Personalized cancer diagnosis 1. Business Problem 1.1. Description Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/ Data: Memorial Sloan Kettering Cancer Center (MSKCC) Download training variants.zip and training text.zip from Kaggle. Context: Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/discussion/35336#198462 Problem statement: Classify the given genetic variations/mutations based on evidence from text-based clinical literature. 1.2. Source/Useful Links Some articles and reference blogs about the problem statement 1. https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almost-everyone- who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25 2. https://www.youtube.com/watch?v=UwbuW7oK8rk

3. https://www.youtube.com/watch?v=qxXRKVompl8
1.3. Real-world/Business objectives and constraints.
 No low-latency requirement. Interpretability is important. Errors can be very costly. Probability of a data-point belonging to each class is needed.
2. Machine Learning Problem Formulation
2.1. Data
2.1.1. Data Overview
 Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/data 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 (vets erythroblastosis virus E26 oncogene homolog 2) transcription factor and inhibits its transcriptional activity through an unknown mechanism (9). CDK10 knockdown derepresses ETS2, which increases the expression of the c-Raf protein kinase, activates the MAPK pathway, and induces resistance of MCF7 cells to tamoxifen (6). 2.2. Mapping the real-world problem to an ML problem 2.2.1. Type of Machine Learning Problem There are nine different classes a genetic mutation can be classified into => Multi class classification problem 2.2.2 Performance Metric Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment#evaluation 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

```
from sklearn.ensemble import VotingClassifier
from sklearn.ensemble import RandomForestClassifier
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
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
```

```
(learn.linear model import SGDClassifier
from imblearn.over sampling import SMOTE
from collections import Counter
from scipy.sparse import hstack
from sklearn.svm import SVC
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
from sklearn.metrics import normalized_mutual_info_score
warnings.filterwarnings("ignore")
from mlxtend.classifier import StackingClassifier
from sklearn import model_selection
from sklearn.linear_model import LogisticRegression
nltk.download('stopwords')
 [nltk_data] Downloading package stopwords to /home/keshav/nltk data...
 [nltk data] Package stopwords is already up-to-date!
 True
```

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

```
data = pd.read csv('training/training variants')
print('Number of data points : ', data.shape[0])
print('Number of features : ', data.shape[1])
print('Features : ', data.columns.values)
data.head()
 Number of data points : 3321
 Number of features: 4
 Features: ['ID' 'Gene' 'Variation' 'Class']
                   Variation Class
       Gene
o 0 FAM58A Truncating Mutations 1
     CBL
            W802*
     CBL
            Q249E
            N454D
     CBL
 4 4 CBL
           L399V
```

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

```
data text =pd.read csv("training/training text",sep="\|\|",engine="python",names=["ID",
"TEXT"], skiprows=1)
print('Number of data points : ', data_text.shape[0])
print('Number of features : ', data_text.shape[1])
print('Features : ', data text.columns.values)
data text head()
 Number of data points : 3321
 Number of features : 2
 Features : ['ID' 'TEXT']
   ID
                                       TEXT
0 O Cyclin-dependent kinases (CDKs) regulate a var...
      Abstract Background Non-small cell lung canc...
2 2 Abstract Background Non-small cell lung canc...
3 3 Recent evidence has demonstrated that acquired...
      Oncogenic mutations in the monomeric Casitas B...
```

3.1.3. Preprocessing of text

```
In [7]: # 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 =
        total text = re.sub('[^a-zA-Z0-9]', ' ', total text)
        total text = re.sub('\s+',' ', total text)
        total text = total text.lower()
        for word in total text.split():
             in not word in stop words:
                  string += word + " "
        data text[column][index] = string
start time = time.clock()
for index, row in data text iterrows():
    if type(row['TEXT']) is str:
        nlp preprocessing(row['TEXT'], index, 'TEXT')
        print("there is no text description for id:",index)
print('Time took for preprocessing the text :',time.clock() - start time, "seconds")
 there is no text description for id: 1109
 there is no text description for id: 1277
 there is no text description for id: 1407
 there is no text description for id: 1639
 there is no text description for id: 2755
 Time took for preprocessing the text: 183.39537900000002 seconds
```

```
result = pd.merge(data, data text,on='ID', how='left')
result head()
        Gene
                      Variation Class
                                                                      TEXT
      FAM58A Truncating Mutations 1
                                     cyclin dependent kinases cdks regulate variety...
      CBL
              W802*
                                     abstract background non small cell lung cancer...
      CBL
                               2
                                     abstract background non small cell lung cancer...
              Q249E
                                     recent evidence demonstrated acquired uniparen...
      CBL
              N454D
     CBL
              L399V
                                     oncogenic mutations monomeric casitas b lineag...
result[result.isnull().any(axis=1)]
           Gene
                         Variation Class TEXT
 1109 1109 FANCA S1088F
                                         NaN
1277 1277 ARID5B Truncating Mutations 1
                                         NaN
 1407 1407 FGFR3 K508M
                                         NaN
 1639 1639 FLT1
                  Amplification
                                         NaN
 2755 2755 BRAF
                  G596C
                                         NaN
result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Variation']
result[result['ID']==1109]
           Gene Variation Class
                                        TEXT
 1109 1109 FANCA S1088F
                                 FANCA S1088F
  3.1.4. Test, Train and Cross Validation Split
```

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

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

```
In [14]: print('Number of data points in train data:', train_df.shape[0])
print('Number of data points in test data:', test_df.shape[0])
print('Number of data points in cross validation data:', cv_df.shape[0])

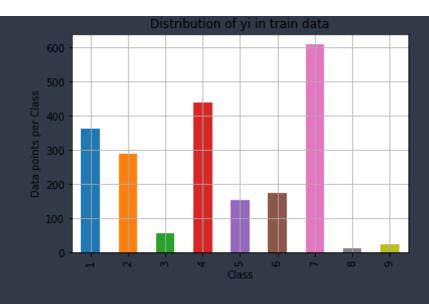
Number of data points in train data: 2124
Number of data points in test data: 665
Number of data points in cross validation data: 532
```

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

```
In [15]: # it returns a dict, keys as class labels and values as the number of data points in tha
    t class
    train_class_distribution = train_df['Class'].value_counts().sortlevel()
```

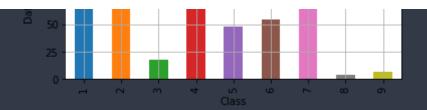
```
test class distribution = test df['Class'].value counts().sortlevel()
cv class distribution = cv df['Class'].value counts().sortlevel()
my colors = 'rgbkymc'
train class distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in train data')
plt.grid()
plt show()
sorted yi = np.argsort(-train class distribution.values)
for i in sorted yi:
   print('Number of data points in class', i+1, ':',train class distribution.values[i],
'(', np.round((train class distribution.values[i]/train df.shape[0]*100), 3), '%)')
print('-'*80)
my colors = 'rgbkymc'
test class distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of vi in test data')
plt.grid()
plt show()
```

```
sorted yi = np.argsort(-test class distribution.values)
for i in sorted yi:
   ncint('Number of data points in class', i+1, ':', test class distribution.values[i],
'(', np.round((test class distribution values[i]/test df.shape[0]*100), 3), '%)')
print('-'*80)
my colors = 'rgbkymc'
cv class distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in cross validation data')
plt grid()
plt.show()
sorted yi = np.argsort(-train class distribution.values)
for i in sorted yi:
   print('Number of data points in class', i+1, ':',cv_class_distribution.values[i],
'(', np.round((cv class distribution.values[i]/cv df.shape[0]*100), 3), '%)')
```



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





```
Number of data points in class 7 : 191 ( 28.722 %)

Number of data points in class 4 : 137 ( 20.602 %)

Number of data points in class 1 : 114 ( 17.143 %)

Number of data points in class 2 : 91 ( 13.684 %)

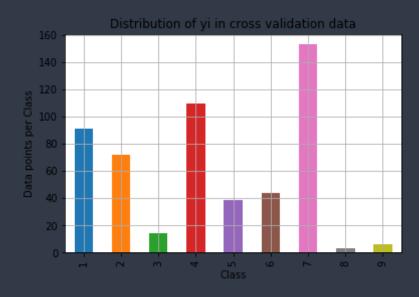
Number of data points in class 6 : 55 ( 8.271 %)

Number of data points in class 5 : 48 ( 7.218 %)

Number of data points in class 3 : 18 ( 2.707 %)

Number of data points in class 9 : 7 ( 1.053 %)

Number of data points in class 8 : 4 ( 0.602 %)
```



Number of data points in class 7 : 153 (28.759 %)

```
Number of data points in class 4 : 110 ( 20.677 %)

Number of data points in class 1 : 91 ( 17.105 %)

Number of data points in class 2 : 72 ( 13.534 %)

Number of data points in class 6 : 44 ( 8.271 %)

Number of data points in class 5 : 39 ( 7.331 %)

Number of data points in class 3 : 14 ( 2.632 %)

Number of data points in class 9 : 6 ( 1.128 %)

Number of data points in class 8 : 3 ( 0.564 %)
```

3.2 Prediction using a 'Random' Model

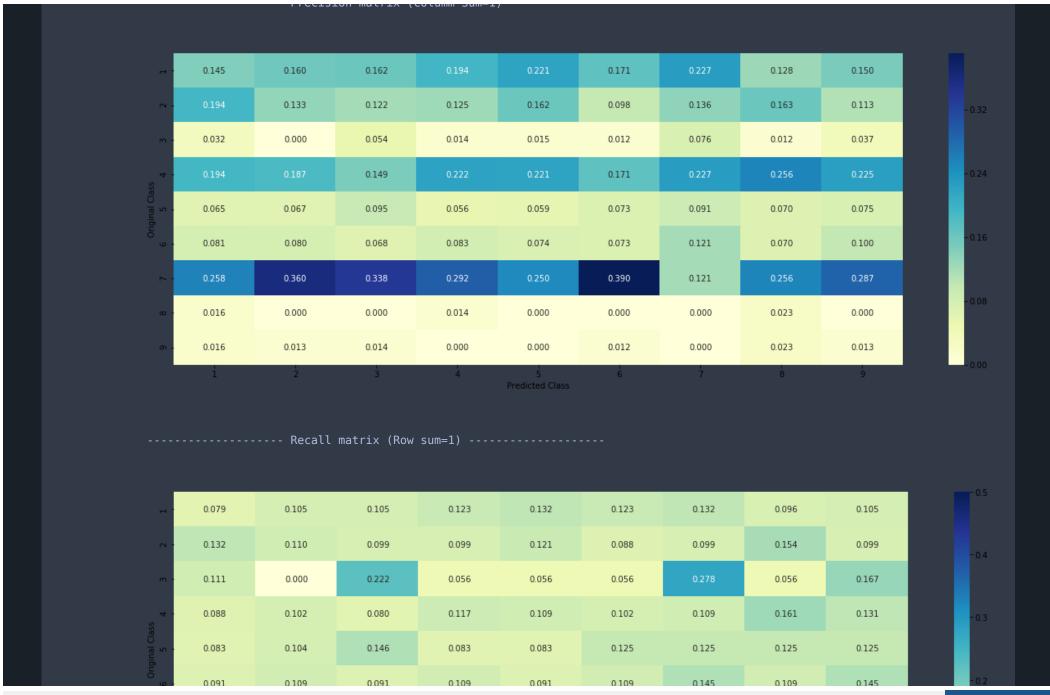
In a 'Random' Model, we generate the NINE class probabilites randomly such that they sum to 1.

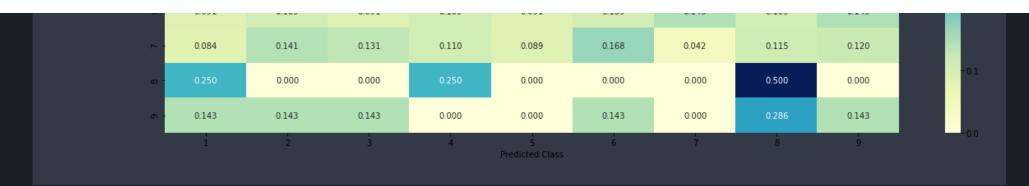
```
((test y, predict y):
C = confusion matrix(test y, predict y)
A = (((C.T)/(C.sum(axis=1))).T)
```

```
B = (C/C.sum(axis=0))
    labels = [1,2,3,4,5,6,7,8,9]
    print("-"*20, "Confusion matrix", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels
=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()
    print("-"*20, "Precision matrix (Column Sum=1)", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels
=labels)
    plt.xlabel('Predicted Class')
```

```
plt.ylabel('Original Class')
    plt.show()
   print("-"*20, "Recall matrix (Row sum=1)", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(A, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels
=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt show()
# ref: https://stackoverflow.com/a/18662466/4084039
test data len = test df.shape[0]
cv data len = cv df.shape[0]
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])
nrint("Log loss on Cross Validation Data using Random Model", log loss(y cv,cv predicted
y, eps=1e-15))
test predicted y = np.zeros((test data len,9))
```

```
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=1
e-15))
predicted y =np.argmax(test predicted y, axis=1)
plot confusion matrix(y test, predicted y+1)
  Log loss on Cross Validation Data using Random Model 2.551212409664783
  Log loss on Test Data using Random Model 2.56965616863993
  ----- Confusion matrix ------
          9.000
                      12.000
                                  12.000
                                                          15.000
                                                                      14.000
                                                                                   15.000
                                              14.000
                                                                                               11.000
                                                                                                           12.000
                                  9.000
                                                          11.000
                                                                                   9.000
                                                                                                           9.000
          12.000
                      10.000
                                               9.000
                                                                       8.000
                                                                                               14.000
          2.000
                      0.000
                                  4.000
                                              1.000
                                                           1.000
                                                                       1.000
                                                                                   5.000
                                                                                               1.000
                                                                                                           3.000
          12.000
                      14.000
                                  11.000
                                                          15.000
                                                                      14.000
                                                                                   15.000
          4.000
                      5.000
                                  7.000
                                               4.000
                                                           4.000
                                                                       6.000
                                                                                   6.000
                                                                                               6.000
                                                                                                           6.000
          5.000
                                  5.000
                                                           5.000
                                                                                   8.000
                      6.000
                                               6.000
                                                                       6.000
                                                                                               6.000
                                                                                                           8.000
                      27.000
                                  25.000
                                                                      32.000
                                                                                   8.000
                                                                                               22.000
                                              21.000
                                                                                                           23.000
          1.000
                      0.000
                                  0.000
                                              1.000
                                                           0.000
                                                                       0.000
                                                                                   0.000
                                                                                               2.000
                                                                                                           0.000
          1.000
                      1.000
                                  1.000
                                               0.000
                                                           0.000
                                                                       1.000
                                                                                   0.000
                                                                                               2.000
                                                                                                           1.000
```





3.3 Univariate Analysis

```
alpha / number of time it occurred in total data+90*alpha)
```

```
(alpha, feature, df):
        KIT 61
        PDGFRA 46
value count = train df[feature].value counts()
```

```
gv_dict = dict()
for i, denominator in value count items():
   vec = []
   for k in range(1,10):
                    BRCA1
       # 2486 2486 BRCA1
       # 2614 2614 BRCA1
       # 2432 2432 BRCA1
       # 2567 2567 BRCA1
                                       T1685A
       cls cnt = train df.loc[(train df['Class']==k) & (train df[feature]==i)]
       vec.append((cls cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
```

```
qv dict[i]=vec
   return gv dict
def get gv feature(alpha, feature, df):
3636363636363635, 0.25, 0.19318181818181818, 0.037878787878788, 0.0378787878787878,
   # 'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 0.2
7040816326530615, 0.061224489795918366, 0.066326530612244902, 0.051020408163265307, 0.05
1020408163265307, 0.0561224489795918371,
177, 0.068181818181818177, 0.0625, 0.34659090909090912, 0.0625, 0.056818181818181816],
   # 'BRCA2': [0.133333333333333333, 0.0606060606060608, 0.0606060606060608, 0.
62893081761006289, 0.062893081761006289],
         'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.07
2847682119205295, 0.066225165562913912, 0.066225165562913912, 0.27152317880794702, 0.066
733333333333334, 0.093333333333333338, 0.0800000000000002, 0.299999999999999, 0.06
   gv dict = get gv fea dict(alpha, feature, df)
```

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

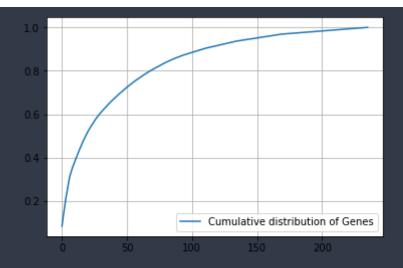
Q2. How many categories are there and How they are distributed?

```
In [19]: unique_genes = train_df['Gene'].value_counts()
    print('Number of Unique Genes :', unique_genes.shape[0])
```

```
print(unique genes.head(10))
         Number of Unique Genes: 236
         BRCA1
                178
         TP53
                100
         PTEN
                 88
         EGFR
                 86
         BRCA2
         BRAF
         KIT
         ERBB2
         ALK
         TSC2
                 34
         Name: Gene, dtype: int64
       print("Ans: There are", unique genes.shape[0] , "different categories of genes in the tra
        in data, and they are distibuted as follows",)
         Ans: There are 236 different categories of genes in the train data, and they are distibuted as follows
In [21]: 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()
```

```
    Histrogram of Genes

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



Q3. How to featurize this Gene feature?

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

- 1. One hot Encoding
- 2. Response coding

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

```
In [23]: #response-coding of the Gene feature
    # alpha is used for laplace smoothing
    alpha = 1
    # train gene feature
    train_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", train_df))
    # test gene feature
    test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", test_df))
```

```
cv gene feature responseCoding = np.array(get gv feature(alpha, "Gene", cv df))
d. The shape of gene feature: ", train gene feature responseCoding.shape)
 train gene feature responseCoding is converted feature using respone coding method. The shape of gene feature: (2124, 9)
gene vectorizer = CountVectorizer()
train gene feature onehotCoding = gene vectorizer.fit transform(train df['Gene'])
test gene feature onehotCoding = gene vectorizer.transform(test_df['Gene'])
cv gene feature onehotCoding = gene vectorizer.transform(cv df['Gene'])
train df['Gene'].head()
 564
        SMAD3
 1400
        FGFR3
 257
        EGFR
 1698
        PMS2
         SM0
 Name: Gene, dtype: object
gene vectorizer get feature names()
 ['abl1',
  'acvr1',
  'ago2',
  'akt1',
  'akt2',
  'akt3',
```

