# Personalized cancer diagnosis

# 1. Business Problem

# 1.1. Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training\_variants.zip and training\_text.zip from Kaggle.

#### Context:

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

#### Problem statement:

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

# 1.2. Source/Useful Links

Some articles and reference blogs about the problem statement

- https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almost-everyone-who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25
- 2. <a href="https://www.youtube.com/watch?v=UwbuW7oK8rk">https://www.youtube.com/watch?v=UwbuW7oK8rk</a>
- 3. https://www.youtube.com/watch?v=qxXRKVompI8

# 1.3. Real-world/Business objectives and constraints.

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

# 2. Machine Learning Problem Formulation

## 2.1. Data

#### 2.1.1. Data Overview

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

# 2.1.2. Example Data Point

#### training\_variants

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

...

#### training\_text

#### ID.Text

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

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

# 2.2.1. Type of Machine Learning Problem

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

#### 2.2.2. Performance Metric

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

Metric(s):

- · Multi class log-loss
- Confusion matrix

## 2.2.3. Machine Learing Objectives and Constraints

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

Constraints:

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

# 2.3. Train, CV and Test Datasets

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

# 3. Exploratory Data Analysis

```
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.feature extraction.text import TfidfVectorizer
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
\textbf{from sklearn.svm import} \ \texttt{SVC}
#from sklearn.cross validation import StratifiedKFold
from collections import Counter, defaultdict
from sklearn.calibration import CalibratedClassifierCV
from sklearn.naive bayes import MultinomialNB
from sklearn.naive bayes import GaussianNB
from sklearn.model selection import train test split
from sklearn.model selection import GridSearchCV
import math
from sklearn.metrics import normalized mutual info score
from sklearn.ensemble import RandomForestClassifier
warnings.filterwarnings("ignore")
from mlxtend.classifier import StackingClassifier
from sklearn import model selection
from sklearn.linear model import LogisticRegression
```

# 3.1. Reading Data

## 3.1.1. Reading Gene and Variation Data

```
In [2]:
```

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

Number of data points : 3321
Number of features : 4
Features : ['ID' 'Gene' 'Variation' 'Class']
Out[2]:
```

ID	Gene	Variation	Class

0	Ю	FA <b>66</b>	Truncating Mutations	class
1	1	CBL	W802*	2
2	2	CBL	Q249E	2
3	3	CBL	N454D	3
4	4	CBL	L399V	4

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

- ID: the id of the row used to link the mutation to the clinical evidence
- Gene: the gene where this genetic mutation is located
- Variation: the aminoacid change for this mutations
- Class: 1-9 the class this genetic mutation has been classified on

# 3.1.2. Reading Text Data

#### In [3]:

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

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

#### Out[3]:

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

# 3.1.3. Preprocessing of text

#### In [4]:

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

#### In [5]:

```
#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
```

In [6]:

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

#### Out[6]:

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

# In [7]:

```
result[result.isnull().any(axis=1)]
```

#### Out[7]:

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

there is no text description for id: 2755

Time took for preprocessing the text: 141.639947 seconds

#### In [8]:

```
result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Variation']
```

# In [9]:

```
result[result['ID']==1109]
```

Out[9]:

1109	1109	<b>Gene</b> FANCA	Variation S1088F	Class	FANCA S1088F

# 3.1.4. Test, Train and Cross Validation Split

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

```
In [10]:
```

```
y_true = result['Class'].values
result.Gene = result.Gene.str.replace('\s+', '_')
result.Variation = result.Variation.str.replace('\s+', '_')
# split the data into test and train by maintaining same distribution of output varaible 'y_true'
[stratify=y_true]
X_1, X_test, y_1, y_test = train_test_split(result, y_true, stratify=y_true, test_size=0.2)
# split the train data into train and cross validation by maintaining same distribution of output
varaible 'y_train' [stratify=y_train]
X_train, X_cv, y_train, y_cv = train_test_split(X_1, y_1, stratify=y_1, test_size=0.2)
```

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

#### In [11]:

```
print('Number of data points in train data:', X_train.shape[0])
print('Number of data points in test data:', X_test.shape[0])
print('Number of data points in cross validation data:', X_cv.shape[0])
```

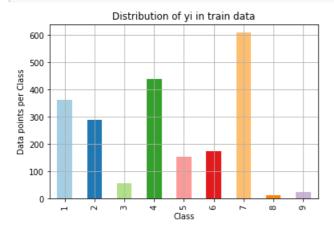
```
Number of data points in train data: 2124
Number of data points in test data: 665
Number of data points in cross validation data: 532
```

#### 3.1.4.2. Distribution of y\_i's in Train, Test and Cross Validation datasets

#### In [12]:

```
#https://stackoverflow.com/questions/50802475/valueerror-invalid-rgba-argument-rgbkymc
# it returns a dict, keys as class labels and values as the number of data points in that class
train_class_distribution = X_train['Class'].value_counts().sort_index()
test class distribution = X test['Class'].value counts().sort index()
cv class distribution = X cv['Class'].value counts().sort index()
paired colors = plt.cm.Paired(range(len(train class distribution)))
train class distribution.plot(kind='bar',color=paired colors)
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in train data')
plt.grid()
plt.show()
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train class distribution.values): the minus sign will give us in decreasing order
sorted yi = np.argsort(-train class distribution.values)
for i in sorted yi:
    print('Number of data points in class', i+1, ':',train_class_distribution.values[i], '(', np.ro
und((train class distribution.values[i]/X train.shape[0]*100), 3), '%)')
print('-'*80)
paired colors = plt.cm.Paired(range(len(test class distribution)))
test class distribution.plot(kind='bar',color=paired_colors)
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in test data')
plt.grid()
plt.show()
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
# -(train class distribution.values): the minus sign will give us in decreasing order
sorted vi = np.argsort(-test class distribution.values)
```

```
for i in sorted yi:
    print('Number of data points in class', i+1, ':',test_class_distribution.values[i], '(', np.rou
nd((test class distribution.values[i]/X test.shape[0]*100), 3), '%)')
print('-'*80)
paired colors = plt.cm.Paired(range(len(cv class distribution)))
cv class distribution.plot(kind='bar',color=paired colors)
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in cross validation data')
plt.grid()
plt.show()
# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.html
 -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted yi:
   print('Number of data points in class', i+1, ':',cv_class_distribution.values[i], '(', np.round
((cv_class_distribution.values[i]/X_cv.shape[0]*100), 3), '%)')
```



```
Number of data points in class 7 : 609 ( 28.672 %)

Number of data points in class 4 : 439 ( 20.669 %)

Number of data points in class 1 : 363 ( 17.09 %)

Number of data points in class 2 : 289 ( 13.606 %)

Number of data points in class 6 : 176 ( 8.286 %)

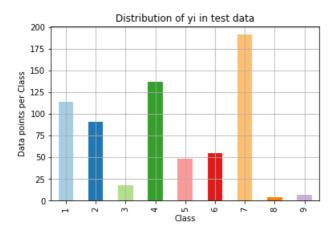
Number of data points in class 5 : 155 ( 7.298 %)

Number of data points in class 3 : 57 ( 2.684 %)

Number of data points in class 9 : 24 ( 1.13 %)

Number of data points in class 8 : 12 ( 0.565 %)
```

-----



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

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

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

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

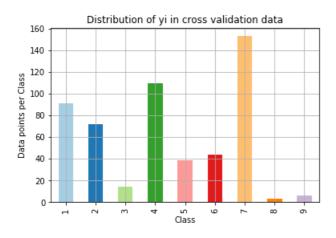
Number of data points in class 6 : 55 ( 8.271 %)

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

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

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

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



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

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

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

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

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

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

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

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

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

# 3.2 Prediction using a 'Random' Model

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

#### In [13]:

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

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

print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
plt.figure(figsize=(20,7))
sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=labels, yticklabels=labels)
plt.xlabel('Predicted Class')
plt.ylabel('Original Class')
plt.show()

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

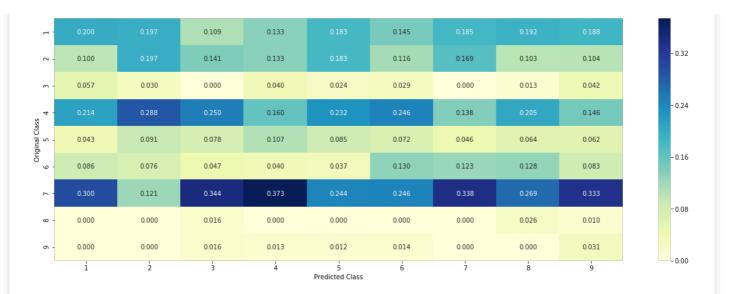
#### In [14]:

```
\# 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 = X test.shape[0]
cv data len = X cv.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)
    \texttt{test\_predicted\_y[i] = ((rand\_probs/sum(sum(rand\_probs)))[0])}
print("Log loss on Test Data using Random Model", log loss(y test, test predicted y, eps=1e-15))
predicted_y =np.argmax(test_predicted_y, axis=1)
plot confusion matrix(y test, predicted y+1)
```

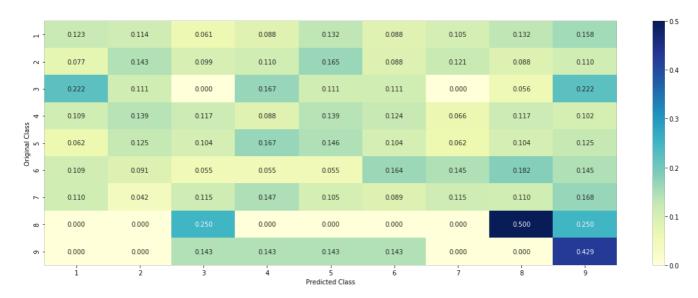
Log loss on Cross Validation Data using Random Model 2.5358430631813267 Log loss on Test Data using Random Model 2.5182132107572777 ------ Confusion matrix ------



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



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



# 3.3 Univariate Analysis

In [15]:

```
# code for response coding with Laplace smoothing.
# alpha : used for laplace smoothing
# feature: ['gene', 'variation']
# df: ['X_train', 'X_test', 'X_cv']
# algorithm
# Consider all unique values and the number of occurances of given feature in train data dataframe
\# build a vector (1*9) , the first element = (number of times it occured in class1 + 10*alpha / nu
mber of time it occurred in total data+90*alpha)
\# gv_dict is like a look up table, for every gene it store a (1*9) representation of it
 for a value of feature in df:
# if it is in train data:
\# we add the vector that was stored in 'gv_dict' look up table to 'gv_fea'
# if it is not there is train:
# we add [1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9] to 'gv_fea'
# return 'gv_fea'
# get gv fea dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
   # value_count: it contains a dict like
   # print(X train['Gene'].value counts())
    # output:
             {BRCA1
                         174
              TP53
```

