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

/opt/conda/lib/python3.7/site-packages/sklearn/utils/deprecation.py:143: FutureWarning: The sklearn.metrics.c lassification module is deprecated in version 0.22 and will be removed in version 0.24. The corresponding cl asses / functions should instead be imported from sklearn.metrics. Anything that cannot be imported from sklearn.metrics is now part of the private API.

warnings.warn(message, FutureWarning)

```
In [2]: # This Python 3 environment comes with many helpful analytics libraries installed
        # It is defined by the kaggle/python Docker image: https://github.com/kaggle/docker-python
        # For example, here's several helpful packages to load
        import numpy as np # linear algebra
        import pandas as pd # data processing, CSV file I/O (e.g. pd.read csv)
        # Input data files are available in the read-only "../input/" directory
        # For example, running this (by clicking run or pressing Shift+Enter) will list all files under the input dir
        ectory
        import os
        for dirname, , filenames in os.walk('/kaggle/input'):
            for filename in filenames:
                print(os.path.join(dirname, filename))
        # You can write up to 5GB to the current directory (/kaggle/working/) that gets preserved as output when you
         create a version using "Save & Run All"
        # You can also write temporary files to /kaggle/temp/, but they won't be saved outside of the current session
        /kaggle/input/msk-redefining-cancer-treatment/stage2 test variants.csv.7z
        /kaggle/input/msk-redefining-cancer-treatment/stage2 sample submission.csv.7z
        /kaggle/input/msk-redefining-cancer-treatment/stage 2 private solution.csv.7z
        /kaggle/input/msk-redefining-cancer-treatment/training text.zip
        /kaggle/input/msk-redefining-cancer-treatment/stage1 solution filtered.csv.7z
        /kaggle/input/msk-redefining-cancer-treatment/test text.zip
        /kaggle/input/msk-redefining-cancer-treatment/stage2 test text.csv.7z
        /kaggle/input/msk-redefining-cancer-treatment/training variants.zip
        /kaggle/input/msk-redefining-cancer-treatment/test variants.zip
In [3]: import pandas as pd
        data = pd.read csv('../input/msk-redefining-cancer-treatment/training variants.zip')
        data text =pd.read csv("../input/msk-redefining-cancer-treatment/training text.zip",sep="\|\|",engine="pytho
        n",names=["ID","TEXT"],skiprows=1)
```

In [4]: data.head()

Out[4]:

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

In [5]: data_text.head()

Out[5]:

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

```
In [6]: print(data.info())
        print(data text.info())
        <class 'pandas.core.frame.DataFrame'>
        RangeIndex: 3321 entries, 0 to 3320
        Data columns (total 4 columns):
                        Non-Null Count Dtype
             Column
             ID
                        3321 non-null
         0
                                       int64
         1
             Gene
                        3321 non-null
                                        object
         2
             Variation 3321 non-null
                                        object
             Class
         3
                        3321 non-null
                                        int64
        dtypes: int64(2), object(2)
        memory usage: 103.9+ KB
        None
        <class 'pandas.core.frame.DataFrame'>
        RangeIndex: 3321 entries, 0 to 3320
        Data columns (total 2 columns):
             Column Non-Null Count Dtype
         0
             ID
                     3321 non-null
                                     int64
                                     object
             TEXT
                     3316 non-null
        dtypes: int64(1), object(1)
        memory usage: 52.0+ KB
        None
```

preprocessing the text data

```
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 = ""
                # replace every special char with space
                total text = re.sub('[^a-zA-Z0-9\n]', ' ', total_text)
                # replace multiple spaces with single space
                total_text = re.sub('\s+',' ', total_text)
                # converting all the chars into lower-case.
                total text = total text.lower()
                for word in total text.split():
                # if the word is a not a stop word then retain that word from the data
                    if not word in stop words:
                         string += word + " "
                data text[column][index] = string
In [8]: | #text processing stage.
        start time = time.clock()
        for index, row in data text.iterrows():
            if type(row['TEXT']) is str:
                nlp preprocessing(row['TEXT'], index, 'TEXT')
            else:
                print("there is no text description for id:",index)
        print('Time took for preprocessing the text :',time.clock() - start time, "seconds")
        there is no text description for id: 1109
        there is no text description for id: 1277
        there is no text description for id: 1407
        there is no text description for id: 1639
```

Time took for preprocessing the text: 59.15178399999999 seconds

there is no text description for id: 2755

```
In [9]: result = pd.merge(data,data_text,on='ID',how='left')
    result.head()
```

Out[9]:

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

filling null values in text data with gene and variation

```
In [10]: k=result[result.isnull().any(axis=1)]
for row in k.values:
    result['TEXT'][row[0]] = result['Gene'][row[0]]+ ''+ result['Variation'][row[0]]
```

EDA

```
In []:

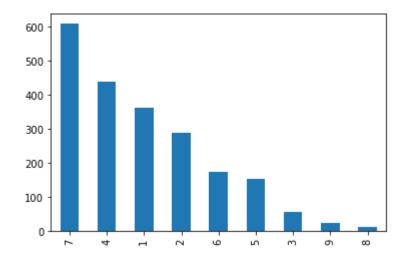
In [11]: # splitting the data into train ,cv,test
    y_true = result['Class']
    #preprocessing Gene and variation ie taking unnecessary spaces and replacing it with just one underscore
    result.Gene = result.Gene.str.replace('\s+',"_")
    result.Variation = result.Variation.str.replace('\s+',"_")
    # splitting dataset into train and test
    X_train,test_df,y_train,y_test=train_test_split(result,y_true,stratify = y_true,test_size=0.2)
    #splitting train data into train and cv
    train_df,cv_df,y_train,y_cv = train_test_split(X_train,y_train,stratify=y_train,test_size=0.2)
```

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

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

In [13]: train_df['Class'].value_counts().plot.bar()

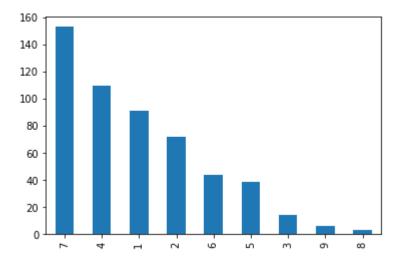
Out[13]: <matplotlib.axes._subplots.AxesSubplot at 0x7f52672613d0>



Here there are more 7th class datapoints

In [14]: cv_df['Class'].value_counts().plot.bar()

Out[14]: <matplotlib.axes._subplots.AxesSubplot at 0x7f5266fe8a50>



so if u look at above graphs we come to notice two things

- 1. data is imbalanced data.
- 2. since we have splitted using startify on class labels the splitting done is same or similar ie, distribution of classes in train,test,cv are almost similar

prediction using a random model

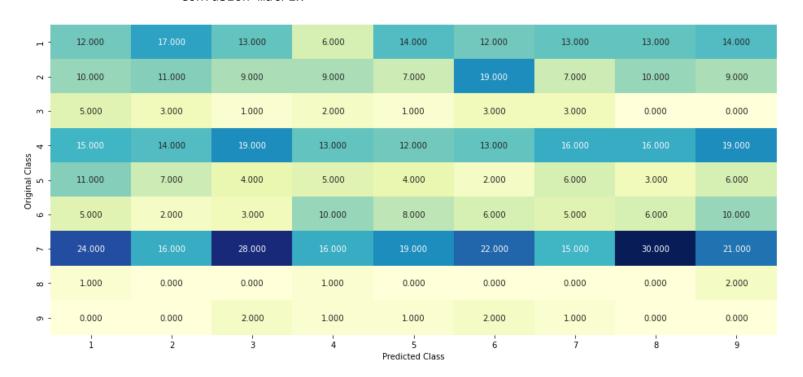
In a 'Random' Model, we generate the NINE class probabilites randomly such that they sum to 1.

```
In [15]: # This function plots the confusion matrices given y i, y i hat.
         def plot confusion_matrix(test_y, predict_y):
             C = confusion matrix(test v, predict v)
             \# C = 9,9 matrix, each cell (i,j) represents number of points of class i are predicted class i
             A = (((C.T)/(C.sum(axis=1))).T)
             #divid each element of the confusion matrix with the sum of elements in that column
             \# C = [[1, 2],
             # [3, 41]
             # C.T = [[1, 3]]
                     [2, 41]
             # C.sum(axis = 1) axis=0 corresonds to columns and axis=1 corresponds to rows in two diamensional array
             # C.sum(axix = 1) = [[3, 7]]
             \# ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
                                         [2/3, 4/711]
             \# ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]]
                                         [3/7, 4/71]
             # sum of row elements = 1
             B = (C/C.sum(axis=0))
             #divid each element of the confusion matrix with the sum of elements in that row
             \# C = [[1, 2],
                   [3, 411]
             # C.sum(axis = 0) axis=0 corresonds to columns and axis=1 corresponds to rows in two diamensional array
             # C.sum(axix = 0) = [[4, 6]]
             \# (C/C.sum(axis=0)) = [[1/4, 2/6],
                                    [3/4, 4/6]]
             labels = [1,2,3,4,5,6,7,8,9]
             # representing A in heatmap format
             print("-"*20, "Confusion matrix", "-"*20)
             plt.figure(figsize=(20,7))
             sns.heatmap(C, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
             plt.xlabel('Predicted Class')
             plt.vlabel('Original Class')
             plt.show()
             print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
             plt.figure(figsize=(20,7))
             sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
```

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

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

```
In [16]: # we need to generate 9 numbers and the sum of numbers should be 1
         # one solution is to genarate 9 numbers and divide each of the numbers by their sum
         # ref: https://stackoverflow.com/a/18662466/4084039
         test data len = test df.shape[0]
         cv data len = cv df.shape[0]
         # we create a output array that has exactly same size as the CV data
         cv predicted y = np.zeros((cv data len,9))
         for i in range(cv data len):
             rand probs = np.random.rand(1,9)
             cv predicted y[i] = ((rand probs/sum(sum(rand probs)))[0])
         print("Log loss on Cross Validation Data using Random Model",log loss(y cv,cv predicted y, eps=1e-15))
         # Test-Set error.
         #we create a output array that has exactly same as the test data
         test predicted y = np.zeros((test data len,9))
         for i in range(test data len):
             rand_probs = np.random.rand(1,9)
             test predicted y[i] = ((rand probs/sum(sum(rand probs)))[0])
         print("Log loss on Test Data using Random Model",log loss(y test,test predicted y, eps=1e-15))
         predicted y =np.argmax(test predicted y, axis=1)
         plot confusion matrix(y test, predicted y+1)
```