```
'aridla',
'arid1b',
'arid5b',
'asxl1',
'atm',
'atrx',
'aurka',
'aurkb',
'axin1',
'b2m',
'bap1',
'bard1',
'bcl10',
'bcl2l11',
'brca1',
'brca2',
'brd4',
'brip1',
'btk',
'card11',
'carm1',
'casp8',
'ccnd1',
'cdk12',
'cdk4',
'cdk8',
'cdkn1a',
```

```
'cebpa',
'crebbp',
'ctla4',
'ddr2',
'dicer1',
'dnmt3a',
'dnmt3b',
'dusp4',
'egfr',
'eiflax',
'ep300',
'epas1',
'epcam',
'erbb2',
'erbb3',
'erbb4',
'ercc3',
'ercc4',
'erg',
'ewsr1',
'fam58a',
'fanca',
'fat1',
'fgf3',
```

```
'fgf4',
'fgfr1',
'fgfr2',
'fgfr3',
'fgfr4',
'foxa1',
'foxl2',
'foxo1',
'foxp1',
'gata3',
'gli1',
'gna11',
'gnas',
'h3f3a',
'hla',
'hnfla',
'hras',
'igf1r',
'il7r',
'kdm5c',
'kdm6a',
'keap1',
'kmt2a',
'kmt2b',
'kmt2c',
'kmt2d',
'knstrn',
```

```
'map2k2',
'map2k4',
'map3k1',
'mapk1',
'med12',
'mef2b',
'mlh1',
'mpl',
'msh6',
'myc',
'mycn',
'myd88',
'myod1',
'nfkbia',
'notch1',
'notch2',
'nras',
'ntrk1',
'ntrk3',
'nup93',
'pbrm1',
'pdgfra',
'pdgfrb',
```

```
'pik3r1',
'pms2',
'pole',
'ppp2r1a',
'ppp6c',
'prdm1',
'ptch1',
'pten',
'ptpn11',
'ptprd',
'ptprt',
'rac1',
'rad21',
'rad50',
'rad51c',
'rad51d',
'rad54l',
'raf1',
'rasa1',
'rbm10',
'ret',
'rheb',
'rnf43',
'ros1',
'setd2',
'sf3b1',
'shq1',
```

```
'smad2',
   'smad3',
   'smad4',
   'smarca4',
   'smarcb1',
   'smo',
   'sox9',
   'spop',
   'src',
   'srsf2',
   'stat3',
   'stk11',
  'tcf3',
   'tcf7l2',
   'tert',
   'tet1',
   'tet2',
   'tgfbr1',
  'tgfbr2',
   'tmprss2',
   'tp53bp1',
   'tsc1',
  'tsc2',
   'u2af1',
  'whsc1',
  'whsc1l1',
  'xpo1',
   'yap1']
d. The shape of gene feature: ", train gene feature onehotCoding shape)
 train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature: (2124, 236)
```

Q4. How good is this gene feature in predicting y_i?

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

```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sk
learn.linear model.SGDClassifier.html
cv log error array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random state=42)
```

```
clf fit(train gene feature onehotCoding, y train)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=llone)
    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, labe
ls=clf.classes , eps=le-15))
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax annotate((alpha[i],np round(txt,3)), (alpha[i],cv log error array[i]))
plt grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best alpha], penalty='l2', loss='log', random state=42)
clf fit(train gene feature onehotCoding, y train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
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 los
s(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 i
```

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

```
For values of alpha = 1e-05 The log loss is: 1.208702688586516

For values of alpha = 0.0001 The log loss is: 1.1953639079706706

For values of alpha = 0.001 The log loss is: 1.2390173936800735

For values of alpha = 0.01 The log loss is: 1.3582071666325053

For values of alpha = 0.1 The log loss is: 1.4463552970448768

For values of alpha = 1 The log loss is: 1.4832238937041724
```



```
For values of best alpha = 0.0001 The train log loss is: 1.0015663922665903
For values of best alpha = 0.0001 The cross validation log loss is: 1.1953639079706706
For values of best alpha = 0.0001 The test log loss is: 1.1652301439734927
```

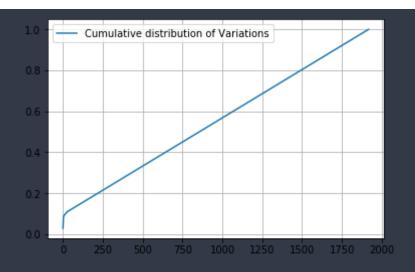
Q5. Is the Gene feature stable across all the data sets (Test, Train, Cross validation)?

Ans. Yes, it is. Otherwise, the CV and Test errors would be significantly more than train error. In [30]: print("Q6. How many data points in Test and CV datasets are covered by the ", unique gen es.shape[0], " genes in train dataset?") test coverage=test df['Gene'].isin(list(set(train_df['Gene'])))].shape[0] cv coverage=cv df[cv df['Gene'].isin(list(set(train df['Gene'])))].shape[0] print('Ans\n1. In test data', test coverage, 'out of', test df.shape[0], ":", (test coverage) e/test df.shape[0])*100) print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_cover age/cv df.shape[0])*100) Q6. How many data points in Test and CV datasets are covered by the 236 genes in train dataset? 1. In test data 647 out of 665 : 97.29323308270676 2. In cross validation data 520 out of 532 : 97.74436090225564 3.2.2 Univariate Analysis on Variation Feature **Q7.** Variation, What type of feature is it? Ans. Variation is a categorical variable **Q8.** How many categories are there? unique variations = train df['Variation'].value counts() print('Number of Unique Variations :', unique variations shape[0]) print(unique variations.head(10)) Number of Unique Variations : 1918

```
Truncating Mutations
         Deletion
         Amplification
         Fusions
         Overexpression
         061L
         061H
         G12V
         061R
         TMPRSS2-ETV1_Fusion
         Name: Variation, dtype: int64
In [32]: print("Ans: There are", unique_variations.shape[0] ,"different categories of variations
         in the train data, and they are distibuted as follows",)
         Ans: There are 1918 different categories of variations in the train data, and they are distibuted as follows
In [33]: 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()
```

```
    Histrogram of Variations

c = np.cumsum(h)
print(c)
plt.plot(c,label='Cumulative distribution of Variations')
plt grid()
plt legend()
plt show()
 [0.02966102 0.05367232 0.07580038 ... 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 both these methods to featurize the Variation Feature

```
In [35]: # alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", tra
in_df))
# test gene feature
test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", test
_df))
# cross validation gene feature
```

```
cv variation feature responseCoding = np.array(get gv feature(alpha, "Variation", cv df
 coding method. The shape of Variation feature: ", train variation feature responseCoding
 shape)
 train_variation_feature_responseCoding is a converted feature using the response coding method. The shape of Variation featu
 re: (2124, 9)
variation vectorizer = CountVectorizer()
train variation feature onehotCoding = variation vectorizer.fit transform(train df['Vari
ation'l)
test variation feature onehotCoding = variation vectorizer.transform(test df['Variation'
1)
cv variation feature onehotCoding = variation vectorizer.transform(cv df['Variation'])
oding method. The shape of Variation feature: ", train variation feature onehotCoding.sha
pe)
 train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method. The shape of Variation featur
 e: (2124, 1944)
  Q10. How good is this Variation feature in predicting y i?
  Let's build a model just like the earlier!
alpha = [10 ** x for x in range(-5, 1)]
```

```
cv log error array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random state=42)
    clf fit(train variation feature onehotCoding, y train)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv="lone")
    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))
```

```
nrint('For values of alpha = ', i, "The log loss is:", log loss(y cv, predict y, labe
ls=clf.classes , eps=1e-15))
fig, ax = plt.subplots()
ax plot(alpha, cv log error array,c='q')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax annotate((alpha[i],np round(txt,3)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best alpha], penalty='l2', loss='log', random state=42)
clf fit(train variation feature onehotCoding, y train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=Nome)
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 los
s(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 i"
s:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test variation feature onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss
(y_test, predict_y, labels=clf.classes , eps=le-15))
 For values of alpha = 1e-05 The log loss is: 1.720094498695089
```

```
For values of alpha = 0.0001 The log loss is: 1.716645969883596

For values of alpha = 0.001 The log loss is: 1.7189894501801914

For values of alpha = 0.01 The log loss is: 1.7335778163205122

For values of alpha = 0.1 The log loss is: 1.750425928585354

For values of alpha = 1 The log loss is: 1.750451737622075
```



```
For values of best alpha = 0.0001 The train log loss is: 0.754021684361103

For values of best alpha = 0.0001 The cross validation log loss is: 1.716645969883596

For values of best alpha = 0.0001 The test log loss is: 1.7044771255131872
```

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 [40]: print("Q12. How many data points are covered by total ", unique_variations.shape[0], " g
enes in test and cross validation data sets?")
test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))].shape
[0]
```

3.2.3 Univariate Analysis on Text Feature

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

```
(df):
   text feature responseCoding = np.zeros((df.shape[0],9))
   for i in range(0,9):
        row index = 0
        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))
d,0)+90))
            text feature responseCoding[row index][i] = math.exp(sum prob/len(row['TEXT'
].split()))
            row index += 1
   return text feature responseCoding
text vectorizer = CountVectorizer(min df=3)
train text feature onehotCoding = text vectorizer.fit transform(train df['TEXT'])
train text features= text vectorizer get feature names()
train text fea counts = train text feature onehotCoding.sum(axis=0).A1
text fea dict = dict(zin(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: 53645
dict list = []
for i in range(1,10):
    cls text = train df[train df['Class']==i]
    dict list.append(extract dictionary paddle(cls text))
total dict = extract dictionary paddle(train df)
confuse array = []
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)
train text feature responseCoding = get text responsecoding(train df)
```

```
test text feature responseCoding = get text responsecoding(test df)
cv text feature responseCoding = get text responsecoding(cv df)
train text feature responseCoding = (train text feature responseCoding T/train text feat
ure responseCoding.sum(axis=1)).T
test text feature responseCoding = (test text feature responseCoding.T/test text feature
 responseCoding.sum(axis=1)).T
cv text feature responseCoding = (cv text feature responseCoding.T/cv text feature responseCoding.T
nseCoding.sum(axis=1)).T
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)
cv text feature onehotCoding = text vectorizer.transform(cv df['TEXT'])
cv text feature onehotCoding = normalize(cv text feature onehotCoding, axis=0)
#https://stackoverflow.com/a/2258273/4084039
sorted text fea dict = dict(sorted(text fea dict.items(), key=lambda x: x[1] , reverse=1
rue))
sorted text occur = np.array(list(sorted text fea dict.values()))
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Counter({3: 5914, 4: 3363, 6: 3015, 5: 2856, 7: 2039, 8: 1879, 9: 1660, 12: 1579, 10: 1472, 15: 1064, 11: 933, 17: 856, 14: 832, 13: 803, 18: 715, 16: 700, 20: 599, 24: 575, 21: 512, 19: 474, 23: 453, 28: 439, 22: 405, 30: 372, 40: 370, 29: 354, 2 5: 348, 26: 336, 27: 306, 36: 294, 31: 276, 53: 275, 33: 261, 34: 261, 32: 255, 35: 246, 37: 216, 42: 211, 41: 202, 38: 197, 39: 189, 47: 185, 45: 179, 60: 179, 54: 169, 48: 168, 44: 167, 46: 165, 56: 162, 43: 159, 51: 159, 57: 155, 52: 150, 50: 14 9, 49: 144, 55: 129, 65: 119, 69: 117, 58: 115, 63: 111, 59: 109, 64: 103, 73: 103, 62: 102, 72: 102, 66: 101, 68: 97, 70: 9 5, 61: 93, 74: 93, 94: 91, 76: 89, 80: 88, 75: 87, 91: 84, 67: 78, 78: 77, 77: 72, 81: 72, 84: 72, 87: 72, 71: 71, 93: 71, 8 5: 70, 89: 68, 86: 67, 102: 67, 90: 65, 99: 65, 96: 64, 106: 64, 79: 60, 92: 59, 120: 59, 83: 58, 95: 58, 101: 58, 108: 56, 88: 55, 109: 54, 82: 53, 97: 52, 105: 52, 112: 50, 113: 50, 110: 49, 98: 48, 116: 48, 119: 47, 130: 47, 100: 46, 107: 46, 11 1: 46, 159: 46, 127: 45, 133: 45, 104: 43, 117: 43, 118: 43, 141: 43, 151: 43, 145: 42, 114: 41, 124: 40, 144: 40, 103: 39, 115: 39, 128: 38, 131: 38, 134: 37, 121: 37, 126: 36, 132: 36, 135: 35, 136: 35, 150: 35, 122: 33, 138: 33, 140: 33, 142: 3 3, 183: 33, 123: 32, 137: 32, 139: 32, 146: 32, 155: 32, 143: 30, 147: 30, 171: 30, 160: 29, 161: 29, 222: 29, 129: 28, 167: 28, 168: 28, 173: 28, 148: 27, 176: 27, 193: 27, 208: 27, 162: 26, 188: 26, 191: 26, 154: 25, 156: 25, 164: 25, 184: 25, 12 5: 24, 166: 24, 182: 24, 225: 24, 149: 23, 153: 23, 177: 23, 180: 23, 181: 23, 192: 23, 196: 23, 207: 23, 277: 23, 165: 22, 189: 22, 205: 22, 211: 22, 234: 22, 258: 22, 157: 21, 158: 21, 178: 21, 199: 21, 206: 21, 209: 21, 216: 21, 152: 20, 163: 2 0, 170: 20, 172: 20, 174: 20, 194: 20, 200: 20, 203: 20, 212: 20, 220: 20, 227: 20, 244: 20, 250: 20, 204: 19, 210: 19, 223: 19, 236: 19, 290: 19, 195: 19, 169: 18, 186: 18, 231: 18, 263: 18, 269: 18, 285: 18, 197: 17, 213: 17, 218: 17, 233: 17, 25 9: 17, 185: 16, 187: 16, 214: 16, 224: 16, 232: 16, 242: 16, 254: 16, 313: 16, 344: 16, 406: 16, 175: 15, 198: 15, 202: 15, 221: 15, 228: 15, 230: 15, 248: 15, 268: 15, 272: 15, 299: 15, 308: 15, 314: 15, 217: 14, 219: 14, 243: 14, 247: 14, 262: 1 4, 288: 14, 301: 14, 311: 14, 320: 14, 329: 14, 190: 13, 237: 13, 245: 13, 249: 13, 251: 13, 257: 13, 265: 13, 296: 13, 297: 13, 303: 13, 315: 13, 229: 12, 239: 12, 261: 12, 264: 12, 270: 12, 271: 12, 273: 12, 276: 12, 286: 12, 289: 12, 291: 12, 30 0: 12, 346: 12, 354: 12, 386: 12, 393: 12, 179: 11, 226: 11, 235: 11, 241: 11, 246: 11, 255: 11, 260: 11, 266: 11, 267: 11, 279: 11, 284: 11, 302: 11, 324: 11, 332: 11, 350: 11, 362: 11, 373: 11, 381: 11, 441: 11, 295: 11, 215: 10, 240: 10, 253: 1 0, 274: 10, 275: 10, 280: 10, 287: 10, 293: 10, 294: 10, 304: 10, 310: 10, 316: 10, 317: 10, 319: 10, 326: 10, 333: 10, 338: 10, 341: 10, 348: 10, 357: 10, 377: 10, 415: 10, 425: 10, 436: 10, 282: 9, 283: 9, 292: 9, 298: 9, 309: 9, 312: 9, 318: 9, 3 55: 9, 364: 9, 368: 9, 392: 9, 403: 9, 442: 9, 446: 9, 481: 9, 489: 9, 500: 9, 278: 8, 281: 8, 307: 8, 323: 8, 325: 8, 328: 8, 330: 8, 331: 8, 337: 8, 342: 8, 343: 8, 360: 8, 361: 8, 365: 8, 372: 8, 374: 8, 378: 8, 380: 8, 387: 8, 394: 8, 399: 8, 4 02: 8, 414: 8, 420: 8, 424: 8, 437: 8, 445: 8, 450: 8, 456: 8, 457: 8, 467: 8, 478: 8, 492: 8, 493: 8, 583: 8, 238: 7, 252: 7, 321: 7, 322: 7, 336: 7, 347: 7, 349: 7, 352: 7, 353: 7, 369: 7, 376: 7, 384: 7, 390: 7, 396: 7, 409: 7, 411: 7, 413: 7, 4 16: 7, 430: 7, 431: 7, 434: 7, 440: 7, 444: 7, 448: 7, 459: 7, 460: 7, 468: 7, 469: 7, 472: 7, 475: 7, 476: 7, 488: 7, 498: 7, 503: 7, 520: 7, 522: 7, 548: 7, 560: 7, 571: 7, 572: 7, 588: 7, 593: 7, 612: 7, 631: 7, 648: 7, 680: 7, 1073: 7, 201: 6, 305: 6, 327: 6, 339: 6, 351: 6, 363: 6, 367: 6, 375: 6, 389: 6, 391: 6, 395: 6, 398: 6, 401: 6, 405: 6, 408: 6, 419: 6, 421: 6, 422: 6, 432: 6, 433: 6, 451: 6, 452: 6, 453: 6, 464: 6, 470: 6, 482: 6, 485: 6, 507: 6, 513: 6, 517: 6, 519: 6, 521: 6, 5 30: 6, 533: 6, 536: 6, 552: 6, 559: 6, 563: 6, 564: 6, 567: 6, 586: 6, 619: 6, 642: 6, 652: 6, 667: 6, 692: 6, 693: 6, 695: 6, 725: 6, 747: 6, 750: 6, 751: 6, 761: 6, 767: 6, 777: 6, 797: 6, 887: 6, 964: 6, 557: 6, 256: 5, 334: 5, 340: 5, 345: 5, 3 56: 5, 359: 5, 371: 5, 382: 5, 404: 5, 412: 5, 418: 5, 427: 5, 428: 5, 435: 5, 462: 5, 465: 5, 471: 5, 505: 5, 512: 5, 515: 5, 524: 5, 537: 5, 541: 5, 542: 5, 556: 5, 558: 5, 562: 5, 584: 5, 596: 5, 603: 5, 608: 5, 609: 5, 610: 5, 620: 5, 638: 5, 6 45: 5, 655: 5, 656: 5, 662: 5, 673: 5, 677: 5, 681: 5, 682: 5, 684: 5, 685: 5, 702: 5, 707: 5, 749: 5, 760: 5, 772: 5, 775:

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 1, 7993: 1, 7994: 1, 9527: 1, 8022: 1, 8042: 1, 16252: 1, 8063: 1, 8095: 1, 8096: 1, 8105: 1, 2723: 1, 8455: 1, 9553: 1, 817
 0: 1, 24566: 1})
alpha = [10 ** x for x in range(-5, 1)]
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sk
learn.linear model.SGDClassifier.html
cv log error array=[]
for i in alpha:
```

