concat([df_gene_var_test, df_geneandvar_test], axis=1)
          df_gene_and_var_cv = pd.concat([df_gene_var_cv, df_geneandvar_cv], axis=1)
          df_train = pd.concat([df_gene_and_var_train, df_text_train], axis=1)
          df_test = pd.concat([df_gene_and_var_test, df_text_test], axis=1)
          df_cv = pd.concat([df_gene_and_var_cv, df_text_cv], axis=1)
          # scaling the text_count feature
          from sklearn.preprocessing import MinMaxScaler
          scaler = MinMaxScaler()
          train_df["Feature_1"] = scaler.fit_transform(train_df["Feature_1"].reshape(-1,1))
          test_df["Feature_1"] = scaler.fit_transform(test_df["Feature_1"].reshape(-1,1))
          cv_df["Feature_1"] = scaler.fit_transform(cv_df["Feature_1"].reshape(-1,1))
          train_df["Feature_2"] = scaler.fit_transform(train_df["Feature_2"].reshape(-1,1))
          test_df["Feature_2"] = scaler.fit_transform(test_df["Feature_2"].reshape(-1,1))
          cv_df["Feature_2"] = scaler.fit_transform(cv_df["Feature_2"].reshape(-1,1))
          train_df["Feature_3"] = scaler.fit_transform(train_df["Feature_3"].reshape(-1,1))
          test_df["Feature_3"] = scaler.fit_transform(test_df["Feature_3"].reshape(-1,1))
          cv_df["Feature_3"] = scaler.fit_transform(cv_df["Feature_3"].reshape(-1,1))
          df_train["Gene_Share"] = train_df.Gene_Share.values
          df_train["Variation_Share"] = train_df.Variation_Share.values
          df_train["Feature_1"] = train_df.Feature_1.values
          df_train["Feature_2"] = train_df.Feature_2.values
          df train["Feature_3"] = train_df.Feature_3.values
          df_test["Gene_Share"] = test_df.Gene_Share.values
          df_test["Variation_Share"] = test_df.Variation_Share.values
          df_test["Feature_1"] = test_df.Feature_1.values
          df_test["Feature_2"] = test_df.Feature_2.values
          df_test["Feature_3"] = test_df.Feature_3.values
          df_cv["Gene_Share"] = cv_df.Gene_Share.values
          df_cv["Variation_Share"] = cv_df.Variation_Share.values
          df_cv["Feature_1"] = cv_df.Feature_1.values
          df_cv["Feature_2"] = cv_df.Feature_2.values
          df_cv["Feature_3"] = cv_df.Feature_3.values
          train_x_onehotCoding = df_train
          test_x_onehotCoding = df_test
          cv_x_onehotCoding = df_cv
In [320]: 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)
```

(number of data points * number of features) in train data = (2124, 6327)
(number of data points * number of features) in test data = (665, 6327)

(number of data points * number of features) in cross validation data = (532, 6327)

```
4.1. Base Line Model
```

One hot encoding features :

4.	1.	1.	1.	Hν	per	parameter	tunina

```
In [280]: # find more about Multinomial Naive base function here http://scikit-learn.org/stable/modules/gene
          rated/sklearn.naive_bayes.MultinomialNB.html
          # default paramters
          # sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_prior=None)
          # some of methods of MultinomialNB()
                                        Fit Naive Bayes classifier according to X, y
          # fit(X, y[, sample_weight])
          # 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-
          alaorithm-1/
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/
          sklearn.calibration.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight]) Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-
          alaorithm-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_y)
          predict_y = sig_clf.predict_proba(train_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
           predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-05

Log Loss: 1.233816172023287

for alpha = 0.0001

Log Loss : 1.2337083709494239

for alpha = 0.001

Log Loss : 1.2343450081698089

for alpha = 0.1

Log Loss : 1.253028536291359

for alpha = 1

Log Loss : 1.2705641127871883

for alpha = 10

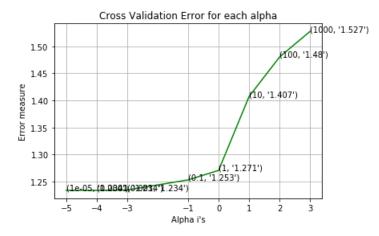
Log Loss : 1.4071878034064196

for alpha = 100

Log Loss : 1.4801906371270999

for alpha = 1000

Log Loss : 1.5274644180242751



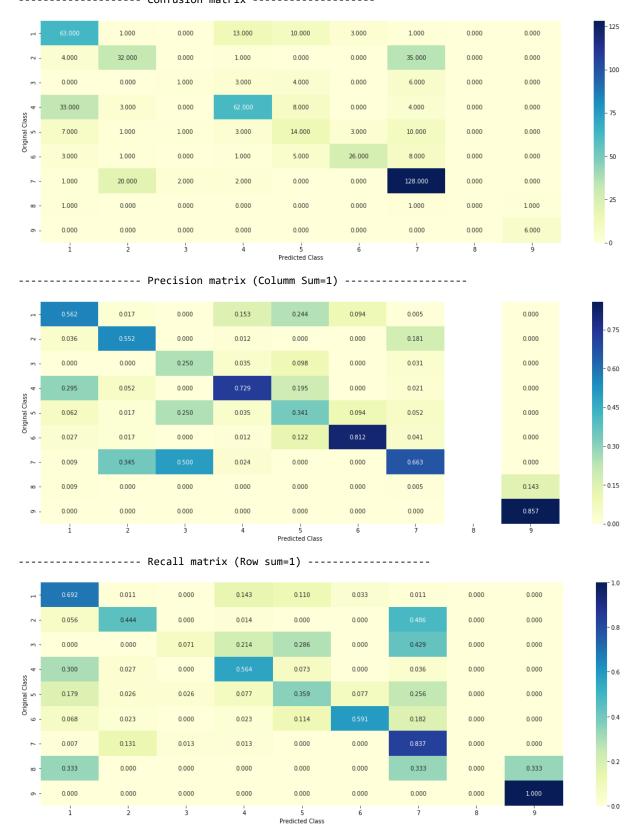
For values of best alpha = 0.0001 The train log loss is: 0.6218903432935438

For values of best alpha = 0.0001 The cross validation log loss is: 1.2337083709494239

For values of best alpha = 0.0001 The test log loss is: 1.2642411605579797

4.1.1.2. Testing the model with best hyper paramters

```
In [287]: # find more about Multinomial Naive base function here http://scikit-learn.org/stable/modules/gene
          rated/sklearn.naive_bayes.MultinomialNB.html
          # default paramters
          # sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_prior=None)
          # some of methods of MultinomialNB()
          # fit(X, y[, sample_weight])
                                        Fit Naive Bayes classifier according to X, y
          \# 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.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          \# fit(X, y[, sample_weight]) Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          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.as matrix()))
```



```
In [289]: test_point_index = 1
          no_feature = 100
          predicted cls = sig clf.predict(test x onehotCoding.iloc[test_point index, :].reshape(1, -1))
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding.iloc[te
          st_point_index, :].reshape(1,-1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_
          point_index],test_df['Variation'].iloc[test_point_index], no_feature)
          Predicted Class: 4
          Predicted Class Probabilities: [[0.0558 0.0437 0.0091 0.6975 0.0316 0.0292 0.1271 0.0028 0.003 ]]
          Actual Class : 4
          75 Text feature [47] present in test data point [True]
          88 Text feature [42] present in test data point [True]
```