```
EGFR
            BRCA2
            PTEN
            KTT
                      61
            BRAF
                      60
            ERBB2
                      47
           PDGFRA
                      46
            . . . }
   # print(X train['Variation'].value counts())
   # output:
   # Truncating Mutations
                                          6.3
   # Deletion
                                          43
   # Amplification
                                          4.3
                                          22
   # Fusions
   # Overexpression
                                          3
                                          3
   # E17K
   # 061L
                                           3
   # S222D
   # P130S
   value_count = X_train[feature].value_counts()
   # gv dict : Gene Variation Dict, which contains the probability array for each gene/variation
   gv dict = dict()
   # denominator will contain the number of time that particular feature occured in whole data
   for i, denominator in value count.items():
      \# vec will contain (p(yi==1/Gi) probability of gene/variation belongs to perticular class
       # vec is 9 diamensional vector
      vec = []
      for k = n  range (1, 10):
          # print(X train.loc[(X train['Class']==1) & (X train['Gene']=='BRCA1')])
          # ID Gene Variation Class
# 2470 2470 BRCA1 S1715C 1
          # 2486 2486 BRCA1
                                         S1841R
          # 2614 2614 BRCA1
                                           M1R
          # 2432 2432 BRCA1
                                         L1657P
                                         T1685A
          # 2567 2567 BRCA1
          # 2583 2583 BRCA1
# 2634 2634 BRCA1
                                         E1660G
                                         W1718T
          # cls cnt.shape[0] will return the number of rows
          cls cnt = X train.loc[(X train['Class']==k) & (X train[feature]==i)]
          # cls cnt.shape[0](numerator) will contain the number of time that particular feature (
ccured in whole data
          vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
       # we are adding the gene/variation to the dict as key and vec as value
      gv dict[i]=vec
   return gv_dict
# Get Gene variation feature
def get gv feature(alpha, feature, df):
   # print(gv_dict)
        {'BRCA1': [0.20075757575757575, 0.0378787878787878, 0.068181818181818177,
0.13636363636363635,\ 0.25,\ 0.1931818181818181818,\ 0.03787878787878788,\ 0.03787878787878788,
0.03787878787878787881,
         'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366,
163265307, 0.056122448979591837],
         'EGFR': [0.05681818181818181816, 0.215909090909091, 0.0625, 0.068181818181818177,
0.068181818181818177, 0.0625, 0.346590909090912, 0.0625, 0.056818181818181816],
         'BRCA2': [0.1333333333333333, 0.0606060606060608, 0.0606060606060608,
0..07878787878787878782,\ 0..13939393939394,\ 0..345454545454546,\ 0..060606060606060608,
0.06060606060606060608, 0.060606060606060608],
         'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917,
761006289, 0.062893081761006289],
         'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295,
0.072847682119205295,\ 0.066225165562913912,\ 0.066225165562913912,\ 0.27152317880794702,
0.066225165562913912, 0.066225165562913912],
        'BRAF': [0.0666666666666666666, 0.17999999999999, 0.073333333333333334,
```

```
gv_dict = get_gv_fea_dict(alpha, feature, df)
    # value count is similar in get gv fea dict
   value_count = X_train[feature].value_counts()
    # gv_fea: Gene_variation feature, it will contain the feature for each feature value in the da
t.a
   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])
             gv fea.append([-1,-1,-1,-1,-1,-1,-1,-1])
   return gv fea
4
```

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

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

# 3.2.1 Univariate Analysis on Gene Feature

Q1. Gene, What type of feature it is?

Ans. Gene is a categorical variable

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

```
In [16]:
```

```
unique genes = X train['Gene'].value counts()
print('Number of Unique Genes :', unique genes.shape[0])
# the top 10 genes that occured most
print(unique_genes.head(10))
Number of Unique Genes: 230
BRCA1 161
TP53
EGFR
         93
         82
PTEN
BRCA2
BRAF
         65
          57
KIT
ERBB2
          44
ALK
         41
         37
FLT3
Name: Gene, dtype: int64
```

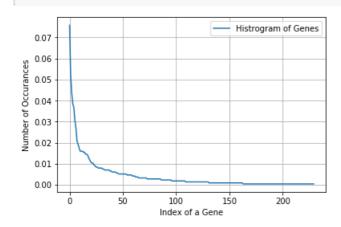
#### In [17]:

```
print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in the train data, an
d they are distibuted as follows",)
```

Ans: There are 230 different categories of genes in the train data, and they are distibuted as fol lows

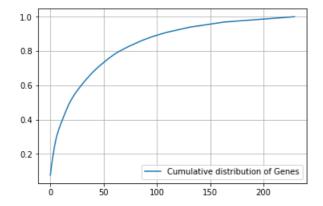
#### In [18]:

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



#### In [19]:

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



# Q3. How to featurize this Gene feature?

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

- 1. One hot Encoding
- 2. Response coding

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

# In [20]:

```
#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", X_train))
# test gene feature
test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", X_test))
# cross validation gene feature
cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", X_cv))
```

#### In [21]:

```
print("train_gene_feature_responseCoding is converted feature using respone coding method. The sha
pe of gene feature:", train_gene_feature_responseCoding.shape)
```

 ${\tt train\_gene\_feature\_responseCoding~is~converted~feature~using~respone~coding~method.~The~shape~of~g}$ 

```
ene feature: (2124, 9)
In [22]:
# one-hot encoding of Gene feature.
gene vectorizer = CountVectorizer(ngram range=(1,2))
train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(X_train['Gene'])
test_gene_feature_onehotCoding = gene_vectorizer.transform(X_test['Gene'])
cv gene feature onehotCoding = gene vectorizer.transform(X cv['Gene'])
In [146]:
# tfidf encoding of Gene feature.
gene tfidf vectorizer = TfidfVectorizer(ngram range=(1,1))
train gene feature tfidf = gene tfidf vectorizer.fit transform(X train['Gene'])
test gene feature tfidf = gene tfidf vectorizer.transform(X test['Gene'])
cv gene feature tfidf = gene tfidf vectorizer.transform(X cv['Gene'])
In [112]:
print("train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The sha
pe of gene feature:", train_gene_feature_tfidf.shape)
train gene feature onehotCoding is converted feature using one-hot encoding method. The shape of g
ene feature: (2124, 230)
```

# **Q4.** How good is this gene feature in predicting y\_i?

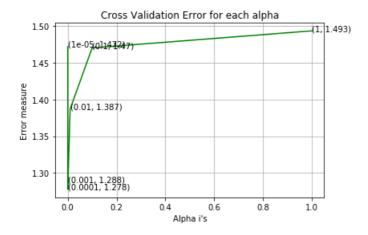
There are many ways to estimate how good a feature is, in predicting y\_i. One of the good methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y\_i.

```
In [25]:
```

```
alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear\ model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link:
cv log error array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
    clf.fit(train gene feature onehotCoding, y train)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig clf.fit(train gene feature onehotCoding, y train)
    predict y = sig clf.predict proba(cv gene feature onehotCoding)
   cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
   print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, labels=clf.clas
ses_, 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.arid()
plt.title("Cross Validation Error for each alpha")
```

```
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
clf.fit(train gene feature onehotCoding, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_gene_feature_onehotCoding, y_train)
predict y = sig clf.predict proba(train gene feature onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
predict y, labels=clf.classes , eps=1e-15))
predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",log loss(y test, p
redict y, labels=clf.classes , eps=1e-15))
For values of alpha = 1e-05 The log loss is: 1.4718910639355252
```

```
For values of alpha = 1e-05 The log loss is: 1.4718910639355252
For values of alpha = 0.0001 The log loss is: 1.2775050083514932
For values of alpha = 0.001 The log loss is: 1.2876432742746475
For values of alpha = 0.01 The log loss is: 1.3870437053419553
For values of alpha = 0.1 The log loss is: 1.4701829768717998
For values of alpha = 1 The log loss is: 1.493404590983701
```



```
For values of best alpha = 0.0001 The train log loss is: 1.039603279111539
For values of best alpha = 0.0001 The cross validation log loss is: 1.2775050083514932
For values of best alpha = 0.0001 The test log loss is: 1.1978393112378956
```

## 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 [26]:

```
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=X_test[X_test['Gene'].isin(list(set(X_train['Gene'])))].shape[0]

cv_coverage=X_cv[X_cv['Gene'].isin(list(set(X_train['Gene'])))].shape[0]

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

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

[*]
```

- Q6. How many data points in Test and CV datasets are covered by the 230 genes in train dataset?
- 1. In test data 645 out of 665 : 96.99248120300751
- 2. In cross validation data 509 out of 532 : 95.67669172932331

# 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 [27]:

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

```
Number of Unique Variations: 1931
Truncating_Mutations
Deletion
                        50
Amplification
                         45
                        16
Fusions
Overexpression
G12V
                         4
061H
                         3
Q61R
                          3
T58T
E17K
Name: Variation, dtype: int64
```

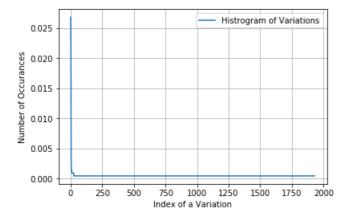
#### In [28]:

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

Ans: There are 1931 different categories of variations in the train data, and they are distibuted as follows

# In [29]:

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

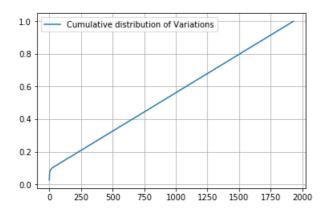


# In [30]:

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

```
plt.show()
```

[0.02683616 0.05037665 0.07156309 ... 0.99905838 0.99952919 1.



#### **Q9.** How to featurize this Variation feature?

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

- 1. One hot Encoding
- 2. Response coding

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

#### In [31]:

```
# alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", X_train))
# test gene feature
test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", X_test))
# cross validation gene feature
cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", X_cv))
```

# In [32]:

```
print("train_variation_feature_responseCoding is a converted feature using the response coding met
hod. The shape of Variation feature:", train_variation_feature_responseCoding.shape)
```

 $train\_variation\_feature\_responseCoding$  is a converted feature using the response coding method. The shape of Variation feature: (2124, 9)

#### In [33]:

```
# one-hot encoding of variation feature.
variation_vectorizer = CountVectorizer(ngram_range=(1,2))
train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(X_train['Variation'])
test_variation_feature_onehotCoding = variation_vectorizer.transform(X_test['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(X_cv['Variation'])
```

#### In [148]:

```
# tfidf encoding of variation feature.
variation_tfidf_vectorizer = TfidfVectorizer(ngram_range=(1,1))
train_variation_feature_tfidf = variation_tfidf_vectorizer.fit_transform(X_train['Variation'])
test_variation_feature_tfidf = variation_tfidf_vectorizer.transform(X_test['Variation'])
cv_variation_feature_tfidf = variation_tfidf_vectorizer.transform(X_cv['Variation'])
```

#### In [114]:

```
od. The shape of Variation feature:", train_variation_feature_tfidf.shape)
```

train\_variation\_feature\_onehotEncoded is converted feature using the onne-hot encoding method. The shape of Variation feature: (2124, 2066)

# Q10. How good is this Variation feature in predicting y i?

Let's build a model just like the earlier!