```
clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random state=42)
    clf.fit(train text feature onehotCoding, y train)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
    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, labe
ls=clf.classes , eps=1e-15))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax annotate((alpha[i],np round(txt,3)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best alpha], penalty='l2', loss='log', random state=42)
clf fit(train text feature onehotCoding, y train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
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 los
s(y train, predict y, labels=clf.classes , eps=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.3381902080683417

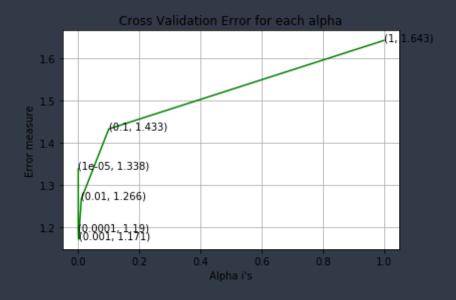
For values of alpha = 0.0001 The log loss is: 1.189774336644601

For values of alpha = 0.001 The log loss is: 1.1711849306609765

For values of alpha = 0.01 The log loss is: 1.2661660207388017

For values of alpha = 0.1 The log loss is: 1.4329881488304357

For values of alpha = 1 The log loss is: 1.6430932501445323
```



```
For values of best alpha = 0.001 The train log loss is: 0.7152773566845694

For values of best alpha = 0.001 The cross validation log loss is: 1.1711849306609765

For values of best alpha = 0.001 The test log loss is: 1.1193142751961653
```

```
Q. Is the Text feature stable across all the data sets (Test, Train, Cross validation)?
  Ans. Yes. it seems like!
def get intersec text(df):
    df text vec = CountVectorizer(min df=3)
    df text fea = df text vec.fit transform(df['TEXT'])
    df text features = df text vec.get feature names()
    df text fea counts = df text fea.sum(axis=0).A1
    df text fea dict = dict(zin(list(df text features), df text fea counts))
    len1 = len(set(df text features))
    len2 = len(set(train_text_features) & set(df_text_features))
    return len1, len2
len1,len2 = get intersec text(test df)
print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data")
len1,len2 = get intersec text(cv df)
print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train dat
 97.061 % of word of test data appeared in train data
 97.854 % of word of Cross Validation appeared in train data
  4. Machine Learning 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",cv =None)
   sig clf fit(train x, train y)
   pred y = sig clf.predict(test x)
   print("Log loss:",log loss(test y, sig clf.predict proba(test x)))
   print("Number of mis-classified points :", np.count nonzero((pred y- test y))/test y
shape[0])
   plot confusion matrix(test_y, pred_y)
                   (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)
                      es(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 < feal 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))
       clif (v < fea1 len+fea2 len):</pre>
           word = var vec.get feature names()[v-(fea1 len)]
           yes no = True if word == var else False
            yes no:
               word present += 1
               print(i, "variation feature [{}] present in test data point [{}]".format
(word, yes_no))
           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 quer
y point")
```

Stacking the three types of features

```
train gene var onehotCoding = hstack((train gene feature onehotCoding,train variation fe
ature onehotCoding))
test gene var onehotCoding = hstack((test gene feature onehotCoding,test variation featu
re onehotCoding))
cv gene var onehotCoding = hstack((cv gene feature onehotCoding,cv variation feature one
hotCoding))
train x onehotCoding = hstack((train gene var onehotCoding, train text feature onehotCod
ing)).tocsr()
train y = np.array(list(train df['Class']))
test x onehotCoding = hstack((test gene var onehotCoding, test text feature onehotCoding
)) tocsr()
test y = np.array(list(test df['Class']))
```

```
cv x onehotCoding = hstack((cv gene var onehotCoding, cv text feature onehotCoding)).toc
sr()
cv y = np.array(list(cv df['Class']))
train gene var responseCoding = np.hstack((train gene feature responseCoding,train varia
tion feature responseCoding))
test gene var responseCoding = np.hstack((test gene feature responseCoding,test variatio
n feature responseCoding))
cv gene var responseCoding = np.hstack((cv gene feature responseCoding,cv variation feat
ure responseCoding))
train x responseCoding = np.hstack((train gene var responseCoding, train text feature re
sponseCoding))
test x responseCoding = np.hstack((test gene var responseCoding, test text feature responseCoding)
nseCoding))
cv x responseCoding = np.hstack((cv gene var responseCoding, cv text feature responseCod
ing))
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train x onehotCod
ing shape)
print("(number of data points * number of features) in test data = ", test x onehotCodin
g shape)
print("(number of data points * number of features) in cross validation data =", cv x on
ehotCoding shape)
 One hot encoding features :
 (number of data points * number of features) in train data = (2124, 55825)
```

```
(number of data points * number of features) in test data = (665, 55825)
 (number of data points * number of features) in cross validation data = (532, 55825)
print("(number of data points * number of features) in train data = ", train x responseC
oding shape)
print("(number of data points * number of features) in test data = ", test_x_responseCod
ing shape)
print("(number of data points * number of features) in cross validation data =", cv x re
sponseCoding shape)
  Response encoding features :
 (number of data points * number of features) in train data = (2124, 27)
 (number of data points * number of features) in test data = (665, 27)
 (number of data points * number of features) in cross validation data = (532, 27)
  4.1. Base Line Model
  4.1.1. Naive Bayes
  4.1.1.1. Hyper parameter tuning
```

```
ive-bayes-algorithm-1/
alpha = [0.00001, 0.0001, 0.001, 0.1, 1, 10, 100,1000]
cv log error array = []
for i in alpha:
   print("for alpha =", i)
```

```
clf = MultinomialNB(alpha=i)
    clf fit(train x onehotCoding, train y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
    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(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",cv=None)
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 los
s(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 i"
s:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss
(y test, predict y, labels=clf.classes , eps=1e-15))
 for alpha = 1e-05
 Log Loss: 1.3019887897106295
 for alpha = 0.0001
 Log Loss: 1.300875080188898
 for alpha = 0.001
 Log Loss: 1.2948544096648285
 for alpha = 0.1
```

Log Loss: 1.2852735223933165

Log Loss: 1.2892465620145752

Log Loss: 1.3708098192870757

Log Loss: 1.365013032962014

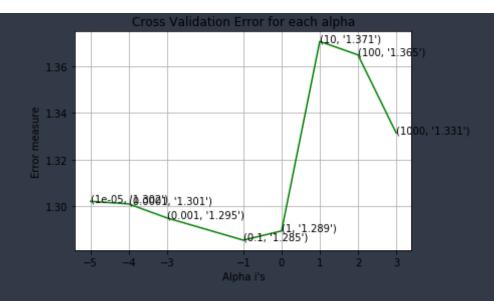
Log Loss: 1.3314332639172644

for alpha = 1

for alpha = 10

for alpha = 100

for alpha = 1000



```
For values of best alpha = 0.1 The train log loss is: 0.9083908465682289

For values of best alpha = 0.1 The cross validation log loss is: 1.2852735223933165

For values of best alpha = 0.1 The test log loss is: 1.2197307184179849
```

4.1.1.2. Testing the model with best hyper paramters

```
ive-bayes-algorithm-1/
clf = MultinomialNB(alpha=alpha[best alpha])
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
sig clf fit(train x onehotCoding, train y)
sig clf probs = sig clf.predict proba(cv x onehotCoding)
print("Log Loss :",log loss(cv y, sig clf probs))
print("Number of missclassified point :", np.count nonzero((sig clf.predict(cv x onehotC))
oding) - cv y))/cv y.shape[0])
plot confusion matrix(cv y, sig_clf.predict(cv_x_onehotCoding.toarray()))
```





4.1.1.3. Feature Importance, Correctly classified point

```
test point index = 1
no feature = 100
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCodi
ng[test point index]),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: 1
  Predicted Class Probabilities: [[0.5555 0.0793 0.0149 0.1164 0.0383 0.0389 0.1487 0.0046 0.0034]]
  Actual Class: 1
  10 Text feature [affect] present in test data point [True]
  11 Text feature [function] present in test data point [True]
  12 Text feature [one] present in test data point [True]
  13 Text feature [dna] present in test data point [True]
  14 Text feature [type] present in test data point [True]
  15 Text feature [protein] present in test data point [True]
  16 Text feature [two] present in test data point [True]
  17 Text feature [region] present in test data point [True]
  19 Text feature [wild] present in test data point [True]
  21 Text feature [containing] present in test data point [True]
  22 Text feature [sequence] present in test data point [True]
  23 Text feature [binding] present in test data point [True]
  24 Text feature [possible] present in test data point [True]
  25 Text feature [large] present in test data point [True]
  26 Text feature [indicate] present in test data point [True]
  27 Text feature [loss] present in test data point [True]
```

```
28 Text Teature [Tour] present in test data point [True]
29 Text feature [present] present in test data point [True]
31 Text feature [gene] present in test data point [True]
32 Text feature [six] present in test data point [True]
34 Text feature [therefore] present in test data point [True]
38 Text feature [specific] present in test data point [True]
39 Text feature [corresponding] present in test data point [True]
40 Text feature [functions] present in test data point [True]
41 Text feature [used] present in test data point [True]
43 Text feature [five] present in test data point [True]
45 Text feature [identified] present in test data point [True]
46 Text feature [involved] present in test data point [True]
47 Text feature [three] present in test data point [True]
48 Text feature [results] present in test data point [True]
51 Text feature [deletion] present in test data point [True]
52 Text feature [change] present in test data point [True]
53 Text feature [data] present in test data point [True]
54 Text feature [define] present in test data point [True]
55 Text feature [form] present in test data point [True]
57 Text feature [using] present in test data point [True]
58 Text feature [structure] present in test data point [True]
59 Text feature [effect] present in test data point [True]
60 Text feature [conserved] present in test data point [True]
61 Text feature [surface] present in test data point [True]
63 Text feature [specifically] present in test data point [True]
65 Text feature [table] present in test data point [True]
66 Text feature [also] present in test data point [True]
67 Text feature [control] present in test data point [True]
68 Text feature [following] present in test data point [True]
69 Text feature [contains] present in test data point [True]
70 Text feature [result] present in test data point [True]
71 Text feature [ability] present in test data point [True]
72 Text feature [determined] present in test data point [True]
75 Text feature [located] present in test data point [True]
76 Text feature [defined] present in test data point [True]
77 Text feature [performed] present in test data point [True]
78 Text feature [terminal] present in test data point [True]
79 Text feature [transcriptional] present in test data point [True]
80 Text feature [reveal] present in test data point [True]
```

```
reature [additional] present in test data point [irue
84 Text feature [indicated] present in test data point [True]
85 Text feature [fig] present in test data point [True]
86 Text feature [changes] present in test data point [True]
87 Text feature [expected] present in test data point [True]
88 Text feature [identify] present in test data point [True]
89 Text feature [discussion] present in test data point [True]
90 Text feature [acids] present in test data point [True]
91 Text feature [possibility] present in test data point [True]
93 Text feature [either] present in test data point [True]
94 Text feature [length] present in test data point [True]
95 Text feature [important] present in test data point [True]
96 Text feature [individual] present in test data point [True]
97 Text feature [addition] present in test data point [True]
98 Text feature [together] present in test data point [True]
99 Text feature [efficiency] present in test data point [True]
Out of the top 100 features 71 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

16 Text feature [presence] present in test data point [True] 17 Text feature [kinase] present in test data point [True] 18 Text feature [downstream] present in test data point [True] 19 Text feature [independent] present in test data point [True] 20 Text feature [inhibitor] present in test data point [True] 21 Text feature [well] present in test data point [True] 23 Text feature [expressing] present in test data point [True] 24 Text feature [cell] present in test data point [True] 25 Text feature [showed] present in test data point [True] 30 Text feature [contrast] present in test data point [True] 31 Text feature [recently] present in test data point [True] 32 Text feature [previously] present in test data point [True] 33 Text feature [compared] present in test data point [True] 34 Text feature [cells] present in test data point [True] 35 Text feature [found] present in test data point [True] 36 Text feature [shown] present in test data point [True] 37 Text feature [obtained] present in test data point [True] 38 Text feature [enhanced] present in test data point [True] 39 Text feature [also] present in test data point [True] 40 Text feature [however] present in test data point [True] 41 Text feature [suggest] present in test data point [True] 42 Text feature [observed] present in test data point [True] 43 Text feature [10] present in test data point [True] 44 Text feature [activation] present in test data point [True] 45 Text feature [higher] present in test data point [True] 46 Text feature [1a] present in test data point [True] 47 Text feature [treated] present in test data point [True] 48 Text feature [similar] present in test data point [True] 49 Text feature [factor] present in test data point [True] 50 Text feature [mutations] present in test data point [True] 51 Text feature [inhibition] present in test data point [True] 52 Text feature [growth] present in test data point [True] 53 Text feature [may] present in test data point [True] 54 Text feature [described] present in test data point [True] 55 Text feature [interestingly] present in test data point [True] 56 Text feature [respectively] present in test data point [True] 57 Text feature [addition] present in test data point [True] 58 Text feature [without] present in test data point [True]

```
59 Text feature [molecular] present in test data point [True]
60 Text feature [new] present in test data point [True]
61 Text feature [including] present in test data point [True]
62 Text feature [studies] present in test data point [True]
63 Text feature [identified] present in test data point [True]
64 Text feature [hours] present in test data point [True]
66 Text feature [approximately] present in test data point [True]
67 Text feature [using] present in test data point [True]
68 Text feature [total] present in test data point [True]
70 Text feature [increased] present in test data point [True]
71 Text feature [figure] present in test data point [True]
72 Text feature [various] present in test data point [True]
73 Text feature [reported] present in test data point [True]
74 Text feature [followed] present in test data point [True]
77 Text feature [3a] present in test data point [True]
78 Text feature [occur] present in test data point [True]
79 Text feature [report] present in test data point [True]
80 Text feature [furthermore] present in test data point [True]
81 Text feature [although] present in test data point [True]
82 Text feature [different] present in test data point [True]
83 Text feature [suggesting] present in test data point [True]
84 Text feature [proliferation] present in test data point [True]
86 Text feature [leading] present in test data point [True]
88 Text feature [whereas] present in test data point [True]
89 Text feature [1b] present in test data point [True]
90 Text feature [recent] present in test data point [True]
91 Text feature [measured] present in test data point [True]
93 Text feature [confirm] present in test data point [True]
94 Text feature [serum] present in test data point [True]
95 Text feature [demonstrated] present in test data point [True]
96 Text feature [three] present in test data point [True]
97 Text feature [active] present in test data point [True]
98 Text feature [within] present in test data point [True]
99 Text feature [inhibitors] present in test data point [True]
Out of the top 100 features 72 are present in query point
```

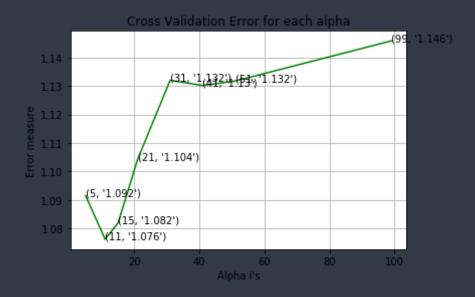
4.2. K Nearest Neighbour Classification

4.2.1. Hyper parameter tuning

```
alpha = [5, 11, 15, 21, 31, 41, 51, 99]
cv log error array = []
for i in alpha:
   print("for alpha =", i)
    clf = KNeighborsClassifier(n neighbors=i)
    clf fit(train x responseCoding, train y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=llone)
    sig clf fit(train x responseCoding, train y)
    sig clf probs = sig clf.predict proba(cv x responseCoding)
    cv log error array append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-
15))
   print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax annotate((alpha[i], str(txt)), (alpha[i],cv log error array[i]))
plt grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
```

```
plt show()
best alpha = np.argmin(cv log error array)
clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
sig clf fit(train x responseCoding, train y)
predict y = sig clf.predict proba(train x responseCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log los
s(y train, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x responseCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss i
s:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x responseCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss
(y test, predict y, labels=clf.classes , eps=1e-15))
 for alpha = 5
 Log Loss: 1.0915141863557163
 for alpha = 11
 Log Loss: 1.0762154185069404
 for alpha = 15
 Log Loss: 1.0819586099996104
 for alpha = 21
 Log Loss: 1.10423728629933
 for alpha = 31
 Log Loss: 1.131985738538
 for alpha = 41
 Log Loss: 1.1301598960132477
 for alpha = 51
 Log Loss: 1.1317179373827864
 for alpha = 99
```

Log Loss: 1.145802056830009

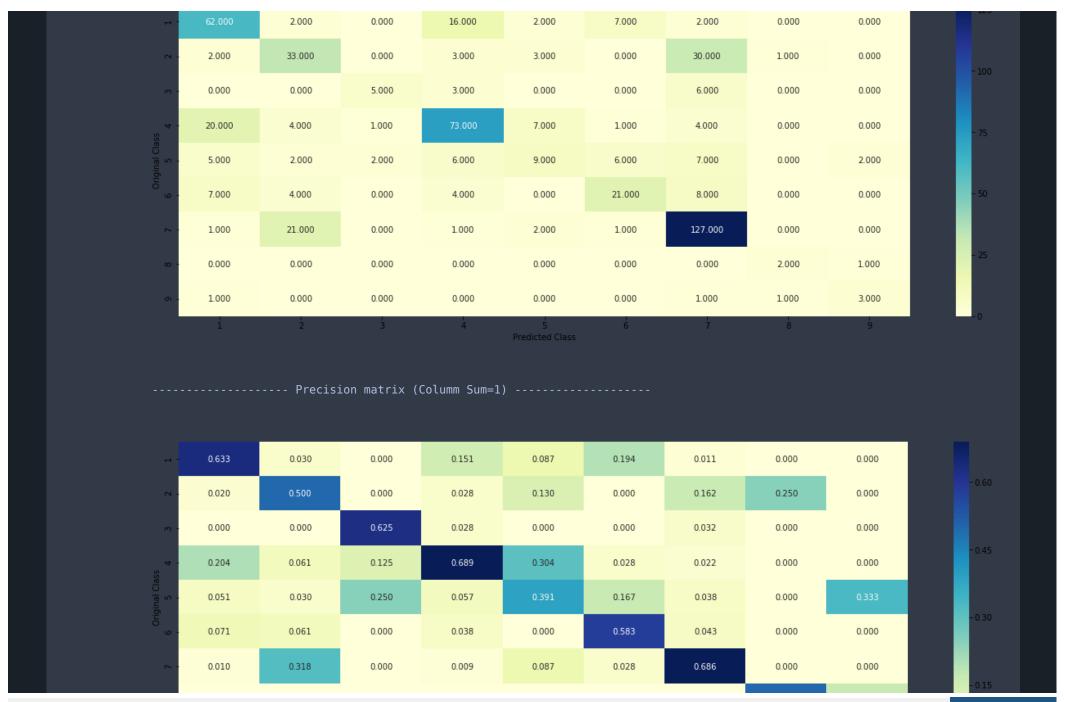


```
For values of best alpha = 11 The train log loss is: 0.6314169517736006

For values of best alpha = 11 The cross validation log loss is: 1.0762154185069404

For values of best alpha = 11 The test log loss is: 1.0163893373522823
```

