Personalized cancer diagnosis

1. Business Problem

1.1. Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training_variants.zip and training_text.zip from Kaggle.

Context:

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

Problem statement :

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

1.2. Source/Useful Links

Some articles and reference blogs about the problem statement

1. https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almost-everyone-who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25

2. https://www.youtube.com/watch?v=UwbuW7oK8rk
3. https://www.youtube.com/watch?v=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: https://www.kaggle.com/c/msk-redefining-cancer-treatment/data
- We have two data files: one conatins the information about the genetic mutations and the other contains the clinical evidence (text) that human experts/pathologists use to classify the genetic mutations.
- Both these data files are have a common column called ID
- Data file's information:
  - training_variants (ID , Gene, Variations, Class)
  - training_text (ID, Text)

2.1.2. Example Data Point

training_variants

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

training_text

ID,Text
0||Cyclin-dependent kinases (CDKs) regulate a variety of fundamental cellular processes. CDK10 stands out as one of the last orphan CDKs for which no activating cyclin has been identified and no kinase activity revealed. Previous work has shown that CDK10 silencing increases ETS2 (v-ets erythroblastosis virus E26 oncogene homolog 2)-driven activation of the MAPK pathway, which confers tamoxifen resistance to breast cancer cells. The precise mechanisms by which CDK10 modulates ETS2 activity, and more generally the functions of CDK10, remain elusive. Here we demonstrate that CDK10 is a cyclin-dependent kinase by identifying cyclin M as an activating cyclin. Cyclin M, an orphan cyclin, is the product of FAM58A, whose mutations cause STAR syndrome, a human developmental anomaly whose features include toe syndactyly, telecanthus, and anogenital and renal malformations. We show that STAR syndrome-associated cyclin M mutants are unable to interact with CDK10. Cyclin M silencing phenocopies CDK10 silencing in increasing c-Raf and in conferring tamoxifen resistance to breast cancer cells. CDK10/cyclin M phosphorylates ETS2 in vitro, and in cells it positively controls ETS2 degradation by the proteasome. ETS2 protein levels are increased in cells derived from a STAR patient, and this increase is attributable to decreased cyclin M levels. Altogether, our results reveal an additional regulatory mechanism for ETS2, which plays key roles in cancer and development. They also shed light on the molecular mechanisms underlying STAR syndrome.Cyclin-dependent kinases (CDKs) play a pivotal role in the control of a number of fundamental cellular processes (1). The human genome contains 21 genes encoding proteins that can be considered as members of the CDK family owing to their sequence similarity with bona fide CDKs, those known to be activated by cyclins (2). Although discovered almost 20 y

ago (3, 4), CDK10 remains one of the two CDKs without an identified cyclin partner. This knowledge gap has largely impeded the exploration of its biological functions. CDK10 can act as a positive cell cycle regulator in some cells (5, 6) or as a tumor suppressor in others (7, 8). CDK10 interacts with the ETS2 (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]:
```
!pip install nltk
!pip install mlxtend
!pip install seaborn
!pip install imblearn
```

```
Collecting nltk
  Downloading https://files.pythonhosted.org/packages/50/09/3b1755d528a
d9156ee7243d52aa5cd2b809ef053a0f31b53d92853dd653a/nltk-3.3.0.zip (1.4M
B)
    100% |################################| 1.4MB 9.2MB/s eta 0:00:01
Requirement already satisfied: six in /opt/conda/envs/py3.6/lib/python
3.6/site-packages (from nltk) (1.11.0)
Building wheels for collected packages: nltk
  Running setup.py bdist_wheel for nltk ... done
  Stored in directory: /home/jovyan/.cache/pip/wheels/d1/ab/40/3bceea46
922767e42986aef7606a600538ca80de6062dc266c
Successfully built nltk
jupyter 1.0.0 requires qtconsole, which is not installed.
ipywidgets 7.0.3 has requirement widgetsnbextension~=3.0.0, but you'll
 have widgetsnbextension 3.2.1 which is incompatible.
```

```
Installing collected packages: nltk
Successfully installed nltk-3.3
You are using pip version 10.0.1, however version 18.0 is available.
You should consider upgrading via the 'pip install --upgrade pip' comma
nd.
Collecting mlxtend
  Downloading https://files.pythonhosted.org/packages/d0/f9/798cb32550d
cbc9e0e3c143dc7144d2631df171423ed143cdb8b38ee2e5e/mlxtend-0.13.0-py2.py
3-none-any.whl (1.3MB)
    100% |################################| 1.3MB 9.1MB/s ta 0:00:011
Requirement already satisfied: setuptools in /opt/conda/envs/py3.6/lib/
python3.6/site-packages (from mlxtend) (36.4.0)
Requirement already satisfied: numpy>=1.10.4 in /opt/conda/envs/py3.6/l
ib/python3.6/site-packages (from mlxtend) (1.12.1)
Requirement already satisfied: scikit-learn>=0.18 in /opt/conda/envs/py
3.6/lib/python3.6/site-packages (from mlxtend) (0.19.0)
Requirement already satisfied: matplotlib>=1.5.1 in /opt/conda/envs/py
3.6/lib/python3.6/site-packages (from mlxtend) (2.1.2)
Requirement already satisfied: pandas>=0.17.1 in /opt/conda/envs/py3.6/
lib/python3.6/site-packages (from mlxtend) (0.20.3)
Requirement already satisfied: scipy>=0.17 in /opt/conda/envs/py3.6/li
b/python3.6/site-packages (from mlxtend) (0.19.1)
Requirement already satisfied: six>=1.10 in /opt/conda/envs/py3.6/lib/p
ython3.6/site-packages (from matplotlib>=1.5.1->mlxtend) (1.11.0)
Requirement already satisfied: python-dateutil>=2.1 in /opt/conda/envs/
py3.6/lib/python3.6/site-packages (from matplotlib>=1.5.1->mlxtend) (2.
7.3)
Requirement already satisfied: pytz in /opt/conda/envs/py3.6/lib/python
3.6/site-packages (from matplotlib>=1.5.1->mlxtend) (2018.4)
Requirement already satisfied: cycler>=0.10 in /opt/conda/envs/py3.6/li
b/python3.6/site-packages (from matplotlib>=1.5.1->mlxtend) (0.10.0)
Requirement already satisfied: pyparsing!=2.0.4,!=2.1.2,!=2.1.6,>=2.0.1
 in /opt/conda/envs/py3.6/lib/python3.6/site-packages (from matplotlib>
=1.5.1->mlxtend) (2.2.0)
jupyter 1.0.0 requires qtconsole, which is not installed.
ipywidgets 7.0.3 has requirement widgetsnbextension~=3.0.0, but you'll
 have widgetsnbextension 3.2.1 which is incompatible.
Installing collected packages: mlxtend
Successfully installed mlxtend-0.13.0
```

```
You are using pip version 10.0.1, however version 18.0 is available.
You should consider upgrading via the 'pip install --upgrade pip' comma
nd.
Collecting seaborn
  Downloading https://files.pythonhosted.org/packages/a8/76/220ba442045
9d9c4c9c9587c6ce607bf56c25b3d3d2de62056efe482dadc/seaborn-0.9.0-py3-non
e-any.whl (208kB)
    100% |################################| 215kB 6.4MB/s ta 0:00:01
Requirement already satisfied: scipy>=0.14.0 in /opt/conda/envs/py3.6/l
ib/python3.6/site-packages (from seaborn) (0.19.1)
Requirement already satisfied: pandas>=0.15.2 in /opt/conda/envs/py3.6/
lib/python3.6/site-packages (from seaborn) (0.20.3)
Requirement already satisfied: numpy>=1.9.3 in /opt/conda/envs/py3.6/li
b/python3.6/site-packages (from seaborn) (1.12.1)
Requirement already satisfied: matplotlib>=1.4.3 in /opt/conda/envs/py
3.6/lib/python3.6/site-packages (from seaborn) (2.1.2)
Requirement already satisfied: python-dateutil>=2 in /opt/conda/envs/py
3.6/lib/python3.6/site-packages (from pandas>=0.15.2->seaborn) (2.7.3)
Requirement already satisfied: pytz>=2011k in /opt/conda/envs/py3.6/li
b/python3.6/site-packages (from pandas>=0.15.2->seaborn) (2018.4)
Requirement already satisfied: six>=1.10 in /opt/conda/envs/py3.6/lib/p
ython3.6/site-packages (from matplotlib>=1.4.3->seaborn) (1.11.0)
Requirement already satisfied: cycler>=0.10 in /opt/conda/envs/py3.6/li
b/python3.6/site-packages (from matplotlib>=1.4.3->seaborn) (0.10.0)
Requirement already satisfied: pyparsing!=2.0.4,!=2.1.2,!=2.1.6,>=2.0.1
 in /opt/conda/envs/py3.6/lib/python3.6/site-packages (from matplotlib>
=1.4.3->seaborn) (2.2.0)
jupyter 1.0.0 requires qtconsole, which is not installed.
ipywidgets 7.0.3 has requirement widgetsnbextension~=3.0.0, but you'll
 have widgetsnbextension 3.2.1 which is incompatible.
Installing collected packages: seaborn
Successfully installed seaborn-0.9.0
You are using pip version 10.0.1, however version 18.0 is available.
You should consider upgrading via the 'pip install --upgrade pip' comma
nd.
Collecting imblearn
  Downloading https://files.pythonhosted.org/packages/81/a7/4179e6ebfd6
54bd0eac0b9c06125b8b4c96a9d0a8ff9e9507eb2a26d2d7e/imblearn-0.0-py2.py3-
none-any.whl
```

```
Collecting imbalanced-learn (from imblearn)
  Downloading https://files.pythonhosted.org/packages/80/a4/900463a3c0a
f082aed9c5a43f4ec317a9469710c5ef80496c9abc26ed0ca/imbalanced_learn-0.3.
3-py3-none-any.whl (144kB)
    100% |################################| 153kB 6.2MB/s ta 0:00:01
Requirement already satisfied: scipy in /opt/conda/envs/py3.6/lib/pytho
n3.6/site-packages (from imbalanced-learn->imblearn) (0.19.1)
Requirement already satisfied: scikit-learn in /opt/conda/envs/py3.6/li
b/python3.6/site-packages (from imbalanced-learn->imblearn) (0.19.0)
Requirement already satisfied: numpy in /opt/conda/envs/py3.6/lib/pytho
n3.6/site-packages (from imbalanced-learn->imblearn) (1.12.1)
jupyter 1.0.0 requires qtconsole, which is not installed.
ipywidgets 7.0.3 has requirement widgetsnbextension~=3.0.0, but you'll
 have widgetsnbextension 3.2.1 which is incompatible.
Installing collected packages: imbalanced-learn, imblearn
Successfully installed imbalanced-learn-0.3.3 imblearn-0.0
You are using pip version 10.0.1, however version 18.0 is available.
You should consider upgrading via the 'pip install --upgrade pip' comma
nd.
```

In [2]:

```
import pandas as pd
import matplotlib.pyplot as plt
import re
import time
import warnings
import numpy as np
import nltk
nltk.download('stopwords')
from nltk.corpus import stopwords
from sklearn.decomposition import TruncatedSVD
from sklearn.preprocessing import normalize
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.manifold import TSNE
import seaborn as sns
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics.classification import accuracy_score, log_loss
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.linear_model import SGDClassifier
```

```
from imblearn.over_sampling import SMOTE
from collections import Counter
from scipy.sparse import hstack
from sklearn.multiclass import OneVsRestClassifier
from sklearn.svm import SVC
from sklearn.cross_validation import StratifiedKFold
from collections import Counter, defaultdict
from sklearn.calibration import CalibratedClassifierCV
from sklearn.naive_bayes import MultinomialNB
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import train_test_split
from sklearn.model_selection import GridSearchCV
import math
from sklearn.metrics import normalized_mutual_info_score
from sklearn.ensemble import RandomForestClassifier
warnings.filterwarnings("ignore")

from mlxtend.classifier import StackingClassifier

from sklearn import model_selection
from sklearn.linear_model import LogisticRegression
```

```
[nltk_data] Downloading package stopwords to /home/jovyan/nltk_data...
[nltk_data]   Unzipping corpora/stopwords.zip.
```

```
/opt/conda/envs/py3.6/lib/python3.6/site-packages/sklearn/cross_validat
ion.py:41: DeprecationWarning: This module was deprecated in version 0.
18 in favor of the model_selection module into which all the refactored
classes and functions are moved. Also note that the interface of the ne
w CV iterators are different from that of this module. This module will
be removed in 0.20.
  "This module will be removed in 0.20.", DeprecationWarning)
```