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

- 25

- 20

- 15

- 10

- 5

-0



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

- 0.35

- 0.30

- 0.25

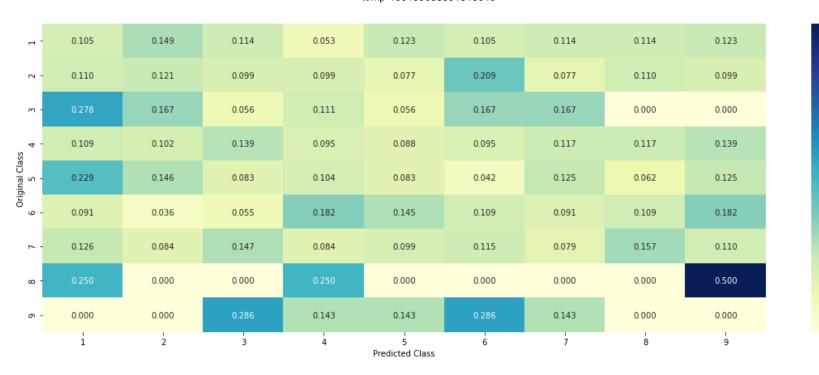
-0.20

-0.15

-0.10

- 0.05

-0.00



univariate analysis

- 0.4

- 0.3

- 0.2

- 0.1

- 0.0

```
In [17]: # code for response coding with Laplace smoothing.
         # alpha: used for laplace smoothing
         # feature: ['gene', 'variation']
         # df: ['train_df', 'test_df', 'cv_df']
         # algorithm
         # -----
         # Consider all unique values and the number of occurances of given feature in train data dataframe
         # build a vector (1*9) , the first element = (number of times it occured in class1 + 10*alpha / number of tim
         e it occurred in total data+90*alpha)
         # av dict is like a look up table, for every gene it store a (1*9) representation of it
         # for a value of feature in df:
         # if it is in train data:
         # we add the vector that was stored in 'qv dict' look up table to 'qv fea'
         # if it is not there is train:
         # we add [1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9] to 'qv fea'
         # return 'av fea'
         # -----
         # get gv fea dict: Get Gene varaition Feature Dict
         def get gv fea dict(alpha, feature, df):
             # value count: it contains a dict like
             # print(train df['Gene'].value counts())
             # output:
             #
                      {BRCA1
                                  174
                       TP53
                                  106
                      EGFR
                                  86
                       BRCA2
                                  75
                      PTEN
                                  69
                      KIT
                                  61
                      BRAF
                                  60
                      ERBB2
                                  47
                       PDGFRA
                                  46
                       ...}
             # print(train df['Variation'].value counts())
             # output:
             # {
             # Truncating Mutations
                                                       63
             # Deletion
                                                       43
             # Amplification
                                                       43
                                                        22
             # Fusions
                                                        3
             # Overexpression
                                                        3
             # E17K
```

```
# Q61L
                                               3
   # S222D
                                               2
   # P130S
                                               2
   # ...
   # }
   value count = train df[feature].value counts()
   # qv dict : Gene Variation Dict, which contains the probability array for each gene/variation
   gv dict = dict()
   # denominator will contain the number of time that particular feature occured in whole data
   for i, denominator in value count.items():
       # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticular class
       # vec is 9 diamensional vector
       vec = []
       for k in range(1,10):
           # print(train df.loc[(train df['Class']==1) & (train df['Gene']=='BRCA1')])
                                           Variation Class
                     ID Gene
           # 2470 2470 BRCA1
                                              S1715C
           # 2486 2486 BRCA1
                                              S1841R
           # 2614 2614 BRCA1
                                                 M1R
                                                          1
           # 2432 2432 BRCA1
                                              L1657P
                                                          1
           # 2567 2567 BRCA1
                                              T1685A
           # 2583 2583 BRCA1
                                              E1660G
                                                          1
           # 2634 2634 BRCA1
                                              W1718L
                                                          1
           # cls cnt.shape[0] will return the number of rows
           cls cnt = train df.loc[(train df['Class']==k) & (train df[feature]==i)]
           # cls cnt.shape[0](numerator) will contain the number of time that particular feature occured in
 whole data
           vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
       # we are adding the gene/variation to the dict as key and vec as value
       gv dict[i]=vec
   return gv dict
# Get Gene variation feature
def get gv feature(alpha, feature, df):
    # print(qv dict)
         {'BRCA1': [0.20075757575757575, 0.037878787878788, 0.0681818181818177, 0.13636363636363635, 0.2
5, 0.193181818181818, 0.0378787878787878, 0.03787878787878, 0.037878787878787878787878,
           'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, 0.27040816326530615, 0.0
```

```
61224489795918366, 0.066326530612244902, 0.051020408163265307, 0.051020408163265307, 0.056122448979591837],
          'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.0681818181818177, 0.068181818181
8177, 0.0625, 0.34659090909090912, 0.0625, 0.056818181818181816],
          'BRCA2': [0.1333333333333333, 0.060606060606060608, 0.060606060606060608, 0.0787878787878782,
0.13939393939394, 0.34545454545454546, 0.060606060606060608, 0.06060606060608, 0.06060606060606060608],
          'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917, 0.46540880503144655, 0.
075471698113207544, 0.062893081761006289, 0.069182389937106917, 0.062893081761006289, 0.062893081761006289],
          'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0.072847682119205295, 0.0
66225165562913912, 0.066225165562913912, 0.27152317880794702, 0.066225165562913912, 0.066225165562913912],
          'BRAF': [0.0666666666666666666, 0.179999999999999, 0.073333333333334, 0.073333333333334, 0.
gv dict = get gv fea dict(alpha, feature, df)
   # value count is similar in get qv fea dict
   value count = train df[feature].value counts()
   # qv fea: Gene variation feature, it will contain the feature for each feature value in the data
   gv fea = []
   # for every feature values in the given data frame we will check if it is there in the train data then we
will add the feature to gv fea
   # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to gv_fea
   for index, row in df.iterrows():
       if row[feature] in dict(value count).keys():
           gv fea.append(gv dict[row[feature]])
       else:
           gv fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
            qv fea.append([-1,-1,-1,-1,-1,-1,-1,-1])
   return gv fea
```

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

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

univariate analysis of gene feature

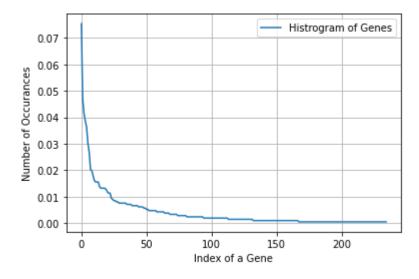
Q1. Gene, What type of feature it is?

Ans. Gene is a categorical variable

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

```
In [18]: | unique_genes = train_df['Gene'].value_counts()
         unique_genes.head(10)
Out[18]: BRCA1
                   160
         TP53
                   100
         EGFR
                    88
         PTEN
                     82
                    77
         BRCA2
         KIT
                    64
         BRAF
                     57
         ALK
                     43
         ERBB2
                    42
         CDKN2A
                     38
         Name: Gene, dtype: int64
```

Ans: There are 235 different categories of genes in the train data, and they are distibuted as follows



Q3. How to featurize this Gene feature?

Ans.there are two ways we can featurize this variable check out this video: <a href="https://www.appliedaicourse.com/course/applied-ai-course-applied-ai-cou

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

```
In [20]: k = time.clock()
         #response-coding of the Gene feature
         # alpha is used for laplace smoothing
         alpha = 1
         # train gene feature
         train_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", train_df))
         # test gene feature
         test gene feature responseCoding = np.array(get gv feature(alpha, "Gene", test df))
         # cross validation gene feature
         cv gene feature responseCoding = np.array(get_gv_feature(alpha, "Gene", cv_df))
         print(time.clock()-k)
         13.441859000000008
In [21]: train gene feature responseCoding.shape
Out[21]: (2124, 9)
In [22]: # one-hot encoding of Gene feature.
         gene vectorizer = CountVectorizer()
         train gene feature onehotCoding = gene vectorizer.fit transform(train df['Gene'])
         test gene feature onehotCoding = gene vectorizer.transform(test df['Gene'])
         cv gene feature onehotCoding = gene vectorizer.transform(cv df['Gene'])
In [23]: train gene feature onehotCoding.shape
Out[23]: (2124, 234)
```

how good is gene feature in predicting yi

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

```
In [24]: | alphavalues = (10 ** x for x in range(-5,5))
         cv log error array=[]
         alphavalueslist = []
         for i in alphavalues:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train gene feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train gene feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv gene feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
             alphavalueslist.append(i)
             print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=
         1e-15))
         fig, ax = plt.subplots()
         ax.plot(alphavalueslist, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alphavalueslist[i],np.round(txt,3)), (alphavalueslist[i],cv log error array[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.vlabel("Error measure")
         plt.show()
         best alpha = np.argmin(cv log error array)
         k = alphavalueslist[best alpha]
         clf = SGDClassifier(alpha=k, penalty='12', loss='log', random_state=42)
         clf.fit(train gene feature onehotCoding, y train)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train gene feature onehotCoding, y train)
         predict y = sig clf.predict proba(train gene feature onehotCoding)
         print('For values of best alpha = ', k, "The train log loss is:",log loss(y train, predict y, labels=clf.clas
         ses, eps=1e-15))
         predict y = sig clf.predict_proba(cv_gene_feature_onehotCoding)
         print('For values of best alpha = ', k, "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 gene feature onehotCoding)
         print('For values of best alpha = ', k, "The test log loss is:",log loss(y test, predict y, labels=clf.classe
         s, eps=1e-15)
```

```
For values of alpha = 1e-05 The log loss is: 1.2117049684254682
For values of alpha = 0.0001 The log loss is: 1.1908227397055235
For values of alpha = 0.001 The log loss is: 1.2378401467277482
For values of alpha = 0.01 The log loss is: 1.3572013524730129
For values of alpha = 0.1 The log loss is: 1.457714046478715
For values of alpha = 10 The log loss is: 1.4874775684765487
For values of alpha = 100 The log loss is: 1.4912783033981398
For values of alpha = 1000 The log loss is: 1.4923078404934584
For values of alpha = 10000 The log loss is: 1.493932150403798
```

Cross Validation Error for each alpha (**(100)**(1**/49902**) 1.492) 1.50 (10000, 1.494) (0.1, 1.458)1.45 1.40 Error measure 0.01, 1.357 1.35 1.30 1.25 0.001, 1.238) 1e-05, 1.212) 1.20 (0.0001, 1.191)2000 4000 6000 0 8000 10000 Alpha i's

```
For values of best alpha = 0.0001 The train log loss is: 0.9985029871072895

For values of best alpha = 0.0001 The cross validation log loss is: 1.1908227397055235

For values of best alpha = 0.0001 The test log loss is: 1.181845666610073
```

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 [25]: print("Q6. How many data points in Test and CV datasets are covered by the ", unique_genes.shape[0], " genes in train dataset?")

test_coverage=test_df[test_df['Gene'].isin(list(set(train_df['Gene'])))].shape[0]

cv_coverage=cv_df[cv_df['Gene'].isin(list(set(train_df['Gene'])))].shape[0]

print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_coverage/test_df.shape[0])*1

00)

print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(cv_coverage/cv_df.shape[0])*1

00)
```

Q6. How many data points in Test and CV datasets are covered by the 235 genes in train dataset? Ans

- 1. In test data 646 out of 665 : 97.14285714285714
- 2. In cross validation data 517 out of 532 : 97.18045112781954

here from above information what we get is.

1. out of 656 gene points in test data 646 of them we have alredy seen them in train data, similarly for test data also

3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it?

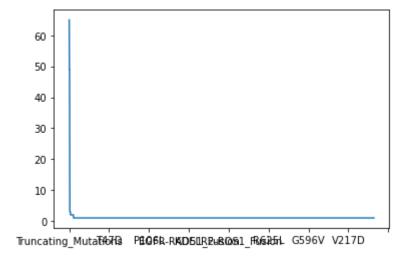
Ans. Variation is a categorical variable

Q8. How many categories are there?

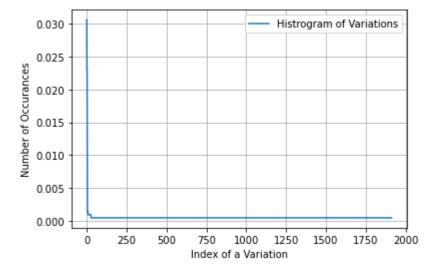
```
In [26]: unique_variations=train_df['Variation'].value_counts()
    print('Number of Unique Variations :', unique_variations.shape[0])
    unique_variations.head(10)
    train_df['Variation'].value_counts().plot()
```

Number of Unique Variations : 1912

Out[26]: <matplotlib.axes._subplots.AxesSubplot at 0x7f5266a70950>



```
In [27]: 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()
```



1. How to featurize this Variation feature?

Ans. There are two ways we can featurize this variable check out this video: <a href="https://www.appliedaicourse.com/course/applied-ai-course-applied-ai-co

One hot Encoding Response coding We will be using both these methods to featurize the Variation Feature

```
In [28]: # alpha is used for Laplace smoothing
    alpha = 1
    # train gene feature
    train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", train_df))
    # test gene feature
    test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", test_df))
    # cross validation gene feature
    cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", cv_df))
```

In [29]: print("train_variation_feature_responseCoding is a converted feature using the response coding method. The sh ape 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 feature: (2124, 9)

```
In [30]: # one-hot encoding of variation feature.
    variation_vectorizer = CountVectorizer()
    train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_df['Variation'])
    test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Variation'])
    cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation'])
```

In [31]: print("train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method. The sha
 pe of Variation feature:", train_variation_feature_onehotCoding.shape)

train_variation_feature_onehotEncoded is converted feature using the onne-hot encoding method. The shape of V ariation feature: (2124, 1940)

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

Let's build a model just like the earlier!

```
In [32]: alpha = [10 ** x for x in range(-5, 1)]
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SG
         DClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, t
         ol=None.
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power
         t=0.5.
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         # predict(X) Predict class labels for samples in X.
         #-----
         # video link:
         #-----
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
             clf.fit(train variation feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train variation feature onehotCoding, v train)
             predict y = sig clf.predict proba(cv variation feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=
         1e-15))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error array[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
```

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

predict_y = sig_clf.predict_proba(train_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_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=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.7064488754244915

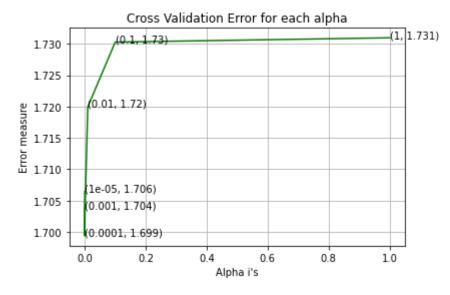
For values of alpha = 0.0001 The log loss is: 1.6993642244269924

For values of alpha = 0.001 The log loss is: 1.7036445792913124

For values of alpha = 0.01 The log loss is: 1.7199632929804176

For values of alpha = 0.1 The log loss is: 1.7302954233640118

For values of alpha = 1 The log loss is: 1.7309817384700747
```



For values of best alpha = 0.0001 The train log loss is: 0.6781213333363376

For values of best alpha = 0.0001 The cross validation log loss is: 1.6993642244269924

For values of best alpha = 0.0001 The test log loss is: 1.7271031183523977

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 [33]: print("Q12. How many data points are covered by total ", unique_variations.shape[0], " genes in test and cros s validation data sets?")
    test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
    cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'])))].shape[0]
    print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_coverage/test_df.shape[0])*1
    00)
    print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(cv_coverage/cv_df.shape[0])*1
    00)
```

Q12. How many data points are covered by total 1912 genes in test and cross validation data sets? Ans

- 1. In test data 60 out of 665 : 9.022556390977442
- 2. In cross validation data 49 out of 532 : 9.210526315789473

Note: variation feature here is not stable across test and train and cv

3.2.3 Univariate Analysis on Text Feature

How many unique words are present in train data?

How are word frequencies distributed?

How to featurize text field?

Is the text feature useful in predicitng y_i?

Is the text feature stable across train, test and CV datasets?