Out of the top 100 features 2 are present in query point

4.1.1.4. Feature Importance, Incorrectly classified point

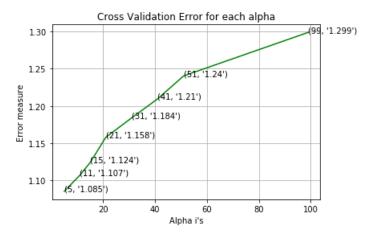
```
In [290]: test point index = 100
         no_feature = 100
         predicted_cls = sig_clf.predict(test_x_onehotCoding.iloc[test_point_index, :].reshape(1,-1))
         print("Predicted Class :", predicted_cls[0])
         st_point_index, :].reshape(1,-1)),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
         print("-"*50)
         get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_
         point_index],test_df['Variation'].iloc[test_point_index], no_feature)
         Predicted Class : 5
         Predicted Class Probabilities: [[0.0899 0.0671 0.0139 0.1098 0.4708 0.0446 0.1952 0.0043 0.0045]]
         Actual Class : 1
         90 Text feature [276300] present in test data point [True]
         Out of the top 100 features 1 are present in query point
```

4.2. K Nearest Neighbour Classification

4.2.1. Hyper parameter tuning

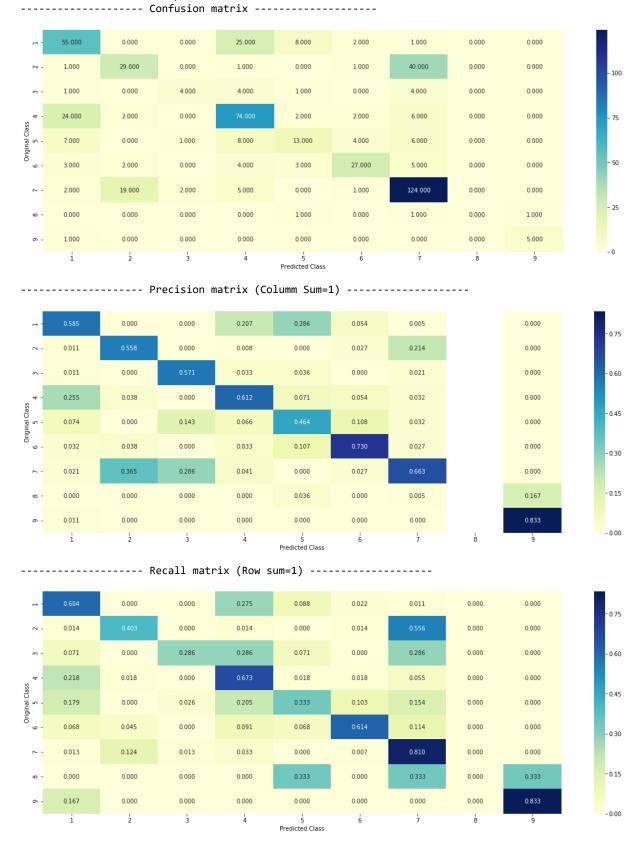
```
In [291]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/generated/skl
          earn.neighbors.KNeighborsClassifier.html
          # default parameter
          \# KNeighborsClassifier(n_neighbors=5, weights='uniform', algorithm='auto', Leaf_size=30, p=2,
          # metric='minkowski', metric_params=None, n_jobs=1, **kwargs)
          # methods of
          # fit(X, y) : Fit the model using X as training data and y 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-ne
          ighbors-geometric-intuition-with-a-toy-example-1/
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/
          sklearn.calibration.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight])
                                         Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          #-----
          # video Link:
          alpha = [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_onehotCoding, train_y)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(train_x_onehotCoding, train_y)
              sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
              cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
              # to avoid rounding error while multiplying probabilites we use log-probability estimates
              print("Log Loss :",log_loss(cv_y, sig_clf_probs))
          fig, ax = plt.subplots()
          ax.plot(alpha, cv_log_error_array,c='g')
          for i, txt in enumerate(np.round(cv_log_error_array,3)):
              ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()
          best_alpha = np.argmin(cv_log_error_array)
          clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
          clf.fit(train_x_onehotCoding, train_y)
          sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(train_x_onehotCoding, train_y)
          predict_y = sig_clf.predict_proba(train_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
           predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 5
Log Loss: 1.0852829601316618
for alpha = 11
Log Loss : 1.1068069609892106
for alpha = 15
Log Loss : 1.1239734112934245
for alpha = 21
Log Loss: 1.157792733394395
for alpha = 31
Log Loss : 1.1840769306698482
for alpha = 41
Log Loss : 1.2095648188645158
for alpha = 51
Log Loss : 1.2403831491653186
for alpha = 99
Log Loss: 1.2988340945993473
```



For values of best alpha = 5 The train log loss is: 0.8589002413672985 For values of best alpha = 5 The cross validation log loss is: 1.0852829601316618 For values of best alpha = 5 The test log loss is: 1.0951620282817154

4.2.2. Testing the model with best hyper paramters



4.3. Logistic Regression

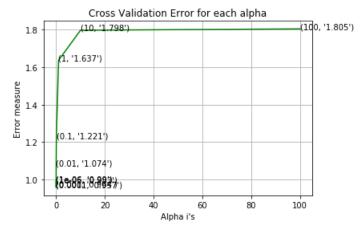
4.3.1. With Class balancing

4.3.1.1. Hyper paramter tuning

```
In [298]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.line
          ar_model.SGDClassifier.html
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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-in
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/
          sklearn.calibration.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight])
                                        Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          # video link:
          #-----
          alpha = [10 ** x for x in range(-6, 3)]
          cv_log_error_array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='12', loss='log', random_state=4
              clf.fit(train_x_onehotCoding, train_y)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(train_x_onehotCoding, train_y)
              sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
              cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
              # to avoid rounding error while multiplying probabilites we use log-probability estimates
              print("Log Loss :",log_loss(cv_y, sig_clf_probs))
          fig, ax = plt.subplots()
          ax.plot(alpha, cv log error_array,c='g')
          for i, txt in enumerate(np.round(cv_log_error_array,3)):
              ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()
          best_alpha = np.argmin(cv_log_error_array)
          clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='log', ra
          ndom_state=42)
          clf.fit(train_x_onehotCoding, train_y)
          sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(train_x_onehotCoding, train_y)
          predict_y = sig_clf.predict_proba(train_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
          predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_x_onehotCoding)
```

print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict_y, labels=clf.classes_, eps=1e-15))

```
for alpha = 1e-06
Log Loss: 0.9904781143992294
for alpha = 1e-05
Log Loss: 0.9832920905787479
for alpha = 0.0001
Log Loss: 0.9572675305625858
for alpha = 0.001
Log Loss: 0.9644174727158827
for alpha = 0.01
Log Loss: 1.0743182035485732
for alpha = 0.1
Log Loss: 1.2214073279561124
for alpha = 1
Log Loss : 1.6370128495942953
for alpha = 10
Log Loss : 1.797721121776716
for alpha = 100
Log Loss: 1.8051691959223746
```