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

In [3]:
```
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[3]:

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

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

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

3.1.2. Reading Text Data

In [4]:
```
# 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[4]:

	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 [5]:

```
# loading stop words from nltk library
stop_words = set(stopwords.words('english'))


def nlp_preprocessing(total_text, index, column):
    if type(total_text) is not int:
        string = ""
        # replace every special char with space
        total_text = re.sub('[^a-zA-Z0-9\n]', ' ', total_text)
        # replace multiple spaces with single space
        total_text = re.sub('\s+',' ', total_text)
        # converting all the chars into lower-case.
        total_text = total_text.lower()
```

```
        for word in total_text.split():
        # if the word is a not a stop word then retain that word from t
he data
            if not word in stop_words:
                string += word + " "

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

In [6]:
```
#text processing stage.
start_time = time.clock()
for index, row in data_text.iterrows():
    nlp_preprocessing(row['TEXT'], index, 'TEXT')
print('Time took for preprocessing the text :',time.clock() - start_tim
e, "seconds")
```

```
Time took for preprocessing the text : 141.573352 seconds
```

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

Out[7]:

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

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 [8]:
```
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 o
f output varaible 'y_true' [stratify=y_true]
X_train, test_df, y_train, y_test = train_test_split(result, y_true, st
ratify=y_true, test_size=0.2)
# split the train data into train and cross validation by maintaining s
ame distribution of output varaible 'y_train' [stratify=y_train]
train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train, str
atify=y_train, 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 [9]:
```
print('Number of data points in train data:', train_df.shape[0])
print('Number of data points in test data:', test_df.shape[0])
print('Number of data points in cross validation data:', cv_df.shape[0
])
```

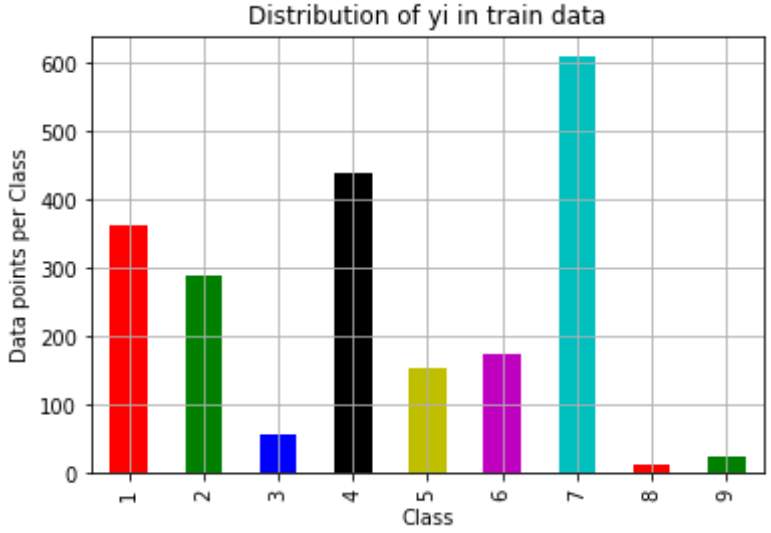
```
Number of data points in train data: 2124
Number of data points in test data: 665
Number of data points in cross validation data: 532
```

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

In [10]:
```
# it returns a dict, keys as class labels and values as the number of d
ata points in that class
train_class_distribution = train_df['Class'].value_counts().sortlevel()
test_class_distribution = test_df['Class'].value_counts().sortlevel()
cv_class_distribution = cv_df['Class'].value_counts().sortlevel()
```

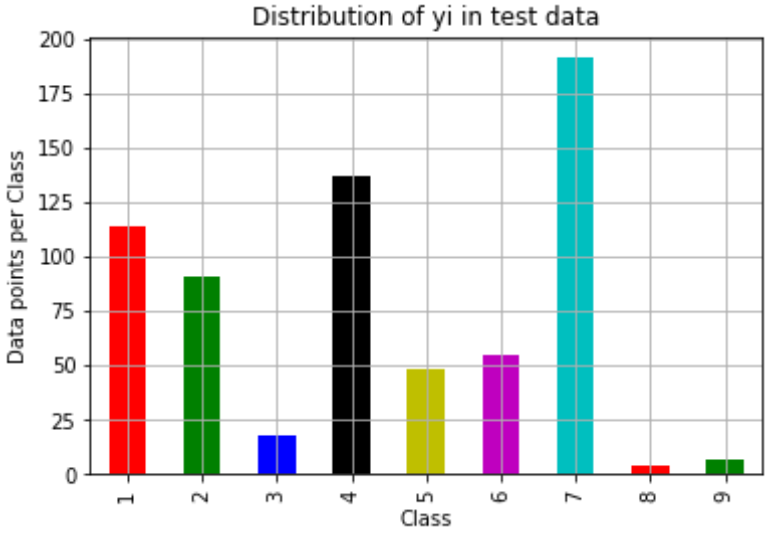
```
my_colors = 'rgbkymc'
train_class_distribution.plot(kind='bar', color=my_colors)
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in train data')
plt.grid()
plt.show()

# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/num
py.argsort.html
# -(train_class_distribution.values): the minus sign will give us in de
creasing 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_distri
bution.values[i], '(', np.round((train_class_distribution.values[i]/tra
in_df.shape[0]*100), 3), '%)')


print('-'*80)
my_colors = 'rgbkymc'
test_class_distribution.plot(kind='bar', color=my_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/num
py.argsort.html
# -(train_class_distribution.values): the minus sign will give us in de
creasing order
sorted_yi = np.argsort(-test_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',test_class_distrib
ution.values[i], '(', np.round((test_class_distribution.values[i]/test_
df.shape[0]*100), 3), '%)')

print('-'*80)
```

```
my_colors = 'rgbkymc'
cv_class_distribution.plot(kind='bar', color=my_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/num
py.argsort.html
# -(train_class_distribution.values): the minus sign will give us in de
creasing 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_distribut
ion.values[i], '(', np.round((cv_class_distribution.values[i]/cv_df.sha
pe[0]*100), 3), '%)')
```

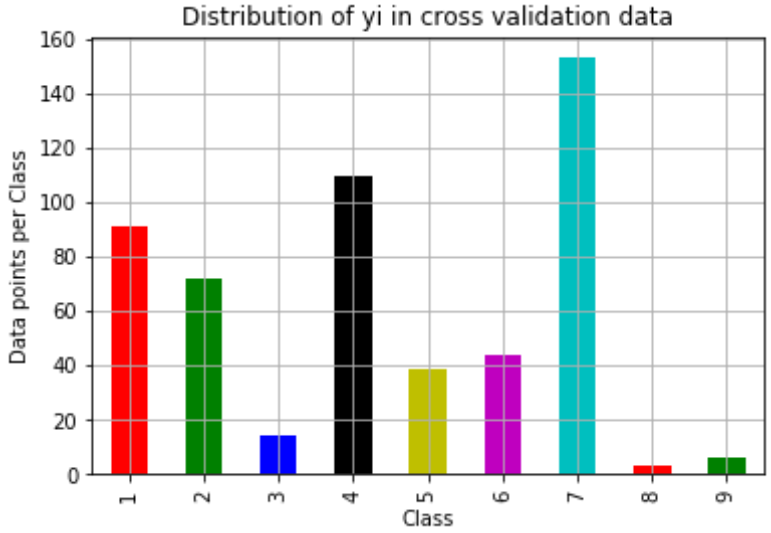



```
Number of data points in class 7 : 609 ( 28.672 %)
Number of data points in class 4 : 439 ( 20.669 %)
Number of data points in class 1 : 363 ( 17.09 %)
Number of data points in class 2 : 289 ( 13.606 %)
Number of data points in class 6 : 176 ( 8.286 %)
```

```
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 [11]:
```
# 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 cl
ass i are predicted class j
```

```
    A =(((C.T)/(C.sum(axis=1))).T)
    #divid each element of the confusion matrix with the sum of element
s 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 correspo
nds 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 element
s in that row
    # C = [[1, 2],
    #     [3, 4]]
    # C.sum(axis = 0)  axis=0 corresonds to columns and axis=1 correspo
nds 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=la
bels, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()
```

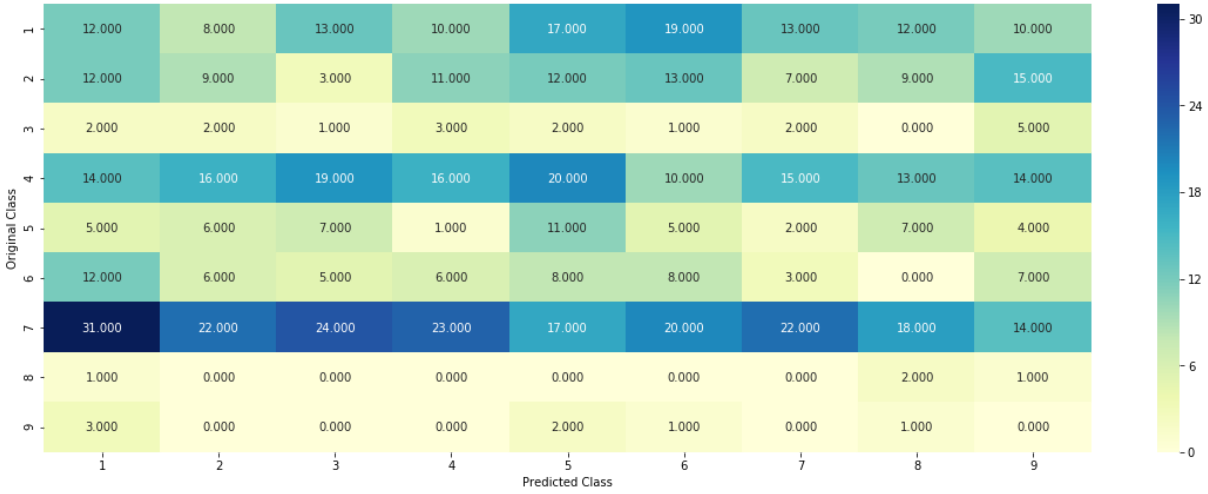
```
    print("-"*20, "Precision matrix (Columm Sum=1)", "-"*20)
    plt.figure(figsize=(20,7))
    sns.heatmap(B, annot=True, cmap="YlGnBu", fmt=".3f", xticklabels=la
bels, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()