4.2.2. Testing the model with best hyper paramters





4.2.3. Sample Query point -1

```
clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
clf fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
sig clf.fit(train x responseCoding, train y)
test point index = 1
predicted cls = sig clf.predict(test x responseCoding[0].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Actual Class :", test y[test point index])
neighbors = clf.kneighbors(test x responseCoding[test point index].reshape(1, -1), alpha
[best alpha])
print("The ",alpha[best alpha]," nearest neighbours of the test points belongs to classe
s",train y[neighbors[1][0]])
print("Feguency of nearest points :",Counter(train y[neighbors[1][0]]))
 Predicted Class: 7
 Actual Class: 1
 The 11 nearest neighbours of the test points belongs to classes [1 1 1 4 1 1 3 1 1 5 1]
 Feguency of nearest points : Counter({1: 8, 3: 1, 4: 1, 5: 1})
```

4.2.4. Sample Query Point-2

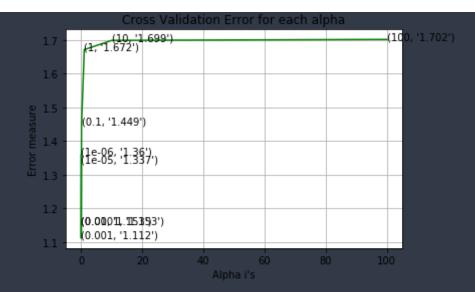
```
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid",cv = None)
sig_clf.fit(train_x_responseCoding, train_y)
test_point_index = 100
```

```
predicted cls = sig clf.predict(test x responseCoding[test point index].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Actual Class :", test y[test point index])
neighbors = clf_kneighbors(test x responseCoding[test point index].reshape(1, -1), alpha
[best alpha])
print("the k value for knn is",alpha[best alpha],"and the nearest neighbours of the test
points belongs to classes",train y[neighbors[1][0]])
print("Fequency of nearest points :",Counter(train y[neighbors[1][0]]))
 Predicted Class: 4
 Actual Class: 4
 the k value for knn is 11 and the nearest neighbours of the test points belongs to classes [4 4 4 4 1 4 4 1 3 2]
 Fequency of nearest points : Counter({4: 7, 1: 2, 2: 1, 3: 1})
  4.3. Logistic Regression
  4.3.1. With Class balancing
  4.3.1.1. Hyper paramter tuning
# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sk
learn.linear model.SGDClassifier.html
```

```
alpha = [10 ** x for x in range(-6, 3)]
cv log error array = []
```

```
i in alpha:
    print("for alpha =", i)
    clf = SGDClassifier(class weight='balanced', alpha=i, penalty='l2', loss='log', rand
om state=42)
    clf fit(train x onehotCoding, train y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=llone)
    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='q')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax annotate((alpha[i], str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv log error_array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='l2', loss
='log', random state=42)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
```

```
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 los
s(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 i
s:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss
(y test, predict y, labels=clf.classes , eps=1e-15))
 for alpha = 1e-06
 Log Loss: 1.359708524387313
 for alpha = 1e-05
 Log Loss: 1.3369311091684417
 for alpha = 0.0001
 Log Loss: 1.1534922241687542
 for alpha = 0.001
 Log Loss: 1.1115439140669414
 for alpha = 0.01
 Log Loss: 1.1533336843091526
 for alpha = 0.1
 Log Loss: 1.4494447193180873
 for alpha = 1
 Log Loss: 1.6717483455468505
 for alpha = 10
 Log Loss: 1.6992865507091743
 for alpha = 100
 Log Loss: 1.7021617847310466
```



```
For values of best alpha = 0.001 The train log loss is: 0.5803577697459831

For values of best alpha = 0.001 The cross validation log loss is: 1.1115439140669414

For values of best alpha = 0.001 The test log loss is: 1.0322990425247833
```

4.3.1.2. Testing the model with best hyper paramters





```
tabulte list = []
incresingorder ind = 0
for i in indices:
    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
        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 [70]: # from tabulate import tabulate
    clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12', loss
    ='log', random_state=42)
    clf.fit(train_x_onehotCoding,train_y)
    test_point_index = 1
    no_feature = 500
    predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCodi
```

```
ng[test point index]),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: 1
 Predicted Class Probabilities: [[0.6475 0.0866 0.0086 0.1298 0.0303 0.0181 0.069 0.0059 0.0041]]
 Actual Class: 1
 159 Text feature [ortholog] present in test data point [True]
 175 Text feature [processing] present in test data point [True]
 197 Text feature [archaebacterial] present in test data point [True]
 218 Text feature [tgs] present in test data point [True]
 233 Text feature [paralog] present in test data point [True]
 319 Text feature [tnrc6b] present in test data point [True]
 322 Text feature [deletion] present in test data point [True]
 338 Text feature [hooks] present in test data point [True]
 342 Text feature [piwi] present in test data point [True]
 369 Text feature [ago1] present in test data point [True]
 376 Text feature [ago] present in test data point [True]
 384 Text feature [hook] present in test data point [True]
 388 Text feature [silencing] present in test data point [True]
 494 Text feature [derepresses] present in test data point [True]
 Out of the top 500 features 14 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

```
In [71]: test_point_index = 100
    no_feature = 500
    predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
```

```
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
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: [[0.2881 0.0839 0.0086 0.3845 0.0304 0.0177 0.1707 0.0099 0.0062]]
Actual Class : 4

170 Text feature [suppressor] present in test data point [True]
309 Text feature [trevigen] present in test data point [True]
314 Text feature [degradation] present in test data point [True]
439 Text feature [neighbouring] present in test data point [True]
014 Text feature [microscopy] present in test data point [True]
015 Out of the top 500 features 5 are present in query point
```

4.3.2. Without Class balancing

4.3.2.1. Hyper paramter tuning

```
alpha = [10 ** x for x in range(-6, 1)]
cv log error array = []
for i in alpha:
```

```
print("for alpha =", i)
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random state=42)
    clf fit(train x onehotCoding, train y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
    sig clf.fit(train x onehotCoding, train y)
    sig clf probs = sig clf.predict proba(cv x onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes , eps=1e-
15))
   print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i], str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best alpha], penalty='l2', loss='log', random state=42)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv = None)
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 los
s(y_train, predict_y, labels=clf.classes , eps=1e-15))
```

Log Loss: 1.1213418687589178

Log Loss: 1.2098805187133874

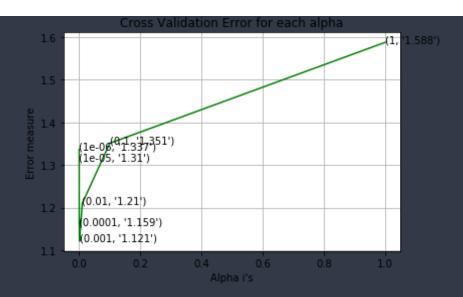
Log Loss: 1.3511788593887577

Log Loss: 1.5878648635479533

for alpha = 0.01

for alpha = 0.1

for alpha = 1



```
For values of best alpha = 0.001 The train log loss is: 0.5805831049211583

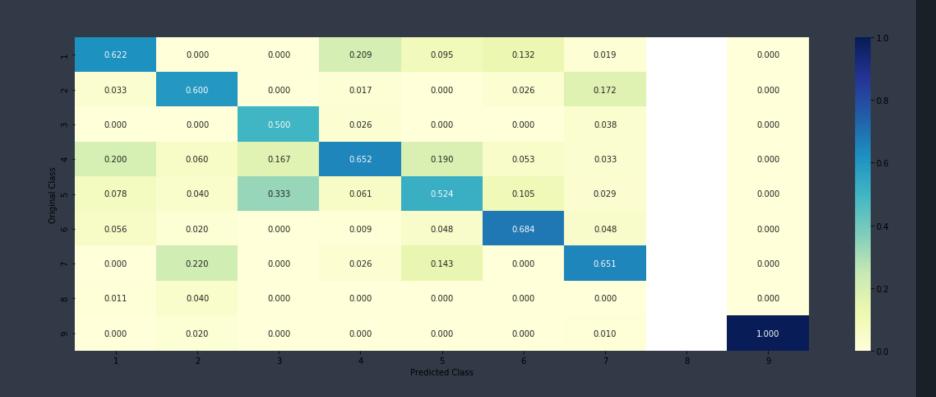
For values of best alpha = 0.001 The cross validation log loss is: 1.1213418687589178

For values of best alpha = 0.001 The test log loss is: 1.0494926777133984
```

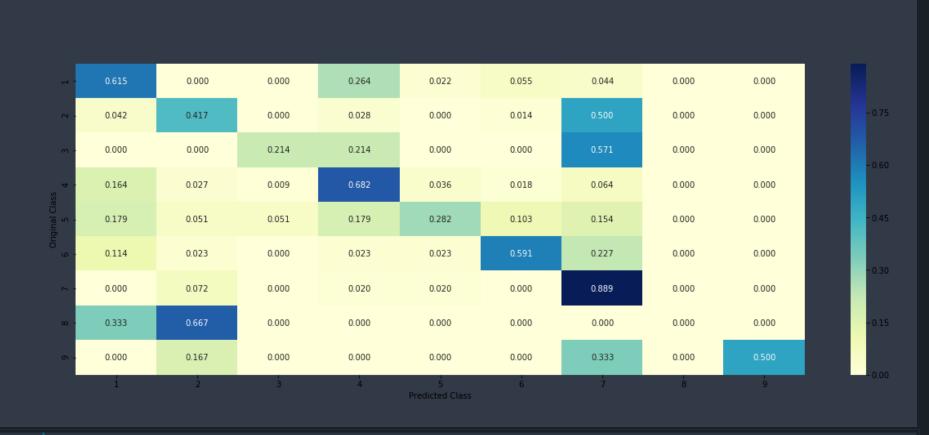
4.3.2.2. Testing model with best hyper parameters



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



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



4.3.2.3. Feature Importance, Correctly Classified point

```
In [74]: clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
    clf.fit(train_x_onehotCoding,train_y)
    test_point_index = 1
    no_feature = 500
    predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding))
```

```
ng[test point index]),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: 1
 Predicted Class Probabilities: [[0.6483 0.0888 0.0089 0.1281 0.0314 0.0194 0.066 0.0059 0.0032]]
 Actual Class : 1
 181 Text feature [ortholog] present in test data point [True]
 215 Text feature [processing] present in test data point [True]
 219 Text feature [archaebacterial] present in test data point [True]
 240 Text feature [paralog] present in test data point [True]
 242 Text feature [tgs] present in test data point [True]
 332 Text feature [tnrc6b] present in test data point [True]
 345 Text feature [hooks] present in test data point [True]
 349 Text feature [piwi] present in test data point [True]
 376 Text feature [ago1] present in test data point [True]
 388 Text feature [ago] present in test data point [True]
 392 Text feature [hook] present in test data point [True]
 397 Text feature [deletion] present in test data point [True]
 409 Text feature [silencing] present in test data point [True]
 Out of the top 500 features 13 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

```
In [75]: test_point_index = 100
    no_feature = 500
    predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
```

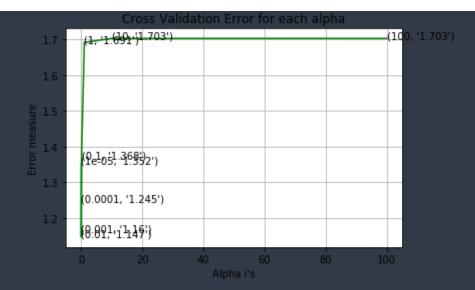
4.4. Linear Support Vector Machines

4.4.1. Hyper paramter tuning

```
generated/sklearn.calibration.CalibratedClassifierCV.html
alpha = [10 ** x for x in range(-5, 3)]
cv log error array = []
for i in alpha:
   print("for C =", i)
```

```
clf = SGDClassifier( class weight='balanced', alpha=i, penalty='l2', loss='hinge', r
andom state=42)
    clf fit(train x onehotCoding, train y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv= None)
    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(class weight='balanced', alpha=alpha[best alpha], penalty='l2', loss
='hinge', random state=42)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
sig clf fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
```

```
t('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log los
s(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 i
s:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss
(y test, predict y, labels=clf.classes , eps=1e-15))
 for C = 1e-05
 Log Loss: 1.3524569724749946
 for C = 0.0001
 Log Loss: 1.2450746542152122
 for C = 0.001
 Log Loss: 1.1600525511390811
 for C = 0.01
 Log Loss: 1.146523550332717
 for C = 0.1
 Log Loss: 1.367641778353358
 Log Loss: 1.691373569950243
 for C = 10
 Log Loss: 1.7027183144245908
 for C = 100
 Log Loss: 1.7026663780978135
```

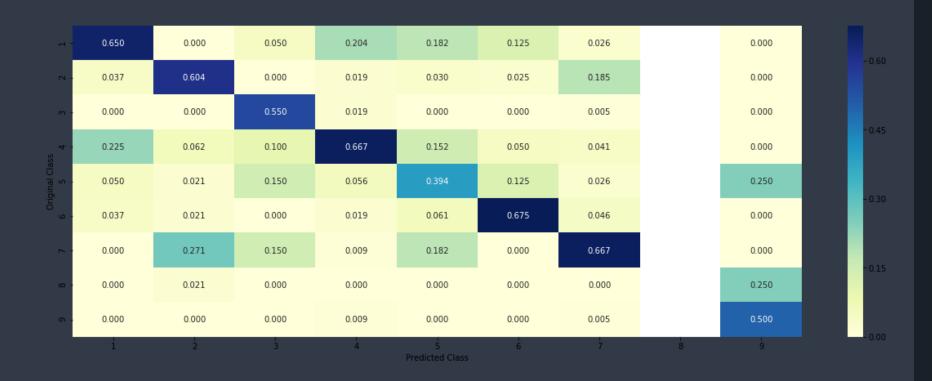


```
For values of best alpha = 0.01 The train log loss is: 0.7712014933162398
For values of best alpha = 0.01 The cross validation log loss is: 1.146523550332717
For values of best alpha = 0.01 The test log loss is: 1.0992427668689382
```

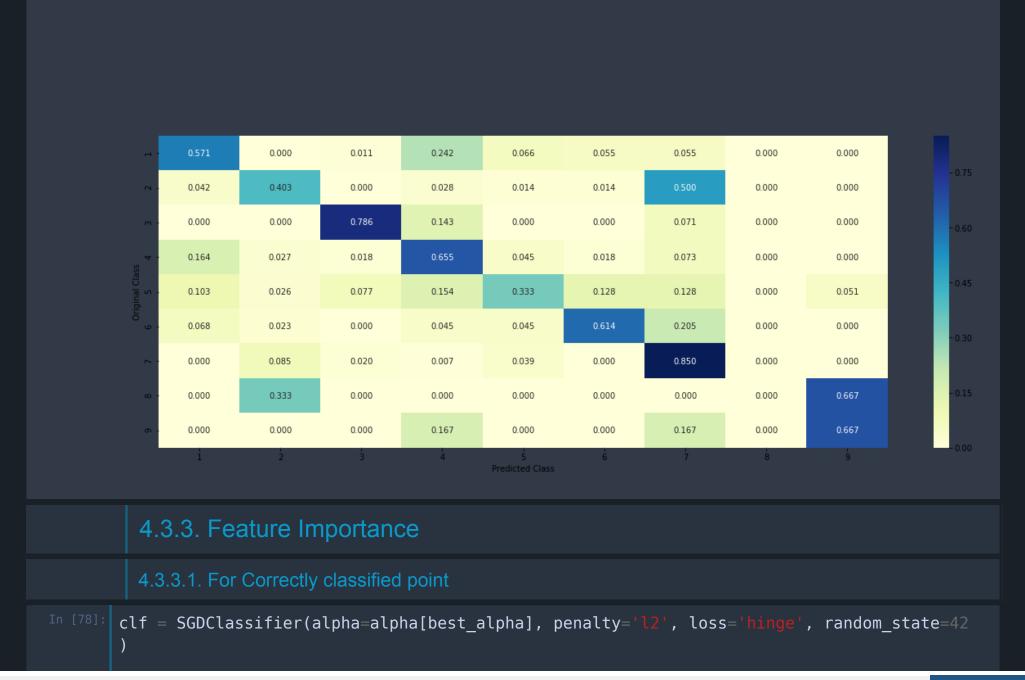
4.4.2. Testing model with best hyper parameters



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



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



```
clf fit(train x onehotCoding,train y)
test point index = 1
no feature = 500
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCodi
ng[test point index]),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: 1
 Predicted Class Probabilities: [[0.599 0.0907 0.0115 0.1321 0.0388 0.0265 0.0919 0.0053 0.0043]]
 Actual Class: 1
 12 Text feature [archaebacterial] present in test data point [True]
 39 Text feature [ortholog] present in test data point [True]
 40 Text feature [tgs] present in test data point [True]
 53 Text feature [tnrc6b] present in test data point [True]
 60 Text feature [piwi] present in test data point [True]
 67 Text feature [processing] present in test data point [True]
 69 Text feature [ago] present in test data point [True]
 75 Text feature [paralog] present in test data point [True]
 79 Text feature [ago1] present in test data point [True]
 106 Text feature [hooks] present in test data point [True]
 111 Text feature [derepresses] present in test data point [True]
 118 Text feature [silencing] present in test data point [True]
 144 Text feature [a260] present in test data point [True]
 149 Text feature [hook] present in test data point [True]
 155 Text feature [a280] present in test data point [True]
 191 Text feature [awg] present in test data point [True]
 195 Text feature [trnas] present in test data point [True]
 199 Text feature [reestablish] present in test data point [True]
```

```
224 Text feature [derepression] present in test data point [True] 292 Text feature [deletion] present in test data point [True] 343 Text feature [mimicry] present in test data point [True] 0ut of the top 500 features 21 are present in query point
```