```
In [34]: # cls text is a data frame
         # for every row in data fram consider the 'TEXT'
         # split the words by space
         # make a dict with those words
         # increment its count whenever we see that word
         def extract dictionary paddle(cls text):
             dictionary = defaultdict(int)
             for index, row in cls text.iterrows():
                 for word in row['TEXT'].split():
                     dictionarv[word] +=1
             return dictionary
         import math
         #https://stackoverflow.com/a/1602964
         def get text responsecoding(df):
             text feature responseCoding = np.zeros((df.shape[0],9))
             for i in range(0,9):
                 row index = 0
                 for index, row in df.iterrows():
                     sum_prob = 0
                     for word in row['TEXT'].split():
                          sum prob += math.log(((dict list[i].get(word,0)+10 )/(total dict.get(word,0)+90)))
                     text feature responseCoding[row index][i] = math.exp(sum prob/len(row['TEXT'].split()))
                     row index += 1
             return text feature responseCoding
         # building a CountVectorizer with all the words that occured minimum 3 times in train data
         text vectorizer = CountVectorizer(min df=3)
         train text feature onehotCoding = text vectorizer.fit transform(train df['TEXT'])
         # getting all the feature names (words)
         train text features = text vectorizer.get feature names()
         # train text feature onehotCoding.sum(axis=0).A1 will sum every row and returns (1*number of features) vector
         train text fea counts = train text feature onehotCoding.sum(axis=0).A1
         # zip(list(text_features), text_fea_counts) will zip a word with its number of times it occured
         text fea dict = dict(zip(list(train text features),train text fea counts))
         print("Total number of unique words in train data :", len(train text features))
         dict list = []
         # dict list =[] contains 9 dictoinaries each corresponds to a class
         for i in range(1,10):
```

```
cls_text = train_df[train_df['Class']==i]
    # build a word dict based on the words in that class
    dict_list.append(extract_dictionary_paddle(cls_text))
    # append it to dict_list

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

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

Total number of unique words in train data : 52990

```
In [35]: #response coding of text features
    train_text_feature_responseCoding = get_text_responsecoding(train_df)
    test_text_feature_responseCoding = get_text_responsecoding(test_df)
    cv_text_feature_responseCoding = get_text_responsecoding(cv_df)
```

```
In [36]: # https://stackoverflow.com/a/16202486
# we convert each row values such that they sum to 1
    train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train_text_feature_responseCoding.su
    m(axis=1)).T
    test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_feature_responseCoding.sum(a
    xis=1)).T
    cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_responseCoding.sum(axis=1
    )).T
```

```
In [37]: # don't forget to normalize every feature
    train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding, axis=0)

# we use the same vectorizer that was trained on train data
    test_text_feature_onehotCoding = text_vectorizer.transform(test_df['TEXT'])
    # don't forget to normalize every feature
    test_text_feature_onehotCoding = normalize(test_text_feature_onehotCoding, axis=0)

# we use the same vectorizer that was trained on train data
    cv_text_feature_onehotCoding = text_vectorizer.transform(cv_df['TEXT'])
# don't forget to normalize every feature
    cv_text_feature_onehotCoding = normalize(cv_text_feature_onehotCoding, axis=0)
```

```
In [38]: #https://stackoverflow.com/a/2258273/4084039
    sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambda x: x[1] , reverse=True))
    sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))
```

```
In [39]: # Train a Logistic regression+Calibration model using text features whicha re on-hot encoded
         alpha = [10 ** x for x in range(-5, 1)]
         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SG
         DClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, t
         ol=None.
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power
         t=0.5.
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y), coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         # predict(X) Predict class labels for samples in X.
         #-----
         # video Link:
         #-----
         cv log error array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
             clf.fit(train text feature onehotCoding, y train)
             sig clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig clf.fit(train text feature onehotCoding, y train)
             predict y = sig clf.predict proba(cv text feature onehotCoding)
             cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
             print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict y, labels=clf.classes , eps=
         1e-15))
         fig, ax = plt.subplots()
         ax.plot(alpha, cv log error array,c='g')
         for i, txt in enumerate(np.round(cv log error array,3)):
             ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error array[i]))
         plt.grid()
         plt.title("Cross Validation Error for each alpha")
         plt.xlabel("Alpha i's")
         plt.ylabel("Error measure")
```

```
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
clf.fit(train_text_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_onehotCoding, y_train)

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

10/2/2020 temp-160165086591545049

```
For values of alpha = 1e-05 The log loss is: 1.3129536147222927

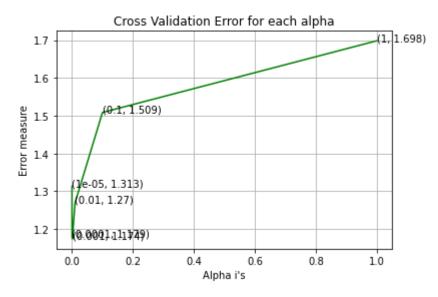
For values of alpha = 0.0001 The log loss is: 1.179386439263951

For values of alpha = 0.001 The log loss is: 1.1742713036156371

For values of alpha = 0.01 The log loss is: 1.269535101075292

For values of alpha = 0.1 The log loss is: 1.5086360076715486

For values of alpha = 1 The log loss is: 1.6983242671241472
```



For values of best alpha = 0.001 The train log loss is: 0.6537559315471534

For values of best alpha = 0.001 The cross validation log loss is: 1.1742713036156371

For values of best alpha = 0.001 The test log loss is: 1.1055922767654471

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

Ans. Yes, it seems like!

```
In [40]: def get_intersec_text(df):
    df_text_vec = CountVectorizer(min_df=3)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_fea = df_text_vec.get_feature_names()

    df_text_fea_dict = df_text_fea.sum(axis=0).A1
    df_text_fea_dict = dict(zip(list(df_text_features),df_text_fea_counts))
    len1 = len(set(df_text_features))
    len2 = len(set(train_text_features) & set(df_text_features))
    return len1,len2

In [41]: len1,len2 = get_intersec_text(test_df)
    print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data")
    len1,len2 = get_intersec_text(cv_df)
    print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train data")

96.536 % of word of test data appeared in train data
98.729 % of word of Cross Validation appeared in train data
```

ML models

```
In [42]: #Data preparation for ML models.

#Misc. functionns for ML models

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

# for calculating log_loss we will provide the array of probabilities belongs to each class
        print("Log loss:",log_loss(test_y, sig_clf.predict_proba(test_x)))
# calculating the number of data points that are misclassified
        print("Number of mis-classified points:", np.count_nonzero((pred_y- test_y))/test_y.shape[0])
        plot_confusion_matrix(test_y, pred_y)
```

```
In [44]: # this function will be used just for naive bayes
         # for the given indices, we will print the name of the features
         # and we will check whether the feature present in the test point text or not
         def get impfeature names(indices, text, gene, var, no features):
             gene count vec = CountVectorizer()
             var count vec = CountVectorizer()
             text count vec = CountVectorizer(min df=3)
             gene vec = gene count vec.fit(train df['Gene'])
             var vec = var count vec.fit(train df['Variation'])
             text_vec = text_count_vec.fit(train df['TEXT'])
             fea1 len = len(gene vec.get feature names())
             fea2 len = len(var count vec.get feature names())
             word present = 0
             for i,v in enumerate(indices):
                 if (v < fea1 len):</pre>
                     word = gene vec.get feature names()[v]
                      ves no = True if word == gene else False
                      if yes no:
                          word present += 1
                          print(i, "Gene feature [{}] present in test data point [{}]".format(word,yes no))
                 elif (v < fea1 len+fea2 len):</pre>
                     word = var vec.get feature names()[v-(fea1 len)]
                      ves no = True if word == var else False
                      if yes no:
                          word present += 1
                          print(i, "variation feature [{}] present in test data point [{}]".format(word,yes no))
                 else:
                      word = text vec.get feature names()[v-(fea1 len+fea2 len)]
                     yes no = True if word in text.split() else False
                      if yes no:
                          word present += 1
                          print(i, "Text feature [{}] present in test data point [{}]".format(word, yes no))
             print("Out of the top ", no features," features ", word present, "are present in query point")
```

Stacking the three types of features

```
In [45]: # merging gene, variance and text features
         # building train, test and cross validation data sets
         # a = [[1, 2]]
               [3, 4]]
         \# b = [4, 5].
           [6, 7]]
         # hstack(a, b) = [[1, 2, 4, 5],
                          Γ 3. 4. 6. 711
         train gene var onehotCoding = hstack((train gene feature onehotCoding,train variation feature onehotCoding))
         test gene var onehotCoding = hstack((test gene feature onehotCoding, test variation feature onehotCoding))
         cv gene var onehotCoding = hstack((cv gene feature onehotCoding,cv variation feature onehotCoding))
         train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train text feature onehotCoding)).tocsr()
         train y = np.array(list(train df['Class']))
         test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test text feature onehotCoding)).tocsr()
         test y = np.array(list(test df['Class']))
         cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text feature onehotCoding)).tocsr()
         cv y = np.array(list(cv df['Class']))
         train gene var responseCoding = np.hstack((train gene feature responseCoding,train variation feature response
         Coding))
         test gene var responseCoding = np.hstack((test gene feature responseCoding,test variation feature responseCod
         ing))
         cv gene var responseCoding = np.hstack((cv gene feature responseCoding,cv variation feature responseCoding))
         train x responseCoding = np.hstack((train gene var responseCoding, train text feature responseCoding))
         test x responseCoding = np.hstack((test gene var responseCoding, test text feature responseCoding))
         cv x responseCoding = np.hstack((cv gene var responseCoding, cv text feature responseCoding))
```

```
In [46]:
         print("One hot encoding features :")
         print("(number of data points * number of features) in train data = ", train x onehotCoding.shape)
         print("(number of data points * number of features) in test data = ", test x onehotCoding.shape)
         print("(number of data points * number of features) in cross validation data =", cv x onehotCoding.shape)
         One hot encoding features :
         (number of data points * number of features) in train data = (2124, 55164)
         (number of data points * number of features) in test data = (665, 55164)
         (number of data points * number of features) in cross validation data = (532, 55164)
In [47]:
         print(" Response encoding features :")
         print("(number of data points * number of features) in train data = ", train x responseCoding.shape)
         print("(number of data points * number of features) in test data = ", test x responseCoding.shape)
         print("(number of data points * number of features) in cross validation data =", cv x responseCoding.shape)
          Response encoding features :
         (number of data points * number of features) in train data = (2124, 27)
         (number of data points * number of features) in test data = (665, 27)
         (number of data points * number of features) in cross validation data = (532, 27)
```

Base Line Model

- 4.1.1. Naive Bayes
- 4.1.1.1. Hyper parameter tuning

```
In [48]: # find more about Multinomial Naive base function here http://scikit-learn.org/stable/modules/generated/sklea
         rn.naive bayes.MultinomialNB.html
        # ------
        # default paramters
         # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=None)
        # some of methods of MultinomialNB()
        # fit(X, y[, sample weight]) Fit Naive Bayes classifier according to X, y
        \# predict(X) Perform classification on an array of test vectors X.
        # predict Log proba(X) Return Log-probability estimates for the test vector X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-algorithm-
         1/
         # -----
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.cal
         ibration.CalibratedClassifierCV.html
        # -----
         # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample_weight])
Fit the calibrated model
        # get params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
        # predict proba(X) Posterior probabilities of classification
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-algorithm-
         1/
         cv log error array = []
         for i in alpha:
            print("for alpha =", i)
            clf = MultinomialNB(alpha=i)
            clf.fit(train x onehotCoding, train y)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train x onehotCoding, train y)
            sig clf probs = sig clf.predict proba(cv x onehotCoding)
```

```
cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
   # to avoid rounding error while multiplying probabilites we use log-probability estimates
   print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(np.log10(alpha), cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv log error array[i]))
plt.grid()
plt.xticks(np.log10(alpha))
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = MultinomialNB(alpha=alpha[best alpha])
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y,
labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, pr
edict 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, 1
abels=clf.classes , eps=1e-15))
```

for alpha = 1e-05

Log Loss: 1.272847835912897

for alpha = 0.0001

Log Loss: 1.2733588050178313

for alpha = 0.001

Log Loss: 1.2743957990020447

for alpha = 0.1

Log Loss: 1.285193204379748

for alpha = 1

Log Loss: 1.2921354813077794

for alpha = 10

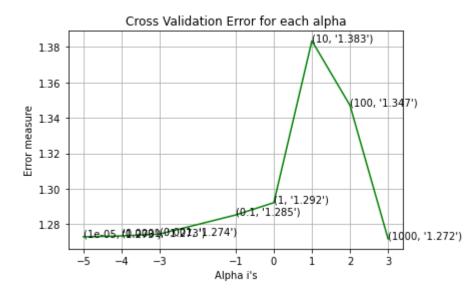
Log Loss: 1.383495729753779

for alpha = 100

Log Loss: 1.3470380026402216

for alpha = 1000

Log Loss: 1.271721858086986