    # 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=la
bels, yticklabels=labels)
    plt.xlabel('Predicted Class')
    plt.ylabel('Original Class')
    plt.show()
```

In [12]:

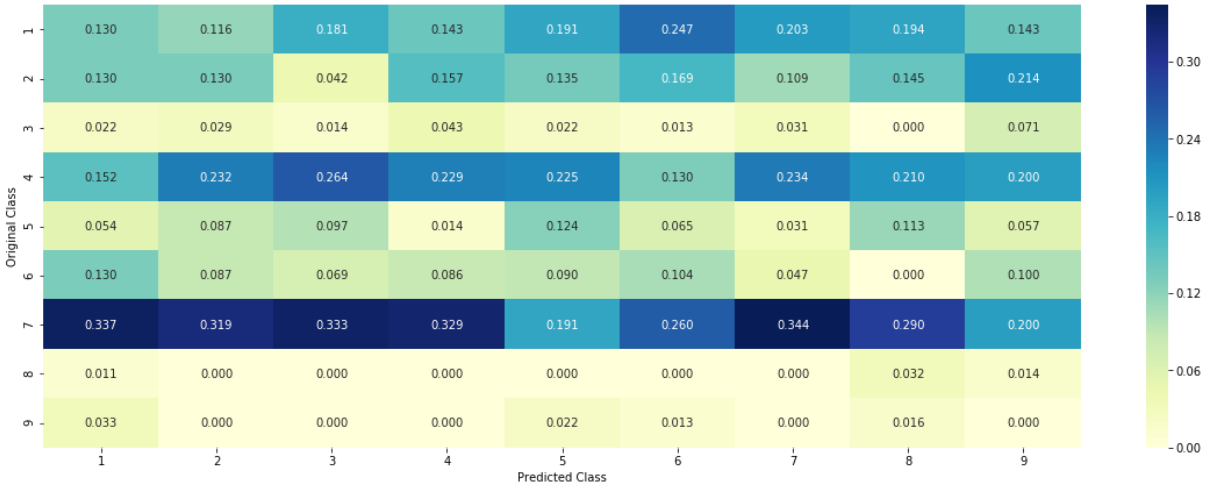
```
# we need to generate 9 numbers and the sum of numbers should be 1
# one solution is to genarate 9 numbers and divide each of the numbers
 by their sum
# ref: https://stackoverflow.com/a/18662466/4084039
test_data_len = test_df.shape[0]
cv_data_len = cv_df.shape[0]

# we create a output array that has exactly same size as the CV data
cv_predicted_y = np.zeros((cv_data_len,9))
for i in range(cv_data_len):
    rand_probs = np.random.rand(1,9)
    cv_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Cross Validation Data using Random Model",log_loss(y
_cv,cv_predicted_y, eps=1e-15))


# Test-Set error.
#we create a output array that has exactly same as the test data
test_predicted_y = np.zeros((test_data_len,9))
for i in range(test_data_len):
    rand_probs = np.random.rand(1,9)
```

```
    test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Test Data using Random Model",log_loss(y_test,test_p
redicted_y, eps=1e-15))

predicted_y =np.argmax(test_predicted_y, axis=1)
plot_confusion_matrix(y_test, predicted_y+1)
```

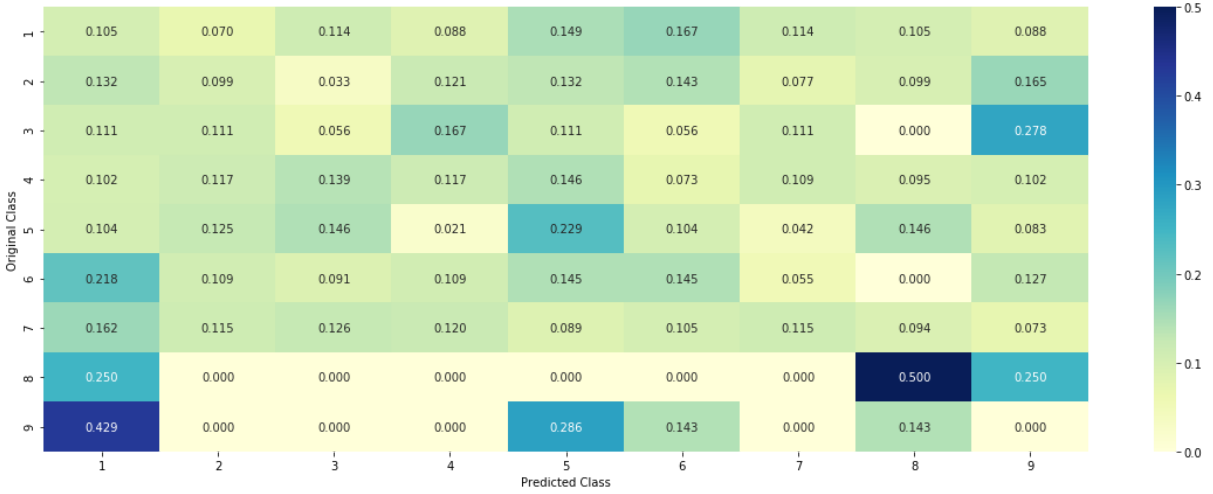
```
Log loss on Cross Validation Data using Random Model 2.48320935811
Log loss on Test Data using Random Model 2.50516026498
-------------------- Confusion matrix --------------------
```




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



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



3.3 Univariate Analysis

In [13]:
```
# code for response coding with Laplace smoothing.
# alpha : used for laplace smoothing
# feature: ['gene', 'variation']
```

```
# df: ['train_df', 'test_df', 'cv_df']
# algorithm
# ----------
# Consider all unique values and the number of occurances of given feat
ure in train data dataframe
# build a vector (1*9) , the first element = (number of times it occure
d in class1 + 10*alpha / number of time it occurred in total data+90*al
pha)
# gv_dict is like a look up table, for every gene it store a (1*9) repr
esentation 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_f
ea'
# 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, 1/9] to 'gv_fea'
# return 'gv_fea'
# ----------------------

# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
    # value_count: it contains a dict like
    # print(train_df['Gene'].value_counts())
    # output:
    #        {BRCA1      174
    #         TP53       106
    #         EGFR        86
    #         BRCA2       75
    #         PTEN        69
    #         KIT         61
    #         BRAF        60
    #         ERBB2       47
    #         PDGFRA      46
    #         ...}
    # print(train_df['Variation'].value_counts())
    # output:
    # {
    # Truncating_Mutations                     63
    # Deletion                                 43
```

```
    # Amplification                             43
    # Fusions                                   22
    # Overexpression                             3
    # E17K                                       3
    # Q61L                                       3
    # S222D                                      2
    # P130S                                      2
    # ...
    # }
    value_count = train_df[feature].value_counts()

    # gv_dict : Gene Variation Dict, which contains the probability arr
ay for each gene/variation
    gv_dict = dict()

    # denominator will contain the number of time that particular featu
re occured in whole data
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation b
elongs to perticular class
        # vec is 9 diamensional vector
        vec = []
        for k in range(1,10):
            # print(train_df.loc[(train_df['Class']==1) & (train_df['Ge
ne']=='BRCA1')])
            #         ID   Gene             Variation  Class
            # 2470  2470  BRCA1                S1715C      1
            # 2486  2486  BRCA1                S1841R      1
            # 2614  2614  BRCA1                   M1R      1
            # 2432  2432  BRCA1                L1657P      1
            # 2567  2567  BRCA1                T1685A      1
            # 2583  2583  BRCA1                E1660G      1
            # 2634  2634  BRCA1                W1718L      1
            # cls_cnt.shape[0] will return the number of rows

            cls_cnt = train_df.loc[(train_df['Class']==k) & (train_df[f
eature]==i)]

            # cls_cnt.shape[0](numerator) will contain the number of ti
```

```
me that particular feature occured in whole data
            vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90
*alpha))

        # we are adding the gene/variation to the dict as key and vec a
s value
        gv_dict[i]=vec
    return gv_dict

# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
    # print(gv_dict)
    #     {'BRCA1': [0.20075757575757575, 0.03787878787878788, 0.068181
818181818177, 0.13636363636363635, 0.25, 0.19318181818181818, 0.0378787
8787878788, 0.03787878787878788, 0.03787878787878788],
    #      'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224
489795918366, 0.27040816326530615, 0.061224489795918366, 0.066326530612
244902, 0.051020408163265307, 0.051020408163265307, 0.05612244897959183
7],
    #      'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625,
 0.06818181818181818177, 0.06818181818181818177, 0.0625, 0.3465909090909091
2, 0.0625, 0.056818181818181816],
    #      'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.06060
6060606060608, 0.078787878787878782, 0.1393939393939394, 0.345454545454
54546, 0.060606060606060608, 0.060606060606060608, 0.0606060606060606060
8],
    #      'PTEN': [0.069182389937106917, 0.062893081761006289, 0.06918
2389937106917, 0.46540880503144655, 0.075471698113207544, 0.06289308176
1006289, 0.069182389937106917, 0.062893081761006289, 0.0628930817610062
89],
    #      'KIT': [0.066225165562913912, 0.25165562913907286, 0.0728476
82119205295, 0.072847682119205295, 0.066225165562913912, 0.066225165562
913912, 0.27152317880794702, 0.066225165562913912, 0.06622516556291391
2],
    #      'BRAF': [0.066666666666666666, 0.17999999999999999, 0.073333
333333333334, 0.073333333333333334, 0.093333333333333338, 0.080000000000
0000002, 0.29999999999999999, 0.066666666666666666, 0.06666666666666666
6],
    #      ...
```

```
    #     }
    gv_dict = get_gv_fea_dict(alpha, feature, df)
    # value_count is similar in get_gv_fea_dict
    value_count = train_df[feature].value_counts()

    # gv_fea: Gene_variation feature, it will contain the feature for e
ach feature value in the data
    gv_fea = []
    # for every feature values in the given data frame we will check if
 it is there in the train data then we will add the feature to gv_fea
    # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to gv_fe
a
    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([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
#             gv_fea.append([-1,-1,-1,-1,-1,-1,-1,-1,-1])
    return gv_fea
```

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

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

3.2.1 Univariate Analysis on Gene Feature

Q1. Gene, What type of feature it is ?

Ans. Gene is a categorical variable

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

In [14]:
```
unique_genes = train_df['Gene'].value_counts()
print('Number of Unique Genes :', unique_genes.shape[0])
```

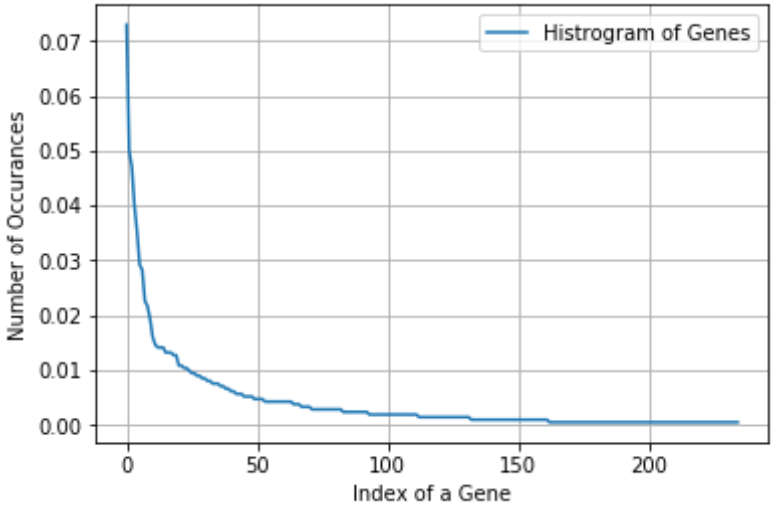
```
# the top 10 genes that occured most
print(unique_genes.head(10))
```