For values of best alpha = 0.0001 The train log loss is: 0.4246640193264304

For values of best alpha = 0.0001 The cross validation log loss is: 0.9572675305625858

For values of best alpha = 0.0001 The test log loss is: 0.9994144760254319

4.3.1.2. Testing the model with best hyper paramters

```
In [299]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.line
          ar_model.SGDClassifier.html
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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-in
          tuition-1/
          #-----
          clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='log', ra
          ndom_state=42)
          \verb|predict_and_plot_confusion_matrix| (train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, clf)|
```

---- Confusion matrix ------ 125 2.000 0.000 19.000 2.000 2.000 1.000 0.000 0.000 31.000 38.000 0.000 0.000 2.000 0.000 1.000 0.000 0.000 100 0.000 0.000 0.000 5.000 3.000 0.000 6.000 0.000 0.000 2.000 16.000 1.000 0.000 0.000 5.000 0.000 0.000 9.000 1.000 1.000 11.000 5.000 0.000 5.000 0.000 3.000 3.000 29.000 4.000 0.000 0.000 0.000 50 13.000 1.000 2.000 3.000 2.000 1.000 0.000 1.000 - 25 1.000 0.000 0.000 0.000 0.000 0.000 1.000 0.000 1.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 6.000 -0 5 Predicted Class ----- Precision matrix (Columm Sum=1) ------0.75 0.154 0.053 0.005 0.000 0.042 0.000 0.087 0.016 0.198 0.000 0.000 0.000 0.026 0.000 - 0.60 0.000 0.000 0.000 0.041 0.130 0.000 0.031 0.000 0.165 0.021 0.000 0.087 0.000 0.026 0.000 - 0.45 Original Class 0.093 0.021 0.333 0.041 0.132 0.036 0.000 0.052 0.000 0.000 0.024 0.130 0.021 0.000 - 0.30 0.010 0.271 0.024 0.087 0.026 0.125 - 0.15 0.010 0.000 0.000 0.000 0.000 0.000 0.005 0.125 0.000 0.000 0.000 0.000 0.000 0.000 - 0.00 2 5 Predicted Class ----- Recall matrix (Row sum=1) ------0.022 0.022 0.011 0.000 0.000 0.209 0.022 0.000



0.6

0.4

0.2

4.3.1.3. Feature Importance

```
In [300]: 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 [302]: # from tabulate import tabulate
          clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', ra
          ndom state=42)
          clf.fit(train_x onehotCoding,train_y)
          test_point_index = 1
          no_feature = 500
          predicted_cls = sig_clf.predict(test_x_onehotCoding.iloc[test_point_index, :].reshape(1, -1))
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding.iloc[te
          st_point_index, :].reshape(1, -1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test
          point_index],test_df['Variation'].iloc[test_point_index], no_feature)
          Predicted Class: 4
          Predicted Class Probabilities: [[0.0153 0.0083 0.1122 0.8122 0.0204 0.0098 0.0174 0.0019 0.0025]]
          Actual Class : 4
          25 Text feature [200] present in test data point [True]
          449 Text feature [31] present in test data point [True]
          460 Text feature [44] present in test data point [True]
          Out of the top 500 features 3 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

```
In [303]: test_point_index = 100
          no_feature = 500
          predicted_cls = sig_clf.predict(test_x_onehotCoding.iloc[test_point_index, :].reshape(1,-1))
          print("Predicted Class :", predicted_cls[0])
          print ("Predicted Class Probabilities:", np.round (sig_clf.predict_proba(test_x\_onehotCoding.iloc[test_x]) \\
          st_point_index,:].reshape(1,-1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_
          point_index],test_df['Variation'].iloc[test_point_index], no_feature)
          Predicted Class : 5
          Predicted Class Probabilities: [[0.1418 0.0297 0.0068 0.2824 0.4927 0.0289 0.0113 0.0031 0.0034]]
          Actual Class : 1
          61 Text feature [144] present in test data point [True]
          152 Text feature [169] present in test data point [True]
          248 Text feature [183] present in test data point [True]
          349 Text feature [276300] present in test data point [True]
          350 Text feature [449] present in test data point [True]
          386 Text feature [217] present in test data point [True]
          434 Text feature [38] present in test data point [True]
          489 Text feature [458] present in test data point [True]
          Out of the top 500 features 8 are present in query point
```

4.3.2. Without Class balancing

```
In [304]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.line
          ar_model.SGDClassifier.html
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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-in
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/
          sklearn.calibration.CalibratedClassifierCV.html
          # ------
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight])
                                         Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          # video link:
          #-----
          alpha = [10 ** x for x in range(-6, 1)]
          cv_log_error_array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier(alpha=i, penalty='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.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-06