4.3.3.2. For Incorrectly classified point

```
test point index = 100
no feature = 500
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted cls[0])
mrint("Predicted Class Probabilities:", np.round(sig clf.predict_proba(test_x_onehotCodi
ng[test point index]),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: [[0.2255 0.1016 0.0168 0.2968 0.052 0.0347 0.2574 0.0075 0.0077]]
 Actual Class: 4
 89 Text feature [microscopy] present in test data point [True]
 94 Text feature [suppressor] present in test data point [True]
 118 Text feature [trevigen] present in test data point [True]
 420 Text feature [degradation] present in test data point [True]
 442 Text feature [phosphatases] present in test data point [True]
 Out of the top 500 features 5 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

```
# Some of methods of RandomForestClassifier()
# some of attributes of RandomForestClassifier()
from sklearn.ensemble import RandomForestClassifier
```

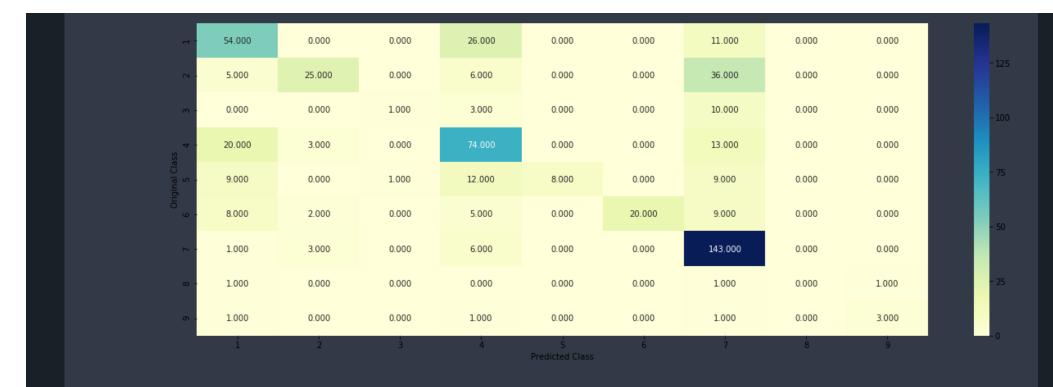
```
alpha = [100,200,500,1000,2000]
max depth = [5, 10]
cv log error array = []
for i in alpha:
   j in max depth:
       print("for n estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, rand
om state=42, n jobs=-1)
        clf fit(train x onehotCoding, train y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv = None)
        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))
```

```
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', ma
x depth=max depth[int(best alpha%2)], random state=42, n jobs=-1)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv =\noic \]
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 i
s:",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 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 in
s:",log loss(y test, predict y, labels=clf.classes , eps=1e-15))
 for n estimators = 100 and max depth = 5
 Log Loss: 1.2688416724170735
```

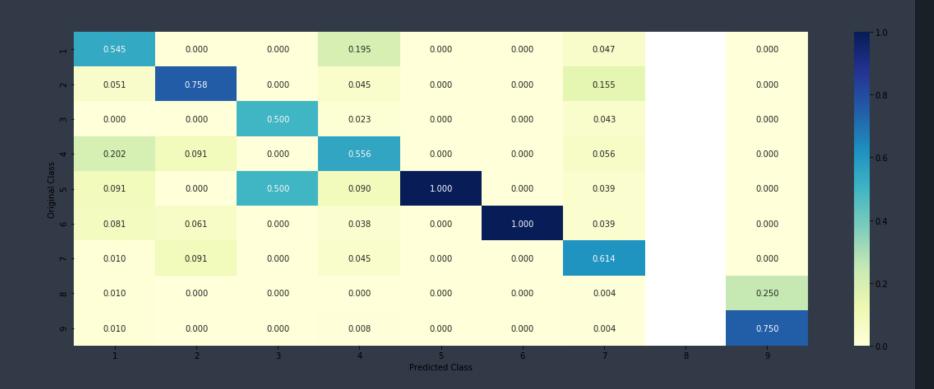
```
Log Loss: 1.2087727655909308
for n estimators = 200 and max depth = 5
Log Loss: 1.258595206386008
for n estimators = 200 and max depth = 10
Log Loss: 1.1950033841946577
for n_{estimators} = 500 and max_{estimator} = 5
Log Loss: 1.243850557415404
for n estimators = 500 and max depth = 10
Log Loss: 1.1866806202017914
for n_estimators = 1000 and max depth = 5
Log Loss: 1.246225714225061
for n_{estimators} = 1000 and max depth = 10
Log Loss: 1.1845336170641814
for n estimators = 2000 and max depth = 5
Log Loss: 1.2457997810987553
for n estimators = 2000 and max depth = 10
Log Loss: 1.1850105655127776
For values of best estimator = 1000 The train log loss is: 0.7158043669972709
For values of best estimator = 1000 The cross validation log loss is: 1.1845336170641814
For values of best estimator = 1000 The test log loss is: 1.1604813292237788
```

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

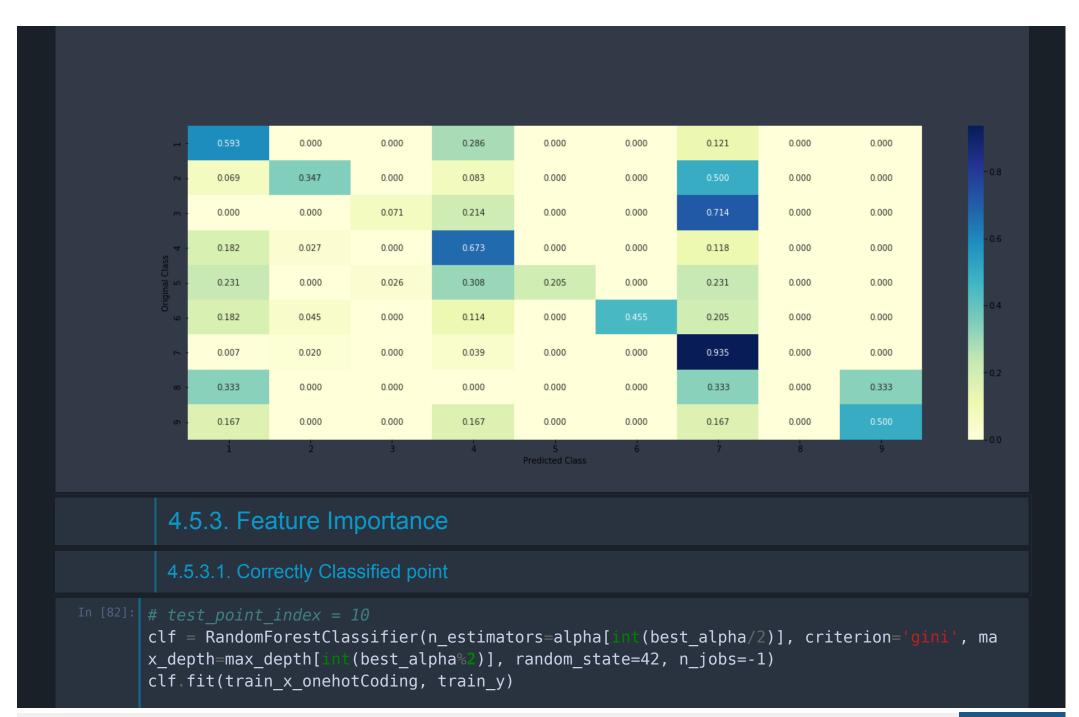
```
In [81]:
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=N
    one, min_samples_split=2,
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=
    None, min_impurity_decrease=0.0,
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None,
    verbose=0, warm_start=False,
# class_weight=None)
# Some of methods of RandomForestClassifier()
```



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



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



```
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf fit(train x onehotCoding, train y)
test point index = 1
no feature = 100
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted cls[0])
nrint("Predicted Class Probabilities:", np.round(sig clf.predict_proba(test_x onehotCodi)
ng[test point index]),4))
print("Actual Class :", test y[test point index])
indices = np.argsort(-clf.feature importances )
print("-"*50)
get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point index],test d
f['Gene'].iloc[test point index], test df['Variation'].iloc[test point index], no feature
 Predicted Class: 1
 Predicted Class Probabilities: [[0.4913 0.0605 0.0194 0.2511 0.058 0.0528 0.0509 0.0075 0.0084]]
 Actual Class: 1
 2 Text feature [tyrosine] present in test data point [True]
 6 Text feature [inhibitor] present in test data point [True]
 14 Text feature [treatment] present in test data point [True]
 27 Text feature [function] present in test data point [True]
 30 Text feature [cells] present in test data point [True]
 35 Text feature [functional] present in test data point [True]
 36 Text feature [loss] present in test data point [True]
 37 Text feature [yeast] present in test data point [True]
 47 Text feature [cell] present in test data point [True]
 64 Text feature [lines] present in test data point [True]
 66 Text feature [nuclear] present in test data point [True]
 68 Text feature [transformation] present in test data point [True]
 72 Text feature [inhibition] present in test data point [True]
 79 Text feature [expression] present in test data point [True]
 84 Text feature [presence] present in test data point [True]
```

```
86 Text feature [dna] present in test data point [True]
99 Text feature [independent] present in test data point [True]
Out of the top 100 features 17 are present in query point
```

4.5.3.2. Inorrectly Classified point

```
test point index = 100
no feature = 100
predicted_cls = sig_clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCodi
ng[test point index]),4))
print("Actuall Class :", test y[test point index])
indices = np.argsort(-clf.feature importances )
print("-"*50)
get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point index],test d
f['Gene'].iloc[test point index], test df['Variation'].iloc[test point index], no feature
  Predicted Class: 7
  Predicted Class Probabilities: [[0.1812 0.0986 0.024 0.1854 0.0545 0.0474 0.3924 0.0076 0.0089]]
  Actuall Class : 4
  O Text feature [kinase] present in test data point [True]
 2 Text feature [tyrosine] present in test data point [True]
  3 Text feature [activation] present in test data point [True]
  4 Text feature [phosphorylation] present in test data point [True]
  6 Text feature [inhibitor] present in test data point [True]
 7 Text feature [suppressor] present in test data point [True]
  8 Text feature [inhibitors] present in test data point [True]
  9 Text feature [activated] present in test data point [True]
  10 Text feature [missense] present in test data point [True]
  14 Text feature [treatment] present in test data point [True]
  15 Text feature [signaling] present in test data point [True]
  17 Text feature [oncogenic] present in test data point [True]
```

```
20 Text feature [receptor] present in test data point [True]
24 Text feature [growth] present in test data point [True]
27 Text feature [function] present in test data point [True]
28 Text feature [downstream] present in test data point [True]
29 Text feature [transforming] present in test data point [True]
30 Text feature [cells] present in test data point [True]
35 Text feature [functional] present in test data point [True]
36 Text feature [loss] present in test data point [True]
38 Text feature [constitutively] present in test data point [True]
41 Text feature [ras] present in test data point [True]
43 Text feature [response] present in test data point [True]
47 Text feature [cell] present in test data point [True]
49 Text feature [phospho] present in test data point [True]
51 Text feature [extracellular] present in test data point [True]
53 Text feature [proliferation] present in test data point [True]
54 Text feature [stability] present in test data point [True]
61 Text feature [expressing] present in test data point [True]
63 Text feature [lung] present in test data point [True]
64 Text feature [lines] present in test data point [True]
66 Text feature [nuclear] present in test data point [True]
72 Text feature [inhibition] present in test data point [True]
73 Text feature [treated] present in test data point [True]
77 Text feature [inhibited] present in test data point [True]
79 Text feature [expression] present in test data point [True]
80 Text feature [serum] present in test data point [True]
82 Text feature [defective] present in test data point [True]
83 Text feature [receptors] present in test data point [True]
84 Text feature [presence] present in test data point [True]
86 Text feature [dna] present in test data point [True]
99 Text feature [independent] present in test data point [True]
Out of the top 100 features 42 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

```
In [84]: # ------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=N)
```

```
generated/sklearn.calibration.CalibratedClassifierCV.html
```

```
alpha = [10,50,100,200,500,1000]
\max depth = [2,3,5,10]
cv log error array = []
for i in alpha:
   for j in max depth:
       print("for n estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, rand
om state=42, n_jobs=-1)
        clf fit(train x responseCoding, train y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig clf fit(train x responseCoding, train y)
        sig clf probs = sig clf.predict proba(cv x responseCoding)
        cv log error array append(log loss(cv y, sig clf probs, labels=clf.classes , eps
=1e-15)
       print("Log Loss :",log loss(cv y, sig clf probs))
```

```
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='gini', ma
x depth=max depth[int(best alpha%4)], random state=42, n jobs=-1)
clf fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x responseCoding, train y)
predict y = sig clf.predict proba(train x responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The train log loss is:",
log loss(y train, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x responseCoding)
print('For values of best alpha = ', alpha[int(best alpha/4)], "The cross validation log
loss is:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x responseCoding)
print('For values of best alpha = ', alpha[int(best alpha/4)], "The test log loss is:", l
og loss(y test, predict y, labels=clf.classes , eps=1e-15))
 for n estimators = 10 and max depth = 2
 Log Loss: 2.2262522292101115
 for n_{estimators} = 10 and max depth = 3
 Log Loss: 1.8880784512904003
 for n estimators = 10 and max depth = 5
 Log Loss: 1.5714491153626275
 for n estimators = 10 and max depth = 10
 Log Loss: 1.7326629999496141
 for n estimators = 50 and max depth = 2
```

```
Log Loss: 1.8127536591736855
for n estimators = 50 and max depth = 3
Log Loss: 1.5681415678395936
for n estimators = 50 and max depth = 5
Log Loss: 1.4261497291469316
for n_{estimators} = 50 and max depth = 10
Log Loss: 1.794551887023849
for n estimators = 100 and max depth = 2
Log Loss: 1.6507421975398098
for n_estimators = 100 and max depth = 3
Log Loss: 1.6100597127674834
for n estimators = 100 and max depth = 5
Log Loss: 1.3501173032947442
for n estimators = 100 and max depth = 10
Log Loss: 1.829196441600451
for n_{estimators} = 200 and max_{estimator} = 2
Log Loss: 1.741510653850449
for n estimators = 200 and max depth = 3
Log Loss: 1.6070235968945639
for n estimators = 200 and max depth = 5
Log Loss: 1.4136503322445506
for n estimators = 200 and max depth = 10
Log Loss: 1.8542733543796914
for n estimators = 500 and max depth = 2
Log Loss: 1.8261744088809844
for n estimators = 500 and max depth = 3
Log Loss: 1.6261711915680421
for n estimators = 500 and max depth = 5
Log Loss: 1.432686149945551
for n_estimators = 500 and max depth = 10
Log Loss: 1.8922637436582896
for n estimators = 1000 and max depth = 2
Log Loss: 1.8175144635668152
for n estimators = 1000 and max depth = 3
Log Loss: 1.6717267309493578
for n estimators = 1000 and max depth = 5
Log Loss: 1.4236694372360745
for n estimators = 1000 and max depth = 10
Log Loss: 1.830948162650952
```

```
For values of best alpha = 100 The train log loss is: 0.05455095461234915

For values of best alpha = 100 The cross validation log loss is: 1.3501173032947442

For values of best alpha = 100 The test log loss is: 1.3050860874683652
```

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

```
# Some of methods of RandomForestClassifier()
```

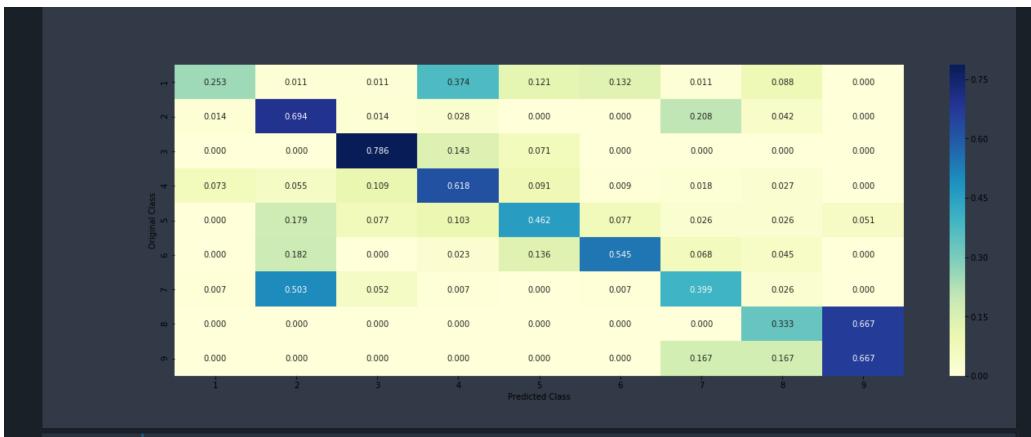
clf = RandomForestClassifier(max_depth=max_depth[:::(best_alpha%:)], n_estimators=alpha
[int(best_alpha/4)], criterion='gini', max_features='auto',random_state=42)
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_responseCoding,cv
_y, clf)



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



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



4.5.5. Feature Importance

4.5.5.1. Correctly Classified point

```
clf = RandomForestClassifier(n_estimators=alpha[im(best_alpha/4)], criterion='gini', ma
x_depth=max_depth[im(best_alpha%)], random_state=42, n_jobs=-1)
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)
```

```
test point index = 1
no feature = 27
predicted cls = sig clf.predict(test x responseCoding[test point index].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_responseCo
ding[test point index] reshape(1,-1)),4))
print("Actual Class :", test y[test point index])
indices = np.argsort(-clf.feature importances )
print("-"*50)
for i in indices:
    ifig
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
        print("Text is important feature")
 Predicted Class: 1
 Predicted Class Probabilities: [[0.2888 0.0717 0.0637 0.1074 0.0381 0.0703 0.0143 0.2146 0.1309]]
 Actual Class : 1
 Variation is important feature
 Variation is important feature
 Variation is important feature
 Variation is important feature
 Gene is important feature
 Variation is important feature
 Variation is important feature
 Text is important feature
 Text is important feature
 Gene is important feature
 Text is important feature
 Text is important feature
```

```
Text is important feature

Gene is important feature

Gene is important feature

Variation is important feature

Text is important feature

Gene is important feature

Gene is important feature

Variation is important feature

Variation is important feature

Variation is important feature

Text is important feature

Text is important feature

Text is important feature

Gene is important feature

Gene is important feature

Gene is important feature
```

4.5.5.2. Incorrectly Classified point

```
In [87]: test_point_index = 100
    predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
    irin ('Predicted Class :", predicted_cls[0])
    irin ('Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_responseCoding[test_point_index].reshape(1,-1)),4))
    irin ('Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.feature_importances_)
    irin ('-:**50)
    ior i in indices:
        if i<9:
            prin ("Gene is important feature")
        elif i<18:
            prin ("Variation is important feature")
        elic:
            prin ("Text is important feature")</pre>
```

```
Predicted Class: 4
Predicted Class Probabilities: [[0.2016 0.0225 0.1241 0.4567 0.0408 0.0716 0.0069 0.0343 0.0414]]
Actual Class: 4
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Gene is important feature
 4.7 Stack the models
4.7.1 testing with hyper parameter tuning
```