```
In [36]:
```

```
alpha = [10 ** x for x in range(-5, 1)]
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link:
cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
    clf.fit(train variation feature onehotCoding, y train)
   sig clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig clf.fit(train variation feature onehotCoding, y train)
    predict y = sig clf.predict proba(cv variation feature onehotCoding)
   cv log error array.append(log loss(y cv, predict y, labels=clf.classes , eps=1e-15))
   print('For values of alpha = ', i, "The log loss is:", log loss(y cv, predict y, labels=clf.clas
ses_, eps=1e-15))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv log error array,3)):
   ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random state=42)
clf.fit(train variation feature onehotCoding, y train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train variation feature onehotCoding, y train)
predict_y = sig_clf.predict_proba(train_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(test variation feature onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The test log loss is: ",log loss(y test, p
redict y, labels=clf.classes , eps=1e-15))
```

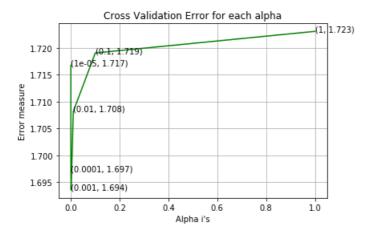
For values of alpha = 1e-05 The log loss is: 1.7167196126504518 For values of alpha = 0.0001 The log loss is: 1.6970744784336635

```
For values of alpha = 0.001 The log loss is: 1.6935926369802465

For values of alpha = 0.01 The log loss is: 1.7081638298695538

For values of alpha = 0.1 The log loss is: 1.7190330123402875

For values of alpha = 1 The log loss is: 1.7230468914787866
```



```
For values of best alpha = 0.001 The train log loss is: 1.0530749177305776
For values of best alpha = 0.001 The cross validation log loss is: 1.6935926369802465
For values of best alpha = 0.001 The test log loss is: 1.7037824676287987
```

# 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 [37]:

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

Q12. How many data points are covered by total 1931 genes in test and cross validation data sets? Ans

1. In test data 66 out of 665 : 9.924812030075188

2. In cross validation data 59 out of 532 : 11.090225563909774

## 3.2.3 Univariate Analysis on Text Feature

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

# In [38]:

```
In [39]:
```

#### In [40]:

```
# building a CountVectorizer with all the words that occured minimum 3 times in train data
text_vectorizer = CountVectorizer(min_df=3,ngram_range=(1,2))
train_text_feature_onehotCoding = text_vectorizer.fit_transform(X_train['TEXT'])
# getting all the feature names (words)
train_text_features= text_vectorizer.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).Al will sum every row and returns (1*number of feature) vector
train_text_fea_counts = train_text_feature_onehotCoding.sum(axis=0).Al
#print(train_text_fea_counts)
# zip(list(text_fea_tures),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(text_fea_dict)

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

Total number of unique words in train data: 766917

#### In [184]:

```
# tfidf encoding of text feature.
text_tfidf_vectorizer = TfidfVectorizer(max_features=1250,ngram_range=(1,1))
train_text_feature_tfidf = text_tfidf_vectorizer.fit_transform(X_train['TEXT'])
test_text_feature_tfidf = text_tfidf_vectorizer.transform(X_test['TEXT'])
cv_text_feature_tfidf = text_tfidf_vectorizer.transform(X_cv['TEXT'])
```

### In [42]:

```
dict list = []
# dict list =[] contains 9 dictoinaries each corresponds to a class
for i in range (1,10):
    cls text = X train[X train['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(X_train)
confuse_array = []
for i in train text features:
    ratios = []
   max_val = -1
    for j in range (0,9):
       ratios.append((dict list[j][i]+10 )/(total dict[i]+90))
    confuse array.append(ratios)
confuse array = np.array(confuse array)
```

#### In [43]:

#roomongo goding of tout footung

```
train_text_feature_responseCoding = get_text_responsecoding(X_train)
test_text_feature_responseCoding = get_text_responsecoding(X_test)
cv_text_feature_responseCoding = get_text_responsecoding(X_cv)
```

#### In [44]:

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

#### In [45]:

```
# don't forget to normalize every feature
train_text_feature_onehotCoding = normalize(train_text_feature_onehotCoding, axis=0)

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

#### In [185]:

```
#normalizing tfidf features
train_text_feature_tfidf = normalize(train_text_feature_tfidf, axis=0)
cv_text_feature_tfidf = normalize(cv_text_feature_tfidf, axis=0)
test_text_feature_tfidf = normalize(test_text_feature_tfidf, axis=0)
```

#### In [47]:

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

# In [48]:

```
# Number of words for a given frequency.
print(Counter(sorted_text_occur))
```

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```

#### In [49]:

```
# Train a Logistic regression+Calibration model using text features which are one-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.SGDC lassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link:
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)
    \verb|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.clas
ses , eps=1e-15))
fig, ax = plt.subplots()
ax.plot(alpha, cv log error array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best alpha = np.argmin(cv log error array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
clf.fit(train text_feature_onehotCoding, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_onehotCoding, y_train)
predict_y = sig_clf.predict_proba(train_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_loss(y_train,
predict y, labels=clf.classes , eps=1e-15))
predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best alpha], "The cross validation log loss is:",log lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_text_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha = 1e-05 The log loss is: 1.5143069505709046

For values of alpha = 0.0001 The log loss is: 1.5117748280810117

For values of alpha = 0.001 The log loss is: 1.4631832833821021

For values of alpha = 0.01 The log loss is: 1.2810406538068342

For values of alpha = 0.1 The log loss is: 1.313435977576093

For values of alpha = 1 The log loss is: 1.375070302009839
```

# Cross Validation Error for each alpha (0.001, 1.463) 1.40 1.35 1.30 (0.1, 1.313) (0.1, 1.313) (0.1, 1.313) (0.1, 1.281) (0.0 0.2 0.4 0.6 0.8 1.0 Alpha i's

```
For values of best alpha = 0.01 The train log loss is: 0.8717855736127258
For values of best alpha = 0.01 The cross validation log loss is: 1.2810406538068342
For values of best alpha = 0.01 The test log loss is: 1.1678793551365518
```

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

Ans. Yes, it seems like!

```
In [50]:
```

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

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

#### In [51]:

```
len1,len2 = get_intersec_text(X_test)
print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data")
len1,len2 = get_intersec_text(X_cv)
print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train data")
```

```
96.978 % of word of test data appeared in train data 97.305 % of word of Cross Validation appeared in train data
```

# 4. Machine Learning Models

#### In [52]:

```
#Data preparation for ML models.

#Misc. functionns for ML models

def predict_and_plot_confusion_matrix(train_x, train_y, test_x, test_y, clf):
    clf.fit(train_x, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x, train_y)
    red w = sig_clf_predict(test_w)
```

```
# 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
global mis_per
mis_per=(np.count_nonzero((pred_y- test_y))/test_y.shape[0])*100
print("Number of mis-classified points:", np.count_nonzero((pred_y- test_y))/test_y.shape[0])
plot_confusion_matrix(test_y, pred_y)
```

In [53]:

```
def report_log_loss(train_x, train_y, test_x, test_y, clf):
    clf.fit(train_x, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x, train_y)
    sig_clf_probs = sig_clf.predict_proba(test_x)
    return log_loss(test_y, sig_clf_probs, eps=le-15)
```

In [54]:

```
# this function will be used just for naive bayes
# for the given indices, we will print the name of the features
# and we will check whether the feature present in the test point text or not
def get impfeature names (indices, text, gene, var, no features):
   gene count vec = CountVectorizer(ngram range=(1,2))
    var count vec = CountVectorizer(ngram range=(1,2))
    text count vec = CountVectorizer(min df=3,ngram range=(1,2))
    gene vec = gene count vec.fit(X train['Gene'])
    var_vec = var_count_vec.fit(X_train['Variation'])
    text_vec = text_count_vec.fit(X_train['TEXT'])
    fea1 len = len(gene vec.get feature names())
    fea2 len = len(var_count_vec.get_feature_names())
    word_present = 0
    for i,v in enumerate(indices):
       if (v < feal len):</pre>
            word = gene_vec.get_feature_names()[v]
            yes no = True if word == gene else False
            if yes no:
                word_present += 1
                print(i, "Gene feature [{}] present in test data point [{}]".format(word,yes no))
        elif (v < fea1 len+fea2 len):</pre>
            word = var vec.get feature names()[v-(fea1 len)]
            yes no = True if word == var else False
            if yes_no:
                word present += 1
                print(i, "variation feature [{}] present in test data point [{}]".format(word, yes_r
0))
            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")
4
```

# Stacking the three types of features

In [186]:

```
# merging gene, variance and text features

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

```
# IISLaCK(a, D) = [[1, 2, 4, 3],
                 [ 3, 4, 6, 7]]
#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(X train['Class']))
#test x onehotCoding = hstack((test gene var onehotCoding,
test text feature onehotCoding)).tocsr()
#test y = np.array(list(X test['Class']))
#cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text_feature_onehotCoding)).tocsr()
\#cv_y = np.array(list(X_cv['Class']))
#train_gene_var_responseCoding =
np.hstack((train gene feature responseCoding, train variation feature responseCoding))
#test gene var responseCoding =
np.hstack((test gene feature responseCoding,test variation feature responseCoding))
#cv gene var responseCoding =
np.hstack((cv gene feature responseCoding,cv variation feature responseCoding))
#train x responseCoding = np.hstack((train gene var responseCoding,
train text feature responseCoding))
#test x responseCoding = np.hstack((test gene var responseCoding,
test_text_feature_responseCoding))
\#cv\_x\_responseCoding = np.hstack((cv\_gene\_var\_responseCoding, cv\_text\_feature\_responseCoding))
train gene var tfidf=hstack((train gene feature tfidf,train variation feature tfidf))
test gene var tfidf=hstack((test gene feature tfidf,test variation feature tfidf))
cv gene var tfidf=hstack((cv gene feature tfidf,cv variation feature tfidf))
train x tfidf=hstack((train gene var tfidf,train text feature tfidf))
test x tfidf=hstack((test gene var tfidf,test text feature tfidf))
cv_x_tfidf=hstack((cv_gene_var_tfidf,cv_text_feature_tfidf))
In [56]:
print("One hot encoding features :")
print("(number of data points * number of features) in train data = ", train x onehotCoding.shape)
print("(number of data points * number of features) in test data = ", test_x_onehotCoding.shape)
print("(number of data points * number of features) in cross validation data =", cv_x_onehotCoding
.shape)
One hot encoding features :
(number of data points * number of features) in train data = (2124, 769211)
(number of data points * number of features) in test data = (665, 769211)
(number of data points * number of features) in cross validation data = (532, 769211)
In [57]:
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ", train x responseCoding.shap
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)
In [187]:
print(" tfidf encoding features :")
```

```
print("(number of data points * number of features) in train data = ", train_x_tridf.snape)
print("(number of data points * number of features) in test data = ", test_x_tfidf.shape)
print("(number of data points * number of features) in cross validation data = ", cv_x_tfidf.shape)

tfidf encoding features:
(number of data points * number of features) in train data = (2124, 3444)
(number of data points * number of features) in test data = (665, 3444)
(number of data points * number of features) in cross validation data = (532, 3444)

In [59]:

#groupDF = [X_train, X_cv, X_test]
#for i in groupDF:
# i.drop(['Class'], axis=1, inplace=True)
```

# 4.1. Base Line Model

# 4.1.1. Naive Bayes

#### 4.1.1.1. Hyper parameter tuning

```
In [60]:
```

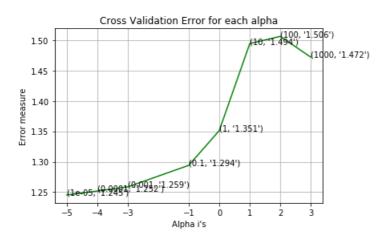
```
from prettytable import PrettyTable
x = PrettyTable()
x.field_names = ["ML Model", "Train Log Loss", "CV Log Loss", "Test Log Loss", "Misclassification %"]
```

#### In [61]:

```
# find more about Multinomial Naive base function here http://scikit-
learn.org/stable/modules/generated/sklearn.naive bayes.MultinomialNB.html
# default paramters
# sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_prior=None)
# some of methods of MultinomialNB()
# fit(X, y[, sample_weight]) Fit Naive Bayes classifier according to X, y
# predict(X) Perform classification on an array of test vectors X.
# predict_log_proba(X) Return log-probability estimates for the test vector X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-
algorithm-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
# 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 tfidf. v train)
```

```
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig clf.fit(train x tfidf, y train)
    sig_clf_probs = sig_clf.predict_proba(cv_x_tfidf)
    \verb|cv_log_error_array.append(log_loss(y_cv, 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(y cv, 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_tfidf, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x tfidf, y train)
predict y = sig clf.predict proba(train x tfidf)
train ll=log loss(y train, predict y, labels=clf.classes , eps=1e-15)
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_tfidf)
cv_ll=log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(test x tfidf)
test_ll=log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict y, labels=clf.classes , eps=1e-15))
```

```
for alpha = 1e-05
Log Loss: 1.245401013356264
for alpha = 0.0001
Log Loss : 1.2518259595269317
for alpha = 0.001
Log Loss: 1.258637606741886
for alpha = 0.1
Log Loss: 1.2940837840410697
for alpha = 1
Log Loss: 1.3512928304426302
for alpha = 10
Log Loss: 1.4943723990295623
for alpha = 100
Log Loss: 1.5062717285108203
for alpha = 1000
Log Loss: 1.4721096315440183
```



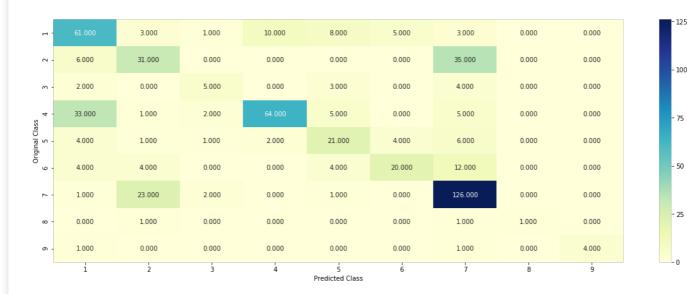
For values of best alpha = 1e-05 The train log loss is: 0.6141817542885196For values of best alpha = 1e-05 The cross validation log loss is: 1.245401013356264

#### 4.1.1.2. Testing the model with best hyper paramters

In [62]:

```
# find more about Multinomial Naive base function here http://scikit-
learn.org/stable/modules/generated/sklearn.naive bayes.MultinomialNB.html
# default paramters
# sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=None)
# some of methods of MultinomialNB()
# fit(X, y[, sample weight]) Fit Naive Bayes classifier according to X, y
# predict(X) Perform classification on an array of test vectors X.
# predict_log_proba(X) Return log-probability estimates for the test vector X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/naive-bayes-
algorithm-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train x tfidf, y train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train_x_tfidf, y_train)
sig clf probs = sig clf.predict proba(cv x tfidf)
# to avoid rounding error while multiplying probabilites we use log-probability estimates
print("Log Loss :",log_loss(y_cv, sig_clf_probs))
mis per=(np.count nonzero((sig clf.predict(cv x tfidf)- y cv))/y cv.shape[0])*100
print("Number of missclassified point:", np.count nonzero((sig clf.predict(cv x tfidf) - y cv))/y
cv.shape[0])
x.add_row(["Naive Bayes(TFIDF)",train_ll,cv_ll,test_ll,mis_per])
plot_confusion_matrix(y_cv, sig_clf.predict(cv_x_tfidf.toarray()))
```

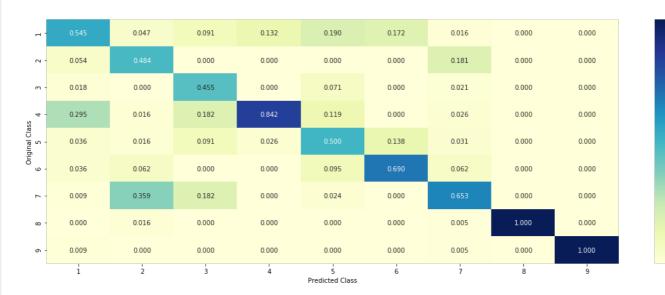
Log Loss: 1.245401013356264 Number of missclassified point : 0.37406015037593987 ----- Confusion matrix -----



75

50





1.0

- 0.8

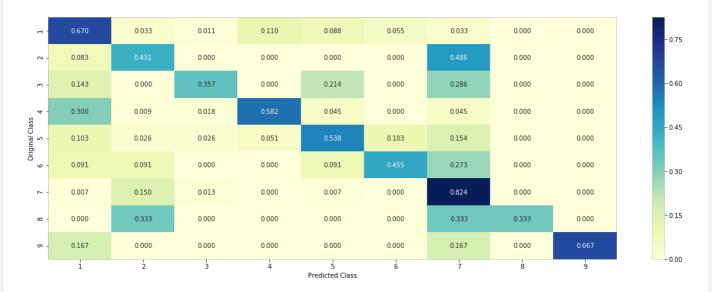
- 0.6

- 0.4

-02

0.0

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



#### 4.1.1.3. Feature Importance, Correctly classified point

```
In [63]:
```

```
test_point_index = 1
no_feature = 100
predicted_cls = sig_clf.predict(test_x_tfidf.tocsr()[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf.tocsr()
[test_point_index]), 4))
print("Actual Class :", y_test[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], X_test['TEXT'].iloc[test_point_index], X_test['Gene'].iloc[test_point_index], X_test['Variation'].iloc[test_point_index], no_feature)

Predicted Class : 7
Predicted Class Probabilities: [[0.0589 0.0547 0.0147 0.0824 0.0418 0.0404 0.7001 0.0045 0.0024]]
Actual Class : 7
```

# 4.1.1.4. Feature Importance, Incorrectly classified point

Out of the top 100 features 0 are present in query point

```
In [64]:
test point index = 100
no feature = 100
predicted cls = sig clf.predict(test x tfidf.tocsr()[test point index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x tfidf.tocsr()
[test point index]),4))
print("Actual Class :", y test[test point index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get impfeature names(indices[0], X test['TEXT'].iloc[test point index], X test['Gene'].iloc[test poi
nt_index], X_test['Variation'].iloc[test_point_index], no_feature)
Predicted Class: 1
Predicted Class Probabilities: [[0.6457 0.0575 0.0155 0.0889 0.044 0.0425 0.0986 0.0048 0.0026]]
Actual Class : 1
Out of the top 100 features 0 are present in query point
```