```
For values of best alpha = 1000 The train log loss is: 1.044492707286355
For values of best alpha = 1000 The cross validation log loss is: 1.271721858086986
For values of best alpha = 1000 The test log loss is: 1.3135797210773767
```

```
In [49]: sig_clf_probs[0]
```

Out[49]: array([0.15239007, 0.22834548, 0.03038728, 0.11576721, 0.06871158, 0.08145478, 0.30373508, 0.00873128, 0.01047724])

```
In [50]: # find more about Multinomial Naive base function here http://scikit-learn.org/stable/modules/generated/sklea
         rn.naive bayes.MultinomialNB.html
         # ------
         # default paramters
         # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=None)
         # some of methods of MultinomialNB()
         # fit(X, y[, sample weight]) Fit Naive Bayes classifier according to X, y
         \# predict(X) Perform classification on an array of test vectors X.
         # predict Log proba(X) Return Log-probability estimates for the test vector X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-algorithm-
         1/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.cal
         ibration.CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample_weight])
Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         clf = MultinomialNB(alpha=alpha[best alpha])
         clf.fit(train x onehotCoding, train y)
         sig clf = CalibratedClassifierCV(clf, method="sigmoid")
         sig clf.fit(train x onehotCoding, train y)
         sig clf probs = sig clf.predict proba(cv x onehotCoding)
         # to avoid rounding error while multiplying probabilites we use log-probability estimates
         print("Log Loss :",log loss(cv y, sig clf probs))
         print("Number of missclassified point :", np.count nonzero((sig clf.predict(cv x onehotCoding)- cv y))/cv y.s
         hape[0])
         plot confusion matrix(cv y, sig clf.predict(cv x onehotCoding.toarray()))
```

Log Loss: 1.271721858086986

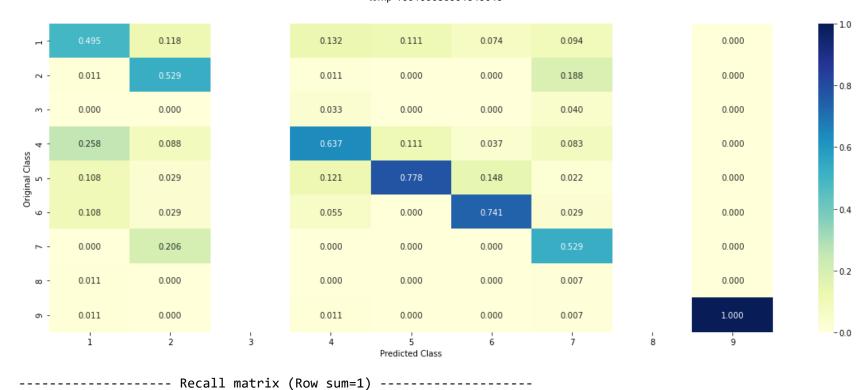
Number of missclassified point : 0.4417293233082707

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

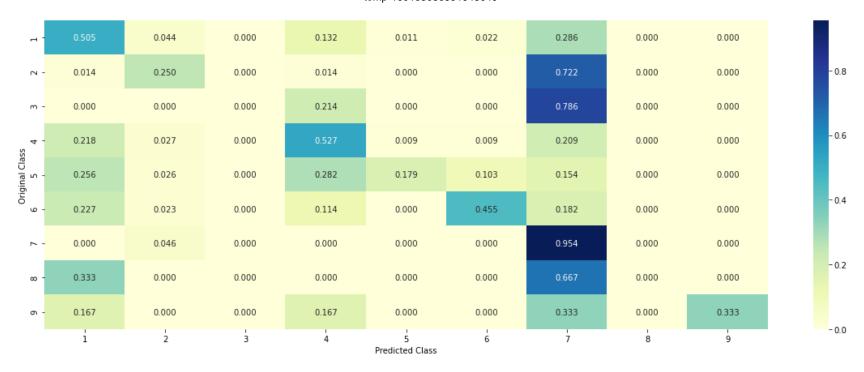
- 1	46.000	4.000	0.000	12.000	1.000	2.000	26.000	0.000	0.000
- 2	1.000	18.000	0.000	1.000	0.000	0.000	52.000	0.000	0.000
m -	0.000	0.000	0.000	3.000	0.000	0.000	11.000	0.000	0.000
55 4 -	24.000	3.000	0.000	58.000	1.000	1.000	23.000	0.000	0.000
Original Class 5	10.000	1.000	0.000	11.000	7.000	4.000	6.000	0.000	0.000
Ori	10.000	1.000	0.000	5.000	0.000	20.000	8.000	0.000	0.000
۲ -	0.000	7.000	0.000	0.000	0.000	0.000	146.000	0.000	0.000
ω -	1.000	0.000	0.000	0.000	0.000	0.000	2.000	0.000	0.000
o -	1.000	0.000	0.000	1.000	0.000	0.000	2.000	0.000	2.000
	1	2	3	4	5 Predicted Class	6	7	8	9

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

- 20



https://htmtopdf.herokuapp.com/ipynbviewer/temp/71cf80f0318527bac9a45271212b1ca2/personalised-cancer-analysis.html?t=1601650867897



4.1.1.3. Feature Importance, Correctly classified point

4.2. K Nearest Neighbour Classification

```
In [52]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/generated/sklearn.neighb
         ors.KNeighborsClassifier.html
         # -----
         # default parameter
         # KNeighborsClassifier(n neighbors=5, weights='uniform', algorithm='auto', leaf size=30, p=2,
         # metric='minkowski', metric params=None, n jobs=1, **kwarqs)
         # methods of
         # fit(X, y) : Fit the model using X as training data and y as target values
         # predict(X):Predict the class labels for the provided data
         # predict proba(X):Return probability estimates for the test data X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/k-nearest-neighbors-geo
         metric-intuition-with-a-toy-example-1/
         #-----
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.cal
         ibration.CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         #-----
         # video Link:
         alpha = [5, 11, 15, 21, 31, 41, 51, 99]
         cv log error array = []
         for i in alpha:
            print("for alpha =", i)
            clf = KNeighborsClassifier(n neighbors=i)
            clf.fit(train x responseCoding, train y)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train x responseCoding, train y)
            sig clf probs = sig clf.predict proba(cv x responseCoding)
```

```
cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
   # to avoid rounding error while multiplying probabilites we use log-probability estimates
   print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
clf.fit(train x responseCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x responseCoding, train y)
predict y = sig clf.predict proba(train x responseCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y,
labels=clf.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 is:",log loss(v cv, pr
edict 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, l
abels=clf.classes , eps=1e-15))
```

for alpha = 5

Log Loss: 1.082610827783673

for alpha = 11

Log Loss: 1.0678613314087946

for alpha = 15

Log Loss: 1.06483168962463

for alpha = 21

Log Loss: 1.0794420070327913

for alpha = 31

Log Loss: 1.09054982239701

for alpha = 41

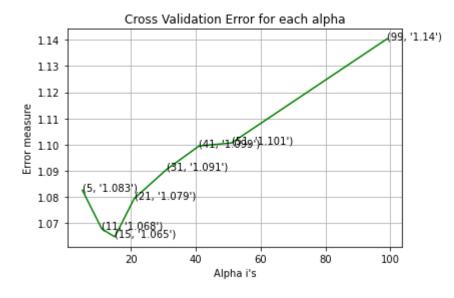
Log Loss: 1.0994936965760644

for alpha = 51

Log Loss: 1.1006399478208193

for alpha = 99

Log Loss: 1.1403548671097543



For values of best alpha = 15 The train log loss is: 0.6523199773832936

For values of best alpha = 15 The cross validation log loss is: 1.06483168962463

For values of best alpha = 15 The test log loss is: 1.0541105125180696

4.2.2. Testing the model with best hyper paramters

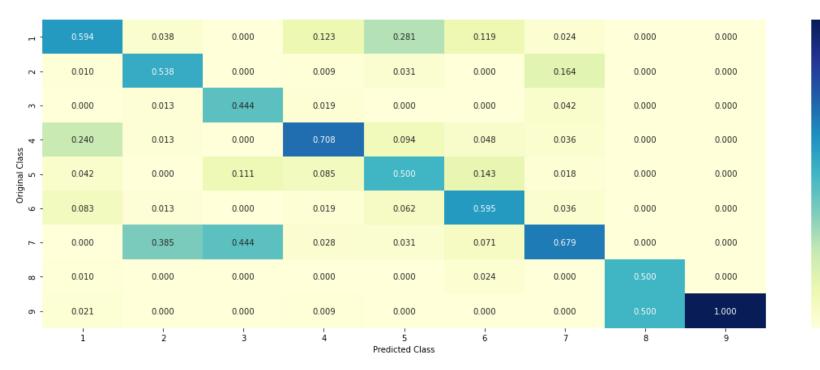
Log loss : 1.06483168962463

Number of mis-classified points : 0.37218045112781956

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

- 1	57.000	3.000	0.000	13.000	9.000	5.000	4.000	0.000	0.000
- 2	1.000	42.000	0.000	1.000	1.000	0.000	27.000	0.000	0.000
m -	0.000	1.000	4.000	2.000	0.000	0.000	7.000	0.000	0.000
4 -	23.000	1.000	0.000	75.000	3.000	2.000	6.000	0.000	0.000
Original Class 5	4.000	0.000	1.000	9.000	16.000	6.000	3.000	0.000	0.000
ori	8.000	1.000	0.000	2.000	2.000	25.000	6.000	0.000	0.000
۲.	0.000	30.000	4.000	3.000	1.000	3.000	112.000	0.000	0.000
ω -	1.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000
6 -	2.000	0.000	0.000	1.000	0.000	0.000	0.000	1.000	2.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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



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

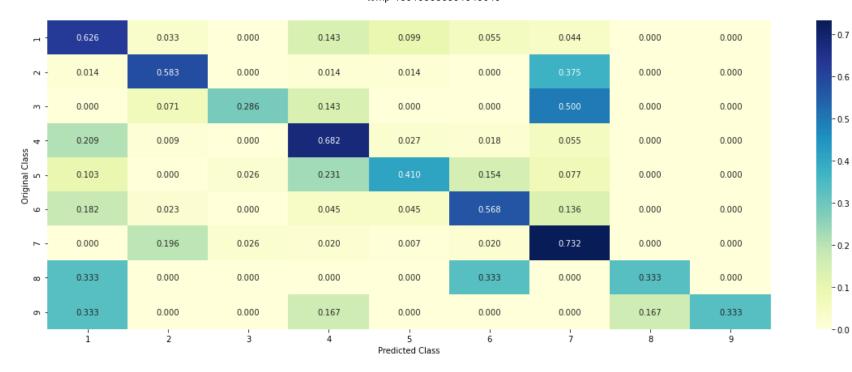
- 0.8

- 0.6

- 0.4

- 0.2

- 0.0



4.2.3. Sample Query point -1

```
In [54]: clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
    clf.fit(train_x_responseCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_responseCoding, train_y)

    test_point_index = 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 classes",train_y[neighbors[1][0]])
    print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

```
Predicted Class : 5
Actual Class : 7
The 15 nearest neighbours of the test points belongs to classes [7 7 7 7 7 6 3 7 7 7 7 7 7 7 7]
Fequency of nearest points : Counter({7: 13, 6: 1, 3: 1})
```

sample2

```
In [55]: clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
    clf.fit(train_x_responseCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_responseCoding, train_y)

    test_point_index = 100

    predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index].reshape(1,-1))
    print("Predicted Class :", predicted_cls[0])
    print("Actual Class :", test_y[test_point_index])
    neighbors = clf.kneighbors(test_x_responseCoding[test_point_index].reshape(1, -1), alpha[best_alpha])
    print("the k value for knn is",alpha[best_alpha], "and the nearest neighbours of the test points belongs to classes",train_y[neighbors[1][0]])
    print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

Predicted Class : 7

Actual Class : 7

the k value for knn is 15 and the nearest neighbours of the test points belongs to classes [7 7 7 7 7 2 7 7 7 2 2 7 7 7 2]

Fequency of nearest points : Counter({7: 11, 2: 4})

4.3. Logistic Regression

with class balancing

```
In [56]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SG
         DCLassifier.html
         # -----
         # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit intercept=True, max iter=None. t
         ol=None.
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power
         t=0.5.
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
        # fit(X, y), coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
        # predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
         #_____
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.cal
         ibration.CalibratedClassifierCV.html
         # -----
         # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='siamoid', cv=3)
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample weight]) Fit the calibrated model
        # get params([deep]) Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
        #-----
        # video Link:
         #-----
         alpha = [10 ** x for x in range(-6, 3)]
         cv log error array = []
         for i in alpha:
            print("for alpha =", i)
            clf = SGDClassifier(class weight='balanced', alpha=i, penalty='12', loss='log', random state=42)
            clf.fit(train x onehotCoding, train y)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train x onehotCoding, train y)
```