```
Number of Unique Genes : 235
BRCA1     155
TP53      106
EGFR      100
BRCA2      85
PTEN       75
BRAF       62
KIT        60
ERBB2      48
ALK        46
PDGFRA     41
Name: Gene, dtype: int64
```

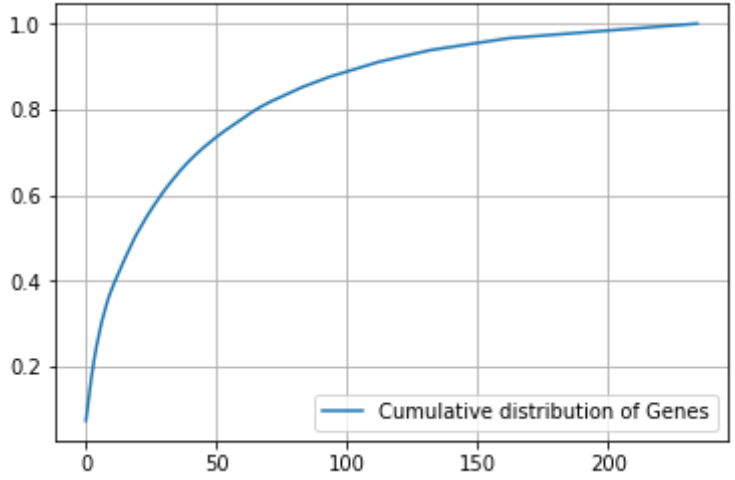
In [15]:
```
print("Ans: There are", unique_genes.shape[0] ,"different categories of
 genes in the train data, and they are distibuted as follows",)
```

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

In [16]:
```
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 [17]:
```
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 [18]:
```
#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, "Gen
e", train_df))
# test gene feature
test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gen
e", test_df))
# cross validation gene feature
cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene",
 cv_df))
```

In [19]:
```
print("train_gene_feature_responseCoding is converted feature using res
pone coding method. The shape of gene feature:", train_gene_feature_res
ponseCoding.shape)
```

```
train_gene_feature_responseCoding is converted feature using respone co
ding method. The shape of gene feature: (2124, 9)
```

In [20]:
```
# one-hot encoding of Gene feature.
gene_vectorizer = TfidfVectorizer()
train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_d
f['Gene'])
```

```
test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gene'])
cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gene'])
```

In [21]:
```
train_df['Gene'].head()
```

Out[21]:
```
3047       KIT
1718    KNSTRN
3201     RASA1
420       TP53
1926       SMO
Name: Gene, dtype: object
```

In [22]:
```
gene_vectorizer.get_feature_names()
```

Out[22]:
```
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
 'akt3',
 'alk',
 'apc',
 'ar',
 'araf',
 'arid1b',
 'arid2',
 'arid5b',
 'asxl1',
 'atm',
 'atr',
 'atrx',
 'aurka',
 'aurkb',
 'axl',
 'b2m',
 'bap1',
 'bard1',
 'bcl10',
```

```
                'bcl2',
                'bcl2l11',
                'bcor',
                'braf',
                'brca1',
                'brca2',
                'brd4',
                'brip1',
                'btk',
                'card11',
                'carm1',
                'casp8',
                'cbl',
                'ccnd1',
                'ccnd2',
                'ccnd3',
                'ccne1',
                'cdh1',
                'cdk12',
                'cdk4',
                'cdk6',
                'cdk8',
                'cdkn1a',
                'cdkn1b',
                'cdkn2a',
                'cdkn2b',
                'cdkn2c',
                'cebpa',
                'chek2',
                'cic',
                'crebbp',
                'ctcf',
                'ctnnb1',
                'ddr2',
                'dicer1',
                'dnmt3a',
                'dnmt3b',
                'dusp4',
                'egfr',
```

```
                'eif1ax',
                'elf3',
                'ep300',
                'epas1',
                'erbb2',
                'erbb3',
                'erbb4',
                'ercc2',
                'ercc3',
                'ercc4',
                'erg',
                'errfi1',
                'esr1',
                'etv6',
                'ewsr1',
                'ezh2',
                'fam58a',
                'fanca',
                'fancc',
                'fat1',
                'fbxw7',
                'fgfr1',
                'fgfr2',
                'fgfr3',
                'fgfr4',
                'flt3',
                'foxa1',
                'foxl2',
                'foxp1',
                'fubp1',
                'gata3',
                'gli1',
                'gna11',
                'gnaq',
                'gnas',
                'h3f3a',
                'hist1h1c',
                'hla',
                'hnf1a',
```

```
                'hras',
                'idh1',
                'idh2',
                'igf1r',
                'ikbke',
                'jak1',
                'jak2',
                'jun',
                'kdm5a',
                'kdm5c',
                'kdm6a',
                'kdr',
                'keap1',
                'kit',
                'klf4',
                'kmt2b',
                'kmt2c',
                'kmt2d',
                'knstrn',
                'kras',
                'lats1',
                'map2k1',
                'map2k2',
                'map2k4',
                'map3k1',
                'mapk1',
                'mdm2',
                'mdm4',
                'med12',
                'mef2b',
                'men1',
                'met',
                'mga',
                'mlh1',
                'mpl',
                'msh2',
                'msh6',
                'mtor',
                'myc',
```

```
                'mycn',
                'myd88',
                'ncor1',
                'nf1',
                'nf2',
                'nfe2l2',
                'nfkbia',
                'nkx2',
                'notch1',
                'notch2',
                'nras',
                'nsd1',
                'ntrk1',
                'ntrk2',
                'ntrk3',
                'nup93',
                'pak1',
                'pax8',
                'pbrm1',
                'pdgfra',
                'pdgfrb',
                'pik3ca',
                'pik3cb',
                'pik3cd',
                'pik3r1',
                'pik3r2',
                'pik3r3',
                'pim1',
                'pms2',
                'pole',
                'ppp2r1a',
                'ppp6c',
                'prdm1',
                'ptch1',
                'pten',
                'ptpn11',
                'ptprd',
                'ptprt',
                'rac1',
```

```
                'rad21',
                'rad50',
                'rad51b',
                'rad51d',
                'rad54l',
                'raf1',
                'rara',
                'rasa1',
                'rb1',
                'rbm10',
                'ret',
                'rheb',
                'rhoa',
                'rictor',
                'rit1',
                'rnf43',
                'ros1',
                'rras2',
                'runx1',
                'rxra',
                'rybp',
                'sdhb',
                'setd2',
                'sf3b1',
                'shq1',
                'smad2',
                'smad3',
                'smad4',
                'smarca4',
                'smarcb1',
                'smo',
                'sos1',
                'sox9',
                'spop',
                'src',
                'stag2',
                'stat3',
                'stk11',
                'tcf3',
```

```
 'tert',
 'tet2',
 'tgfbr1',
 'tgfbr2',
 'tmprss2',
 'tp53',
 'tp53bp1',
 'tsc1',
 'tsc2',
 'u2af1',
 'vhl',
 'whsc1',
 'whsc1l1',
 'xpo1',
 'yap1']
```

In [23]:
```
print("train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature:", train_gene_feature_onehotCoding.shape)
```

```
train_gene_feature_onehotCoding is converted feature using one-hot encoding method. The shape of gene feature: (2124, 234)
```

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

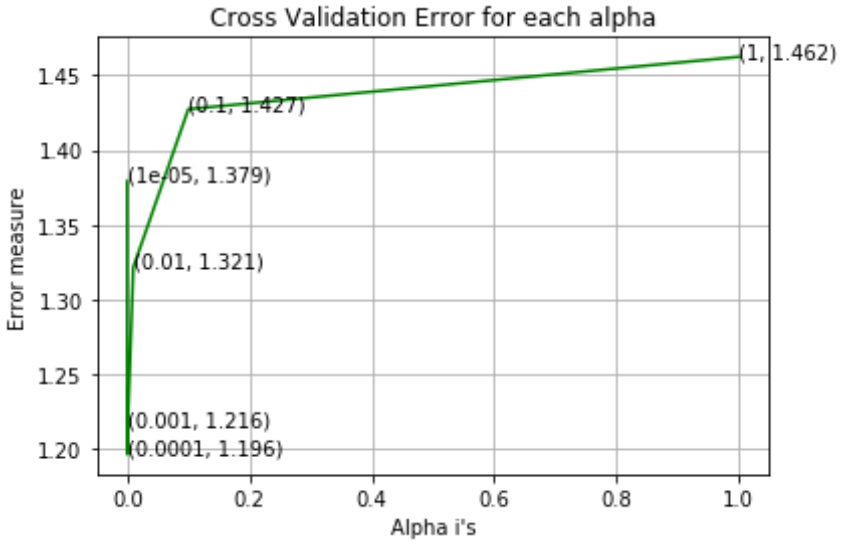
There are many ways to estimate how good a feature is, in predicting y_i. One of the good methods is to build a proper ML model using just this feature. In this case, we will build a logistic regression model using only Gene feature (one hot encoded) to predict y_i.

In [24]:
```
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='l2', alpha=0.0001, l1_ratio=0.1
```

```
5, fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, le
arning_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 S
tochastic 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='l2', 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.clas
ses_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv
, predict_y, labels=clf.classes_, eps=1e-15))

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_arra
y[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
```

```
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log',
random_state=42)
clf.fit(train_gene_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
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 vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_gene_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha =  1e-05 The log loss is: 1.37911356073
For values of alpha =  0.0001 The log loss is: 1.19627105323
For values of alpha =  0.001 The log loss is: 1.21612042334
For values of alpha =  0.01 The log loss is: 1.32138730934
For values of alpha =  0.1 The log loss is: 1.42730073501
For values of alpha =  1 The log loss is: 1.46229930808
```




```
For values of best alpha =  0.0001 The train log loss is: 1.04458769375
For values of best alpha =  0.0001 The cross validation log loss is: 1.
19627105323
For values of best alpha =  0.0001 The test log loss is: 1.20524149888
```

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

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

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

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

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

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

```
Q6. How many data points in Test and CV datasets are covered by the  23
5  genes in train dataset?
Ans
1. In test data 641 out of 665 : 96.39097744360903
2. In cross validation data 517 out of  532 : 97.18045112781954
```

3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it ?

Ans. Variation is a categorical variable

Q8. How many categories are there?

In [26]:
```
unique_variations = train_df['Variation'].value_counts()
print('Number of Unique Variations :', unique_variations.shape[0])
# the top 10 variations that occured most
print(unique_variations.head(10))
```

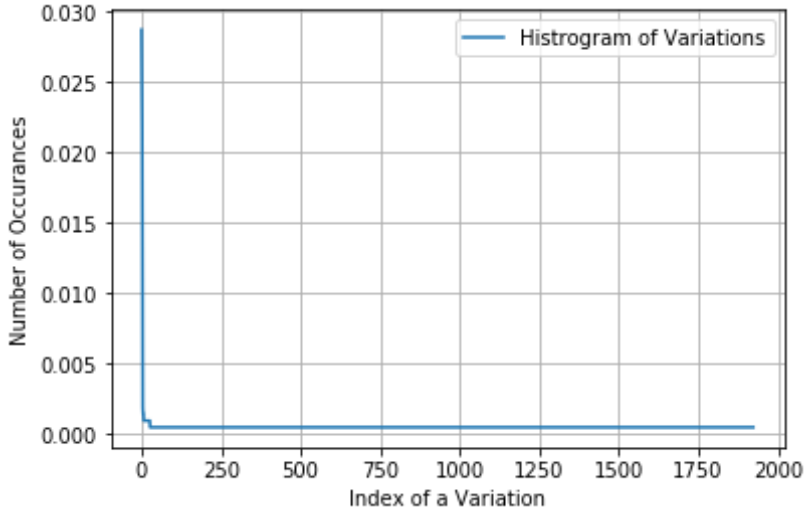
```
Number of Unique Variations : 1923
Truncating_Mutations    61
Deletion                52
Amplification           46
Fusions                 19
Overexpression           4
Q61L                     3
Q61R                     3
C618R                    2
P130S                    2
I31M                     2
Name: Variation, dtype: int64
```

In [27]:
```
print("Ans: There are", unique_variations.shape[0] ,"different categori
es of variations in the train data, and they are distibuted as follows"
```