# 4.2. K Nearest Neighbour Classification

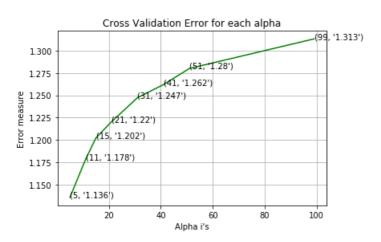
# 4.2.1. Hyper parameter tuning

In [65]:

```
# find more about KNeighborsClassifier() here http://scikit-
learn.org/stable/modules/generated/sklearn.neighbors. \textit{KN} eighborsClassifier.html \\
# default parameter
# KNeighborsClassifier(n neighbors=5, weights='uniform', algorithm='auto', leaf size=30, p=2,
# metric='minkowski', metric params=None, n jobs=1, **kwargs)
# methods of
# fit(X, y) : Fit the model using X as training data and y as target values
# predict(X): Predict the class labels for the provided data
# predict proba(X): Return probability estimates for the test data X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/k-nearest-ne
ighbors-geometric-intuition-with-a-toy-example-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample weight]) Fit the calibrated model
# get params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
# video link:
alpha = [5, 11, 15, 21, 31, 41, 51, 99]
cv_log_error_array = []
for i in alpha:
   print("for alpha =", i)
   clf = KNeighborsClassifier(n neighbors=i)
   clf.fit(train x tfidf, y train)
   sig clf = CalibratedClassifierCV(clf, method="sigmoid")
   sig clf.fit(train_x_tfidf, y_train)
   sig clf probs = sig clf.predict proba(cv x tfidf)
   cv_log_error_array.append(log_loss(y_cv, 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(y_cv, sig_clf_probs))
fig av = nlt euhnlote()
```

```
IIY, ax - pic.suppious()
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_tfidf, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x tfidf, y train)
predict y = sig clf.predict proba(train x tfidf)
train_ll=log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15)
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_tfidf)
cv_ll=log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(test x tfidf)
test_ll=log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict y, labels=clf.classes , eps=1e-15))
```

```
for alpha = 5
Log Loss: 1.135750482766513
for alpha = 11
Log Loss : 1.178231428538192
for alpha = 15
Log Loss: 1.2022566993612505
for alpha = 21
Log Loss: 1.2203849319429523
for alpha = 31
Log Loss: 1.2472904249925698
for alpha = 41
Log Loss: 1.2619254722221698
for alpha = 51
Log Loss: 1.2799913128119973
for alpha = 99
Log Loss: 1.3130887392595583
```



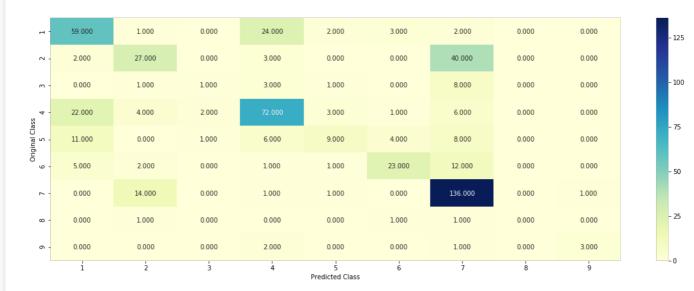
```
For values of best alpha = 5 The train log loss is: 0.9110478758175219

For values of best alpha = 5 The cross validation log loss is: 1.135750482766513

For values of best alpha = 5 The test log loss is: 1.0775710518751482
```

# 4.2.2. Testing the model with best hyper paramters

```
In [66]:
```



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



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

<b>-</b> -	0.648	0.011	0.000	0.264	0.022	0.033	0.022	0.000	0.000
2 -	0.028	0.375	0.000	0.042	0.000	0.000		0.000	0.000
m -	0.000	0.071	0.071	0.214	0.071	0.000	0.571	0.000	0.000



# 4.2.3. Sample Query point -1

```
In [67]:
```

```
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train_x_tfidf, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_tfidf, y_train)

test_point_index = 1
predicted_cls = sig_clf.predict(test_x_tfidf.tocsr()[0].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Actual Class :", y_test[test_point_index])
neighbors = clf.kneighbors(test_x_tfidf.tocsr()[test_point_index].reshape(1, -1), alpha[best_alpha])
print("The ",alpha[best_alpha]," nearest neighbours of the test points belongs to classes",y_train
[neighbors[1][0]])
print("Fequency of nearest points :",Counter(y_train[neighbors[1][0]]))

Predicted Class : 4
Actual Class : 7
The 5 nearest neighbours of the test points belongs to classes [7 7 2 7 7]
Fequency of nearest points : Counter({7: 4, 2: 1})
```

# 4.2.4. Sample Query Point-2

#### In [68]:

```
clf = KNeighborsClassifier(n neighbors=alpha[best alpha])
clf.fit(train_x_tfidf, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_tfidf, y_train)
test point index = 100
predicted cls = sig clf.predict(test x tfidf.tocsr()[test point index].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Actual Class :", y_test[test_point_index])
neighbors = clf.kneighbors(test x tfidf.tocsr()[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 be
longs to classes",y train[neighbors[1][0]])
print("Fequency of nearest points :",Counter(y_train[neighbors[1][0]]))
Predicted Class: 2
Actual Class: 1
the k value for knn is 5 and the nearest neighbours of the test points belongs to classes [1 2 7 2
Fequency of nearest points : Counter({2: 2, 7: 2, 1: 1})
```

# 4.3. Logistic Regression

# 4.3.1. With Class balancing

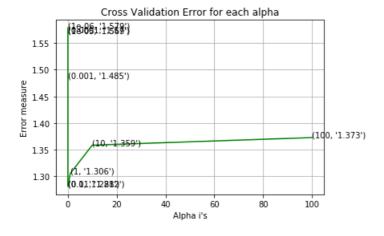
### 4.3.1.1. Hyper paramter tuning

```
In [102]:
```

```
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class weight=None, warm start=False, average=False, n iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample weight]) Fit the calibrated model
# get params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
# video link:
alpha = [10 ** x for x in range(-6, 3)]
cv log error array = []
for i in alpha:
   print("for alpha =", i)
    clf = SGDClassifier(class_weight='balanced', alpha=i, penalty='12', loss='log', random state=42
    clf.fit(train x onehotCoding, y train)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig clf.fit(train x onehotCoding, y train)
    sig clf probs = sig clf.predict proba(cv x onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, 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(y_cv, 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', ran
dom state=42)
clf.fit(train_x_onehotCoding, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, y train)
predict y = sig clf.predict proba(train x onehotCoding)
train ll=log loss(y train, predict y, labels=clf.classes , eps=1e-15)
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)
cv_ll=log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15)
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_x_onehotCoding)
test_ll=log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.5785169808056114
for alpha = 1e-05
Log Loss: 1.5691834800645295
for alpha = 0.0001
Log Loss: 1.5702423695151086
for alpha = 0.001
Log Loss : 1.4850516296136442
for alpha = 0.01
Log Loss : 1.2819931301433514
for alpha = 0.1
Log Loss: 1.2812676609291282
for alpha = 1
Log Loss: 1.3055326215302245
for alpha = 10
Log Loss : 1.3586130305840243
for alpha = 100
Log Loss: 1.3728137804682896
```



```
For values of best alpha = 0.1 The train log loss is: 0.8577608101533614
For values of best alpha = 0.1 The cross validation log loss is: 1.2812676609291282
For values of best alpha = 0.1 The test log loss is: 1.1527262672860776
```

### 4.3.1.2. Testing the model with best hyper paramters

#### In [103]:

dom\_state=42)
predict\_and\_plot\_confusion\_matrix(train\_x\_onehotCoding, y\_train, cv\_x\_onehotCoding, y\_cv, clf)
x.add\_row(["LR\_Class\_Balancing(one hot)",train\_ll,cv\_ll,test\_ll,mis\_per])

125

- 100

75

50

- 25

1.0

- 0.8

0.6

- 0.4

- 0.2

0.0

0.75

- 0.60

- 0.45

0.30

-0.15

-0.00

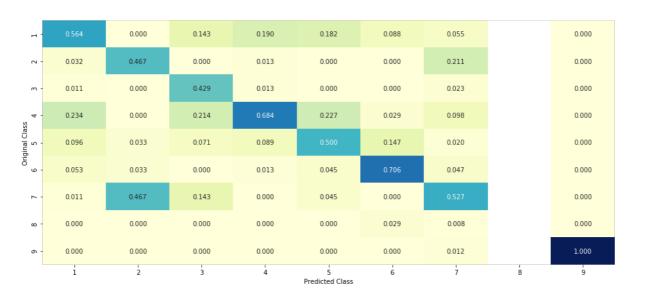
Log loss: 1.2812676609291282

Number of mis-classified points : 0.43609022556390975

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



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



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



#### 4.3.1.3. Feature Importance

```
In [75]:
```

```
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 [76]:
```

```
# from tabulate import tabulate
clf = SGDClassifier(class weight='balanced', alpha=alpha[best alpha], penalty='l2', loss='log', ran
dom state=42)
clf.fit(train x onehotCoding,y train)
test_point_index = 1
no feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", y_test[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get impfeature names(indices[0], X test['TEXT'].iloc[test point index], X test['Gene'].iloc[test poi
nt index], X test['Variation'].iloc[test point index], no feature)
Predicted Class: 7
Predicted Class Probabilities: [[4.600e-03 1.640e-02 3.000e-04 8.000e-04 1.600e-03 2.000e-04 9.742
e-01
  1.800e-03 2.000e-04]]
Actual Class : 7
117 Text feature [constitutive] present in test data point [True]
Out of the top 500 features 1 are present in query point
```

#### 4.3.1.3.2. Incorrectly Classified point

#### In [77]:

```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", y_test[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get impfeature names(indices[0], X test['TEXT'].iloc[test point index],X test['Gene'].iloc[test point]
```

# 4.3.2. Without Class balancing

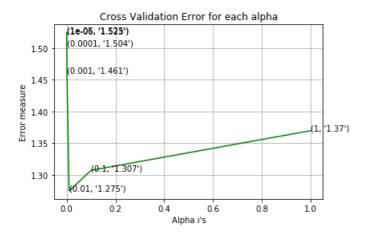
#### 4.3.2.1. Hyper paramter tuning

```
In [105]:
```

```
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear model.SGDClassifier.html
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11_ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Gradient Descent.
# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample weight]) Fit the calibrated model
# get_params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict proba(X) Posterior probabilities of classification
# video link:
alpha = [10 ** x for x in range(-6, 1)]
cv_log_error_array = []
for i in alpha:
   print("for alpha =", i)
   clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
   clf.fit(train_x_onehotCoding, y_train)
    sig clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, y_train)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv log error array.append(log loss(y cv, sig clf probs, labels=clf.classes , eps=1e-15))
   print("Log Loss :",log loss(y cv, 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, y train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x onehotCoding, y train)
predict y = sig clf.predict proba(train x onehotCoding)
train ll=log loss(y train, predict y, labels=clf.classes , eps=1e-15)
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)
cv_ll=log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict y = sig clf.predict proba(test x onehotCoding)
test_ll=log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict y, labels=clf.classes , eps=1e-15))
```

for alpha = 1e-06
Log Loss : 1.5225157573594494
for alpha = 1e-05
Log Loss : 1.5247006469599462
for alpha = 0.0001
Log Loss : 1.504366862163659
for alpha = 0.001
Log Loss : 1.4609712541867417
for alpha = 0.01
Log Loss : 1.274626138776145
for alpha = 0.1
Log Loss : 1.3071379420420022
for alpha = 1
Log Loss : 1.3696589011726492



```
For values of best alpha = 0.01 The train log loss is: 0.8481051995163802
For values of best alpha = 0.01 The cross validation log loss is: 1.274626138776145
For values of best alpha = 0.01 The test log loss is: 1.157109029212211
```