```
sig clf probs = sig clf.predict proba(cv x onehotCoding)
   cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
   # to avoid rounding error while multiplying probabilites we use log-probability estimates
   print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', random state=
42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y,
labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, pr
edict 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, 1
abels=clf.classes , eps=1e-15))
```

for alpha = 1e-06

Log Loss : 1.36294138079984

for alpha = 1e-05

Log Loss: 1.3012417620859105

for alpha = 0.0001

Log Loss: 1.149313586281625

for alpha = 0.001

Log Loss: 1.1077235053590766

for alpha = 0.01

Log Loss: 1.1925155918669383

for alpha = 0.1

Log Loss: 1.4654834143237738

for alpha = 1

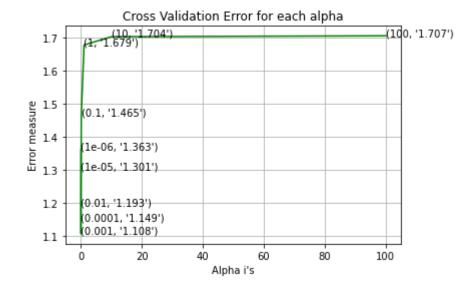
Log Loss: 1.6788734324468384

for alpha = 10

Log Loss: 1.7041432979496354

for alpha = 100

Log Loss: 1.7067955464743005



For values of best alpha = 0.001 The train log loss is: 0.5258212724205154 For values of best alpha = 0.001 The cross validation log loss is: 1.1077235053590766

For values of best alpha = 0.001 The test log loss is: 1.0331173361507624

4.3.1.2. Testing the model with best hyper paramters

```
In [57]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.SG
         DClassifier.html
         # -----
         # default parameters
         # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, t
         ol=None.
         # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power
         t=0.5.
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
         # fit(X, y), coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
         clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', random state=
         42)
         predict and plot confusion matrix(train x onehotCoding, train y, cv x onehotCoding, cv y, clf)
```

Log loss : 1.1077235053590766

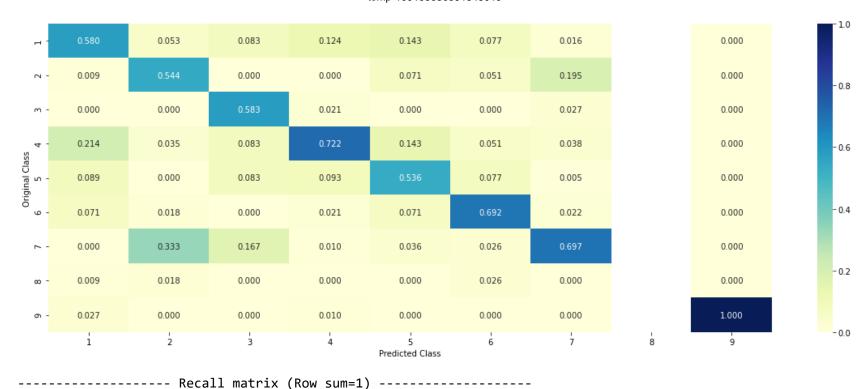
Number of mis-classified points : 0.34962406015037595

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

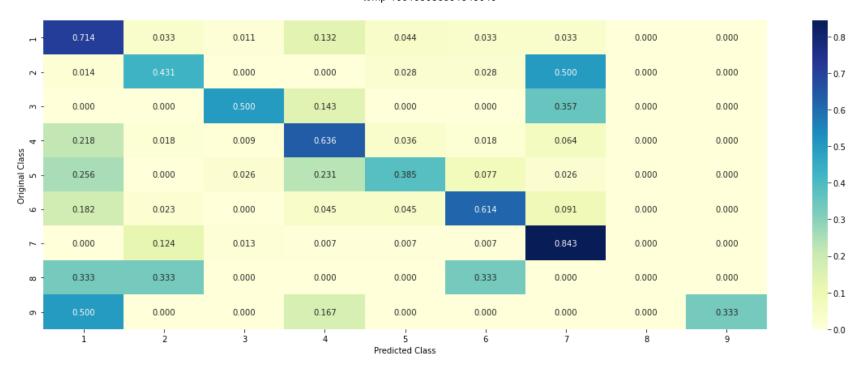
_									
H -	65.000	3.000	1.000	12.000	4.000	3.000	3.000	0.000	0.000
- 2	1.000	31.000	0.000	0.000	2.000	2.000	36.000	0.000	0.000
m -	0.000	0.000	7.000	2.000	0.000	0.000	5.000	0.000	0.000
4 -	24.000	2.000	1.000	70.000	4.000	2.000	7.000	0.000	0.000
Original Class 5	10.000	0.000	1.000	9.000	15.000	3.000	1.000	0.000	0.000
Original Property	8.000	1.000	0.000	2.000	2.000	27.000	4.000	0.000	0.000
7 -	0.000	19.000	2.000	1.000	1.000	1.000	129.000	0.000	0.000
ω -	1.000	1.000	0.000	0.000	0.000	1.000	0.000	0.000	0.000
ი -	3.000	0.000	0.000	1.000	0.000	0.000	0.000	0.000	2.000
	1	2	3	4	5 Predicted Class	6	7	8	9

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

- 20



https://htmtopdf.herokuapp.com/ipynbviewer/temp/71cf80f0318527bac9a45271212b1ca2/personalised-cancer-analysis.html?t=1601650867897



4.3.1.3. Feature Importance

```
In [58]: def get imp feature names(text, indices, removed ind = []):
             word present = 0
             tabulte list = []
             incresingorder ind = 0
             for i in indices:
                 if i < train gene feature onehotCoding.shape[1]:</pre>
                     tabulte list.append([incresingorder ind, "Gene", "Yes"])
                 elif i< 18:
                     tabulte list.append([incresingorder ind, "Variation", "Yes"])
                 if ((i > 17) & (i not in removed ind)) :
                     word = train text features[i]
                     yes no = True if word in text.split() else False
                     if yes no:
                          word present += 1
                     tabulte list.append([incresingorder ind,train text features[i], yes no])
                 incresingorder ind += 1
             print(word present, "most importent features are present in our query point")
             print("-"*50)
             print("The features that are most importent of the ",predicted cls[0]," class:")
             print (tabulate(tabulte list, headers=["Index", 'Feature name', 'Present or Not']))
```

4.3.1.3.1. Correctly Classified point

```
In [59]: # from tabulate import tabulate
         clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='log', random state=
         42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index
         1),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index
         1,test df['Variation'].iloc[test point index], no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.0997 0.1616 0.0287 0.1419 0.076 0.1318 0.3433 0.0078 0.0092]]
         Actual Class: 7
         70 Text feature [constitutive] present in test data point [True]
         100 Text feature [missense] present in test data point [True]
         122 Text feature [activated] present in test data point [True]
         181 Text feature [activating] present in test data point [True]
         191 Text feature [constitutively] present in test data point [True]
         266 Text feature [function] present in test data point [True]
         272 Text feature [rbd] present in test data point [True]
         277 Text feature [expressing] present in test data point [True]
         334 Text feature [transformation] present in test data point [True]
         345 Text feature [variation] present in test data point [True]
         354 Text feature [nude] present in test data point [True]
         392 Text feature [downstream] present in test data point [True]
         422 Text feature [activation] present in test data point [True]
         457 Text feature [overexpression] present in test data point [True]
         487 Text feature [stably] present in test data point [True]
         Out of the top 500 features 15 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

Predicted Class: 7

```
Predicted Class Probabilities: [[0.035     0.0746     0.0084     0.075     0.0288     0.0113     0.7558     0.0068     0.0043]]
Actual Class : 7
70 Text feature [constitutive] present in test data point [True]
91 Text feature [transforming] present in test data point [True]
113 Text feature [3t3] present in test data point [True]
114 Text feature [transform] present in test data point [True]
122 Text feature [activated] present in test data point [True]
129 Text feature [grew] present in test data point [True]
133 Text feature [stat5] present in test data point [True]
155 Text feature [independence] present in test data point [True]
181 Text feature [activating] present in test data point [True]
186 Text feature [technology] present in test data point [True]
191 Text feature [constitutively] present in test data point [True]
217 Text feature [oncogene] present in test data point [True]
230 Text feature [proliferate] present in test data point [True]
247 Text feature [loss] present in test data point [True]
266 Text feature [function] present in test data point [True]
272 Text feature [rbd] present in test data point [True]
276 Text feature [mitogen] present in test data point [True]
277 Text feature [expressing] present in test data point [True]
319 Text feature [cysteine] present in test data point [True]
334 Text feature [transformation] present in test data point [True]
376 Text feature [ligand] present in test data point [True]
392 Text feature [downstream] present in test data point [True]
397 Text feature [predicted] present in test data point [True]
422 Text feature [activation] present in test data point [True]
436 Text feature [deliver] present in test data point [True]
457 Text feature [overexpression] present in test data point [True]
470 Text feature [conserved] present in test data point [True]
475 Text feature [phospho] present in test data point [True]
487 Text feature [stably] present in test data point [True]
Out of the top 500 features 29 are present in query point
```

4.3.2. Without Class balancing

```
In [61]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear model.SG
        DClassifier.html
         # -----
        # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit intercept=True, max iter=None. t
         ol=None.
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power
         t=0.5.
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
        # fit(X, y), coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
         \# predict(X) Predict class labels for samples in X.
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
         #_____
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.cal
         ibration.CalibratedClassifierCV.html
         # -----
        # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='siamoid', cv=3)
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample weight]) Fit the calibrated model
        # get_params([deep]) Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
        # predict proba(X) Posterior probabilities of classification
         #-----
         # video link:
         alpha = [10 ** x for x in range(-6, 1)]
        cv log error array = []
         for i in alpha:
            print("for alpha =", i)
            clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
            clf.fit(train x onehotCoding, train y)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
```

```
sig clf.fit(train x onehotCoding, train y)
   sig clf probs = sig clf.predict proba(cv x onehotCoding)
   cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
   print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
   ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y,
labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_loss(y_cv, pr
edict 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, 1
abels=clf.classes , eps=1e-15))
```

for alpha = 1e-06

Log Loss: 1.3187500585146055

for alpha = 1e-05

Log Loss: 1.269409828851998

for alpha = 0.0001

Log Loss: 1.1343203408531495

for alpha = 0.001

Log Loss: 1.1129013200136924

for alpha = 0.01

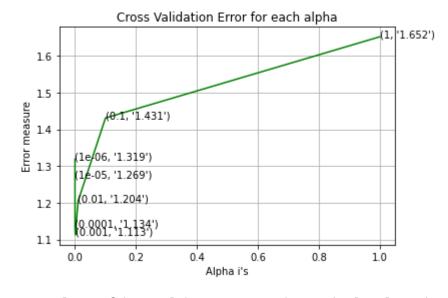
Log Loss: 1.2042891998421648

for alpha = 0.1

Log Loss: 1.430907857712483

for alpha = 1

Log Loss: 1.6518348990681004



For values of best alpha = 0.001 The train log loss is: 0.5224967351264701 For values of best alpha = 0.001 The cross validation log loss is: 1.1129013200136924

For values of best alpha = 0.001 The test log loss is: 1.047232370782306

4.3.2.2. Testing model with best hyper parameters

```
In [62]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.SG
        DClassifier.html
         # ------
         # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max iter=None, t
         ol=None.
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power
         t=0.5.
        # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
        # fit(X, y), coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
        # predict(X) Predict class labels for samples in X.
         #----
         # video Link:
         #-----
        clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
        predict and plot confusion matrix(train x onehotCoding, train y, cv x onehotCoding, cv y, clf)
```

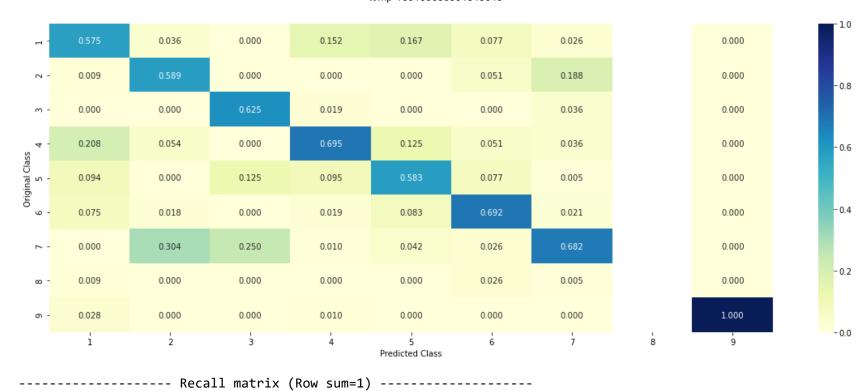
Log loss : 1.1129013200136924

Number of mis-classified points : 0.34962406015037595

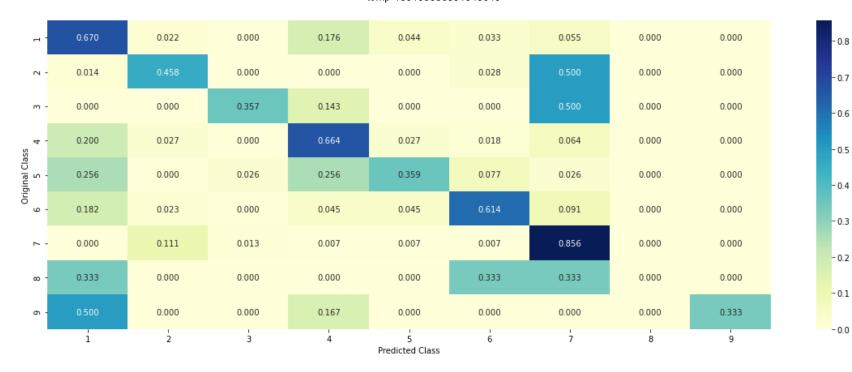
----- Confusion matrix -----

. ·	61.000	2.000	0.000	16.000	4.000	3.000	5.000	0.000	0.000
- 2	1.000	33.000	0.000	0.000	0.000	2.000	36.000	0.000	0.000
m -	0.000	0.000	5.000	2.000	0.000	0.000	7.000	0.000	0.000
4 -	22.000	3.000	0.000	73.000	3.000	2.000	7.000	0.000	0.000
Original Class 5	10.000	0.000	1.000	10.000	14.000	3.000	1.000	0.000	0.000
Orig 6	8.000	1.000	0.000	2.000	2.000	27.000	4.000	0.000	0.000
7 -	0.000	17.000	2.000	1.000	1.000	1.000	131.000	0.000	0.000
ω -	1.000	0.000	0.000	0.000	0.000	1.000	1.000	0.000	0.000
6 -	3.000	0.000	0.000	1.000	0.000	0.000	0.000	0.000	2.000
	1	2	3	4	5 Predicted Class	6	7	8	9