```
,)
```

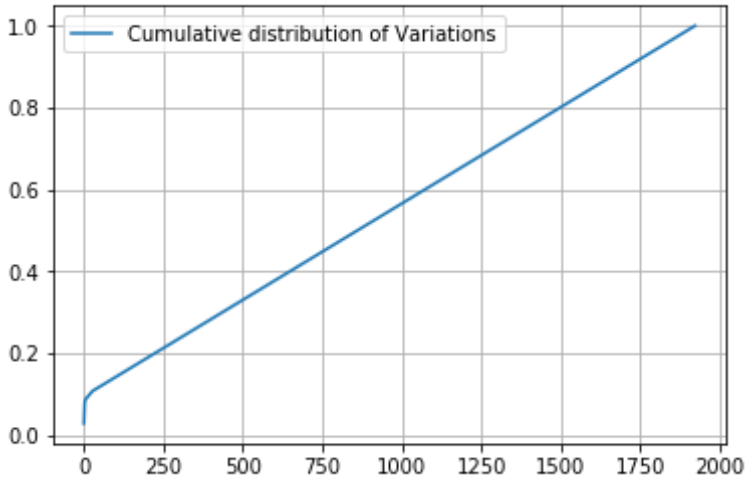
```
Ans: There are 1923 different categories of variations in the train dat
a, and they are distibuted as follows
```

In [28]:
```
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 [29]:
```
c = np.cumsum(h)
print(c)
plt.plot(c,label='Cumulative distribution of Variations')
plt.grid()
plt.legend()
plt.show()
```

```
[ 0.0287194   0.05320151  0.07485876 ...,  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 [30]:
```
# alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(alpha,
 "Variation", train_df))
# test gene feature
test_variation_feature_responseCoding = np.array(get_gv_feature(alpha,
"Variation", test_df))
# cross validation gene feature
```

```
cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "V
ariation", cv_df))
```

In [31]:
```
print("train_variation_feature_responseCoding is a converted feature us
ing the response coding method. The shape of Variation feature:", train
_variation_feature_responseCoding.shape)
```

```
train_variation_feature_responseCoding is a converted feature using the
response coding method. The shape of Variation feature: (2124, 9)
```

In [32]:
```
# one-hot encoding of variation feature.
variation_vectorizer = TfidfVectorizer()
train_variation_feature_onehotCoding = variation_vectorizer.fit_transfo
rm(train_df['Variation'])
test_variation_feature_onehotCoding = variation_vectorizer.transform(te
st_df['Variation'])
cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_d
f['Variation'])
```

In [33]:
```
print("train_variation_feature_onehotEncoded is converted feature using
 the onne-hot encoding method. The shape of Variation feature:", train_
variation_feature_onehotCoding.shape)
```

```
train_variation_feature_onehotEncoded is converted feature using the on
ne-hot encoding method. The shape of Variation feature: (2124, 1953)
```

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

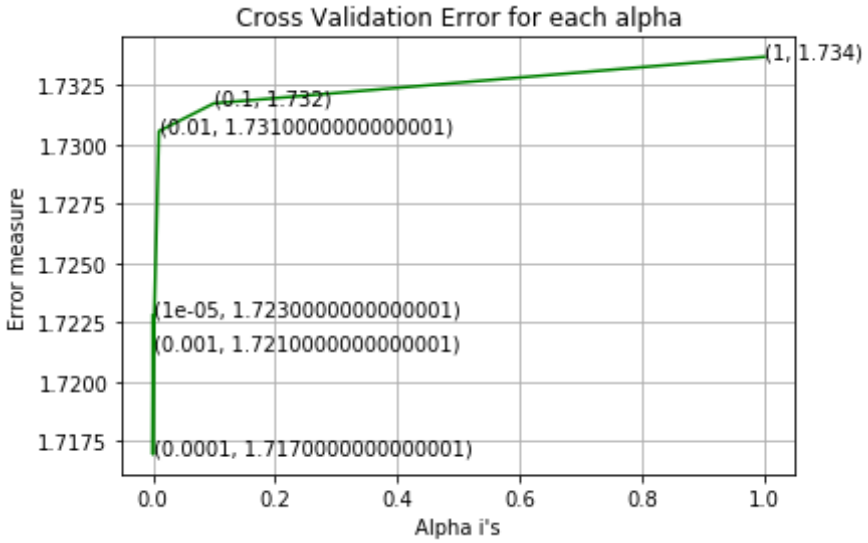
Let's build a model just like the earlier!

In [34]:
```
alpha = [10 ** x for x in range(-5, 1)]

# read more about SGDClassifier() at http://scikit-learn.org/stable/mod
ules/generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.1
```

```
5, fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, le
arning_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 S
tochastic 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='l2', 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.clas
ses_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv
, predict_y, labels=clf.classes_, eps=1e-15))

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_arra
y[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
```

```
plt.ylabel("Error measure")
plt.show()


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log',
random_state=42)
clf.fit(train_variation_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
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 vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_variation_feature_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
For values of alpha =  1e-05 The log loss is: 1.7227877398
For values of alpha =  0.0001 The log loss is: 1.71693140941
For values of alpha =  0.001 The log loss is: 1.7213348536
For values of alpha =  0.01 The log loss is: 1.73055856639
For values of alpha =  0.1 The log loss is: 1.73173323699
For values of alpha =  1 The log loss is: 1.73369419393
```




```
For values of best alpha =  0.0001 The train log loss is: 0.77919277244
4
For values of best alpha =  0.0001 The cross validation log loss is: 1.
71693140941
For values of best alpha =  0.0001 The test log loss is: 1.71821500756
```

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 [35]:
```
print("Q12. How many data points are covered by total ", unique_variati
ons.shape[0], " genes in test and cross validation data sets?")
test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Vari
ation'])))].shape[0]
cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'
])))].shape[0]
print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0],
":",(test_coverage/test_df.shape[0])*100)
print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[
0],":" ,(cv_coverage/cv_df.shape[0])*100)
```

```
Q12. How many data points are covered by total  1923  genes in test and
cross validation data sets?
Ans
1. In test data 72 out of 665 : 10.827067669172932
2. In cross validation data 46 out of  532 : 8.646616541353383
```

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 [36]:
```
# cls_text is a data frame
# for every row in data fram consider the 'TEXT'
# split the words by space
# make a dict with those words
# increment its count whenever we see that word

def extract_dictionary_paddle(cls_text):
    dictionary = defaultdict(int)
    for index, row in cls_text.iterrows():
        for word in row['TEXT'].split():
            dictionary[word] +=1
    return dictionary
```

In [37]:
```
import math
#https://stackoverflow.com/a/1602964
def get_text_responsecoding(df):
    text_feature_responseCoding = np.zeros((df.shape[0],9))
    for i in range(0,9):
        row_index = 0
        for index, row in df.iterrows():
            sum_prob = 0
            for word in row['TEXT'].split():
```

```
                sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(t
otal_dict.get(word,0)+90)))
            text_feature_responseCoding[row_index][i] = math.exp(sum_pr
ob/len(row['TEXT'].split()))
            row_index += 1
    return text_feature_responseCoding
```

In [38]:

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

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

# zip(list(text_features),text_fea_counts) will zip a word with its num
ber of times it occured
text_fea_dict = dict(zip(list(train_text_features),train_text_fea_count
s))


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

```
Total number of unique words in train data : 51839
```

In [39]:

```
dict_list = []
# dict_list =[] contains 9 dictoinaries each corresponds to a class
for i in range(1,10):
    cls_text = train_df[train_df['Class']==i]
    # build a word dict based on the words in that class
    dict_list.append(extract_dictionary_paddle(cls_text))
    # append it to dict_list

# dict_list[i] is build on i'th  class text data
```

```
# total_dict is buid on whole training text data
total_dict = extract_dictionary_paddle(train_df)


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

In [40]:
```
#response coding of text features
train_text_feature_responseCoding  = get_text_responsecoding(train_df)
test_text_feature_responseCoding  = get_text_responsecoding(test_df)
cv_text_feature_responseCoding  = get_text_responsecoding(cv_df)
```

In [41]:
```
# 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_t
ext_feature_responseCoding.sum(axis=1)).T
```

In [42]:
```
# don't forget to normalize every feature
train_text_feature_onehotCoding = normalize(train_text_feature_onehotCo
ding, axis=0)

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

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

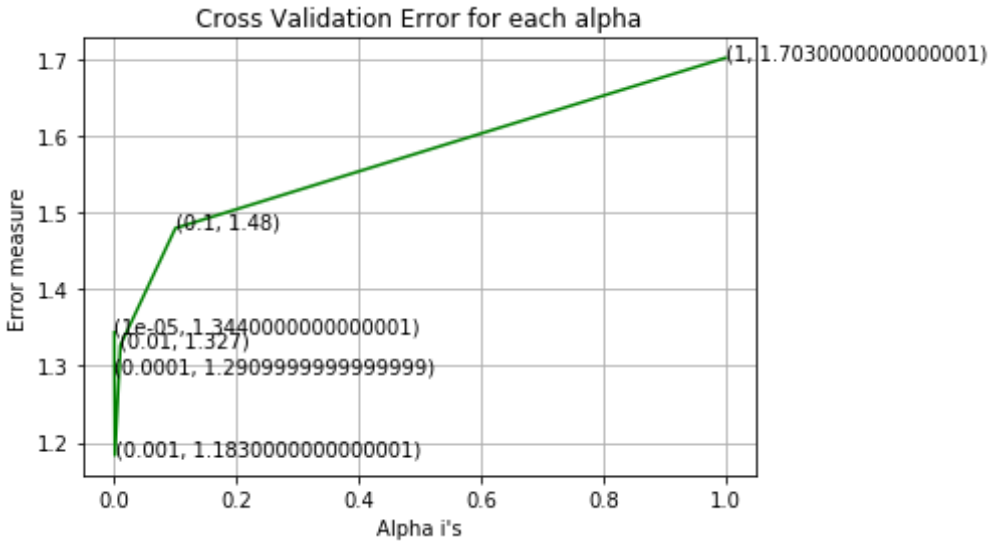
In [43]:
```
#https://stackoverflow.com/a/2258273/4084039
sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambda x:
 x[1] , reverse=True))
sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))
```

In [45]:
```
# Train a Logistic regression+Calibration model using text features whi
cha re on-hot encoded
alpha = [10 ** x for x in range(-5, 1)]

# read more about SGDClassifier() at http://scikit-learn.org/stable/mod
ules/generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.1
5, fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, le
arning_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 S
tochastic 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='l2', loss='log', random_state
```

```
=42)
    clf.fit(train_text_feature_onehotCoding, y_train)

    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_text_feature_onehotCoding, y_train)
    predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.clas
ses_, eps=1e-15))
    print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv
, predict_y, labels=clf.classes_, eps=1e-15))

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_arra
y[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log',
random_state=42)
clf.fit(train_text_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
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 vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_text_feature_onehotCoding)
```

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

```
For values of alpha =  1e-05 The log loss is: 1.34399052783
For values of alpha =  0.0001 The log loss is: 1.29055736307
For values of alpha =  0.001 The log loss is: 1.18321939761
For values of alpha =  0.01 The log loss is: 1.32695353535
For values of alpha =  0.1 The log loss is: 1.47998884321
For values of alpha =  1 The log loss is: 1.70256046272
```




```
For values of best alpha =  0.001 The train log loss is: 0.673578449794
For values of best alpha =  0.001 The cross validation log loss is: 1.1
8321939761
For values of best alpha =  0.001 The test log loss is: 1.15667533864
```

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

Ans. Yes, it seems like!

In [46]:
```
def get_intersec_text(df):
    df_text_vec = TfidfVectorizer(min_df=3)
```

```
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

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

In [47]:
```
len1,len2 = get_intersec_text(test_df)
print(np.round((len2/len1)*100, 3), "% of word of test data appeared in
 train data")
len1,len2 = get_intersec_text(cv_df)
print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appe
ared in train data")
```

```
96.295 % of word of test data appeared in train data
96.608 % of word of Cross Validation appeared in train data
```

4. Machine Learning Models

In [48]:
```
#Data preparation for ML models.

#Misc. functionns for ML models


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

    # for calculating log_loss we willl provide the array of probabilit
ies belongs to each class
    print("Log loss :",log_loss(test_y, sig_clf.predict_proba(test_x)))
```

```
    # calculating the number of data points that are misclassified
    print("Number of mis-classified points :", np.count_nonzero((pred_y
- test_y))/test_y.shape[0])
    plot_confusion_matrix(test_y, pred_y)
```