#### 4.3.2.2. Testing model with best hyper parameters

#### In [106]:

```
#------
# video link:
#------
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, y_train, cv_x_onehotCoding, y_cv, clf)
x.add_row(["LR_Without_Class_Balancing(one hot)",train_ll,cv_ll,test_ll,mis_per])
```

125

- 100

75

- 50

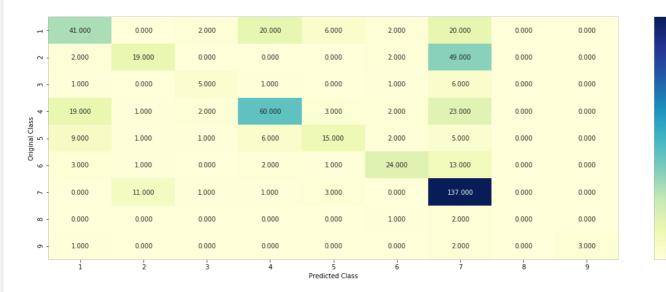
- 25

- 0.75

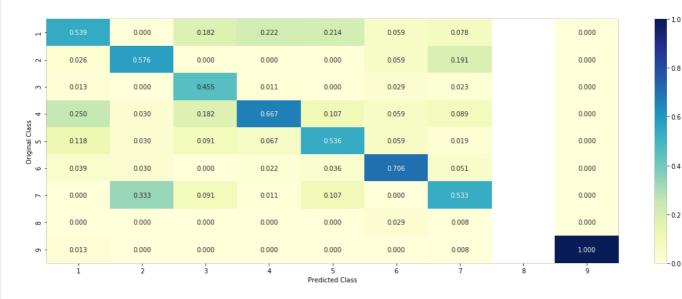
- 0.60

- 0.45

0.30



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



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

- 1		0.000	0.022	0.220	0.066	0.022	0.220	0.000	0.000
- 5	0.028	0.264	0.000	0.000	0.000	0.028	0.681	0.000	0.000
m -	0.071	0.000	0.357	0.071	0.000	0.071	0.429	0.000	0.000
- 4 -	0.173	0.009	0.018	0.545	0.027	0.018	0.209	0.000	0.000
Original Class 5	0.231	0.026	0.026	0.154	0.385	0.051	0.128	0.000	0.000
oric	0.068	0.023	0.000	0.045	0.023	0.545	0.295	0.000	0.000
۲ -	0.000	0.072	0.007	0.007	0.020	0.000	0.895	0.000	0.000
<b>~</b> -	0.000	0.000	0.000	0.000	0.000	U 333	0.667	0.000	0.000

#### 4.3.2.3. Feature Importance, Correctly Classified point

```
In [80]:
```

```
clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random state=42)
clf.fit(train x onehotCoding,y train)
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:",
\verb"np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]), 4)")"
print("Actual Class :", y_test[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get impfeature names(indices[0], X test['TEXT'].iloc[test point index], X test['Gene'].iloc[test poi
nt_index], X_test['Variation'].iloc[test_point_index], no_feature)
Predicted Class: 7
Predicted Class Probabilities: [[1.400e-02 3.850e-02 5.000e-04 4.400e-03 3.900e-03 1.000e-03 9.366
e - 01
  9.000e-04 1.000e-04]]
Actual Class : 7
226 Text feature [nf] present in test data point [True]
266 Text feature [3t3] present in test data point [True]
Out of the top 500 features 2 are present in query point
```

### 4.3.2.4. Feature Importance, Inorrectly Classified point

```
In [81]:
```

```
test point index = 100
no feature = 500
predicted cls = sig clf.predict(test x onehotCoding[test point index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:",
np.round(sig_clf.predict_proba(test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", y_test[test_point_index])
indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
print("-"*50)
get_impfeature_names(indices[0], X_test['TEXT'].iloc[test_point_index], X_test['Gene'].iloc[test_poi
nt index], X test['Variation'].iloc[test point index], no feature)
Predicted Class : 1
Predicted Class Probabilities: [[0.4702 0.109 0.0168 0.1138 0.0506 0.0426 0.1873 0.0055 0.0042]]
Actual Class : 1
405 Text feature [histologic] present in test data point [True]
Out of the top 500 features 1 are present in query point
```

# 4.4. Linear Support Vector Machines

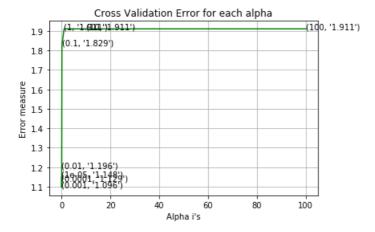
# 4.4.1. Hyper paramter tuning

```
In [82]:
```

```
# read more about support vector machines with linear kernals here http://scikit-
learn.org/stable/modules/generated/sklearn.svm.SVC.html
# default parameters
```

```
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, t
# cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', ra
ndom state=None)
# Some of methods of SVM()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/mathematical-derivation-copy-8/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight]) Fit the calibrated model
# get params([deep]) Get parameters for this estimator.
# predict(X) Predict the target of new samples.
# predict_proba(X) Posterior probabilities of classification
# video link:
alpha = [10 ** x for x in range(-5, 3)]
cv log error array = []
for i in alpha:
   print("for C =", i)
     clf = SVC(C=i,kernel='linear',probability=True, class weight='balanced')
   clf = SGDClassifier( class weight='balanced', alpha=i, penalty='12', loss='hinge', random state
    clf.fit(train x tfidf, y train)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_tfidf, y_train)
    sig clf probs = sig clf.predict proba(cv x tfidf)
    cv_log_error_array.append(log_loss(y_cv, sig_clf_probs, labels=clf.classes_, eps=1e-15))
    print("Log Loss :",log loss(y cv, 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', r
andom state=42)
clf.fit(train_x_tfidf, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x tfidf, y train)
predict y = sig clf.predict proba(train x tfidf)
train ll=log loss(y train, predict y, labels=clf.classes , eps=1e-15)
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 tfidf)
cv ll=log loss(y cv, predict y, labels=clf.classes , eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss is:",log_lo
ss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_tfidf)
test_ll=log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_loss(y_test, p
redict y, labels=clf.classes_, eps=1e-15))
```

```
for C = 1e-05
Log Loss : 1.148465860963182
for C = 0.0001
Log Loss: 1.129262197787261
for C = 0.001
Log Loss: 1.095803788579623
for C = 0.01
Log Loss: 1.1958044397641217
for C = 0.1
Log Loss: 1.8292089972766103
for C = 1
Log Loss: 1.9114331929676418
for C = 10
Log Loss: 1.9114331977442678
for C = 100
Log Loss: 1.911433271213524
```



```
For values of best alpha = 0.001 The train log loss is: 0.5476666709175846
For values of best alpha = 0.001 The cross validation log loss is: 1.095803788579623
For values of best alpha = 0.001 The test log loss is: 0.9970739162371267
```

# 4.4.2. Testing model with best hyper parameters

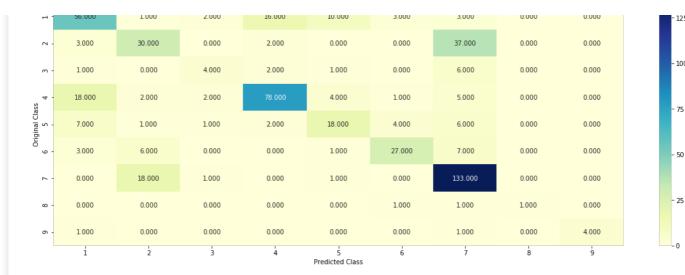
Number of mis-classified points: 0.34022556390977443

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

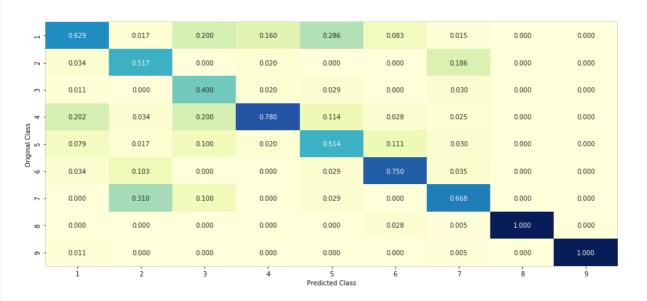
In [83]:

```
# read more about support vector machines with linear kernals here http://scikit-
learn.org/stable/modules/generated/sklearn.svm.SVC.html
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, t
# cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', ra
ndom state=None)
# Some of methods of SVM()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/mathematical-derivation-copy-8/
# clf = SVC(C=alpha[best_alpha], kernel='linear', probability=True, class_weight='balanced')
clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge',
random_state=42,class_weight='balanced')
predict and plot confusion matrix(train x tfidf, y train,cv x tfidf,y cv, clf)
x.add row(["Linear SVM(TFIDF)",train ll,cv ll,test ll,mis per])
Log loss: 1.095803788579623
```