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



https://htmtopdf.herokuapp.com/ipynbviewer/temp/71cf80f0318527bac9a45271212b1ca2/personalised-cancer-analysis.html?t=1601650867897



4.3.2.3. Feature Importance, Correctly Classified point

```
In [63]: | clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         no feature = 500
         predicted cls = sig clf.predict(test x onehotCoding[test point index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index
         1),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index
         ],test_df['Variation'].iloc[test_point index], no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.0975 0.1655 0.0342 0.136 0.0813 0.1355 0.3316 0.0084 0.0101]]
         Actual Class : 7
         108 Text feature [constitutive] present in test data point [True]
         232 Text feature [activating] present in test data point [True]
         251 Text feature [activated] present in test data point [True]
         287 Text feature [constitutively] present in test data point [True]
         332 Text feature [missense] present in test data point [True]
         359 Text feature [expressing] present in test data point [True]
         387 Text feature [transformation] present in test data point [True]
         445 Text feature [rbd] present in test data point [True]
         486 Text feature [nude] present in test data point [True]
         Out of the top 500 features 9 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

```
In [64]: | 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
         1),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-1*abs(clf.coef_))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index
         1,test df['Variation'].iloc[test point index], no feature)
         Predicted Class : 7
         Predicted Class Probabilities: [[0.0341 0.0723 0.0074 0.0752 0.0268 0.011 0.7642 0.0054 0.0038]]
         Actual Class : 7
         108 Text feature [constitutive] present in test data point [True]
         128 Text feature [transforming] present in test data point [True]
         189 Text feature [3t3] present in test data point [True]
         201 Text feature [transform] present in test data point [True]
         225 Text feature [independence] present in test data point [True]
         232 Text feature [activating] present in test data point [True]
         251 Text feature [activated] present in test data point [True]
         269 Text feature [stat5] present in test data point [True]
         287 Text feature [constitutively] present in test data point [True]
         289 Text feature [technology] present in test data point [True]
         294 Text feature [grew] present in test data point [True]
         356 Text feature [cysteine] present in test data point [True]
         359 Text feature [expressing] present in test data point [True]
         387 Text feature [transformation] present in test data point [True]
         399 Text feature [oncogene] present in test data point [True]
         400 Text feature [proliferate] present in test data point [True]
         445 Text feature [rbd] present in test data point [True]
         Out of the top 500 features 17 are present in query point
```

4.4. Linear Support Vector Machines

```
In [65]: # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/gen
        erated/sklearn.svm.SVC.html
        # -----
        # default parameters
        # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001,
        # cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', random state=
        None)
        # Some of methods of SVM()
        # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
        \# predict(X) Perform classification on samples in X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathematical-derivation
        # -----
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.cal
        ibration.CalibratedClassifierCV.html
        # -----
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample weight]) Fit the calibrated model
        # get params([deep]) Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
        # predict proba(X) Posterior probabilities of classification
        #-----
        # video Link:
        #-----
        alpha = [10 ** x for x in range(-5, 3)]
        cv log error array = []
        for i in alpha:
            print("for C =", i)
           clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced')
            clf = SGDClassifier( class weight='balanced', alpha=i, penalty='12', loss='hinge', random state=42)
            clf.fit(train x onehotCoding, train y)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
```

```
sig clf.fit(train x onehotCoding, train y)
   sig clf probs = sig clf.predict proba(cv x onehotCoding)
   cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
   print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
   ax.annotate((alpha[i],str(txt)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
# clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced')
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='12', loss='hinge', random stat
e = 42)
clf.fit(train x onehotCoding, train y)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, train y)
predict y = sig clf.predict proba(train x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The train log loss is:",log loss(y train, predict y,
labels=clf.classes , eps=1e-15))
predict y = sig clf.predict proba(cv x onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log loss(y cv, pr
edict 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, 1
abels=clf.classes , eps=1e-15))
```

for C = 1e-05

Log Loss: 1.314728993307713

for C = 0.0001

Log Loss: 1.2502178546124403

for C = 0.001

Log Loss: 1.1500876328835536

for C = 0.01

Log Loss: 1.1637865648100139

for C = 0.1

Log Loss: 1.3733430875163954

for C = 1

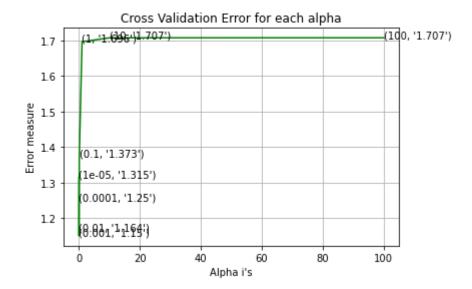
Log Loss: 1.6962686297971055

for C = 10

Log Loss: 1.7072212602074643

for C = 100

Log Loss : 1.7072693840971944



For values of best alpha = 0.001 The train log loss is: 0.5297204834298374

For values of best alpha = 0.001 The cross validation log loss is: 1.1500876328835536

For values of best alpha = 0.001 The test log loss is: 1.1038364842102042

4.4.2. Testing model with best hyper parameters

In [66]: # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/gen erated/sklearn.svm.SVC.html # -----# default parameters # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001, # cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', random state= None) # Some of methods of SVM() # fit(X, y, [sample weight]) Fit the SVM model according to the given training data. # predict(X) Perform classification on samples in X. # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathematical-derivation # -----# clf = SVC(C=alpha[best alpha],kernel='linear',probability=True, class weight='balanced') clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', random state=42,class weight='balanc ed') predict and plot confusion matrix(train x onehotCoding, train y,cv x onehotCoding,cv y, clf)

Log loss : 1.1500876328835536

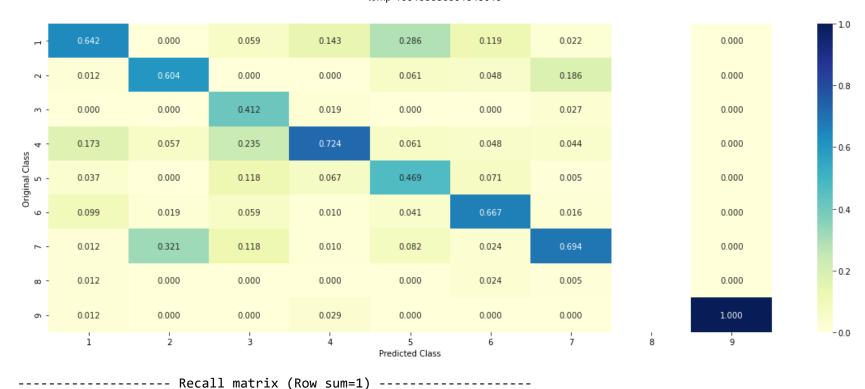
Number of mis-classified points : 0.34774436090225563

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

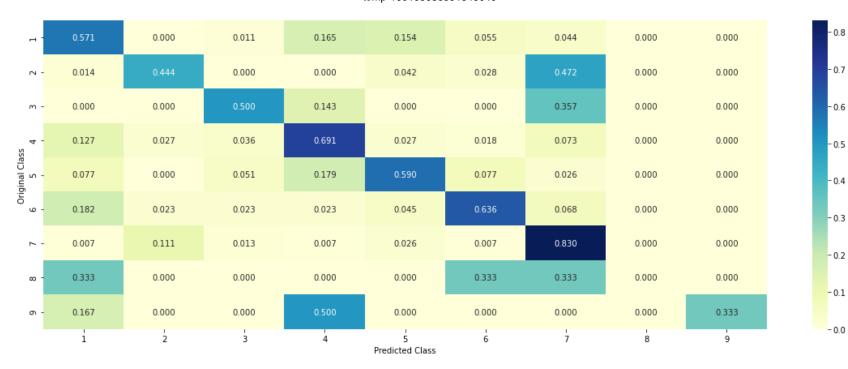
н -	52.000	0.000	1.000	15.000	14.000	5.000	4.000	0.000	0.000
- 2	1.000	32.000	0.000	0.000	3.000	2.000	34.000	0.000	0.000
m -	0.000	0.000	7.000	2.000	0.000	0.000	5.000	0.000	0.000
4 -	14.000	3.000	4.000	76.000	3.000	2.000	8.000	0.000	0.000
Original Class 5	3.000	0.000	2.000	7.000	23.000	3.000	1.000	0.000	0.000
Ori	8.000	1.000	1.000	1.000	2.000	28.000	3.000	0.000	0.000
۲ -	1.000	17.000	2.000	1.000	4.000	1.000	127.000	0.000	0.000
ω -	1.000	0.000	0.000	0.000	0.000	1.000	1.000	0.000	0.000
თ -	1.000	0.000	0.000	3.000	0.000	0.000	0.000	0.000	2.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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

- 20



https://htmtopdf.herokuapp.com/ipynbviewer/temp/71cf80f0318527bac9a45271212b1ca2/personalised-cancer-analysis.html?t=1601650867897



4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

```
In [67]: clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', random state=42)
         clf.fit(train x onehotCoding,train y)
         test point index = 1
         # test point index = 100
         no feature = 500
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index
         1),4))
         print("Actual Class :", test_y[test_point_index])
         indices = np.argsort(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index
         ],test df['Variation'].iloc[test point index], no feature)
         Predicted Class: 7
         Predicted Class Probabilities: [[0.1134 0.1152 0.0325 0.1662 0.0836 0.1927 0.2793 0.0088 0.0082]]
         Actual Class : 7
         415 Text feature [constitutive] present in test data point [True]
         Out of the top 500 features 1 are present in query point
```

4.3.3.2. For Incorrectly classified point

```
In [68]: | 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
         1),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-1*abs(clf.coef ))[predicted cls-1][:,:no feature]
         print("-"*50)
         get impfeature names(indices[0], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test point index
         ],test df['Variation'].iloc[test point index], no feature)
         Predicted Class : 7
         Predicted Class Probabilities: [[0.0538 0.0592 0.0132 0.1053 0.0424 0.0125 0.7036 0.0051 0.0048]]
         Actual Class : 7
         415 Text feature [constitutive] present in test data point [True]
         436 Text feature [3t3] present in test data point [True]
         437 Text feature [transform] present in test data point [True]
         439 Text feature [independence] present in test data point [True]
         Out of the top 500 features 4 are present in query point
```

- 4.5 Random Forest Classifier
- 4.5.1. Hyper paramter tuning (With One hot Encoding)

```
In [69]: # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples spli
         t=2.
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity de
         crease=0.0.
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm star
         t=False.
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         \# predict proba (X) Perform classification on samples in X.
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their
         -construction-2/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.cal
         ibration.CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
         #
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample_weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         \# predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         #-----
         # video Link:
         alpha = [100,200,500,1000,2000]
         \max depth = [5, 10]
```

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

```
for n estimators = 100 and max depth = 5
Log Loss: 1.2510752385857697
for n estimators = 100 and max depth = 10
Log Loss: 1.1710949046215324
for n estimators = 200 and max depth = 5
Log Loss: 1.2425918514711494
for n estimators = 200 and max depth = 10
Log Loss: 1.1658030263909924
for n estimators = 500 and max depth = 5
Log Loss: 1.232035305318242
for n estimators = 500 and max depth = 10
Log Loss: 1.160224784941954
for n estimators = 1000 and max depth = 5
Log Loss: 1.226966071110765
for n estimators = 1000 and max depth = 10
Log Loss: 1.1566287006971108
for n estimators = 2000 and max depth = 5
Log Loss: 1.2255781767795293
for n estimators = 2000 and max depth = 10
Log Loss: 1.1559219378180812
For values of best estimator = 2000 The train log loss is: 0.6955228505989779
For values of best estimator = 2000 The cross validation log loss is: 1.1559219378180812
For values of best estimator = 2000 The test log loss is: 1.1411004344682578
```

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