In [49]:
```
def report_log_loss(train_x, train_y, test_x, test_y,  clf):
    clf.fit(train_x, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x, train_y)
    sig_clf_probs = sig_clf.predict_proba(test_x)
    return log_loss(test_y, sig_clf_probs, eps=1e-15)
```

In [50]:
```
# 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 = TfidfVectorizer()
    var_count_vec = TfidfVectorizer()
    text_count_vec = TfidfVectorizer(min_df=3)

    gene_vec = gene_count_vec.fit(train_df['Gene'])
    var_vec  = var_count_vec.fit(train_df['Variation'])
    text_vec = text_count_vec.fit(train_df['TEXT'])

    fea1_len = len(gene_vec.get_feature_names())
    fea2_len = len(var_count_vec.get_feature_names())

    word_present = 0
    for i,v in enumerate(indices):
        if (v < fea1_len):
            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):
```

```
            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 p
oint [{}]".format(word,yes_no))
        else:
            word = text_vec.get_feature_names()[v-(fea1_len+fea2_len)]
            yes_no = True if word in text.split() else False
            if yes_no:
                word_present += 1
                print(i, "Text feature [{}] present in test data point
 [{}]".format(word,yes_no))

    print("Out of the top ",no_features," features ", word_present, "ar
e present in query point")
```

Stacking the three types of features

In [51]:
```
# merging gene, variance and text features

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

train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCoding,t
rain_variation_feature_onehotCoding))
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,tes
t_variation_feature_onehotCoding))
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_vari
ation_feature_onehotCoding))
```

```
train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_text_
feature_onehotCoding)).tocsr()
train_y = np.array(list(train_df['Class']))

test_x_onehotCoding = hstack((test_gene_var_onehotCoding, test_text_fea
ture_onehotCoding)).tocsr()
test_y = np.array(list(test_df['Class']))

cv_x_onehotCoding = hstack((cv_gene_var_onehotCoding, cv_text_feature_o
nehotCoding)).tocsr()
cv_y = np.array(list(cv_df['Class']))


train_gene_var_responseCoding = np.hstack((train_gene_feature_responseC
oding,train_variation_feature_responseCoding))
test_gene_var_responseCoding = np.hstack((test_gene_feature_responseCod
ing,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, trai
n_text_feature_responseCoding))
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_t
ext_feature_responseCoding))
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_fe
ature_responseCoding))
```

In [52]:

```
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 = ", t
est_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, 54
026)
(number of data points * number of features) in test data =  (665, 5402
```

```
6)
(number of data points * number of features) in cross validation data =
(532, 54026)
```

In [53]:
```
print(" Response encoding features :")
print("(number of data points * number of features) in train data = ",
train_x_responseCoding.shape)
print("(number of data points * number of features) in test data = ", t
est_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, 2
7)
(number of data points * number of features) in test data =  (665, 27)
(number of data points * number of features) in cross validation data =
(532, 27)
```

4.1. Base Line Model

4.1.1. Naive Bayes

4.1.1.1. Hyper parameter tuning

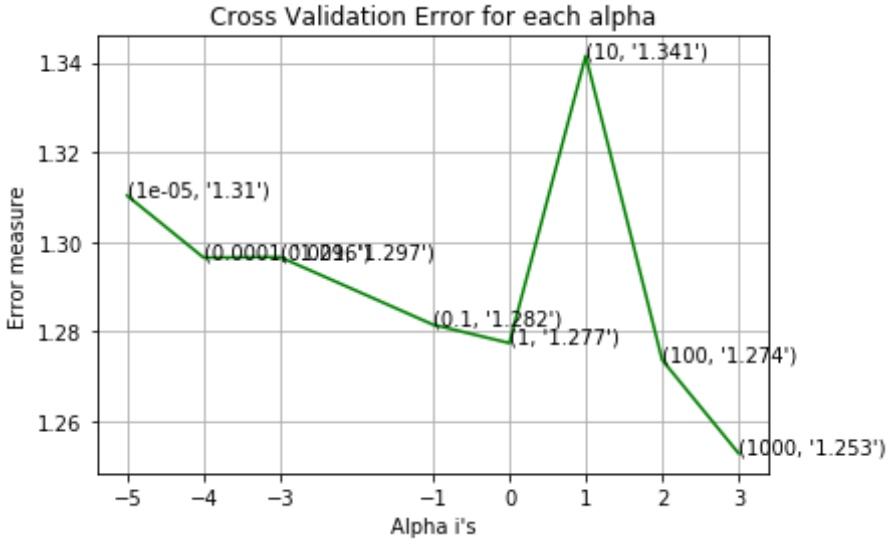
In [54]:
```
# find more about Multinomial Naive base function here http://scikit-le
arn.org/stable/modules/generated/sklearn.naive_bayes.MultinomialNB.html
# -------------------------
# default paramters
# sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_pr
ior=None)

# 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 v
ector 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.or
g/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.h
tml
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, metho
d='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/
# -----------------------


alpha = [0.00001, 0.0001, 0.001, 0.1, 1, 10, 100,1000]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = MultinomialNB(alpha=i)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.
classes_, eps=1e-15))
```

```
    # to avoid rounding error while multiplying probabilites we use log
-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

fig, ax = plt.subplots()
ax.plot(np.log10(alpha), cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv_log_error_a
rray[i]))
plt.grid()
plt.xticks(np.log10(alpha))
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()


best_alpha = np.argmin(cv_log_error_array)
clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)


predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log
 loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15
))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-05
Log Loss : 1.31031054888
for alpha = 0.0001

Log Loss : 1.29649607352
```

```
Log Loss : 1.29649607352
for alpha = 0.001
Log Loss : 1.29661873635
for alpha = 0.1
Log Loss : 1.28156382095
for alpha = 1
Log Loss : 1.27744246175
for alpha = 10
Log Loss : 1.34147071088
for alpha = 100
Log Loss : 1.27368025616
for alpha = 1000
Log Loss : 1.25287190653
```




```
For values of best alpha =  1000 The train log loss is: 0.916118616687
For values of best alpha =  1000 The cross validation log loss is: 1.25
287190653
For values of best alpha =  1000 The test log loss is: 1.1963415613
```

4.1.1.2. Testing the model with best hyper paramters

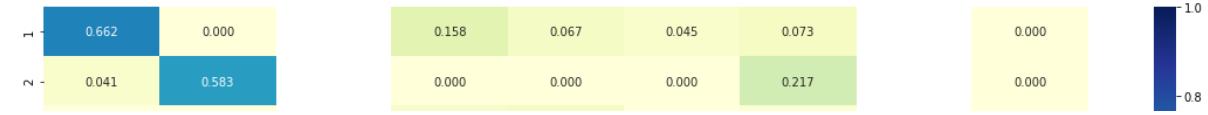
```
In [55]: # find more about Multinomial Naive base function here http://scikit-le
```

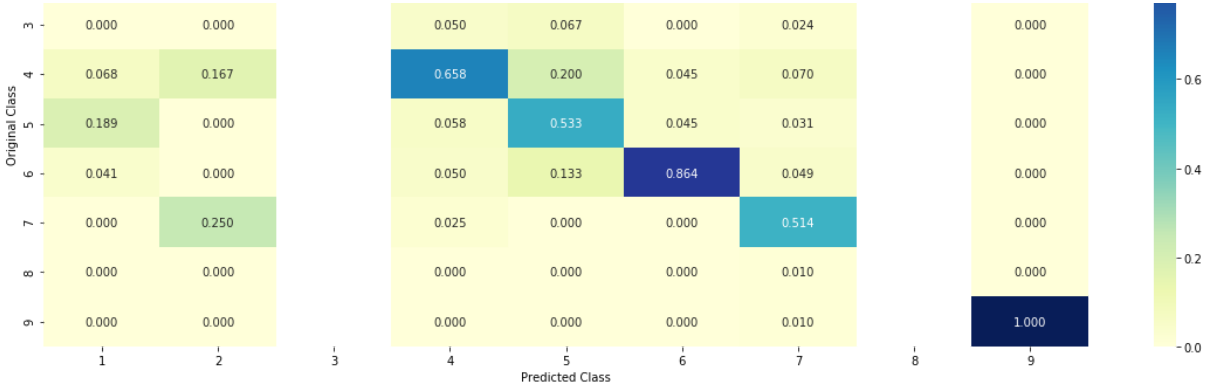
```
arn.org/stable/modules/generated/sklearn.naive_bayes.MultinomialNB.html
# -------------------------
# default paramters
# sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_pr
ior=None)

# 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 v
ector 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.or
g/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.h
tml
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, metho
d='sigmoid', cv=3)
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])    Fit the calibrated model
# get_params([deep])    Get parameters for this estimator.
# predict(X)    Predict the target of new samples.
# predict_proba(X)      Posterior probabilities of classification
# ----------------------------

clf = MultinomialNB(alpha=alpha[best_alpha])
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
# to avoid rounding error while multiplying probabilites we use log-pro
```

```
bability estimates
print("Log Loss :",log_loss(cv_y, sig_clf_probs))
print("Number of missclassified point :", np.count_nonzero((sig_clf.pre
dict(cv_x_onehotCoding)- cv_y))/cv_y.shape[0])
plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray
()))
```

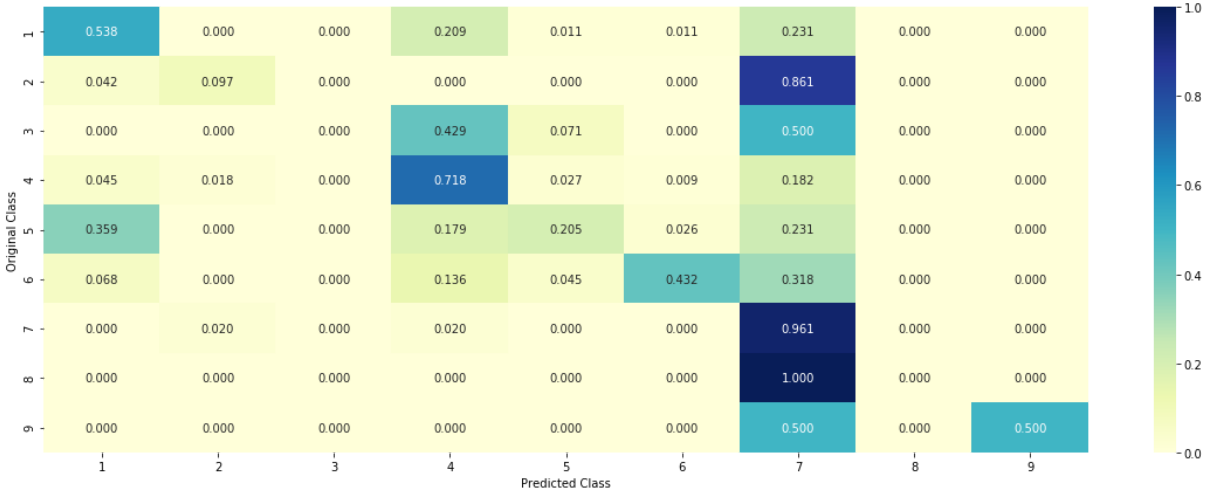
```
Log Loss : 1.25287190653
Number of missclassified point : 0.41353383458646614
-------------------- Confusion matrix --------------------
```