FC 000 1 000 2 000 10 000 2 000 2 000 0000



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



- 0.8

- 0.6

- 0.4

- 0.2

0.75

0.60

- 0.45

-0.15

- 0.00

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



# 4.3.3. Feature Importance

#### 4.3.3.1. For Correctly classified point

```
clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='hinge', random state=42)
clf.fit(train x tfidf,y train)
test point index = 1
# test_point_index = 100
no_feature = 500
predicted cls = sig clf.predict(test x tfidf.tocsr()[test point index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x tfidf.tocsr())
[test point index]),4))
print("Actual Class :", y_test[test_point_index])
indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
print("-"*50)
get impfeature names(indices[0], X test['TEXT'].iloc[test point index], X test['Gene'].iloc[test poi
nt index], X test['Variation'].iloc[test point index], no feature)
Predicted Class: 7
Predicted Class Probabilities: [[1.550e-02 8.800e-03 2.500e-03 1.350e-02 5.600e-03 2.800e-03 9.497
e-01
 1.300e-03 3.000e-04]]
Actual Class : 7
11 Text feature [002] 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 [85]:
```

```
test point index = 100
no feature = 500
predicted_cls = sig_clf.predict(test_x_tfidf.tocsr()[test_point_index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig clf.predict proba(test x tfidf.tocsr())
[test point index]),4))
print("Actual Class :", y_test[test_point_index])
indices = np.argsort(-clf.coef )[predicted cls-1][:,:no feature]
print("-"*50)
get impfeature names(indices[0], X test['TEXT'].iloc[test point index], X test['Gene'].iloc[test poi
nt_index], X_test['Variation'].iloc[test_point_index], no_feature)
Predicted Class: 1
Predicted Class Probabilities: [[7.861e-01 4.100e-03 2.100e-03 1.365e-01 5.600e-03 2.500e-03 5.510
e-02
 7.700e-03 3.000e-04]]
Actual Class : 1
Out of the top 500 features 0 are present in query point
```

# 4.5 Random Forest Classifier

# 4.5.1. Hyper paramter tuning (With tfidf Encoding)

```
In [87]:
```

```
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
\# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid', cv=3)
# some of the methods of CalibratedClassifierCV()
\# fit(X, y[, sample weight]) Fit the calibrated model
# get params([deep]) Get parameters for this estimator.
# predict(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,class weight='balanced')
       clf.fit(train x tfidf, y train)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig clf.fit(train_x_tfidf, y_train)
        sig clf probs = sig clf.predict proba(cv x tfidf)
        cv_log_error_array.append(log_loss(y_cv, sig_clf_probs, labels=clf.classes_, eps=1e-15))
        print("Log Loss :",log_loss(y_cv, 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, class weight='balanced')
clf.fit(train_x_tfidf, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig clf.fit(train x tfidf, y train)
predict_y = sig_clf.predict proba(train x tfidf)
train ll=log loss(y train, predict y, labels=clf.classes , eps=1e-15)
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 tfidf)
cv_ll=log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best estimator = ', alpha[int(best alpha/2)], "The cross validation log loss
is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_tfidf)
test_ll=log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log loss
is:",log loss(y test, predict y, labels=clf.classes , eps=1e-15))
for n_{estimators} = 100 and max depth = 5
```

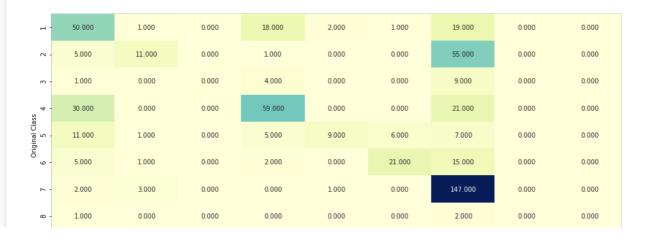
```
for n_estimators = 100 and max depth = 5 Log Loss: 1.302655926934186 for n_estimators = 100 and max depth = 10 Log Loss: 1.2560688345949846
```

```
nog nobb . 1.2000000010010010
for n estimators = 200 and max depth = 5
Log Loss: 1.2796901438406838
for n estimators = 200 and max depth = 10
Log Loss : 1.2426942891240191
for n estimators = 500 and max depth = 5
Log Loss: 1.2549310327900702
for n estimators = 500 and max depth = 10
Log Loss: 1.2386824693281837
for n_{estimators} = 1000 and max depth = 5
Log Loss: 1.2461103699655953
for n estimators = 1000 and max depth = 10
Log Loss : 1.2389164363183003
for n estimators = 2000 and max depth = 5
Log Loss : 1.2418125372380113
for n estimators = 2000 and max depth = 10
Log Loss: 1.234955159365341
For values of best estimator = 2000 The train log loss is: 0.653987824666976
For values of best estimator = 2000 The cross validation log loss is: 1.2349551593653405
For values of best estimator = 2000 The test log loss is: 1.1407676316053723
```

# 4.5.2. Testing model with best hyper parameters (Tfidf Encoding)

```
In [88]:
```

```
# -----
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max depth=None, min s
amples split=2.
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min
impurity decrease=0.0,
# min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None,
verbose=0, warm_start=False,
# class weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gini', max_depth=max
_depth[int(best_alpha%2)], random_state=42, n_jobs=-1,class_weight='balanced')
predict_and_plot_confusion_matrix(train_x_tfidf, y_train,cv_x_tfidf,y_cv, clf)
x.add row(["RF(TFIDF)",train ll,cv ll,test ll,mis per])
```



- 125

- 100

75

- 50



0.4

- 0.2

# 4.5.3. Feature Importance

0.114

0.013

0.333

0.167

0.023

0.020

0.000

0.000

0.000

0.000

0.000

0.000

0.045

0.000

0.000

0.000

0.000

0.007

0.000

0.000

Predicted Class

0.000

0.000

0.000

0.341

0.333

0.000

0.000

0.000

0.167

0.000

0.000

0.000

0.333

# 4.5.3.1. Correctly Classified point

```
In [89]:
```

```
# 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_tfidf, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_tfidf, y_train)

test_point_index = 1
no_feature = 100
predicted_cls = sig_clf.predict(test_x_tfidf.tocsr()[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf.tocsr()
[test_point_index]),4))
print("Actual Class :", y_test[test_point_index])
```

#### 4.5.3.2. Inorrectly Classified point

```
In [90]:
test point index = 100
no feature = 100
predicted_cls = sig_clf.predict(test_x_tfidf.tocsr()[test_point_index])
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_tfidf.tocsr())
[test point index]),4))
print("Actuall Class :", y_test[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
get impfeature names (indices[:no feature],
X test['TEXT'].iloc[test point index], X test['Gene'].iloc[test point index], X test['Variation'].ilo
c[test point index], no feature)
Predicted Class: 1
Predicted Class Probabilities: [[0.5259 0.0835 0.0202 0.1494 0.0564 0.0463 0.1 0.008 0.0104]]
Actuall Class : 1
51 Text feature [10] present in test data point [True]
Out of the top 100 features 1 are present in query point
```

#### 4.5.3. Hyper paramter tuning (With Response Coding)

# In [91]:

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
amples split=2,
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min
impurity decrease=0.0,
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, random_state=None,
verbose=0, warm start=False,
# class weight=None)
# Some of methods of RandomForestClassifier()
\# fit(X, y, [sample_weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
# find more about CalibratedClassifierCV here at http://scikit-
learn.org/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.html \\
# default paramters
          calibration CalibratedClassificaCV/base actimates_None method=/sigmoid/ av=2
```

```
# SKIEdIN.CdllDIdllON.CdllDIdleQCldSSllleICV(DdSe_eStlMdLOI=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, y_train)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_responseCoding, y_train)
        sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
        cv log error array.append(log loss(y cv, sig clf probs, labels=clf.classes , eps=1e-15))
        print("Log Loss :",log loss(y cv, 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, y train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, y_train)
predict y = sig clf.predict proba(train x responseCoding)
train_ll=log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The train log loss is:",log_loss(y
_train, predict_y, labels=clf.classes_, eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
cv_ll=log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15)
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)
test_ll=log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The test log loss is:",log_loss(y_
test, predict y, labels=clf.classes , eps=1e-15))
for n estimators = 10 and max depth = 2
Log Loss: 2.188530340508745
for n estimators = 10 and max depth = 3
Log Loss: 1.748193647254023
for n estimators = 10 and max depth = 5
Log Loss: 1.632479501054656
for n estimators = 10 and max depth = 10
Log Loss : 2.201958840078249
for n estimators = 50 and max depth = 2
Log Loss: 1.87258595336106
for n estimators = 50 and max depth = 3
Log Loss : 1.5545571255191124
for n_{estimators} = 50 and max depth = 5
Log Loss: 1.4420123688716178
for n estimators = 50 and max depth = 10
Log Loss: 1.8962925250887253
for n estimators = 100 and max depth = 2
Log Loss : 1.6926489169904406
```

```
for n estimators = 100 and max depth = 3
Log Loss: 1.592482410598662
for n estimators = 100 and max depth = 5
Log Loss: 1.3796124081630734
for n estimators = 100 and max depth = 10
Log Loss: 1.7886967936040354
for n estimators = 200 and max depth = 2
Log Loss: 1.769698453440723
for n estimators = 200 and max depth = 3
Log Loss: 1.6278959473741905
for n estimators = 200 and max depth = 5
Log Loss : 1.4031163407777034
for n estimators = 200 and max depth = 10
Log Loss: 1.7641361184815787
for n estimators = 500 and max depth = 2
Log Loss: 1.813643059147104
for n_{estimators} = 500 and max depth = 3
Log Loss: 1.6599112409597458
for n estimators = 500 and max depth = 5
Log Loss : 1.4008074801944548
for n_{estimators} = 500 and max depth = 10
Log Loss: 1.758912668483596
for n estimators = 1000 and max depth = 2
Log Loss: 1.8301927475252897
for n estimators = 1000 and max depth = 3
Log Loss : 1.6361184724061835
for n estimators = 1000 and max depth = 5
Log Loss : 1.381657436749045
for n_{estimators} = 1000 and max depth = 10
Log Loss: 1.738327583994187
For values of best alpha = 100 The train log loss is: 0.05492990842923589
For values of best alpha = 100 The cross validation log loss is: 1.3796124081630734
For values of best alpha = 100 The test log loss is: 1.3250060963257428
```

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

## In [92]:

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='gini', max depth=None, min s
amples split=2,
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min
impurity decrease=0.0,
# min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None,
verbose=0, warm start=False,
# class_weight=None)
# Some of methods of RandomForestClassifier()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict_proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
\verb|clf = RandomForestClassifier(max_depth=max_depth[int(best_alpha%4)]|, |
n estimators=alpha[int(best alpha/4)], criterion='gini', max features='auto',random state=42)
predict_and_plot_confusion_matrix(train_x_responseCoding, y_train,cv_x_responseCoding,y_cv, clf)
x.add_row(["RF(Response Coding)",train_ll,cv_ll,test_ll,mis_per])
```