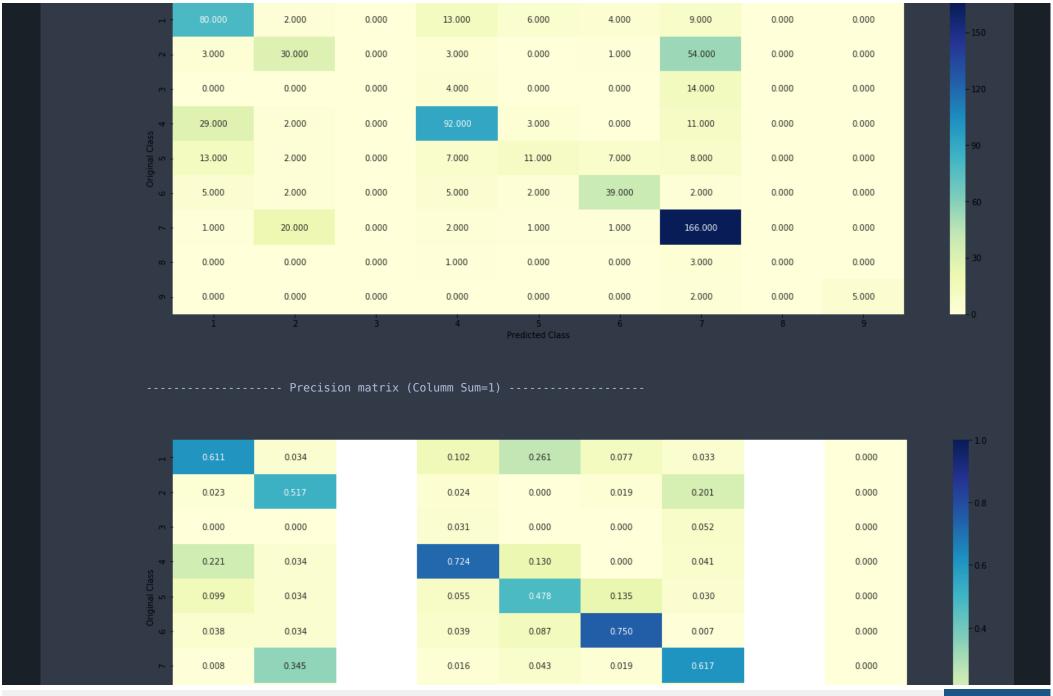
```
clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class weight='balanced', ran
dom state=0)
clf1 fit(train x onehotCoding, train y)
sig clf1 = CalibratedClassifierCV(clf1, method="sigmoid",cv=None)
clf2 = SGDClassifier(alpha=1, penalty='l2', loss='hinge', class_weight='balanced', rando
m state=0)
clf2 fit(train x onehotCoding, train y)
sig clf2 = CalibratedClassifierCV(clf2, method="sigmoid",cv=None)
clf3 = MultinomialNB(alpha=0.001)
clf3 fit(train x onehotCoding, train y)
sig clf3 = CalibratedClassifierCV(clf3, method="sigmoid",cv=None)
sig clf1 fit(train x onehotCoding, train y)
print("Logistic Regression : Log Loss: %0.2f" % (log loss(cv y, sig clf1.predict proba())
cv x onehotCoding))))
sig clf2 fit(train x onehotCoding, train y)
print("Support vector machines : Log Loss: %0.2f" % (log loss(cv y, sig clf2.predict pro
ba(cv x onehotCoding))))
sig clf3 fit(train x onehotCoding, train y)
nrint("Naive Bayes : Log Loss: %0.2f" % (log loss(cv_y, sig_clf3.predict_proba(cv_x_oneh
otCoding))))
```

```
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 classifie
r=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 lo
ss(cv y, sclf predict proba(cv x onehotCoding))))
    log error =log loss(cv y, sclf predict proba(cv x onehotCoding))
    best alpha > log error:
         best alpha = log error
 Logistic Regression : Log Loss: 1.10
 Support vector machines : Log Loss: 1.69
 Naive Bayes : Log Loss: 1.29
 Stacking Classifer: for the value of alpha: 0.000100 Log Loss: 2.179
 Stacking Classifer: for the value of alpha: 0.001000 Log Loss: 2.042
 Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.534
 Stacking Classifer: for the value of alpha: 0.100000 Log Loss: 1.139
 Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.241
 Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.552
```

4.7.2 testing the model with the best hyper parameters

```
In [89]: lr = LogisticRegression(C=0.1)
    sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=lr
    , use_probas="rue")
    sclf.fit(train_x_onehotCoding, train_y)
```

```
log error = log loss(train y, sclf.predict proba(train x onehotCoding))
print("Log loss (train) on the stacking classifier :",log error)
log error = log loss(cv y, sclf.predict proba(cv x onehotCoding))
print("Log loss (CV) on the stacking classifier :",log error)
log error = log loss(test y, sclf.predict proba(test x onehotCoding))
print("Log loss (test) on the stacking classifier :",log error)
print("Number of missclassified point :", np.count nonzero((sclf.predict(test x onehotCo
ding) - test y))/test y.shape[0])
plot confusion matrix(test y=test y, predict y=sclf.predict(test x onehotCoding))
 Log loss (train) on the stacking classifier: 0.6511543219100392
 Log loss (CV) on the stacking classifier: 1.138621819206958
 Log loss (test) on the stacking classifier: 1.1158439148954673
 Number of missclassified point: 0.36390977443609024
 ----- Confusion matrix -----
```





```
vclf = VotingClassifier(estimators=[('lr', sig_clf1), ('svc', sig_clf2), ('rf', sig_clf3)
)], voting='soft')
vclf fit(train x onehotCoding, train y)
print("Log loss (train) on the VotingClassifier :", log loss(train y, vclf.predict proba
(train x onehotCoding)))
print("Log loss (CV) on the VotingClassifier :", log loss(cv y, vclf.predict proba(cv x
onehotCoding)))
print("Log loss (test) on the VotingClassifier :", log_loss(test_y, vclf.predict_proba(t
est x onehotCoding)))
print("Number of missclassified point :", np.count nonzero((vclf.predict(test x onehotCo
ding) - test y))/test y.shape[0])
plot confusion matrix(test y=test y, predict y=vclf.predict(test x onehotCoding))
 Log loss (train) on the VotingClassifier: 0.9154669881995511
 Log loss (CV) on the VotingClassifier: 1.216326492097411
 Log loss (test) on the VotingClassifier: 1.1894053126330026
 Number of missclassified point : 0.362406015037594
 ----- Confusion matrix ------
```





1. Apply All the models with tf-idf features (Replace CountVectorizer with tfidfVectorizer and run the

- same cells)
- 2. Instead of using all the words in the dataset, use only the top 1000 words based of tf-idf values
- 3. Apply Logistic regression with CountVectorizer Features, including both unigrams and bigrams
- 4. Try any of the feature engineering techniques discussed in the course to reduce the CV and test logloss to a value less than 1.0

1. Using TF-IDF features

```
from sklearn.feature_extraction.text import TfidfTransformer
from sklearn.feature extraction.text import TfidfVectorizer
tfidf text vectorizer = TfidfVectorizer(min df=3, max features=1000)
train text feature onehotCoding = tfidf text vectorizer.fit transform(train df['TEXT'])
train text features = tfidf text vectorizer get feature names()
train text fea counts = train text feature onehotCoding.sum(axis=0).A1
text fea dict = dist(zin(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: 1000
```

```
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 = tfidf text vectorizer.transform(test df['TEXT'])
test text feature onehotCoding = normalize(test text feature onehotCoding, axis=0)
cv text feature onehotCoding = tfidf text vectorizer.transform(cv df['TEXT'])
cv text feature onehotCoding = normalize(cv text feature onehotCoding, axis=0)
train gene var onehotCoding = hstack((train gene feature onehotCoding,train variation fe
ature onehotCoding))
test gene var onehotCoding = hstack((test gene feature onehotCoding,test variation featu
re onehotCoding))
cv gene var onehotCoding = hstack((cv gene feature onehotCoding,cv variation feature one
hotCoding))
train x onehotCoding = hstack((train gene var onehotCoding, train text feature onehotCod
ing)) tocsr()
train y = np.array(list(train df['Class']))
test x onehotCoding = hstack((test gene var onehotCoding, test text feature onehotCoding)
)) tocsr()
test y = np.array(list(test df['Class']))
cv x onehotCoding = hstack((cv gene var onehotCoding, cv text feature onehotCoding)).toc
```

```
sr()
cv_y = np.array(lis (cv_df['Class']))

In [95]: print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train_x_onehotCod
ing.shape)
print("(number of data points * number of features) in test data = ", test_x_onehotCodin
g.shape)
print("(number of data points * number of features) in cross validation data =", cv_x_on
ehotCoding.shape)

One hot encoding features:
(number of data points * number of features) in train data = (2124, 3180)
(number of data points * number of features) in test data = (665, 3180)
(number of data points * number of features) in cross validation data = (532, 3180)
```

Base line models

```
In [120]: doi get_impfeature_names(indices, text, gene, var, no_features):
    gene_count_vec = CountVectorizer()
    var_count_vec = CountVectorizer(min_df=3,max_features=1000)

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'])

feal_len = lon(gene_vec.get_feature_names())
    fea2_len = lon(var_count_vec.get_feature_names())
```

```
word present = 0
   for i,v in enumerate(indices):
       if (v < feal len):
           word = gene vec.get feature names()[v]
           yes no = True if word == gene else False
           if yes no:
               word present += 1
               print(i, "Gene feature [{}] present in test data point [{}]".format(word
,yes_no))
       (v < fea1 len+fea2 len):</pre>
           word = var vec.get feature names()[v-(fea1 len)]
           yes no = True if word == var else False
           yes no:
               word present += 1
               print(i, "variation feature [{}] present in test data point [{}]".format
(word, yes no))
           word = text vec.get feature names()[v-(fea1 len+fea2 len)]
           yes no = True if word in text.split() else False
           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 quer
y point")
```

KNN

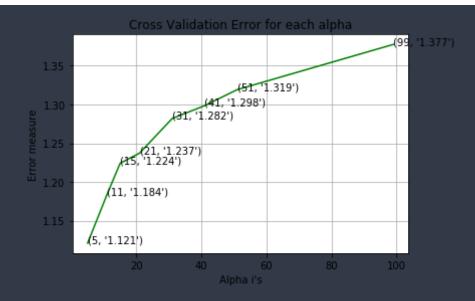
```
In [122]: alpha = [5, 11, 15, 21, 31, 41, 51, 99]
```

```
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",cv=llone)
    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 = KNeighborsClassifier(n neighbors=alpha[best alpha])
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None)
sig clf fit(train x onehotCoding, train y)
```

```
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
num('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_los
s(y_train, predict_y, labels=clf.classes_, eps=le-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
num('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss i
s:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=le-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
num('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss
(y_test, predict_y, labels=clf.classes_, eps=le-15))

for alpha = 5
```

```
for alpha = 5
Log Loss : 1.121096758757845
for alpha = 11
Log Loss : 1.1841272563519538
for alpha = 15
Log Loss : 1.2241019311062764
for alpha = 21
Log Loss : 1.237253833990515
for alpha = 31
Log Loss : 1.2818356626838434
for alpha = 41
Log Loss : 1.29846607972916
for alpha = 51
Log Loss : 1.3190793528025297
for alpha = 99
Log Loss : 1.3774120339020592
```



```
For values of best alpha = 5 The train log loss is: 0.8837266026345719

For values of best alpha = 5 The cross validation log loss is: 1.121096758757845

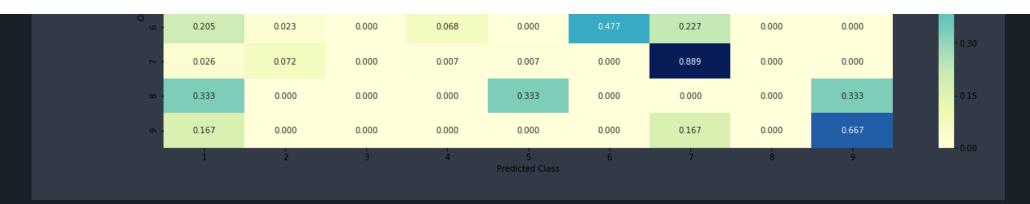
For values of best alpha = 5 The test log loss is: 1.0846021648704152
```

Testing on te best Hyperparameter



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





Sample query point: 1

```
clf = KNeighborsClassifier(n neighbors=alpha[best_alpha])
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv = None)
sig clf fit(train x onehotCoding, train y)
test point index = 12
predicted cls = sig clf.predict(test x onehotCoding[test point index].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Actual Class :", test y[test point index])
neighbors = clf.kneighbors(test x onehotCoding[test point index].reshape(1, -1), alpha[b]
est alpha])
print("the k value for knn is",alpha[best alpha],"and the nearest neighbours of the test
 points belongs to classes", train y[neighbors[1][0]])
print("Fequency of nearest points :",Counter(train y[neighbors[1][0]]))
 Predicted Class: 1
 Actual Class: 1
 the k value for knn is 5 and the nearest neighbours of the test points belongs to classes [1 1 1 1 1]
 Fequency of nearest points : Counter({1: 5})
```

Naive Bayes

```
alpha = [10**i \text{ for } i \text{ in range}(-6,5)]
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",cv=5)
    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 = MultinomialNB(alpha=alpha[best alpha])
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=5)
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 los
s(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 i
s:",log_loss(y_cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss
(y test, predict y, labels=clf.classes , eps=1e-15))
 for alpha = 1e-06
 Log Loss: 1.2395266864541712
 for alpha = 1e-05
 Log Loss: 1.2391177285616148
 for alpha = 0.0001
 Log Loss: 1.23705695574075
 for alpha = 0.001
 Log Loss: 1.2351322057219916
 for alpha = 0.01
 Log Loss: 1.2331628169706605
 for alpha = 0.1
 Log Loss: 1.2826340573844566
 for alpha = 1
 Log Loss: 1.33388184634762
 for alpha = 10
 Log Loss: 1.5555782261278808
 for alpha = 100
 Log Loss: 1.5470773319894693
 for alpha = 1000
 Log Loss: 1.526283548098692
```

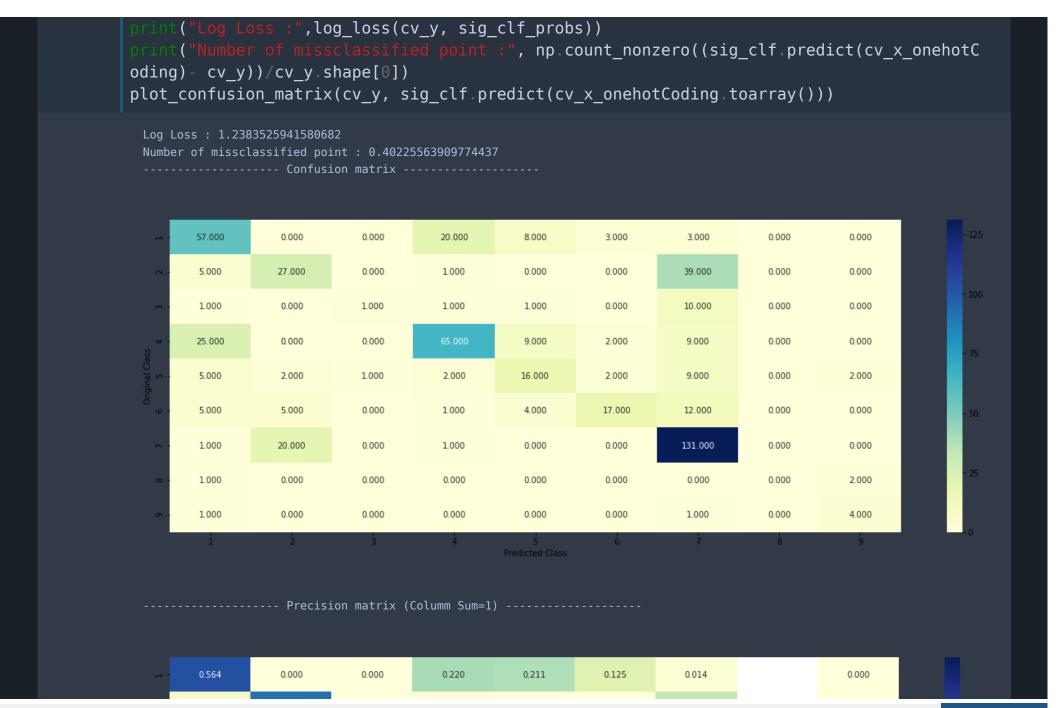
for alpha = 10000Log Loss: 1.5258339075182996 Cross Validation Error for each alpha (1900¹ • \$554) (1000 1 526) 10000, '1.526') anse 1.45 (1, '1.334') (0.1, '1.283') For values of best alpha = 0.01 The train log loss is: 0.46355254883333985

Testing on the best Hyperparameter

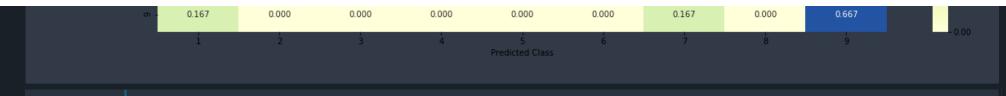
For values of best alpha = 0.01 The cross validation log loss is: 1.2331628169706605

For values of best alpha = 0.01 The test log loss is: 1.183924618014031

```
In [128]: clf = MultinomialNB(alpha=alpha[best_alpha])
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid",cv=lone)
    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 estimate
    s
```