```
In [70]:
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples spli
         t=2.
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity de
         crease=0.0.
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm star
         t=False.
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
                                Perform classification on samples in X.
         # predict proba (X)
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their
         -construction-2/
         clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max_depth[int
         (best alpha%2)], random state=42, n jobs=-1)
         predict and plot confusion matrix(train x onehotCoding, train y,cv x onehotCoding,cv y, clf)
```

Log loss : 1.1559219378180812

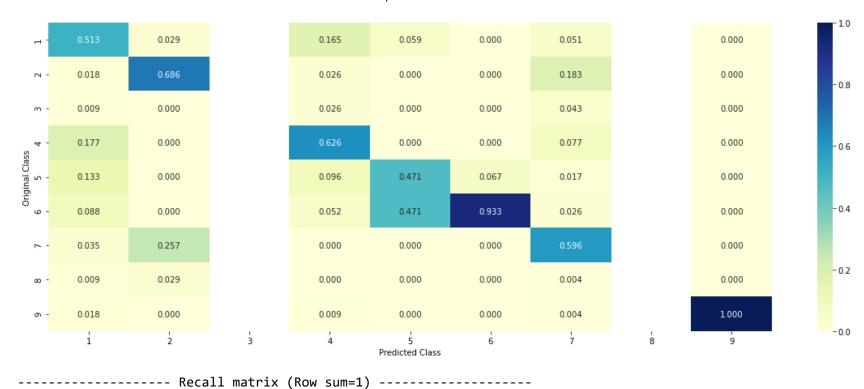
Number of mis-classified points : 0.40225563909774437

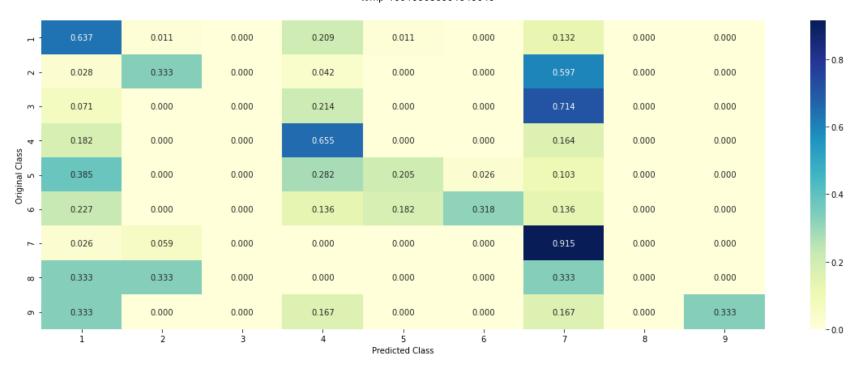
----- Confusion matrix -----

1	58.000	1.000	0.000	19.000	1.000	0.000	12.000	0.000	0.000
- 2	2.000	24.000	0.000	3.000	0.000	0.000	43.000	0.000	0.000
m -	1.000	0.000	0.000	3.000	0.000	0.000	10.000	0.000	0.000
SS 4 -	20.000	0.000	0.000	72.000	0.000	0.000	18.000	0.000	0.000
Original Class 5	15.000	0.000	0.000	11.000	8.000	1.000	4.000	0.000	0.000
Orie	10.000	0.000	0.000	6.000	8.000	14.000	6.000	0.000	0.000
۲ -	4.000	9.000	0.000	0.000	0.000	0.000	140.000	0.000	0.000
ω -	1.000	1.000	0.000	0.000	0.000	0.000	1.000	0.000	0.000
თ -	2.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	2.000
	í	2	3	4	5 Predicted Class	6	7	8	9

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

- 20





4.5.3. Feature Importance

4.5.3.1. Correctly Classified point

```
In [71]: # test point index = 10
         clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gini', max 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")
         sig clf.fit(train x onehotCoding, train y)
         test point index = 1
         no feature = 100
         predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
         print("Predicted Class :", predicted_cls[0])
         print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x onehotCoding[test point index
         1),4))
         print("Actual Class :", test y[test point index])
         indices = np.argsort(-clf.feature importances )
         print("-"*50)
         get impfeature names(indices[:no feature], test df['TEXT'].iloc[test point index],test df['Gene'].iloc[test p
         oint index],test df['Variation'].iloc[test point index], no feature)
```

Predicted Class: 7 Predicted Class Probabilities: [[0.0943 0.2246 0.0245 0.0926 0.0611 0.0488 0.4377 0.0086 0.0077]] Actual Class : 7 0 Text feature [activating] present in test data point [True] 1 Text feature [kinase] present in test data point [True] 4 Text feature [missense] 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 [activated] present in test data point [True] 9 Text feature [function] present in test data point [True] 13 Text feature [constitutive] present in test data point [True] 15 Text feature [erk] present in test data point [True] 16 Text feature [growth] present in test data point [True] 18 Text feature [signaling] present in test data point [True] 20 Text feature [oncogenic] present in test data point [True] 24 Text feature [functional] present in test data point [True] 25 Text feature [receptor] present in test data point [True] 27 Text feature [akt] present in test data point [True] 29 Text feature [cells] present in test data point [True] 31 Text feature [therapy] present in test data point [True] 35 Text feature [activate] present in test data point [True] 40 Text feature [patients] present in test data point [True] 48 Text feature [lines] present in test data point [True] 49 Text feature [constitutively] present in test data point [True] 51 Text feature [mek] present in test data point [True] 52 Text feature [expression] present in test data point [True] 53 Text feature [expressing] present in test data point [True] 55 Text feature [protein] present in test data point [True] 58 Text feature [egfr] present in test data point [True] 59 Text feature [variants] present in test data point [True] 60 Text feature [downstream] present in test data point [True] 62 Text feature [advanced] present in test data point [True] 64 Text feature [resistance] present in test data point [True] 65 Text feature [cell] present in test data point [True] 66 Text feature [patient] present in test data point [True] 67 Text feature [defective] present in test data point [True] 71 Text feature [phosphorylated] present in test data point [True] 74 Text feature [factor] present in test data point [True] 80 Text feature [erk1] present in test data point [True] 81 Text feature [dna] present in test data point [True] 85 Text feature [extracellular] present in test data point [True] 88 Text feature [proliferation] present in test data point [True]

91 Text feature [clinical] present in test data point [True] 93 Text feature [transformation] present in test data point [True] Out of the top 100 features 41 are present in query point

4.5.3.2. Inorrectly Classified point

```
Predicted Class: 7
Predicted Class Probabilities: [[0.0486 0.1125 0.02 0.0497 0.0463 0.0356 0.6762 0.005 0.006 ]]
Actuall Class : 7
0 Text feature [activating] present in test data point [True]
1 Text feature [kinase] present in test data point [True]
2 Text feature [tyrosine] present in test data point [True]
3 Text feature [inhibitors] 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 [activated] present in test data point [True]
9 Text feature [function] present in test data point [True]
10 Text feature [phosphorylation] present in test data point [True]
12 Text feature [inhibitor] present in test data point [True]
13 Text feature [constitutive] present in test data point [True]
15 Text feature [erk] present in test data point [True]
16 Text feature [growth] present in test data point [True]
17 Text feature [loss] present in test data point [True]
18 Text feature [signaling] present in test data point [True]
20 Text feature [oncogenic] present in test data point [True]
24 Text feature [functional] present in test data point [True]
25 Text feature [receptor] present in test data point [True]
27 Text feature [akt] present in test data point [True]
28 Text feature [kinases] present in test data point [True]
29 Text feature [cells] present in test data point [True]
30 Text feature [transforming] present in test data point [True]
35 Text feature [activate] present in test data point [True]
37 Text feature [therapeutic] present in test data point [True]
40 Text feature [patients] present in test data point [True]
41 Text feature [treated] present in test data point [True]
43 Text feature [mitogen] present in test data point [True]
46 Text feature [oncogene] present in test data point [True]
48 Text feature [lines] present in test data point [True]
49 Text feature [constitutively] present in test data point [True]
51 Text feature [mek] present in test data point [True]
52 Text feature [expression] present in test data point [True]
53 Text feature [expressing] present in test data point [True]
55 Text feature [protein] present in test data point [True]
56 Text feature [3t3] present in test data point [True]
60 Text feature [downstream] present in test data point [True]
61 Text feature [ligand] present in test data point [True]
63 Text feature [drug] present in test data point [True]
65 Text feature [cell] present in test data point [True]
```

```
66 Text feature [patient] present in test data point [True]
70 Text feature [phospho] present in test data point [True]
71 Text feature [phosphorylated] present in test data point [True]
73 Text feature [il] present in test data point [True]
74 Text feature [factor] present in test data point [True]
77 Text feature [variant] present in test data point [True]
81 Text feature [dna] present in test data point [True]
84 Text feature [transform] present in test data point [True]
85 Text feature [extracellular] present in test data point [True]
86 Text feature [starved] present in test data point [True]
88 Text feature [proliferation] present in test data point [True]
89 Text feature [survival] present in test data point [True]
90 Text feature [serum] present in test data point [True]
93 Text feature [transformation] present in test data point [True]
97 Text feature [independence] present in test data point [True]
99 Text feature [respond] present in test data point [True]
Out of the top 100 features 55 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

```
In [73]: # -----
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples spli
         t=2.
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity de
         crease=0.0.
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm star
         t=False.
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
         \# predict proba (X) Perform classification on samples in X.
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their
         -construction-2/
         # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.cal
         ibration.CalibratedClassifierCV.html
         # -----
         # default paramters
         # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid', cv=3)
         # some of the methods of CalibratedClassifierCV()
         # fit(X, y[, sample_weight]) Fit the calibrated model
         # get params([deep]) Get parameters for this estimator.
         # predict(X) Predict the target of new samples.
         # predict proba(X) Posterior probabilities of classification
         #-----
         # video Link:
         alpha = [10,50,100,200,500,1000]
         max depth = [2,3,5,10]
```

```
cv log error array = []
for i in alpha:
   for j in max depth:
       print("for n estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n estimators=i, criterion='gini', max depth=j, random state=42, n jobs=-
1)
        clf.fit(train x responseCoding, train y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig clf.fit(train x responseCoding, train y)
       sig clf probs = sig clf.predict proba(cv x responseCoding)
       cv log error array.append(log loss(cv y, sig clf probs, labels=clf.classes , eps=1e-15))
       print("Log Loss :",log loss(cv y, sig clf probs))
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ravel()
ax.plot(features, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
   ax.annotate((alpha[int(i/4)],max depth[int(i%4)],str(txt)), (features[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = RandomForestClassifier(n estimators=alpha[int(best alpha/4)], criterion='gini', max depth=max depth[int
(best alpha%4)], 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, pre
dict 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:",log loss(y test, predi
ct y, labels=clf.classes , eps=1e-15))
```

for n estimators = 10 and max depth = 2Log Loss: 1.9861677450954627 for n estimators = 10 and max depth = 3Log Loss: 1.5435362939196324 for n estimators = 10 and max depth = 5Log Loss: 1.4469034978342659 for n estimators = 10 and max depth = 10 Log Loss: 1.6132637947462776 for n estimators = 50 and max depth = 2Log Loss: 1.6004693454582304 for n estimators = 50 and max depth = 3Log Loss: 1.3614347051222064 for n_estimators = 50 and max depth = 5 Log Loss: 1.3081183334077289 for n estimators = 50 and max depth = 10 Log Loss: 1.5830274330364542 for n estimators = 100 and max depth = 2Log Loss: 1.4976846855755506 for n estimators = 100 and max depth = 3Log Loss: 1.4331341767337324 for n estimators = 100 and max depth = 5 Log Loss: 1.2500037185500072 for n estimators = 100 and max depth = 10 Log Loss: 1.6364236736649644 for n estimators = 200 and max depth = 2Log Loss: 1.4868282085215685 for n estimators = 200 and max depth = 3Log Loss: 1.4073936352601721 for n estimators = 200 and max depth = 5 Log Loss: 1.2823744982928649 for n estimators = 200 and max depth = 10 Log Loss: 1.6522884335788173 for n estimators = 500 and max depth = 2Log Loss: 1.5485391457158015 for n estimators = 500 and max depth = 3Log Loss: 1.4436126700101428 for n estimators = 500 and max depth = 5Log Loss: 1.3055032547490981 for n estimators = 500 and max depth = 10Log Loss: 1.6589038057131122 for n estimators = 1000 and max depth = 2Log Loss: 1.5380263905561016 for n estimators = 1000 and max depth = 3

```
Log Loss : 1.4575548295767202
```

for $n_{estimators} = 1000$ and max depth = 5

Log Loss: 1.2937629123104881

for n_estimators = 1000 and max depth = 10

Log Loss: 1.633210876353533

For values of best alpha = 100 The train log loss is: 0.07003743430006942

For values of best alpha = 100 The cross validation log loss is: 1.2500037185500075

For values of best alpha = 100 The test log loss is: 1.2708388825255514

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

```
In [74]:
         # default parameters
         # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples spli
         t=2.
         # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity de
         crease=0.0.
         # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm star
         t=False.
         # class weight=None)
         # Some of methods of RandomForestClassifier()
         # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
         \# predict(X) Perform classification on samples in X.
                                Perform classification on samples in X.
         # predict proba (X)
         # some of attributes of RandomForestClassifier()
         # feature importances : array of shape = [n features]
         # The feature importances (the higher, the more important the feature).
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their
         -construction-2/
         clf = RandomForestClassifier(max depth=max depth[int(best alpha%4)], n estimators=alpha[int(best alpha/4)], c
         riterion='gini', max features='auto', random state=42)
         predict and plot confusion matrix(train x responseCoding, train y,cv x responseCoding,cv y, clf)
```