Log Loss: 0.9815371302328314

for alpha = 1e-05

Log Loss : 0.990057605040871

for alpha = 0.0001

Log Loss : 0.9612007738504138

for alpha = 0.001

Log Loss : 0.9554467161147713

for alpha = 0.01

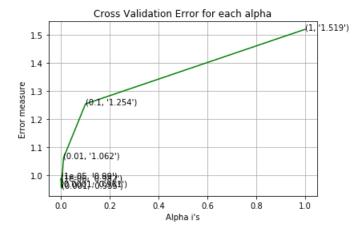
Log Loss: 1.0623456849935953

for alpha = 0.1

Log Loss : 1.2541979620273025

for alpha = 1

Log Loss : 1.5191871641718004



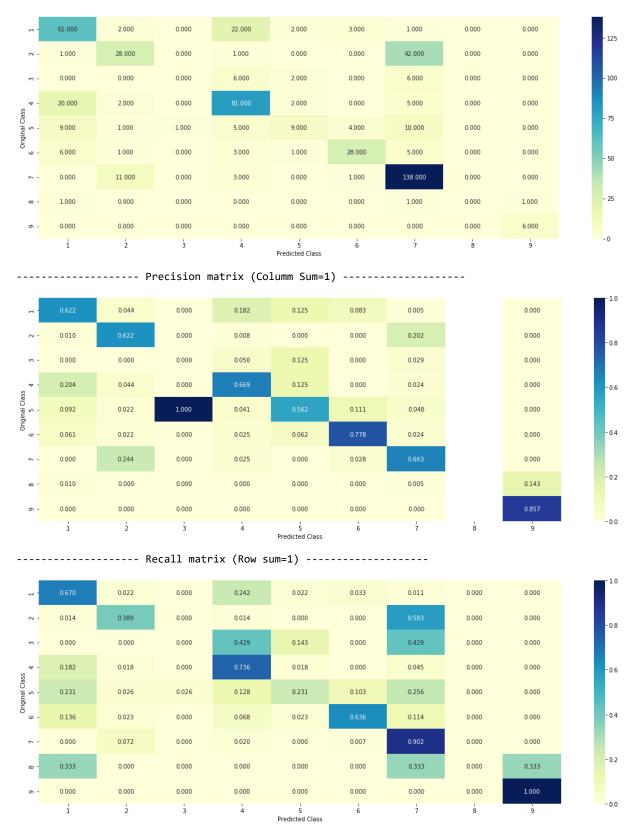
For values of best alpha = 0.001 The train log loss is: 0.5775468155510546
For values of best alpha = 0.001 The cross validation log loss is: 0.9554467161147713
For values of best alpha = 0.001 The test log loss is: 0.995044452598985

4.3.2.2. Testing model with best hyper parameters

```
In [305]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.line
          ar_model.SGDClassifier.html
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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 class labels for samples in X.
          # predict(X)
          #-----
          # video link:
          clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
          predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, clf)
```

Number of mis-classified points : 0.34022556390977443

----- Confusion matrix -----



4.3.2.3. Feature Importance, Correctly Classified point

```
In [306]: 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.iloc[test_point_index, :].reshape(1,-1))
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding.iloc[te
          st_point_index, :].reshape(1,-1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_
          point_index],test_df['Variation'].iloc[test_point_index], no_feature)
          Predicted Class: 4
          Predicted Class Probabilities: [[0.0099 0.0071 0.0348 0.9187 0.0124 0.0065 0.0049 0.0023 0.0034]]
          Actual Class : 4
          78 Text feature [200] present in test data point [True]
          334 Text feature [44] present in test data point [True]
          430 Text feature [42] present in test data point [True]
          Out of the top 500 features 3 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

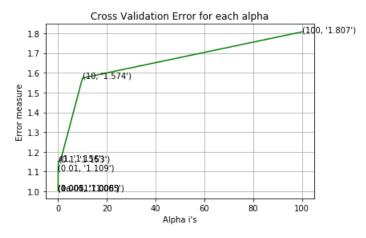
```
In [307]: test_point_index = 100
          no feature = 500
          predicted_cls = sig_clf.predict(test_x_onehotCoding.iloc[test_point_index, :].reshape(1,-1))
          print("Predicted Class :", predicted_cls[0])
          print ("Predicted Class Probabilities:", np.round (sig_clf.predict_proba(test_x\_onehotCoding.iloc[test_x]) \\
          st_point_index, :].reshape(1, -1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_
          point_index],test_df['Variation'].iloc[test_point_index], no_feature)
          Predicted Class : 5
          Predicted Class Probabilities: [[0.1657 0.0239 0.0103 0.3466 0.4094 0.0305 0.0059 0.0028 0.0048]]
          Actual Class : 1
          49 Text feature [144] present in test data point [True]
          170 Text feature [169] present in test data point [True]
          322 Text feature [276300] present in test data point [True]
          335 Text feature [183] present in test data point [True]
          350 Text feature [217] present in test data point [True]
          362 Text feature [449] present in test data point [True]
          414 Text feature [458] present in test data point [True]
          479 Text feature [38] present in test data point [True]
          Out of the top 500 features 8 are present in query point
```

4.4. Linear Support Vector Machines

4.4.1. Hyper paramter tuning

```
In [308]: # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/
          modules/generated/sklearn.svm.SVC.html
          # ------
          # default parameters
          # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, t
          # cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_shape='ovr', ra
          ndom_state=None)
          # Some of methods of SVM()
          # fit(X, y, [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.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight])
                                        Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          # video link:
          alpha = [10 ** x for x in range(-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_stat
          e = 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.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_x_onehotCoding)
```

```
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict_y, labels=clf.classes_, eps=1e-15))
for C = 1e-05
Log Loss : 1.0050996043348637
for C = 0.0001
Log Loss: 1.0049497899468287
for C = 0.001
Log Loss: 1.0057111730892607
for C = 0.01
Log Loss : 1.1087508187419475
for C = 0.1
Log Loss : 1.15333090064045
for C = 1
Log Loss : 1.1555740267992154
for C = 10
Log Loss: 1.5735290247210454
for C = 100
Log Loss: 1.8068729052762467
```



For values of best alpha = 0.0001 The train log loss is: 0.48413403866838484

For values of best alpha = 0.0001 The cross validation log loss is: 1.0049497899468287

For values of best alpha = 0.0001 The test log loss is: 1.0301017311061773

4.4.2. Testing model with best hyper parameters

```
In [309]: # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/
          modules/generated/sklearn.svm.SVC.html
          # ------
          # default parameters
          # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, t
          # cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_shape='ovr', ra
          ndom_state=None)
          # Some of methods of SVM()
          # fit(X, y, [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/
          # clf = SVC(C=alpha[best_alpha],kernel='linear',probability=True, class_weight='balanced')
          clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='hinge', random_state=42,class_wei
          ght='balanced')
          predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf)
```

Predicted Class

4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

Log loss: 1.0049497899468287

Number of mis-classified points : 0.32894736842105265

```
In [311]: 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.iloc[test_point_index, :].reshape(1, -1))
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding.iloc[te
          st_point_index, :].reshape(1,-1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_
          point_index],test_df['Variation'].iloc[test_point_index], no_feature)
          Predicted Class: 4
          Predicted Class Probabilities: [[0.0313 0.016 0.0338 0.8273 0.0258 0.0116 0.0495 0.002 0.0027]]
          Actual Class : 4
          5 Text feature [200] present in test data point [True]
          467 Text feature [44] present in test data point [True]
          486 Text feature [31] present in test data point [True]
          Out of the top 500 features 3 are present in query point
```

4.3.3.2. For Incorrectly classified point