Important features of predicted points

```
test point index = 1
no feature = 100
predicted cls = sig clf.predict(test x onehotCoding[test point index].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCodi")
ng[test point index]),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: 1
 Predicted Class Probabilities: [[0.5939 0.0429 0.0144 0.1861 0.036 0.0344 0.0852 0.0045 0.0026]]
 Actual Class: 1
 7 Text feature [one] present in test data point [True]
 10 Text feature [results] present in test data point [True]
 11 Text feature [function] present in test data point [True]
 12 Text feature [loss] present in test data point [True]
 13 Text feature [protein] present in test data point [True]
 14 Text feature [two] present in test data point [True]
 15 Text feature [therefore] present in test data point [True]
 16 Text feature [role] present in test data point [True]
 17 Text feature [table] present in test data point [True]
 18 Text feature [type] present in test data point [True]
 19 Text feature [region] present in test data point [True]
 20 Text feature [large] present in test data point [True]
```

```
21 Text feature [also] present in test data point [True]
22 Text feature [however] present in test data point [True]
23 Text feature [functions] present in test data point [True]
25 Text feature [using] present in test data point [True]
26 Text feature [possible] present in test data point [True]
27 Text feature [used] present in test data point [True]
28 Text feature [affect] present in test data point [True]
29 Text feature [gene] present in test data point [True]
30 Text feature [either] present in test data point [True]
31 Text feature [determined] present in test data point [True]
32 Text feature [discussion] present in test data point [True]
33 Text feature [25] present in test data point [True]
35 Text feature [specific] present in test data point [True]
37 Text feature [well] present in test data point [True]
38 Text feature [wild] present in test data point [True]
39 Text feature [binding] present in test data point [True]
40 Text feature [control] present in test data point [True]
41 Text feature [may] present in test data point [True]
44 Text feature [following] present in test data point [True]
45 Text feature [three] present in test data point [True]
46 Text feature [whether] present in test data point [True]
47 Text feature [dna] present in test data point [True]
48 Text feature [containing] present in test data point [True]
49 Text feature [four] present in test data point [True]
50 Text feature [data] present in test data point [True]
52 Text feature [human] present in test data point [True]
54 Text feature [present] present in test data point [True]
55 Text feature [deletion] present in test data point [True]
56 Text feature [expression] present in test data point [True]
57 Text feature [defined] present in test data point [True]
59 Text feature [performed] present in test data point [True]
60 Text feature [important] present in test data point [True]
61 Text feature [shown] present in test data point [True]
62 Text feature [result] present in test data point [True]
63 Text feature [addition] present in test data point [True]
64 Text feature [effect] present in test data point [True]
65 Text feature [although] present in test data point [True]
67 Text feature [several] present in test data point [True]
68 Text feature [10] present in test data point [True]
```

```
69 Text feature [similar] present in test data point [True]
70 Text feature [suggest] present in test data point [True]
71 Text feature [30] present in test data point [True]
73 Text feature [identify] present in test data point [True]
75 Text feature [within] present in test data point [True]
76 Text feature [observed] present in test data point [True]
77 Text feature [fig] present in test data point [True]
78 Text feature [mutations] present in test data point [True]
79 Text feature [sufficient] present in test data point [True]
80 Text feature [studies] present in test data point [True]
81 Text feature [indicate] present in test data point [True]
82 Text feature [example] present in test data point [True]
83 Text feature [corresponding] present in test data point [True]
84 Text feature [mutation] present in test data point [True]
85 Text feature [together] present in test data point [True]
86 Text feature [37] present in test data point [True]
87 Text feature [first] present in test data point [True]
88 Text feature [15] present in test data point [True]
92 Text feature [essential] present in test data point [True]
93 Text feature [whereas] present in test data point [True]
95 Text feature [single] present in test data point [True]
98 Text feature [involved] present in test data point [True]
99 Text feature [identified] present in test data point [True]
Out of the top 100 features 74 are present in query point
```

Logistic Regression with Class Balancing

Hyperparameter Tuning

```
alpha = [10**i for i in range(-6,5) ]
    cv_log_error_array = []
    ior i in alpha:
        print("for alpha =", i)
        clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='log', rand
    om_state=42)
```

```
clf fit(train x onehotCoding, train y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=5)
    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(class weight='balanced', alpha=alpha[best alpha, penalty='l2', loss=
'log', random state=42)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=5)
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 los
```

```
s(y train, predict y, labels=clf.classes , eps=le-15))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss i
s:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss
(y test, predict y, labels=clf.classes , eps=1e-15))
 for alpha = 1e-06
 Log Loss: 1.1833372846150654
 for alpha = 1e-05
 Log Loss: 1.081871226987801
 for alpha = 0.0001
 Log Loss: 1.0454118043451743
 for alpha = 0.001
 Log Loss: 1.0792975068099502
 for alpha = 0.01
```

Log Loss: 1.2325664282406343

Log Loss: 1.6713610997408757

Log Loss: 1.8338267436569837

Log Loss: 1.851506095921084

Log Loss: 1.8534581553710916

Log Loss: 1.8531024977108297

Log Loss: 1.8975771018736085

for alpha = 0.1

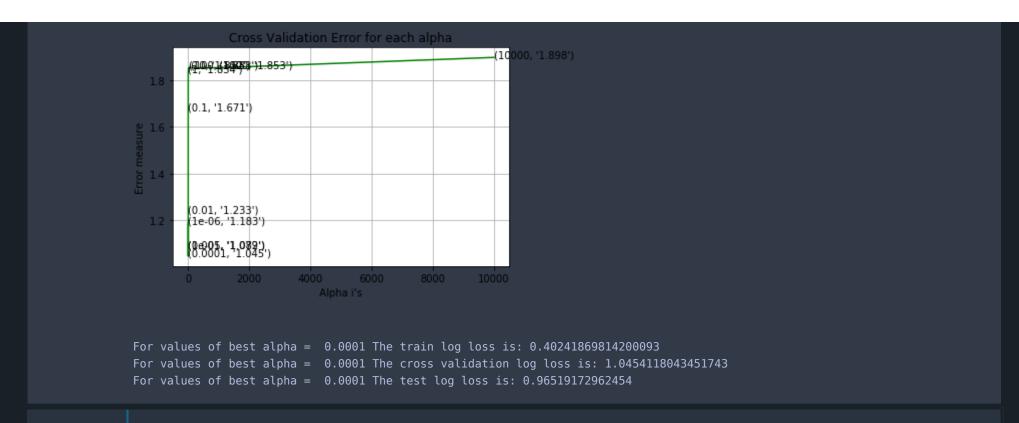
for alpha = 1

for alpha = 10

for alpha = 100

for alpha = 1000

for alpha = 10000



Testing on best Hyperparameter





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



Important Features of Predicted point

```
In [146]: test_point_index = 10
    no_feature = 100
    predicted_cls = sig_clf.predict(test_x_onehotCoding[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[test_point_index]),4))
    print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
```

Logistic regression without class balancing

Hyperparameter Tuning

```
ax.plot(alpha, cv log error array,c='q')
for i, txt in enumerate(np.round(cv log error array,3)):
    ax.annotate((alpha[i], str(txt)), (alpha[i],cv log error array[i]))
plt grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier( alpha=alpha[best alpha], penalty='l2', loss='log', random state=42)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=5)
sig clf fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
nrint('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_los
s(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 i
s:",log_loss(y_cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss
(y test, predict y, labels=clf.classes , eps=1e-15))
 for alpha = 1e-06
 Log Loss: 1.1559549264282034
 for alpha = 1e-05
 Log Loss: 1.1149171483211784
 for alpha = 0.0001
 Log Loss: 1.0712633464177883
```

for alpha = 0.001Log Loss: 1.1403290818739777 for alpha = 0.01Log Loss: 1.3889956724146117 for alpha = 0.1Log Loss: 1.7672218790771852 for alpha = 1Log Loss: 1.8565490594889116 for alpha = 10Log Loss: 1.870332384337331 for alpha = 100Log Loss: 1.871927143298842 for alpha = 1000 Log Loss: 1.8736052213365837 for alpha = 10000Log Loss: 1.8286287881278562

Cross Validation Error for each alpha



For values of best alpha = 0.0001 The train log loss is: 0.3920800535702973

For values of best alpha = 0.0001 The cross validation log loss is: 1.0712633464177883

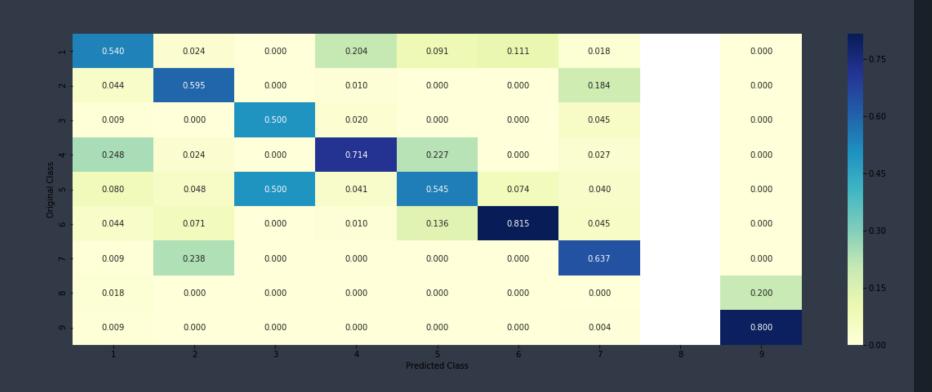
For values of best alpha = 0.0001 The test log loss is: 0.9783379895169934

Testing on Best Hyperparameter

```
In [149]:
    clf = SGDClassifier( alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid",cv=hone)
    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 estimate
    s
    print("Log_Loss:",log_loss(cv_y, sig_clf_probs))
    noint("Number of missclassified point:", np.count_nonzero((sig_clf.predict(cv_x_onehotCoding) - cv_y))/cv_y.shape[0])
    plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray()))
```



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



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



```
In [151]: test_point_index = 200
    no_feature = 100
    predicted_cls = sig_clf.predict(test_x_onehotCoding[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[test_point_index]),4))
    print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
```

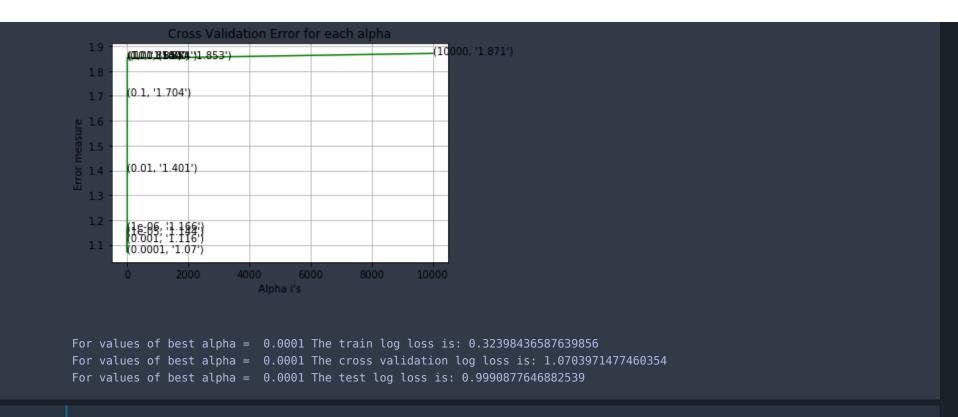
```
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test point index],test_df['Gene'].
iloc[test point index], test df['Variation'].iloc[test point index], no feature)
 Predicted Class: 7
 Predicted Class Probabilities: [[1.040e-02 6.000e-03 7.300e-03 5.000e-03 2.810e-02 3.200e-03 9.379e-01
   2.000e-03 1.000e-04]]
 Actual Class : 7
 15 Text feature [downstream] present in test data point [True]
 27 Text feature [activate] present in test data point [True]
 35 Text feature [activation] present in test data point [True]
 38 Text feature [activated] present in test data point [True]
 41 Text feature [constitutive] present in test data point [True]
 44 Text feature [insertion] present in test data point [True]
 71 Text feature [ras] present in test data point [True]
 77 Text feature [activating] present in test data point [True]
 80 Text feature [versus] present in test data point [True]
 96 Text feature [overexpression] present in test data point [True]
 Out of the top 100 features 10 are present in query point
```

Linear Support Vector Machine

```
alpha = [10**i for i in range(-6,5) ]
    cv_log_error_array = []
    in alpha:
        print("for alpha =", i)
         clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='hinge', ra
        ndom_state=42)
        clf.fit(train_x_onehotCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid",cv=5)
        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(class weight='balanced', alpha=alpha[best alpha], penalty='l2', loss
='hinge', random state=42)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=5)
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 los
s(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 i
s:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
```

```
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss
(y_test, predict_y, labels=clf.classes_, eps=1e-15))
 for alpha = 1e-06
 Log Loss: 1.1659292412707971
 for alpha = 1e-05
 Log Loss: 1.1442115091152125
 for alpha = 0.0001
 Log Loss: 1.0703971477460354
 for alpha = 0.001
 Log Loss: 1.1157960521419852
 for alpha = 0.01
 Log Loss: 1.400609694723615
 for alpha = 0.1
 Log Loss: 1.7035406847783277
 for alpha = 1
 Log Loss: 1.85386080399216
 for alpha = 10
 Log Loss: 1.8538620745497503
 for alpha = 100
 Log Loss: 1.8538621739712606
 for alpha = 1000
 Log Loss: 1.8529450409693369
 for alpha = 10000
 Log Loss: 1.8710899229375983
```



Testing on best Hyperparameter

```
In [154]: clf = SGDClassifier(class_weight='balanced' ,alpha=alpha[best_alpha], penalty='l2', loss
='hinge', random_state=42)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid",cv="lone)
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 estimate
s
print("Log_Loss :",log_loss(cv_y, sig_clf_probs))
print("Number of missclassified point :", np.count_nonzero((sig_clf.predict(cv_x_onehotCoding))
```





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



Important features for predicted point

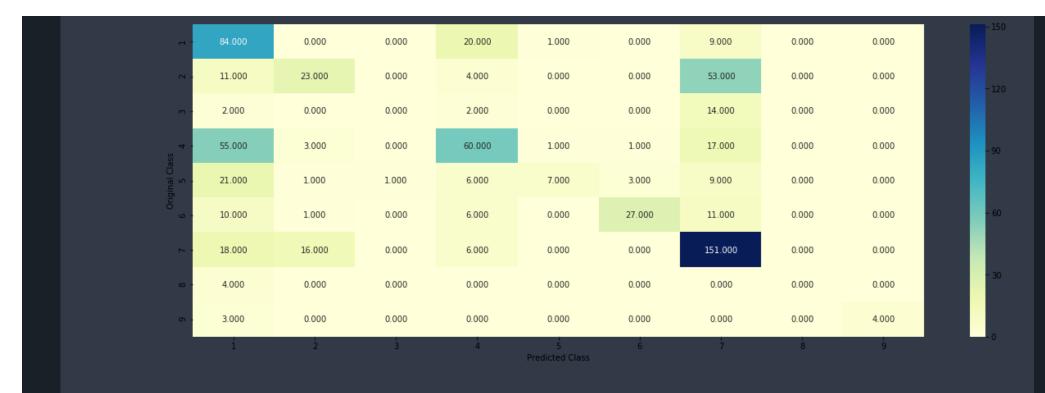
```
In [157]: test_point_index = 500
    no_feature = 100
    predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index].reshape(1,-1))
    print("Predicted Class :", predicted_cls[0])
    print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
    print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
```

Random Forest Classifier

```
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[in (best alpha/2)], criterion='gini', ma
x depth=max depth[ini(best alpha%)], random state=42, n jobs=-1)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv =\noic \]
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 i
s:",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 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 i
s:",log loss(y test, predict y, labels=clf.classes , eps=1e-15))
 for n estimators = 100 and max depth = 5
 Log Loss: 1.2541660340473217
 for n estimators = 100 and max depth = 10
 Log Loss: 1.2596999017093822
 for n estimators = 200 and max depth = 5
 Log Loss: 1.2530940065971095
 for n_{estimators} = 200 and max depth = 10
 Log Loss: 1.2570530443599808
 for n estimators = 500 and max depth = 5
 Log Loss: 1.2447175777923838
 for n estimators = 500 and max depth = 10
 Log Loss: 1.2520506545712338
 for n estimators = 1000 and max depth = 5
 Log Loss: 1.2356188827440346
 for n estimators = 1000 and max depth = 10
 Log Loss: 1.2529955421254342
 for n estimators = 2000 and max depth = 5
 Log Loss: 1.2356419291049852
```

```
for n_estimators = 2000 and max depth = 10
Log Loss : 1.252482517148329
For values of best estimator = 1000 The train log loss is: 0.8568784269766475
For values of best estimator = 1000 The cross validation log loss is: 1.2356188827440346
For values of best estimator = 1000 The test log loss is: 1.2043254095369837
```

Testing on best Hyperparameter



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



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



Feature importance of predicted point

```
In [167]: test_point_index = 120
    no_feature = 100
    predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index].reshape(1,-1))
    indin ("Predicted Class :", predicted_cls[0])
    indin ("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
    indic ("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.feature_importances_)
    indices = np.argsort(-clf.feature_importances_)
    indices = np.argsort(-clf.feature_importances_)
```

```
f['Gene'].iloc[test point index], test df['Variation'].iloc[test point index], no feature
 Predicted Class: 2
 Predicted Class Probabilities: [[0.0226 0.562 0.0099 0.0208 0.0278 0.0253 0.326 0.0042 0.0015]]
 Actual Class : 2
 O Text feature [kinase] present in test data point [True]
 1 Text feature [activating] present in test data point [True]
 2 Text feature [tyrosine] present in test data point [True]
 5 Text feature [activation] present in test data point [True]
 6 Text feature [treatment] present in test data point [True]
 7 Text feature [phosphorylation] present in test data point [True]
 8 Text feature [function] present in test data point [True]
 9 Text feature [loss] present in test data point [True]
 12 Text feature [activated] present in test data point [True]
 13 Text feature [oncogenic] present in test data point [True]
 21 Text feature [akt] present in test data point [True]
 22 Text feature [cells] present in test data point [True]
 23 Text feature [signaling] present in test data point [True]
 24 Text feature [growth] present in test data point [True]
 28 Text feature [cell] present in test data point [True]
 29 Text feature [therapy] present in test data point [True]
 31 Text feature [protein] present in test data point [True]
 35 Text feature [kinases] present in test data point [True]
 43 Text feature [oncogene] present in test data point [True]
 46 Text feature [months] present in test data point [True]
 48 Text feature [expression] present in test data point [True]
 51 Text feature [drug] present in test data point [True]
 53 Text feature [patients] present in test data point [True]
 54 Text feature [survival] present in test data point [True]
 56 Text feature [downstream] present in test data point [True]
 58 Text feature [inhibition] present in test data point [True]
 60 Text feature [treated] present in test data point [True]
 63 Text feature [dna] present in test data point [True]
 65 Text feature [expressing] present in test data point [True]
 66 Text feature [imatinib] present in test data point [True]
 68 Text feature [mapk] present in test data point [True]
 73 Text feature [response] present in test data point [True]
```

```
75 Text feature [clinical] present in test data point [True]
76 Text feature [resistance] present in test data point [True]
82 Text feature [advanced] present in test data point [True]
84 Text feature [ic50] present in test data point [True]
85 Text feature [inhibited] present in test data point [True]
87 Text feature [metastatic] present in test data point [True]
88 Text feature [assays] present in test data point [True]
90 Text feature [sensitivity] present in test data point [True]
91 Text feature [lines] present in test data point [True]
92 Text feature [harboring] present in test data point [True]
99 Text feature [partial] present in test data point [True]
0ut of the top 100 features 43 are present in query point
```