- 35.000 2.000 7.000 29.000 12.000 5.000 0.000 1.000 0.00



- 40

- 30

- 20

- 10

- 0.8

- 0.6

- 0.2

- 0.60

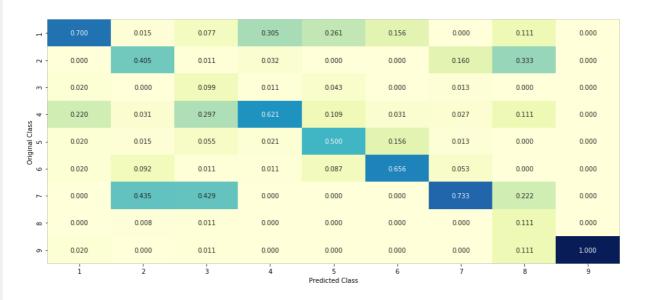
- 0.45

- 0.30

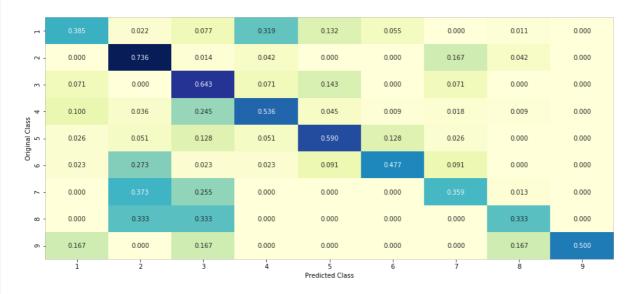
-0.15

- 0.00

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



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



# 4.5.5. Feature Importance

# 4.5.5.1. Correctly Classified point

In [93]:

```
|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, y_train)
sig clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, y_train)
test_point_index = 1
no feature = 27
predicted cls = sig clf.predict(test x responseCoding[test point index].reshape(1,-1))
print("Predicted Class :", predicted cls[0])
print("Predicted Class Probabilities:",
np.round(sig clf.predict proba(test x responseCoding[test point index].reshape(1,-1)),4))
print("Actual Class :", y_test[test_point_index])
indices = np.argsort(-clf.feature importances )
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
       print("Variation is important feature")
    else:
        print("Text is important feature")
Predicted Class: 7
Predicted Class Probabilities: [[0.0179 0.1497 0.3234 0.0169 0.0248 0.0428 0.3851 0.0249 0.0146]]
Actual Class: 7
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Variation is important feature
Gene is important feature
Gene is important feature
Text is important feature
Gene is important feature
```

#### 4.5.5.2. Incorrectly Classified point

# In [94]:

```
httur/ levr to imhorrant learnie )
Predicted Class: 1
Predicted Class Probabilities: [[0.3716 0.0422 0.1404 0.1479 0.047 0.0643 0.0142 0.091 0.0814]]
Actual Class : 1
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Text is important feature
Text is important feature
Variation is important feature
Gene is important feature
Gene is important feature
Text is important feature
Gene is important feature
```

# 4.7 Stack the models

#### 4.7.1 testing with hyper parameter tuning

In [95]:

```
# read more about SGDClassifier() at http://scikit-
learn.org/stable/modules/generated/sklearn.linear\_model.SGDClassifier.html \\
# default parameters
# SGDClassifier(loss='hinge', penalty='12', alpha=0.0001, 11 ratio=0.15, fit intercept=True, max i
ter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate='optimal', eta0
=0.0, power t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)
# some of methods
# fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Gradient Descent.
\# predict(X) Predict class labels for samples in X.
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-in
tuition-1/
# read more about support vector machines with linear kernals here http://scikit-
learn.org/stable/modules/generated/sklearn.svm.SVC.html
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, probability=False, t
01=0.001,
# cache size=200, class weight=None, verbose=False, max iter=-1, decision function shape='ovr', ra
ndom state=None)
# Some of methods of SVM()
# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
\# predict(X) Perform classification on samples in X.
```

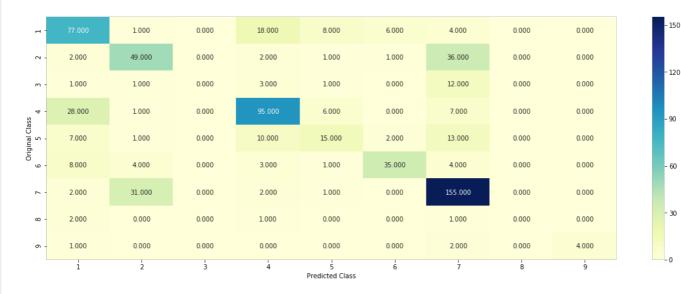
```
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/mathematical-derivation-copy-8/
# read more about support vector machines with linear kernals here http://scikit-
learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='gini', max_depth=None, min_s
amples split=2,
# min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf nodes=None, min
impurity decrease=0.0,
# min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state=None,
verbose=0, warm start=False,
# class weight=None)
# Some of methods of RandomForestClassifier()
\# fit(X, y, [sample weight]) Fit the SVM model according to the given training data.
# predict(X) Perform classification on samples in X.
# predict proba (X) Perform classification on samples in X.
# some of attributes of RandomForestClassifier()
# feature importances : array of shape = [n features]
# The feature importances (the higher, the more important the feature).
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-fores
t-and-their-construction-2/
clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class_weight='balanced', random_state=0
clf1.fit(train x tfidf, y train)
sig clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
clf2 = SGDClassifier(alpha=1, penalty='12', loss='hinge', class weight='balanced', random state=0)
clf2.fit(train_x_tfidf, y_train)
sig clf2 = CalibratedClassifierCV(clf2, method="sigmoid")
clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train_x_tfidf, y_train)
sig clf3 = CalibratedClassifierCV(clf3, method="sigmoid")
sig_clf1.fit(train_x_tfidf, y_train)
print("Logistic Regression : Log Loss: %0.2f" % (log loss(y cv, sig clf1.predict proba(cv x tfidf))
)))
sig clf2.fit(train x tfidf, y train)
print("Support vector machines : Log Loss: %0.2f" % (log loss(y cv,
sig clf2.predict proba(cv x tfidf))))
sig clf3.fit(train x tfidf, y train)
print("Naive Bayes : Log Loss: %0.2f" % (log loss(y cv, sig clf3.predict proba(cv x tfidf))))
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 p
robas=True)
    sclf.fit(train x tfidf, y train)
    print ("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" % (i, log loss(y cv, sc
lf.predict proba(cv x tfidf))))
    log error =log loss(y cv, sclf.predict proba(cv x tfidf))
    if best_alpha > log_error:
       best alpha = log error
                                                                                                | |
4
Logistic Regression : Log Loss: 1.08
Support vector machines : Log Loss: 1.91
Naive Bayes : Log Loss: 1.26
Stacking Classifer: for the value of alpha: 0.000100 Log Loss: 2.178
Stacking Classifer: for the value of alpha: 0.001000 Log Loss: 2.032
Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.504
Stacking Classifer: for the value of alpha: 0.100000 Log Loss: 1.179
```

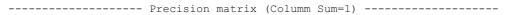
```
Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.32/ Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.608
```

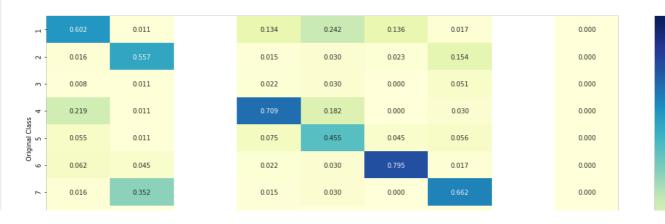
# 4.7.2 testing the model with the best hyper parameters

```
In [96]:
```

```
lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig clf1, sig clf2, sig clf3], meta classifier=lr, use proba
s=True)
sclf.fit(train_x_tfidf, y_train)
log_error = log_loss(y_train, sclf.predict_proba(train_x_tfidf))
train_ll=log_error
print("Log loss (train) on the stacking classifier: ", log error)
log_error = log_loss(y_cv, sclf.predict_proba(cv_x_tfidf))
cv ll=log_error
print("Log loss (CV) on the stacking classifier :",log error)
log_error = log_loss(y_test, sclf.predict_proba(test_x_tfidf))
test ll=log_error
print("Log loss (test) on the stacking classifier :",log error)
mis_per=(np.count_nonzero((sclf.predict(test_x_tfidf)- y_test))/y_test.shape[0]*100)
print("Number of missclassified point :", np.count_nonzero((sclf.predict(test_x_tfidf)- y_test))/y
test.shape[0])
plot confusion matrix(test y=y test, predict y=sclf.predict(test x tfidf))
x.add row(["Stacking(TFIDF)", train ll, cv ll, test ll, mis per])
```







1.0

- 0.8

0.6

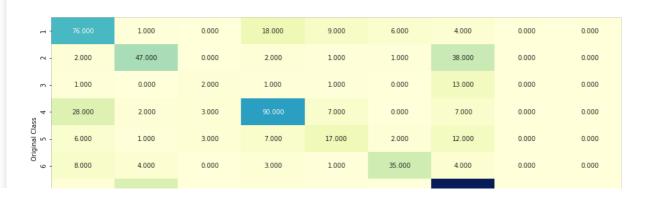
- 0.4



# 4.7.3 Maximum Voting classifier

In [110]:

```
#Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassifier.html
from sklearn.ensemble import VotingClassifier
vclf = VotingClassifier(estimators=[('lr', sig clf1), ('svc', sig clf2), ('rf', sig clf3)], voting=
'soft')
vclf.fit(train_x_tfidf, y_train)
print("Log loss (train) on the VotingClassifier:", log loss(y train,
vclf.predict_proba(train_x_tfidf)))
train_ll=log_loss(y_train, vclf.predict_proba(train_x_tfidf))
print("Log loss (CV) on the VotingClassifier :", log loss(y cv, vclf.predict proba(cv x tfidf)))
cv_ll=log_loss(y_cv, vclf.predict_proba(cv_x_tfidf))
print("Log loss (test) on the VotingClassifier: ", log loss(y test,
vclf.predict proba(test x tfidf)))
test_ll= log_loss(y_test, vclf.predict_proba(test_x_tfidf))
mis_per=(np.count_nonzero((vclf.predict(test_x_tfidf) - y_test))/y_test.shape[0]*100)
print("Number of missclassified point :", np.count_nonzero((vclf.predict(test_x_tfidf) - y_test))/y
test.shape[0])
plot_confusion_matrix(test_y=y_test, predict_y=vclf.predict(test_x_tfidf))
x.add_row(["Maximum Voting(TFIDF)",train_ll,cv_ll,test_ll,mis_per])
print(x)
Log loss (train) on the VotingClassifier: 0.868066769583388
```



- 120

- 90



# 5. Assignments

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