```
In [312]: test_point_index = 100
          no_feature = 500
          predicted_cls = sig_clf.predict(test_x_onehotCoding.iloc[test_point_index, :].reshape(1,-1))
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding.iloc[te
          st point index, :].reshape(1,-1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
          print("-"*50)
          get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].iloc[test_
          point_index],test_df['Variation'].iloc[test_point_index], no_feature)
          Predicted Class : 5
          Predicted Class Probabilities: [[0.0818 0.0313 0.0092 0.333 0.4988 0.0263 0.0134 0.0031 0.0031]]
          Actual Class : 1
          41 Text feature [144] present in test data point [True]
          228 Text feature [169] present in test data point [True]
          247 Text feature [183] present in test data point [True]
          329 Text feature [217] present in test data point [True]
          424 Text feature [458] present in test data point [True]
          449 Text feature [276300] present in test data point [True]
          473 Text feature [36] present in test data point [True]
          Out of the top 500 features 7 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

```
In [313]: # -----
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
          amples_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 the SVM model according to the given training data.
          # fit(X, y, [sample_weight])
                        Perform classification on samples in X.
          # predict(X)
                                 Perform classification on samples in X.
          # predict_proba (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-fores
          t-and-their-construction-2/
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/
          sklearn.calibration.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight]) Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
                       Predict the target of new samples.
          # predict(X)
          # 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=4
          2, n_jobs=-1)
                  clf.fit(train_x_onehotCoding, train_y)
                  sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
                  sig_clf.fit(train_x_onehotCoding, train_y)
                  sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
                  cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
                  print("Log Loss :",log_loss(cv_y, sig_clf_probs))
          '''fig, ax = plt.subplots()
          features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
          ax.plot(features, cv_log_error_array,c='g')
          for i, txt in enumerate(np.round(cv_log_error_array,3)):
              ax. annotate ((alpha[int(i/2)], max\_depth[int(i\%2)], str(txt)), \ (features[i], cv\_log\_error\_array)) \\
          [i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()
          best_alpha = np.argmin(cv_log_error_array)
          clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=ma
          x_depth[int(best_alpha%2)], 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)
          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_lo
ss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross validation log loss
is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
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_los
s(y_test, predict_y, labels=clf.classes_, eps=1e-15))
for n_estimators = 100 and max depth = 5
Log Loss: 1.1865379885037166
for n_estimators = 100 and max depth = 10
Log Loss: 1.2113440910020055
for n_estimators = 200 and max depth = 5
Log Loss: 1.1771037364330132
for n_estimators = 200 and max depth = 10
Log Loss : 1.2016233974573611
for n estimators = 500 and max depth = 5
Log Loss: 1.1708950541902716
for n_estimators = 500 and max_estimators = 10
Log Loss: 1.1929406664084856
for n_{estimators} = 1000 and max depth = 5
Log Loss : 1.16636908224111
for n_estimators = 1000 and max depth = 10
Log Loss: 1.1875663609912825
for n estimators = 2000 and max depth = 5
Log Loss: 1.1677238032096364
for n_{estimators} = 2000 and max depth = 10
Log Loss: 1.1875390569194275
For values of best estimator = 1000 The train log loss is: 0.865313677705407
For values of best estimator = 1000 The cross validation log loss is: 1.16636908224111
For values of best estimator = 1000 The test log loss is: 1.1736019632678938
```

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

```
In [314]: # -----
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
          amples_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.
                        Perform classification on samples in X.
          # predict(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-fores
          t-and-their-construction-2/
          clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=ma
          x_depth[int(best_alpha%2)], random_state=42, n_jobs=-1)
          predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf)
```

0.167

4

0.000

0.000

2

0.000

0.000

0.000

0.000

Predicted Class

0.333

- 0.00

4.5.3. Feature Importance

4.5.3.1. Correctly Classified point

```
In [315]: # test_point_index = 10
          clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=ma
          x_depth[int(best_alpha%2)], 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)
          test_point_index = 1
          no_feature = 100
          predicted_cls = sig_clf.predict(test_x_onehotCoding.iloc[test_point_index, :].reshape(1,-1))
          print("Predicted Class :", predicted_cls[0])
          print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding.iloc[te
          st_point_index, :].reshape(1, -1)),4))
          print("Actual Class :", test_y[test_point_index])
          indices = np.argsort(-clf.feature_importances_)
          print("-"*50)
          get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].
          iloc[test_point_index],test_df['Variation'].iloc[test_point_index], no_feature)
          Predicted Class: 4
          Predicted Class Probabilities: [[0.0259 0.0089 0.0237 0.8624 0.0283 0.024 0.021 0.0024 0.0036]]
          Actual Class : 4
          25 Text feature [42] present in test data point [True]
          Out of the top 100 features 1 are present in query point
```

4.5.3.2. Inorrectly Classified point

```
In [316]: test_point_index = 100
                                 no_feature = 100
                                 predicted_cls = sig_clf.predict(test_x_onehotCoding.iloc[test_point_index, :].reshape(1, -1))
                                  print("Predicted Class :", predicted_cls[0])
                                  print("Predicted \ Class \ Probabilities:", \ np.round(sig\_clf.predict\_proba(test\_x\_onehotCoding.iloc[tended])) and the probabilities in the probabilities
                                  st_point_index, :].reshape(1, -1)),4))
                                  print("Actuall Class :", test_y[test_point_index])
                                  indices = np.argsort(-clf.feature_importances_)
                                  print("-"*50)
                                  get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_point_index],test_df['Gene'].
                                  iloc[test_point_index],test_df['Variation'].iloc[test_point_index], no_feature)
                                 Predicted Class : 4
                                 Predicted Class Probabilities: [[0.2868 0.0169 0.018 0.3335 0.1777 0.1312 0.0249 0.0038 0.0072]]
                                 Actuall Class : 1
                                 25 Text feature [42] present in test data point [True]
                                 Out of the top 100 features 1 are present in query point
```

4.7 Stack the models

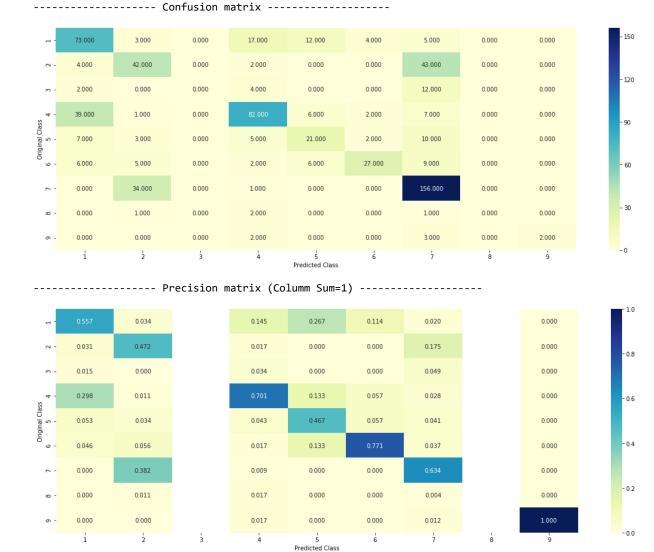
4.7.1 testing with hyper parameter tuning