Stacking the models

```
clf1 = SGDClassifier(alpha=0.0001, penalty='12', loss='log', class_weight='balanced', ra
ndom_state=0)
clf1.fit(train_x_onehotCoding, train_y)
sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid",cv=lons)

clf2 = SGDClassifier(alpha=.0001, penalty='l2', loss='hinge', class_weight='balanced', r
andom_state=0)
clf2.fit(train_x_onehotCoding, train_y)
sig_clf2 = CalibratedClassifierCV(clf2, method="sigmoid",cv=lone)

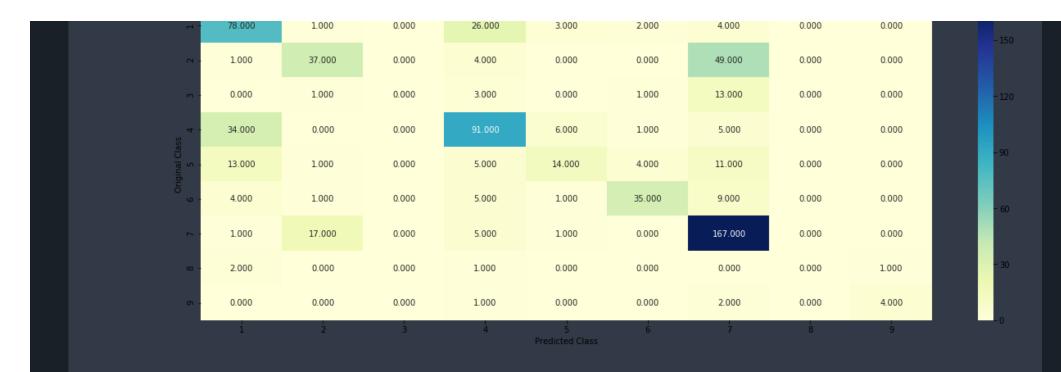
clf3 = MultinomialNB(alpha=0.01)
clf3.fit(train_x_onehotCoding, train_y)
sig_clf3 = CalibratedClassifierCV(clf3, method="sigmoid",cv=lone)

sig_clf1.fit(train_x_onehotCoding, train_y)
sig_clf3 = CalibratedClassifierCV(clf3, method="sigmoid",cv=lone)
```

```
cv x onehotCoding))))
sig clf2 fit(train x onehotCoding, train y)
print("Support vector machines : Log Loss: %0.2f" % (log loss(cv y, sig clf2.predict pro
ba(cv x onehotCoding))))
sig clf3 fit(train x onehotCoding, train y)
print("Naive Bayes : Log Loss: %0.2f" % (log loss(cv y, sig clf3.predict proba(cv x oneh)
otCoding))))
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 classifie
r=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 lo
ss(cv_y, sclf.predict proba(cv x onehotCoding))))
    log error =log loss(cv y, sclf predict proba(cv x onehotCoding))
    best alpha > log error:
         best alpha = log error
 Logistic Regression : Log Loss: 1.04
 Support vector machines : Log Loss: 1.07
 Naive Bayes : Log Loss: 1.24
 Stacking Classifer: for the value of alpha: 0.000100 Log Loss: 2.171
 Stacking Classifer: for the value of alpha: 0.001000 Log Loss: 1.980
 Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.398
 Stacking Classifer: for the value of alpha: 0.100000 Log Loss: 1.165
 Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.418
 Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.871
```

Testing on the best Hyperparameter

```
lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig clf1, sig clf2, sig clf3], meta classifier=lr
, use probas=True)
sclf fit(train x onehotCoding, train y)
log error = log loss(test y, sclf.predict proba(test x onehotCoding))
print("Log loss (train) on the stacking classifier :",log error)
log error = log loss(test y, sclf.predict proba(test x onehotCoding))
print("Log loss (CV) on the stacking classifier :",log_error)
log error = log loss(test y, sclf.predict proba(test x onehotCoding))
print("Log loss (test) on the stacking classifier :",log error)
print("Number of missclassified point :", np.count nonzero((sclf.predict(test x onehotCo
ding) - test y))/test y shape[0])
plot confusion matrix(test y=test y, predict y=sclf.predict(test x onehotCoding))
 Log loss (train) on the stacking classifier : 1.1132412722560951
 Log loss (CV) on the stacking classifier: 1.1132412722560951
 Log loss (test) on the stacking classifier: 1.1132412722560951
 Number of missclassified point: 0.3593984962406015
  ----- Confusion matrix ------
```



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



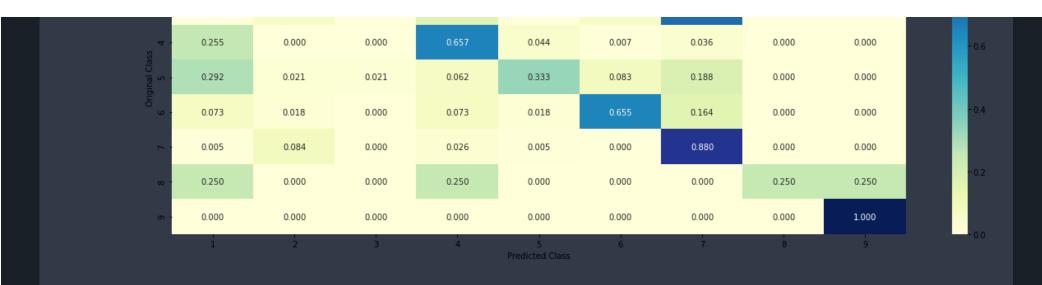


Voting Classifier

```
vclf = VotingClassifier(estimators=[('lr', sig clf1), ('svc', sig clf2), ('rf', sig clf3)
)], voting='soft')
vclf fit(train x onehotCoding, train y)
print("Log loss (train) on the VotingClassifier :", log loss(train y, vclf.predict proba
(train x onehotCoding)))
print("Log loss (CV) on the VotingClassifier :", log loss(cv y, vclf.predict proba(cv x)
onehotCoding)))
print("Log loss (test) on the VotingClassifier :", log loss(test y, vclf.predict proba(t
est x onehotCoding)))
print("Number of missclassified point :", np.count nonzero((vclf.predict(test x onehotCo
ding) - test y))/test y.shape[0])
plot confusion matrix(test y=test y, predict y=vclf.predict(test x onehotCoding))
 Log loss (train) on the VotingClassifier: 0.45087866459950166
 Log loss (CV) on the VotingClassifier: 1.0634424403380565
 Log loss (test) on the VotingClassifier: 1.0035931814918881
 Number of missclassified point: 0.34887218045112783
 ----- Confusion matrix ------
```







2 Applying Logistic Regression to count Vectorizer inclusing bigrams and unigrams

```
text_vectorizer = CountVectorizer(ngram_range=(1,2),min_df=3,max_features=50000)
train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()

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

# zip(list(text_features),text_fea_counts) will zip a word with its number of times it o ccured
text_fea_dict = dict(ap(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 : 50000
train text feature onehotCoding = normalize(train text feature onehotCoding, axis=0)
test text feature onehotCoding = text vectorizer.transform(test df['TEXT'])
test text feature onehotCoding = normalize(test text feature onehotCoding, axis=0)
cv text feature onehotCoding = text vectorizer.transform(cv df['TEXT'])
cv text feature onehotCoding = normalize(cv text feature onehotCoding, axis=0)
train gene var onehotCoding = hstack((train gene feature onehotCoding,train variation fe
ature onehotCoding))
test gene var onehotCoding = hstack((test gene feature onehotCoding,test variation featu
re onehotCoding))
cv gene var onehotCoding = hstack((cv gene feature onehotCoding,cv variation feature one
hotCoding))
train x onehotCoding = hstack((train gene var onehotCoding, train text feature onehotCod
ing)).tocsr()
train y = np.array(list(train df['Class']))
test x onehotCoding = hstack((test gene var onehotCoding, test text feature onehotCoding
)).tocsr()
test y = np.array(list(test df['Class']))
```

```
cv x onehotCoding = hstack((cv gene var onehotCoding, cv text feature onehotCoding)).toc
sr()
cv y = np.array(list(cv df['Class']))
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train x onehotCod
ing shape)
print("(number of data points * number of features) in test data = ", test x onehotCodin
g shape)
print("(number of data points * number of features) in cross validation data =", cv x on
ehotCoding shape)
 One hot encoding features :
 (number of data points * number of features) in train data = (2124, 52180)
 (number of data points * number of features) in test data = (665, 52180)
 (number of data points * number of features) in cross validation data = (532, 52180)
```

Logistic Regression

```
alpha = [10**i for i in range(-6,5) ]
    cv_log_error_array = []
    for i in alpha:
        print("for alpha =", i)
        clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='l2', loss='log', rand
    om_state=42)
        clf.fit(train_x_onehotCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid",cv=5)
```

```
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(class weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss
='log', random state=42)
clf fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=5)
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 los
s(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 i
s:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=le-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss
(y_test, predict_y, labels=clf.classes_, eps=le-15))

for alpha = le-06
Log Loss : 1.312663941693749
for alpha = le-05
Log Loss : 1.3247906772361884
for alpha = 0.0001
Log Loss : 1.1669836354987388
for alpha = 0.001
```

Log Loss : 1.0972744832951915

Log Loss: 1.1089677254632957

Log Loss: 1.4488449769734313

Log Loss : 1.667153066145188

Log Loss: 1.7063336201869346

Log Loss: 1.7109424308321661

Log Loss: 1.7114709100427037

Log Loss: 1.7109768627363455

for alpha = 0.01

for alpha = 0.1

for alpha = 1

for alpha = 10

for alpha = 100

for alpha = 1000

for alpha = 10000

Cross Validation Error for each alpha (1000:1/1000011)1 7111) (10000, '1.711') (1. '1.667') (0.1, '1.449') 16:08: 11:3251) (0.0001, '1.167') 0.084,131097 For values of best alpha = 0.001 The train log loss is: 0.5411039563708149 For values of best alpha = 0.001 The cross validation log loss is: 1.0972744832951915 For values of best alpha = 0.001 The test log loss is: 1.0145501408978073 clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='l2', loss ='log', random state=42) clf fit(train x onehotCoding, train y) sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=None) sig clf fit(train x onehotCoding, train y) sig clf probs = sig clf.predict proba(test x onehotCoding) print("Log Loss :",log_loss(test y, sig clf probs)) print("Number of missclassified point :", np.count nonzero((sig clf.predict(test x oneho)) tCoding) - test y))/test y.shape[0]) plot confusion matrix(test y, sig clf.predict(test x onehotCoding toarray()))





Important features for predicted points

```
def get impfeature names(indices, text, gene, var, no features):
   gene count vec = CountVectorizer()
    var count vec = CountVectorizer()
    text count vec = TfidfVectorizer(ngram range=(1,2),min df=3,max features=50000)
    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 = ben(var count vec.get feature names())
   word present = 0
   for i,v in enumerate(indices):
       (v < fea1 len):
           word = gene vec.get feature names()[v]
           yes no = True if word == gene else False
            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
            yes no:
                word present += 1
               print(i, "variation feature [{}] present in test data point [{}]".format
(word, yes no))
```

```
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 quer
y point")
test point index = 100
no feature = 1000
predicted cls = sig clf.predict(test x onehotCoding[test point index].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCodi
ng[test point index]),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: [[0.3212 0.0471 0.0059 0.4865 0.0192 0.008 0.1005 0.009 0.0025]]
 Actual Class: 4
 186 Text feature [suppressor] present in test data point [True]
 279 Text feature [dn] present in test data point [True]
 427 Text feature [phosphatases] present in test data point [True]
 437 Text feature [degradation] present in test data point [True]
 609 Text feature [microscopy] present in test data point [True]
 669 Text feature [pcmv] present in test data point [True]
```

```
857 Text feature [tgfbr1] present in test data point [True]
888 Text feature [bsa] present in test data point [True]
915 Text feature [pcdna3] present in test data point [True]
928 Text feature [lacks] present in test data point [True]
931 Text feature [tagged] present in test data point [True]
965 Text feature [tgf] present in test data point [True]
0ut of the top 1000 features 12 are present in query point
```

Experimienting some feature engineering techniques

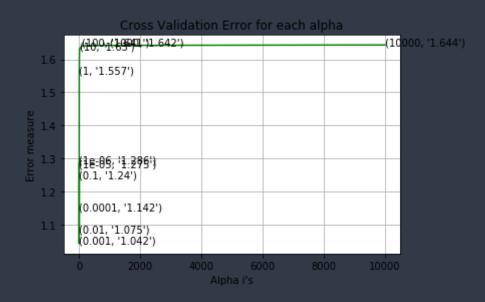
Combining thid final Bow vectorizer with unigram and bigrams and also the response coding feature and applying balanced Logistic Regression

```
t("Total number of unique words in train data :", len(tfidf train text features))
tfidf train text feature onehotCoding = normalize(tfidf train text feature onehotCoding,
 axis=0)
# we use the same vectorizer that was trained on train data
tfidf test text feature onehotCoding = tfidf text vectorizer.transform(test df['TEXT'])
tfidf test text feature onehotCoding = normalize(tfidf test text feature onehotCoding, a
xis=0)
tfidf cv text feature onehotCoding = tfidf text vectorizer.transform(cv df['TEXT'])
# don't forget to normalize every feature
tfidf cv text feature onehotCoding = normalize(tfidf cv text feature onehotCoding, axis=
 Total number of unique words in train data: 53645
train x onehotCoding = hstack((train x onehotCoding,tfidf train text feature onehotCodin
g)) tocsr()
test x onehotCoding = hstack((test x onehotCoding, tfidf test text feature onehotCoding
)) tocsr()
cv x onehotCoding = hstack((cv x onehotCoding, tfidf cv text feature onehotCoding)).tocs
r()
train x onehotCoding = hstack((train x onehotCoding,train x responseCoding)).tocsr()
test x onehotCoding = hstack((test x onehotCoding, test x responseCoding)).tocsr()
cv x onehotCoding = hstack((cv x onehotCoding, cv x responseCoding)).tocsr()
```

```
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train x onehotCod
ing shape)
print("(number of data points * number of features) in test data = ", test x onehotCodin
g.shape)
print("(number of data points * number of features) in cross validation data =", cv x on
ehotCoding shape)
 One hot encoding features :
 (number of data points * number of features) in train data = (2124, 105852)
 (number of data points * number of features) in test data = (665, 105852)
 (number of data points * number of features) in cross validation data = (532, 105852)
alpha = [10**i \text{ for } i \text{ in range}(-6.5)]
cv log error array = []
for i in alpha:
   print("for alpha =", i)
    clf = SGDClassifier(class weight='balanced', alpha=i, penalty='l2', loss='log', rand
om state=42)
    clf fit(train x onehotCoding, train y)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=3)
    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], ser(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='l2', loss
='log', random state=42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid",cv=3)
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 los
s(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 i"
s:",log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss
(y test, predict y, labels=clf.classes , eps=1e-15))
 for alpha = 1e-06
 Log Loss: 1.2855738303938442
```

for alpha = 1e-05Log Loss: 1.2750659790760819 for alpha = 0.0001Log Loss: 1.1418386735464319 for alpha = 0.001Log Loss : 1.041743220913038 for alpha = 0.01Log Loss: 1.0753196088837385 for alpha = 0.1Log Loss : 1.2398815001593497 for alpha = 1Log Loss: 1.5569954355547513 for alpha = 10Log Loss: 1.630400609890844 for alpha = 100 Log Loss : 1.64094499589639 for alpha = 1000 Log Loss: 1.6421676663646674 for alpha = 10000Log Loss: 1.6435043726220684

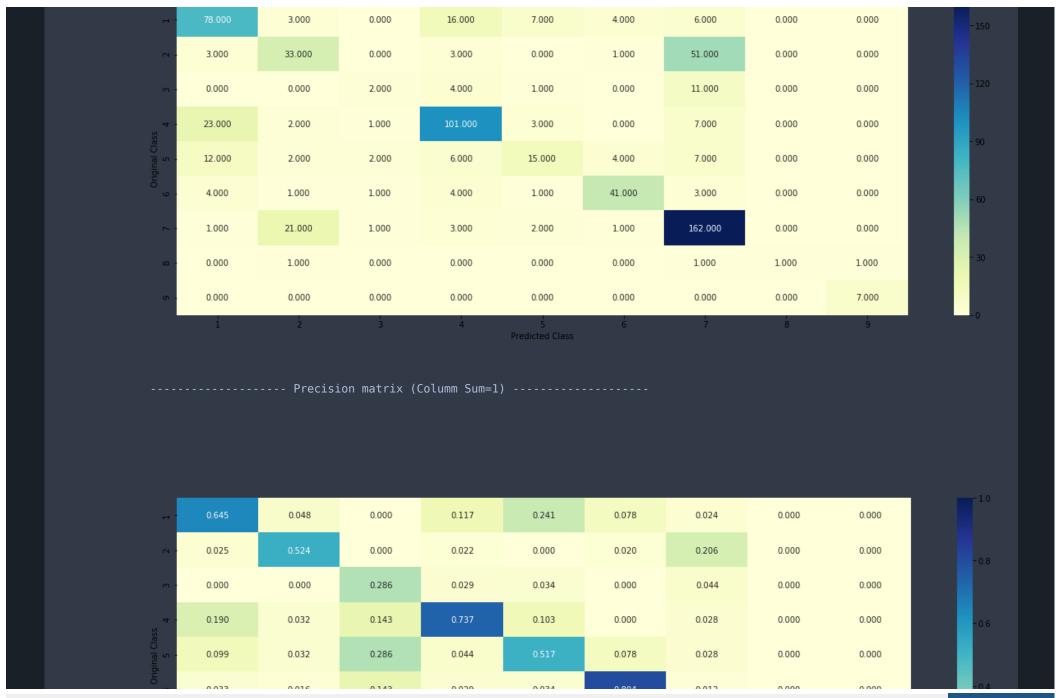


```
For values of best alpha = 0.001 The train log loss is: 0.5403156525032562

For values of best alpha = 0.001 The cross validation log loss is: 1.041743220913038

For values of best alpha = 0.001 The test log loss is: 0.9706049728214963
```

Here we can see that we are able to reduce the test log_loss to 0.97060 less than 1





Conclusion

This model is the best model we have got with test logg_loss of 0.97 and wrong prediction percentage of 33%