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





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



4.1.1.3. Feature Importance, Correctly classified point

In [56]:
```
test_point_index = 1
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
```

```
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.3754  0.0019  0.      0.4275  0.147
4  0.0325  0.0142  0.0011  0.    ]]
Actual Class : 5
--------------------------------------------------
11 Text feature [proteins] present in test data point [True]
12 Text feature [protein] present in test data point [True]
13 Text feature [activity] present in test data point [True]
14 Text feature [experiments] present in test data point [True]
15 Text feature [indicated] present in test data point [True]
17 Text feature [acid] present in test data point [True]
18 Text feature [whereas] present in test data point [True]
22 Text feature [results] present in test data point [True]
23 Text feature [amino] present in test data point [True]
24 Text feature [function] present in test data point [True]
25 Text feature [shown] present in test data point [True]
26 Text feature [determined] present in test data point [True]
27 Text feature [important] present in test data point [True]
28 Text feature [type] present in test data point [True]
29 Text feature [mammalian] present in test data point [True]
30 Text feature [reduced] present in test data point [True]
31 Text feature [loss] present in test data point [True]
32 Text feature [ability] present in test data point [True]
33 Text feature [described] present in test data point [True]
34 Text feature [functions] present in test data point [True]
35 Text feature [whether] present in test data point [True]
37 Text feature [levels] present in test data point [True]
38 Text feature [indicate] present in test data point [True]
41 Text feature [partially] present in test data point [True]
42 Text feature [wild] present in test data point [True]
43 Text feature [expressed] present in test data point [True]
45 Text feature [missense] present in test data point [True]
46 Text feature [two] present in test data point [True]
47 Text feature [bind] present in test data point [True]
```

```
48 Text feature [also] present in test data point [True]
51 Text feature [transfected] present in test data point [True]
52 Text feature [mutations] present in test data point [True]
53 Text feature [abrogate] present in test data point [True]
55 Text feature [either] present in test data point [True]
58 Text feature [containing] present in test data point [True]
59 Text feature [standard] present in test data point [True]
60 Text feature [analyzed] present in test data point [True]
61 Text feature [thus] present in test data point [True]
63 Text feature [transfection] present in test data point [True]
64 Text feature [percentage] present in test data point [True]
66 Text feature [contribute] present in test data point [True]
67 Text feature [purified] present in test data point [True]
68 Text feature [expression] present in test data point [True]
69 Text feature [vitro] present in test data point [True]
71 Text feature [using] present in test data point [True]
73 Text feature [may] present in test data point [True]
74 Text feature [indicates] present in test data point [True]
75 Text feature [see] present in test data point [True]
76 Text feature [determine] present in test data point [True]
78 Text feature [made] present in test data point [True]
80 Text feature [functional] present in test data point [True]
81 Text feature [associated] present in test data point [True]
82 Text feature [amount] present in test data point [True]
83 Text feature [suggest] present in test data point [True]
84 Text feature [lack] present in test data point [True]
85 Text feature [yeast] present in test data point [True]
87 Text feature [within] present in test data point [True]
88 Text feature [vivo] present in test data point [True]
89 Text feature [although] present in test data point [True]
91 Text feature [effects] present in test data point [True]
92 Text feature [previously] present in test data point [True]
93 Text feature [cells] present in test data point [True]
94 Text feature [critical] present in test data point [True]
95 Text feature [discussion] present in test data point [True]
96 Text feature [correspond] present in test data point [True]
98 Text feature [performed] present in test data point [True]
99 Text feature [three] present in test data point [True]
Out of the top  100  features  67 are present in query point
```

4.1.1.4. Feature Importance, Incorrectly classified point

In [57]:
```
test_point_index = 100
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 1
Predicted Class Probabilities: [[  5.00400000e-01   6.70000000e-03   2.
00000000e-04   4.38900000e-01
    1.22000000e-02   1.36000000e-02   2.60000000e-02   1.90000000e-03
    1.00000000e-04]]
Actual Class : 1
--------------------------------------------------
12 Text feature [dna] present in test data point [True]
13 Text feature [protein] present in test data point [True]
14 Text feature [type] present in test data point [True]
16 Text feature [two] present in test data point [True]
17 Text feature [one] present in test data point [True]
19 Text feature [wild] present in test data point [True]
20 Text feature [involved] present in test data point [True]
21 Text feature [also] present in test data point [True]
22 Text feature [results] present in test data point [True]
23 Text feature [expression] present in test data point [True]
25 Text feature [binding] present in test data point [True]
26 Text feature [containing] present in test data point [True]
27 Text feature [loss] present in test data point [True]
28 Text feature [role] present in test data point [True]
29 Text feature [function] present in test data point [True]
30 Text feature [either] present in test data point [True]
```

```
31 Text feature [specific] present in test data point [True]
32 Text feature [reduced] present in test data point [True]
33 Text feature [shown] present in test data point [True]
34 Text feature [region] present in test data point [True]
35 Text feature [indicated] present in test data point [True]
36 Text feature [using] present in test data point [True]
37 Text feature [ability] present in test data point [True]
38 Text feature [result] present in test data point [True]
40 Text feature [important] present in test data point [True]
41 Text feature [sequences] present in test data point [True]
42 Text feature [table] present in test data point [True]
43 Text feature [gene] present in test data point [True]
44 Text feature [however] present in test data point [True]
45 Text feature [control] present in test data point [True]
46 Text feature [determined] present in test data point [True]
47 Text feature [possible] present in test data point [True]
48 Text feature [present] present in test data point [True]
49 Text feature [essential] present in test data point [True]
50 Text feature [similar] present in test data point [True]
51 Text feature [three] present in test data point [True]
52 Text feature [affect] present in test data point [True]
54 Text feature [four] present in test data point [True]
55 Text feature [reporter] present in test data point [True]
57 Text feature [several] present in test data point [True]
59 Text feature [suggest] present in test data point [True]
60 Text feature [may] present in test data point [True]
62 Text feature [described] present in test data point [True]
63 Text feature [human] present in test data point [True]
64 Text feature [complex] present in test data point [True]
66 Text feature [analysis] present in test data point [True]
67 Text feature [indicating] present in test data point [True]
68 Text feature [full] present in test data point [True]
69 Text feature [previously] present in test data point [True]
70 Text feature [indicate] present in test data point [True]
72 Text feature [length] present in test data point [True]
74 Text feature [addition] present in test data point [True]
76 Text feature [proteins] present in test data point [True]
77 Text feature [amino] present in test data point [True]
78 Text feature [observed] present in test data point [True]
```

```
79 Text feature [domain] present in test data point [True]
80 Text feature [within] present in test data point [True]
82 Text feature [contain] present in test data point [True]
85 Text feature [form] present in test data point [True]
88 Text feature [performed] present in test data point [True]
89 Text feature [critical] present in test data point [True]
90 Text feature [mutant] present in test data point [True]
91 Text feature [together] present in test data point [True]
93 Text feature [10] present in test data point [True]
94 Text feature [discussion] present in test data point [True]
95 Text feature [respectively] present in test data point [True]
97 Text feature [15] present in test data point [True]
99 Text feature [contains] present in test data point [True]
Out of the top  100  features  68 are present in query point
```

4.2. K Nearest Neighbour Classification

4.2.1. Hyper parameter tuning

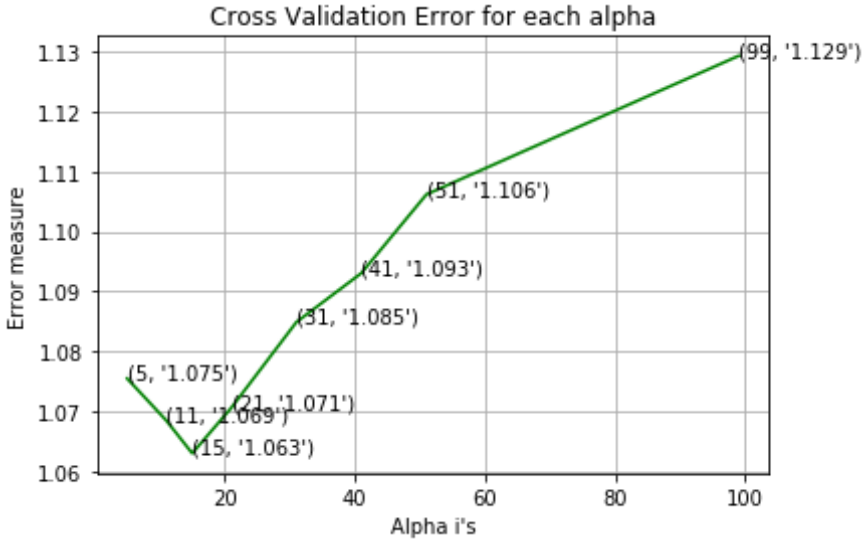
In [58]:
```
# find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KNeighborsClassifier.html
# -------------------------
# default parameter
# KNeighborsClassifier(n_neighbors=5, weights='uniform', algorithm='auto', leaf_size=30, p=2,
# metric='minkowski', metric_params=None, n_jobs=1, **kwargs)

# methods of
# fit(X, y) : Fit the model using X as training data and y as target values
# predict(X):Predict the class labels for the provided data
# predict_proba(X):Return probability estimates for the test data X.
#-----------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/k-nearest-neighbors-geometric-intuition-with-a-toy-example-1/
```

```
#-------------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.or
g/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.h
tml
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, metho
d='sigmoid', cv=3)
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])    Fit the calibrated model
# get_params([deep])    Get parameters for this estimator.
# predict(X)    Predict the target of new samples.
# predict_proba(X)      Posterior probabilities of classification
#-------------------------------------
# video link:
#-------------------------------------


alpha = [5, 11, 15, 21, 31, 41, 51, 99]
cv_log_error_array = []
for i in alpha:
    print("for alpha =", i)
    clf = KNeighborsClassifier(n_neighbors=i)
    clf.fit(train_x_responseCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_responseCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.
classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log
-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
```

```
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()


best_alpha = np.argmin(cv_log_error_array)
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log
 loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15
))
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 5
Log Loss : 1.07549531851
for alpha = 11
Log Loss : 1.06851966809
for alpha = 15
Log Loss : 1.0630263263
for alpha = 21
Log Loss : 1.07060466829
for alpha = 31
Log Loss : 1.0848798558
for alpha = 41
Log Loss : 1.09306218911
for alpha = 51
Log Loss : 1.10618164342
```

```
for alpha = 99
Log Loss : 1.12928817419
```



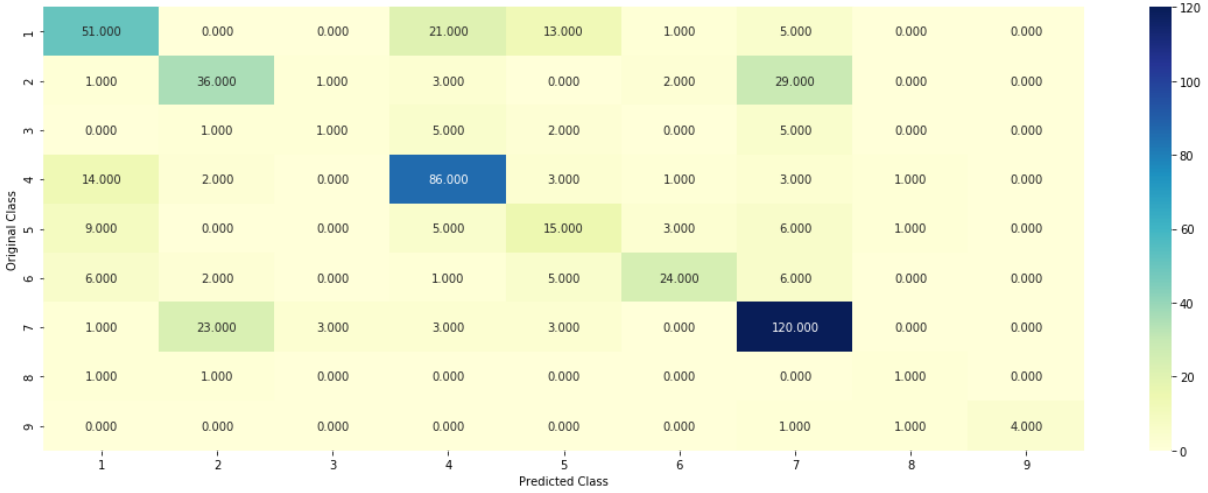

```
For values of best alpha =  15 The train log loss is: 0.703118108403
For values of best alpha =  15 The cross validation log loss is: 1.0630
263263
For values of best alpha =  15 The test log loss is: 1.10774863855
```