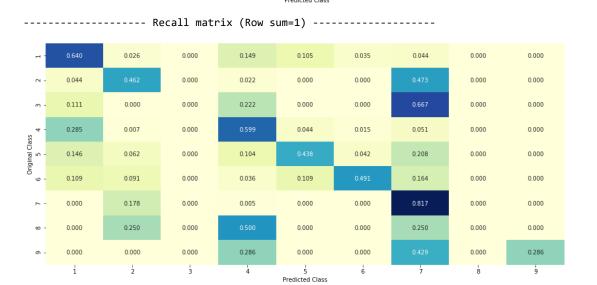
```
In [317]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.line
          ar_model.SGDClassifier.html
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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-in
          # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/
          modules/generated/sklearn.svm.SVC.html
          # default parameters
          # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, t
          # cache_size=200, class_weight=None, verbose=False, max_iter=-1, decision_function_shape='ovr', ra
          ndom state=None)
          # Some of methods of SVM()
          # fit(X, y, [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/sklearn.ensemble.RandomForestClassifier.html
          # default parameters
          # sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None, min_s
          amples 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.
                                 Perform classification on samples in X.
          # predict_proba (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-fores
          t-and-their-construction-2/
          clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class_weight='balanced', random_state=
          clf1.fit(train_x_onehotCoding, train_y)
          sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
          clf2 = SGDClassifier(alpha=1, penalty='12', 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_oneho
tCoding))))
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_on
ehotCoding))))
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, s
clf.predict_proba(cv_x_onehotCoding))))
    log_error =log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    if best_alpha > log_error:
        best_alpha = log_error
Logistic Regression : Log Loss: 0.97
Support vector machines : Log Loss: 1.17
Naive Bayes : Log Loss: 1.23
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 2.176
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 2.020
Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.467
Stacking Classifer : for the value of alpha: 0.100000 Log Loss: 1.110
Stacking Classifer : for the value of alpha: 1.000000 Log Loss: 1.309
Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.788
```

4.7.2 testing the model with the best hyper parameters

Log loss (train) on the stacking classifier : 0.5373966434229661 Log loss (CV) on the stacking classifier : 1.1096531140060404 Log loss (test) on the stacking classifier : 1.1483411935398586 Number of missclassified point : 0.39398496240601505





0.75

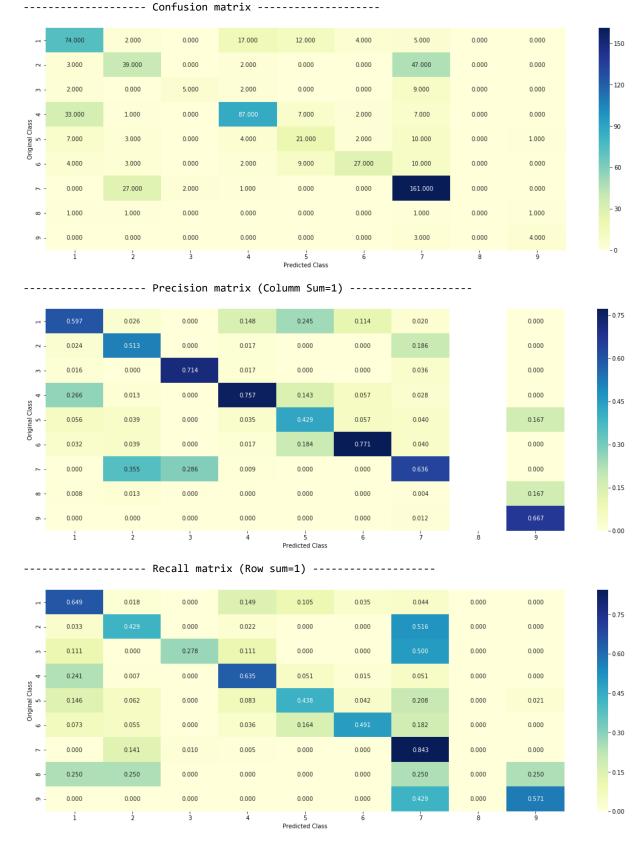
0.60

- 0.45

- 0.30

- 0.15

Log loss (train) on the VotingClassifier: 0.6874087688400785 Log loss (CV) on the VotingClassifier: 1.0753424620453356 Log loss (test) on the VotingClassifier: 1.100137241027604 Number of missclassified point: 0.37142857142857144



```
In [315]: # Train your own Word2Vec model using your own text corpus for train Data
import gensim
i=0
list_of_sent_train=[]
for sent in train_df['TEXT'].values:
    filtered_sentence=[]
    sent=cleanhtml(sent)
    for w in sent.split():
        for cleaned_words in cleanpunc(w).split():
            if(cleaned_words.isalpha()):
                filtered_sentence.append(cleaned_words.lower())
                else:
                      continue
list_of_sent_train.append(filtered_sentence)
```

```
In [316]: # min_count = 5 considers only words that occured atleast 5 times
import gensim
from gensim import models
from gensim.models import Word2Vec, KeyedVectors
w2v_model=Word2Vec(list_of_sent_train,min_count=5,size=200, workers=4)
w2v_words = list(w2v_model.wv.vocab)
print("number of words that occured minimum 5 times ",len(w2v_words))
print("sample words ", w2v_words[0:200])
```

number of words that occured minimum 5 times 31649
sample words ['hub', 'proteins', 'connected', 'binding', 'interactions', 'many', 'mediator', 'sig
nal', 'transduction', 'induced', 'transforming', 'growth', 'factor', 'beta', 'tgf', 'b', 'serves',
'protein', 'different', 'cellular', 'responses', 'mediated', 'product', 'cell', 'type', 'context',
'dependent', 'nucleated', 'complexes', 'acting', 'concert', 'hypothesis', 'perturbation', 'spectru
mt', 'mutation', 'single', 'hot', 'spots', 'distinct', 'consequences', 'methodology', 'principal',
'findings', 'mutated', 'amino', 'acids', 'surface', 'domain', 'identified', 'variants', 'reduced',
'subsets', 'including', 'sara', 'ski', 'mutations', 'defective', 'e', 'g', 'nucleocytoplasmic', 's
huttling', 'compromised', 'modulating', 'expression', 'levels', 'reporter', 'gene', 'six', 'endoge
nous', 'responsive', 'genes', 'however', 'mutants', 'differences', 'signaling', 'example', 'activa
tion', 'inducibilty', 'contrast', 'inducibility', 'severely', 'increased', 'caused', 'higher', 'ba
sal', 'lower', 'conclusions', 'significance', 'interacting', 'range', 'quantitative', 'changes',
'approach', 'useful', 'unraveling', 'critical', 'specific', 'biological', 'citation', 'schiro', 'm
mt', 'stauber', 'se', 'peterson', 'tl', 'krueger', 'c', 'darnell', 'sj', 'et', 'al', 'differentiall
y', 'affect', 'regulated', 'plos', 'one', 'doi', 'journal', 'pone', 'editor', 'dhyan', 'chandra',
'roswell', 'park', 'cancer', 'institute', 'united', 'states', 'amenica', 'received', 'june', 'acce
pted', 'august', 'published', 'september', 'copyright', 'open', 'access', 'article', 'distribute
d', 'terms', 'creative', 'commons', 'attribution', 'license', 'permits', 'unrestricted', 'distribute'
d', 'terms', 'creative', 'commons', 'attribution', 'license', 'permits', 'unrestricted', 'funding', 'work', 'supported', 'muscular', 'dystrophy', 'association', 'www', 'maa', 'org', 'gran
t', 'juvenile', 'dabetes', 'research', 'foundation', 'jfrf', 'national', 'gov', 'funders', 'rol
e', 'study', 'design', 'data',

```
In [317]: # average Word2Vec
          # compute average word2vec for each review.
          sent_vectors_train = []; # the avg-w2v for each sentence/review is stored in this list
          for sent in list_of_sent_train: # for each review/sentence
              sent_vec = np.zeros(200) # as word vectors are of zero Length
              cnt words =0; # num of words with a valid vector in the sentence/review
              for word in sent: # for each word in a review/sentence
                  if word in w2v_words:
                      vec = w2v_model.wv[word]
                       sent_vec += vec
                      cnt_words += 1
              if cnt_words != 0:
                  sent_vec /= cnt_words
              sent_vectors_train.append(sent_vec)
          print(len(sent_vectors_train))
          print(len(sent_vectors_train[0]))
```