Log loss : 1.2500037185500072

Number of mis-classified points : 0.4398496240601504

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

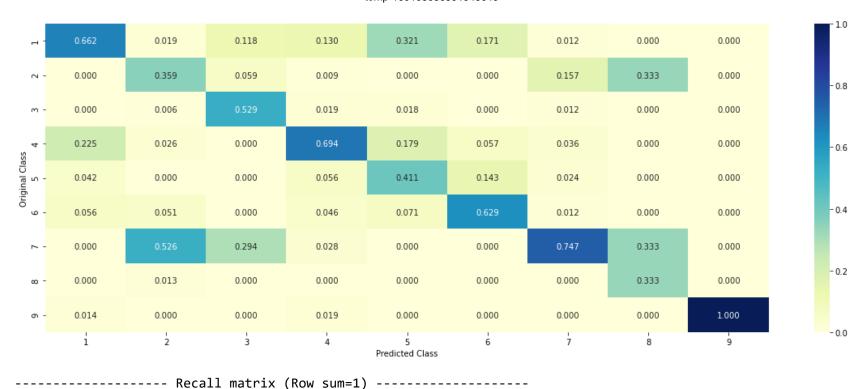
_									
- T	47.000	3.000	2.000	14.000	18.000	6.000	1.000	0.000	0.000
2 -	0.000	56.000	1.000	1.000	0.000	0.000	13.000	1.000	0.000
m -	0.000	1.000	9.000	2.000	1.000	0.000	1.000	0.000	0.000
88 4 -	16.000	4.000	0.000	75.000	10.000	2.000	3.000	0.000	0.000
Original Class 5	3.000	0.000	0.000	6.000	23.000	5.000	2.000	0.000	0.000
Orig 6	4.000	8.000	0.000	5.000	4.000	22.000	1.000	0.000	0.000
۲ -	0.000	82.000	5.000	3.000	0.000	0.000	62.000	1.000	0.000
ω -	0.000	2.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000
თ -	1.000	0.000	0.000	2.000	0.000	0.000	0.000	0.000	3.000
	i	2	3	4	5 Predicted Class	6	7	8	9

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

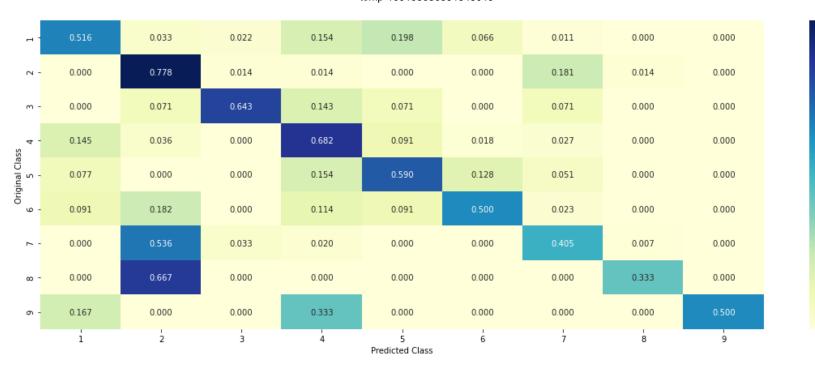
- 20

- 10

-0



https://htmtopdf.herokuapp.com/ipynbviewer/temp/71cf80f0318527bac9a45271212b1ca2/personalised-cancer-analysis.html?t=1601650867897



4.7 Stack the models

- 0.7

- 0.6

- 0.5

- 0.4

- 0.3

- 0.2

-0.1

- 0.0

```
In [75]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/sklearn.linear_model.SG
         DClassifier.html
         # -----
         # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit intercept=True, max iter=None, t
         ol=None.
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0=0.0, power
         t=0.5.
         # class weight=None, warm start=False, average=False, n iter=None)
         # some of methods
        # fit(X, y), coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
        # predict(X) Predict class labels for samples in X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
         # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/gen
        erated/sklearn.svm.SVC.html
         # -----
         # default parameters
        # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, tol=0.001,
        # cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', random state=
         None)
         # Some of methods of SVM()
        # fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
        \# predict(X) Perform classification on samples in X.
        # -----
         # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/mathematical-derivation
         -copy-8/
         # -----
         # read more about support vector machines with linear kernals here http://scikit-learn.org/stable/modules/gen
         erated/sklearn.ensemble.RandomForestClassifier.html
         # -----
         # default parameters
        # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min samples spli
         t=2.
```

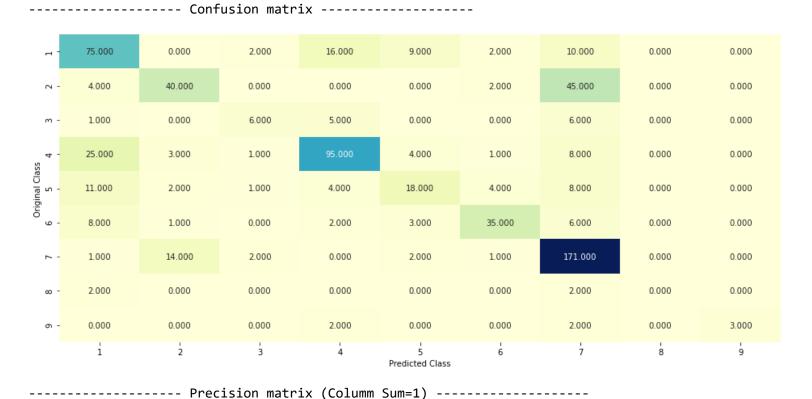
```
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min impurity de
crease=0.0.
# min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None, verbose=0, warm star
t=False.
# class weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
\# predict(X) Perform classification on samples in X.
\# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their
-construction-2/
# -----
clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class weight='balanced', random state=0)
clf1.fit(train x onehotCoding, train y)
sig clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
clf2 = SGDClassifier(alpha=1, penalty='12', loss='hinge', class weight='balanced', random state=0)
clf2.fit(train x onehotCoding, train y)
sig clf2 = CalibratedClassifierCV(clf2, method="sigmoid")
clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train_x_onehotCoding, train y)
sig clf3 = CalibratedClassifierCV(clf3, method="sigmoid")
sig clf1.fit(train x onehotCoding, train y)
print("Logistic Regression : Log Loss: %0.2f" % (log loss(cv y, sig clf1.predict proba(cv x onehotCoding))))
sig clf2.fit(train x onehotCoding, train y)
print("Support vector machines: Log Loss: %0.2f" % (log loss(cv y, sig clf2.predict proba(cv x onehotCoding
))))
sig clf3.fit(train x onehotCoding, train y)
print("Naive Bayes : Log Loss: %0.2f" % (log loss(cv y, sig clf3.predict proba(cv x onehotCoding))))
print("-"*50)
alpha = [0.0001, 0.001, 0.01, 0.1, 1, 10]
```

```
best alpha = 999
for i in alpha:
    lr = LogisticRegression(C=i)
   sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classifier=lr, use_probas=True
    sclf.fit(train x onehotCoding, train y)
   print("Stacking Classifer: for the value of alpha: %f Log Loss: %0.3f" % (i, log loss(cv y, sclf.predict
proba(cv x onehotCoding))))
   log error =log loss(cv y, sclf.predict proba(cv x onehotCoding))
    if best alpha > log error:
       best alpha = log error
Logistic Regression : Log Loss: 1.11
Support vector machines : Log Loss: 1.70
Naive Bayes : Log Loss: 1.27
Stacking Classifer: for the value of alpha: 0.000100 Log Loss: 1.818
Stacking Classifer: for the value of alpha: 0.001000 Log Loss: 1.724
Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.334
Stacking Classifer: for the value of alpha: 0.100000 Log Loss: 1.180
```

4.7.2 testing the model with the best hyper parameters

Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.469 Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.825

Log loss (train) on the stacking classifier: 0.49601922782285474 Log loss (CV) on the stacking classifier: 1.179513082089586 Log loss (test) on the stacking classifier: 1.129657222184161 Number of missclassified point: 0.33383458646616543



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- 160

- 140

- 120

- 100

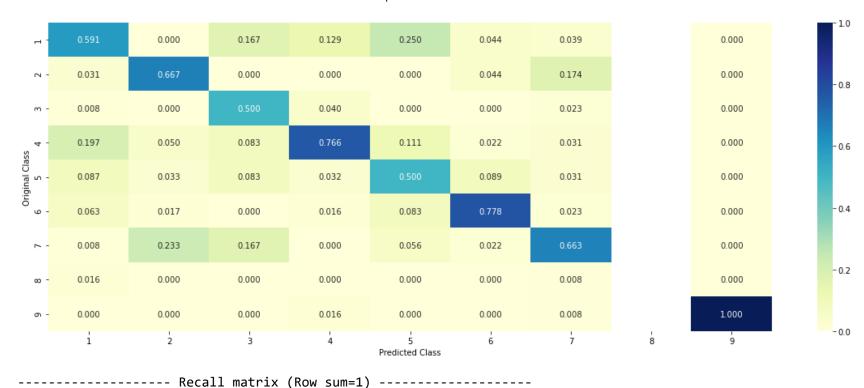
- 80

- 60

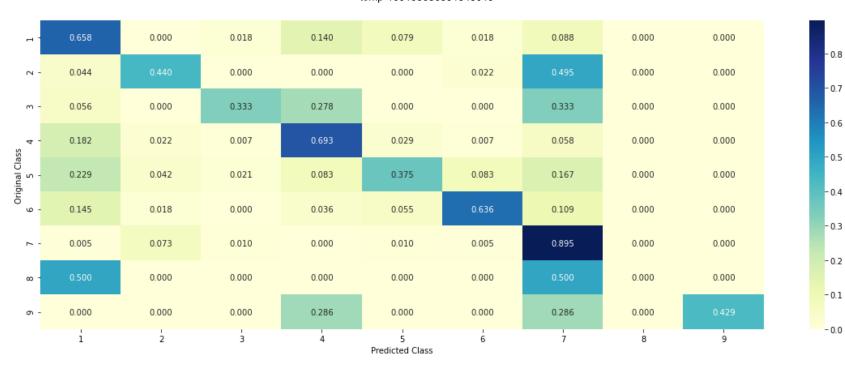
- 40

- 20

-0



https://htmtopdf.herokuapp.com/ipynbviewer/temp/71cf80f0318527bac9a45271212b1ca2/personalised-cancer-analysis.html?t=1601650867897



4.7.3 Maximum Voting classifier

Log loss (train) on the VotingClassifier: 0.8625166091555341 Log loss (CV) on the VotingClassifier: 1.181574347676941 Log loss (test) on the VotingClassifier: 1.1582256363681527 Number of missclassified point: 0.3458646616541353

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

- 1	76.000	0.000	2.000	13.000	9.000	3.000	11.000	0.000	0.000
- 2	4.000	38.000	0.000	0.000	0.000	2.000	47.000	0.000	0.000
m -	1.000	0.000	6.000	5.000	0.000	0.000	6.000	0.000	0.000
. 4 4	32.000	2.000	1.000	87.000	4.000	1.000	10.000	0.000	0.000
Original Class 5	10.000	2.000	1.000	4.000	17.000	5.000	9.000	0.000	0.000
ori	8.000	1.000	0.000	1.000	4.000	35.000	6.000	0.000	0.000
۲ -	1.000	13.000	3.000	0.000	2.000	1.000	171.000	0.000	0.000
∞ -	0.000	0.000	0.000	0.000	0.000	0.000	4.000	0.000	0.000
6 -	0.000	0.000	0.000	0.000	0.000	0.000	1.000	1.000	5.000
	í	2	3	4	5 Predicted Class	6	7	8	9

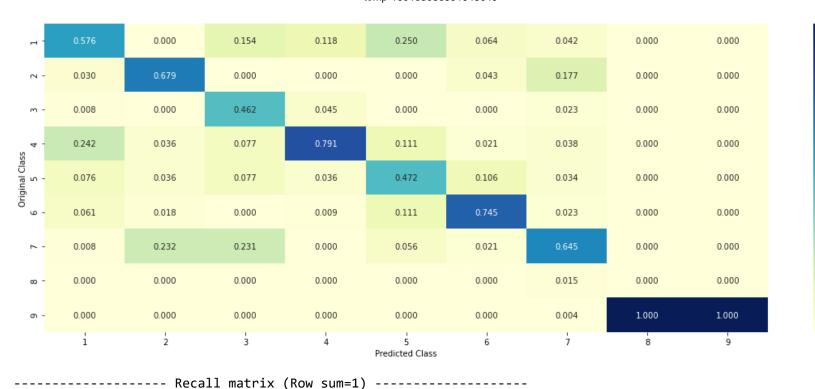
----- Precision matrix (Columm Sum=1) -----

- 60

- 40

- 20

-0



- 0.8

- 0.6

- 0.4

- 0.2

- 0.0