2124 200

Test Data

```
In [318]: # Train your own Word2Vec model using your own text corpus for test Data
import gensim
i=0
list_of_sent_test=[]
for sent in test_df['TEXT'].values:
    filtered_sentence=[]
    sent=cleanhtml(sent)
    for w in sent.split():
        for cleaned_words in cleanpunc(w).split():
            if(cleaned_words.isalpha()):
                filtered_sentence.append(cleaned_words.lower())
            else:
                continue
list_of_sent_test.append(filtered_sentence)
```

```
In [319]: # min_count = 5 considers only words that occured atleast 5 times
    w2v_model=Word2Vec(list_of_sent_test,min_count=5,size=200, workers=4)
    w2v_words = list(w2v_model.wv.vocab)
    print("number of words that occured minimum 5 times ",len(w2v_words))
    print("sample words ", w2v_words[0:50])
```

number of words that occured minimum 5 times 19076 sample words ['purpose', 'kit', 'major', 'oncogenic', 'driver', 'gastrointestinal', 'stromal', 't umors', 'gists', 'imatinib', 'sunitinib', 'regorafenib', 'approved', 'therapies', 'however', 'effi cacy', 'often', 'limited', 'acquisition', 'polyclonal', 'secondary', 'resistance', 'mutations', 'l ocated', 'activation', 'loop', 'exons', 'particularly', 'problematic', 'explored', 'inhibitory', 'activity', 'ponatinib', 'preclinical', 'models', 'describe', 'initial', 'characterization', 'gis t', 'patients', 'experimental', 'design', 'cellular', 'vivo', 'activities', 'mutant', 'evaluated', 'using', 'accelerated', 'mutagenesis']

```
In [320]: # average Word2Vec
          # compute average word2vec for each review.
          sent vectors test = []; # the avg-w2v for each sentence/review is stored in this list
          for sent in list_of_sent_test: # for each review/sentence
              sent_vec = np.zeros(200) # as word vectors are of zero Length
              cnt words =0; # num of words with a valid vector in the sentence/review
              for word in sent: # for each word in a review/sentence
                  if word in w2v_words:
                      vec = w2v_model.wv[word]
                      sent_vec += vec
                      cnt_words += 1
              if cnt_words != 0:
                  sent_vec /= cnt_words
              sent_vectors_test.append(sent_vec)
          print(len(sent_vectors_test))
          print(len(sent_vectors_test[0]))
          665
          200
```

CV data

```
In [321]: # Train your own Word2Vec model using your own text corpus for test Data
import gensim
i=0
list_of_sent_cv=[]
for sent in cv_df['TEXT'].values:
    filtered_sentence=[]
    sent=cleanhtml(sent)
    for w in sent.split():
        for cleaned_words in cleanpunc(w).split():
            if(cleaned_words.isalpha()):
                filtered_sentence.append(cleaned_words.lower())
            else:
                continue
    list_of_sent_cv.append(filtered_sentence)
```

```
In [322]: # min_count = 5 considers only words that occured atleast 5 times
w2v_model=Word2Vec(list_of_sent_cv,min_count=5,size=200, workers=4)
w2v_words = list(w2v_model.wv.vocab)
print("number of words that occured minimum 5 times ",len(w2v_words))
print("sample words ", w2v_words[0:50])
```

number of words that occured minimum 5 times 16875 sample words ['activation', 'canonical', 'tgf', 'signaling', 'pathway', 'provides', 'growth', 'in hibitory', 'signals', 'normal', 'intestinal', 'epithelium', 'colorectal', 'cancers', 'crcs', 'freq uently', 'harbor', 'somatic', 'mutations', 'members', 'extent', 'contribute', 'tumorigenesis', 'un clear', 'cohort', 'primary', 'crc', 'cell', 'lines', 'sequenced', 'analyzed', 'allelic', 'loss', 'single', 'nucleotide', 'polymorphism', 'snp', 'microarray', 'analysis', 'mutation', 'spectra', 'c ompared', 'genes', 'pathogenicity', 'assessed', 'relationships', 'clinicopathologic', 'features', 'examined', 'prevalence']

```
In [323]: # average Word2Vec
          # compute average word2vec for each review.
          sent_vectors_cv = []; # the avg-w2v for each sentence/review is stored in this list
          for sent in list_of_sent_cv: # for each review/sentence
              sent_vec = np.zeros(200) # as word vectors are of zero length
              cnt_words =0; # num of words with a valid vector in the sentence/review
              for word in sent: # for each word in a review/sentence
                  if word in w2v_words:
                      vec = w2v_model.wv[word]
                      sent_vec += vec
                      cnt_words += 1
              if cnt words != 0:
                  sent_vec /= cnt_words
              sent_vectors_cv.append(sent_vec)
          print(len(sent_vectors_cv))
          print(len(sent_vectors_cv[0]))
```

```
In [324]: # merging gene, variance and text features
          # building train, test and cross validation data sets
          # a = [[1, 2],
                 [3, 4]]
          #b = [[4, 5],
                [6, 7]]
          \# hstack(a, b) = [[1, 2, 4, 5],
                           [ 3, 4, 6, 7]]
          train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,train_variation_feature_oneh
          test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variation_feature_onehotC
          oding))
          cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feature_onehotCoding
          ))
          train_x_onehotCoding = hstack((train_gene_var_onehotCoding,sent_vectors_train)).tocsr()
          train_y = np.array(list(train_df['Class']))
          test_x_onehotCoding = hstack((test_gene_var_onehotCoding, sent_vectors_test)).tocsr()
          test_y = np.array(list(test_df['Class']))
          cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding,sent_vectors_cv)).tocsr()
          cv_y = np.array(list(cv_df['Class']))
```

```
In [325]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.line
          ar_model.SGDClassifier.html
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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-in
          # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/
          sklearn.calibration.CalibratedClassifierCV.html
          # default paramters
          # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
          # some of the methods of CalibratedClassifierCV()
          # fit(X, y[, sample_weight])
                                         Fit the calibrated model
          # get_params([deep]) Get parameters for this estimator.
          # predict(X) Predict the target of new samples.
          # predict_proba(X) Posterior probabilities of classification
          # video link:
          alpha = [10 ** x for x in range(-6, 3)]
          cv_log_error_array = []
          for i in alpha:
              print("for alpha =", i)
              clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='12', loss='log', random_state=4
          2)
              clf.fit(train_x_onehotCoding, train_y)
              sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
              sig_clf.fit(train_x_onehotCoding, train_y)
              sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
              cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_, eps=1e-15))
              # to avoid rounding error while multiplying probabilites we use log-probability estimates
              print("Log Loss :",log_loss(cv_y, sig_clf_probs))
          fig, ax = plt.subplots()
          ax.plot(alpha, cv_log_error_array,c='g')
          for i, txt in enumerate(np.round(cv_log_error_array,3)):
              ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
          plt.grid()
          plt.title("Cross Validation Error for each alpha")
          plt.xlabel("Alpha i's")
          plt.ylabel("Error measure")
          plt.show()
          best_alpha = np.argmin(cv_log_error_array)
          clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='log', ra
          ndom state=42)
          clf.fit(train_x_onehotCoding, train_y)
          sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
          sig_clf.fit(train_x_onehotCoding, train_y)
          predict_y = sig_clf.predict_proba(train_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
           predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
          ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
          predict_y = sig_clf.predict_proba(test_x_onehotCoding)
          print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
          redict_y, labels=clf.classes_, eps=1e-15))
```

for alpha = 1e-06

Log Loss : 1.7458173513766055

for alpha = 1e-05

Log Loss : 1.8258168695785402

for alpha = 0.0001

Log Loss : 1.7745596603630562

for alpha = 0.001

Log Loss : 1.6970338684358992

for alpha = 0.01

Log Loss: 1.7708477037124097

for alpha = 0.1

Log Loss : 1.917326871281069

for alpha = 1

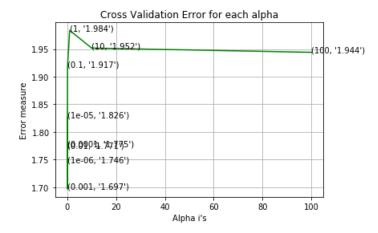
Log Loss : 1.9837670827139646

for alpha = 10

Log Loss: 1.951773139339752

for alpha = 100

Log Loss : 1.9441062620102016



For values of best alpha = 0.001 The train log loss is: 0.8271757247127755

For values of best alpha = 0.001 The cross validation log loss is: 1.6970338684358992

For values of best alpha = 0.001 The test log loss is: 1.465678659743184

```
In [326]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.line
          ar_model.SGDClassifier.html
          # default parameters
          # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_intercept=True, max_i
          ter=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-in
          tuition-1/
          #-----
          clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss='log', ra
          ndom_state=42)
          \verb|predict_and_plot_confusion_matrix| (train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, clf)|
```

Number of mis-classified points : 0.5977443609022557

----- Confusion matrix -----

п-	27.000	11.000	0.000	46.000	3.000	0.000	1.000	0.000	3.000
۲ -	0.000		0.000	1.000	0.000	0.000	5.000	0.000	1.000
m -	0.000	9.000	0.000	3.000	1.000	0.000	1.000	0.000	0.000
- 4 -	1.000	17.000	0.000	87.000	0.000	0.000	1.000	1.000	3.000
Original Class 5	0.000	9.000	0.000	16.000	9.000	0.000	2.000	1.000	2.000
orii	1.000	12.000	0.000	26.000	4.000	0.000	0.000	0.000	1.000
۲.	0.000	122.000	0.000	7.000	1.000	0.000	22.000	0.000	1.000
œ -	0.000	1.000	0.000	0.000	0.000	0.000	0.000	0.000	2.000
თ -	0.000	2.000	0.000	0.000	0.000	0.000	0.000	0.000	4.000
	i	2	3	4	5 Predicted Class	6	7	8	9

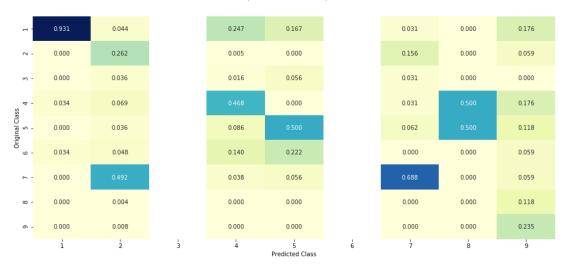
- 25

- 0.2

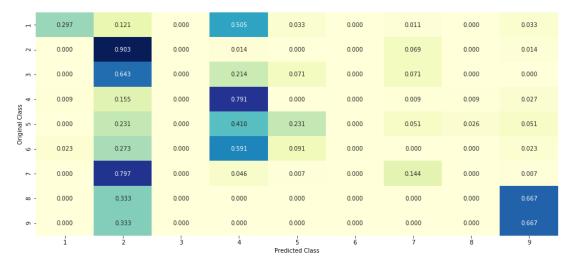
- 0.2

- 0.0

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



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



Conclusion Of 1st Section:-

We tried many models but with Tf-ldf Vectoriser in Bi-grams and for 2000 most important words, we were best able to classify Cancer into its actual classes with minimum error :-

- Stacking Model and Maximum Vote classifier model are hard to interpret.
- Best Model For this Dataset is :- Logistic Regression with Class Balancing
- Train Log-Loss:-0.4246
- CV Log-Loss:-0.9572
- Test Log-Loss:-0.9994
- Percentage Misclassified:-0.3270

Model	Train	cv	Test	Percentage Misclassified
Naive Bayes	0.6218	1.2337	1.2642	0.3759
KNN (Best K=11)	0.8589	1.0852	1.0951	0.3778
LR (With Class Balancing)	0.4246	0.9572	0.9994	0.3270
LR (Without Class Balancing)	0.5775	0.9554	0.9950	0.3402
LINEAR SVM	0.4841	1.0049	1.0301	0.3289
Random Forest	0.8653	1.1663	1.1736	0.4078
Stacking Clasifier (Log Reg+ SVM + Naive Bayes)	0.5373	1.1096	1.1483	0.3939
Maximum Voting Classifier (Log Reg+ SVM + RF)	0.6874	1.0753	1.001	0.3714
Word2Vec(Logistic Regression)	0.8271	1.6970	1.7656	0.5977