4.2.2. Testing the model with best hyper paramters

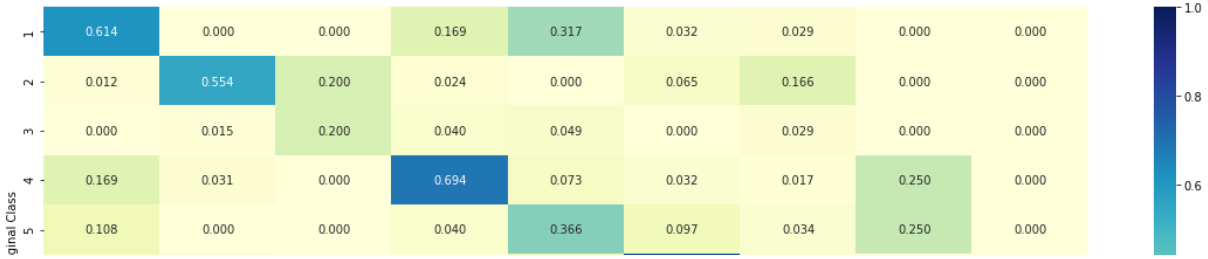
In [59]:
```
# find more about KNeighborsClassifier() here http://scikit-learn.org/s
table/modules/generated/sklearn.neighbors.KNeighborsClassifier.html
# -------------------------
# default parameter
# KNeighborsClassifier(n_neighbors=5, weights='uniform', algorithm='aut
o', leaf_size=30, p=2,
# metric='minkowski', metric_params=None, n_jobs=1, **kwargs)

# methods of
# fit(X, y) : Fit the model using X as training data and y as target va
lues
```

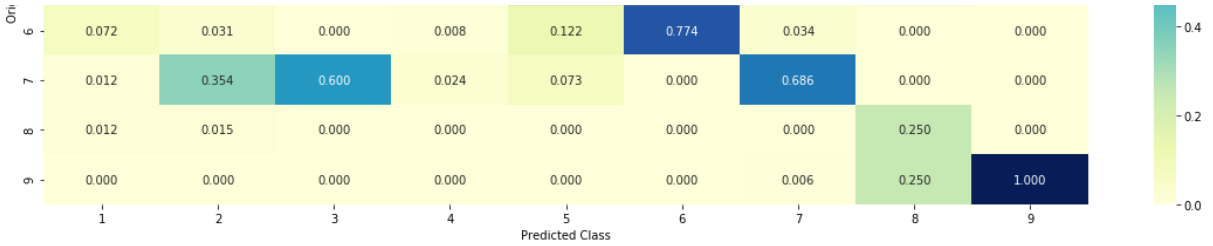
```
# predict(X):Predict the class labels for the provided data
# predict_proba(X):Return probability estimates for the test data X.
#--------------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/k-nearest-neighbors-geometric-intuition-with-a-toy-example-1/
#--------------------------------------
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y, cv_x_responseCoding, cv_y, clf)
```

```
Log loss : 1.0630263263
Number of mis-classified points : 0.36466165413533835
-------------------- Confusion matrix --------------------
```

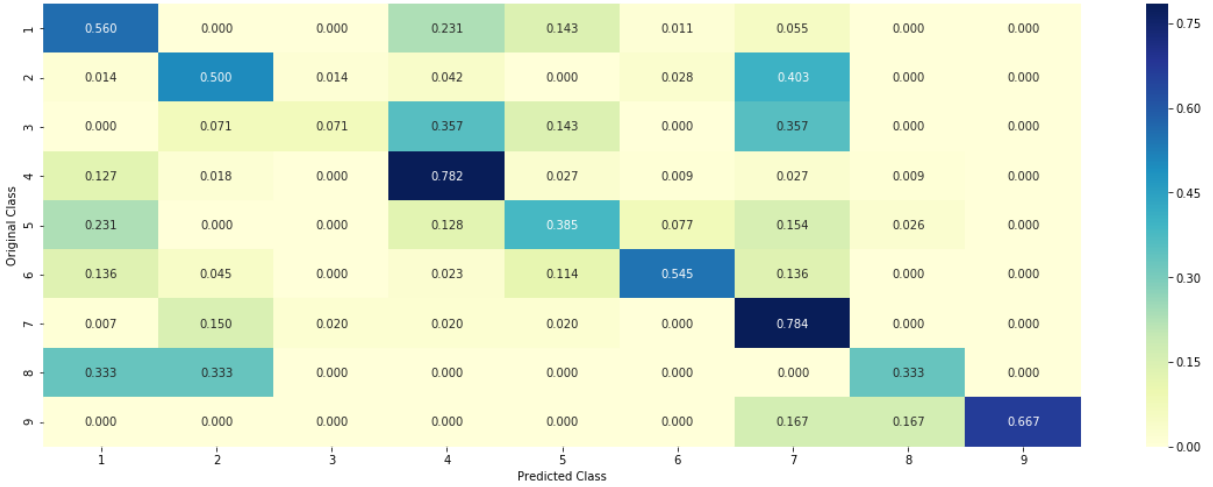



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```





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



4.2.3.Sample Query point -1

In [60]:
```
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

test_point_index = 1
predicted_cls = sig_clf.predict(test_x_responseCoding[0].reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Actual Class :", test_y[test_point_index])
neighbors = clf.kneighbors(test_x_responseCoding[test_point_index].resh
ape(1, -1), alpha[best_alpha])
```

```
print("The ",alpha[best_alpha]," nearest neighbours of the test points
 belongs to classes",train_y[neighbors[1][0]])
print("Fequency of nearest points :",Counter(train_y[neighbors[1][0]]))
```

```
Predicted Class : 1
Actual Class : 5
The  15  nearest neighbours of the test points belongs to classes [4 4
5 4 1 6 5 1 1 1 1 1 5 5 5]
Fequency of nearest points : Counter({1: 6, 5: 5, 4: 3, 6: 1})
```

4.2.4. Sample Query Point-2

In [61]:
```
clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

test_point_index = 100

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

```
Predicted Class : 1
Actual Class : 1
the k value for knn is 15 and the nearest neighbours of the test points
belongs to classes [1 1 4 4 4 4 4 1 4 1 4 1 1 1 1]
Fequency of nearest points : Counter({1: 8, 4: 7})
```

4.3. Logistic Regression

4.3.1. With Class balancing

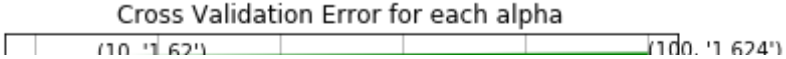
4.3.1.1. Hyper paramter tuning

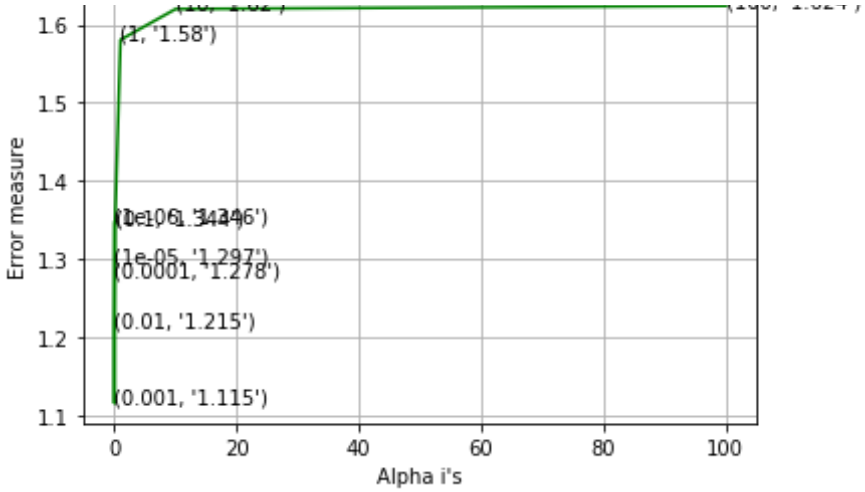
In [62]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/mod
ules/generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.1
5, fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, le
arning_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 S
tochastic Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/geometric-intuition-1/
#------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.or
g/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.h
tml
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, metho
d='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='l2',
 loss='log', random_state=42)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.
classes_, eps=1e-15))
    # to avoid rounding error while multiplying probabilites we use log
-probability estimates
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()


best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], p
enalty='l2', loss='log', random_state=42)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)
```

```
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log
 loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15
))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.34646104956
for alpha = 1e-05
Log Loss : 1.29686965935
for alpha = 0.0001
Log Loss : 1.27823981226
for alpha = 0.001
Log Loss : 1.11521126992
for alpha = 0.01
Log Loss : 1.21493277611
for alpha = 0.1
Log Loss : 1.34427370885
for alpha = 1
Log Loss : 1.58040246588
for alpha = 10
Log Loss : 1.61975452432
for alpha = 100
Log Loss : 1.62387243967
```






```
For values of best alpha =  0.001 The train log loss is: 0.591227515329
For values of best alpha =  0.001 The cross validation log loss is: 1.1
1521126992
For values of best alpha =  0.001 The test log loss is: 1.0941579762
```

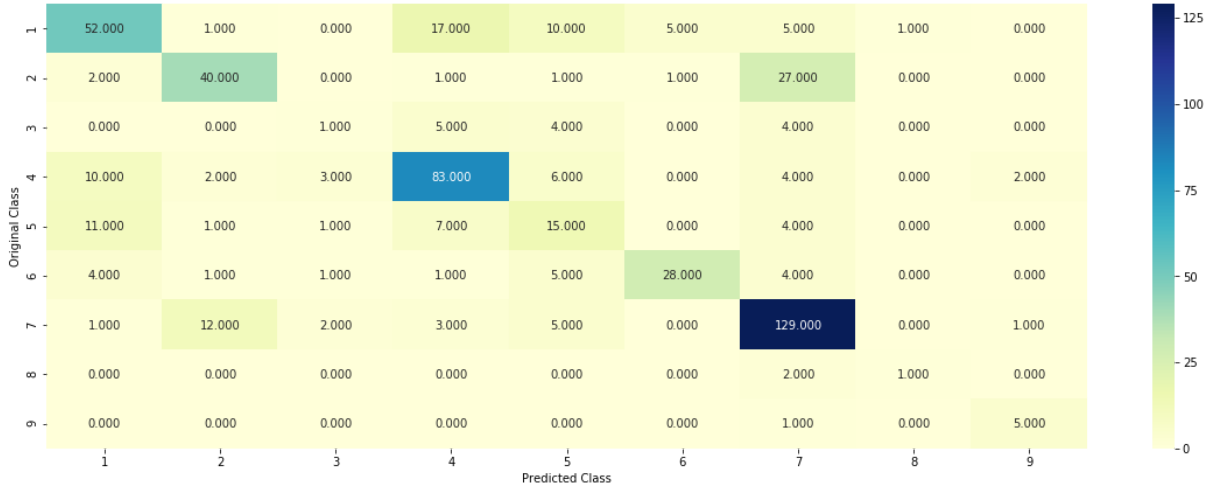
4.3.1.2. Testing the model with best hyper paramters

In [63]:

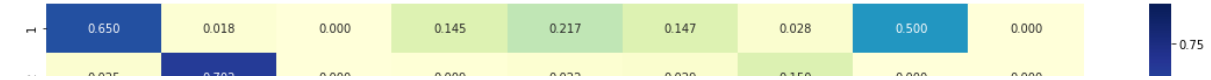
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/mod
ules/generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.1
5, fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, le
arning_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 S
tochastic Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#------------------------------
```

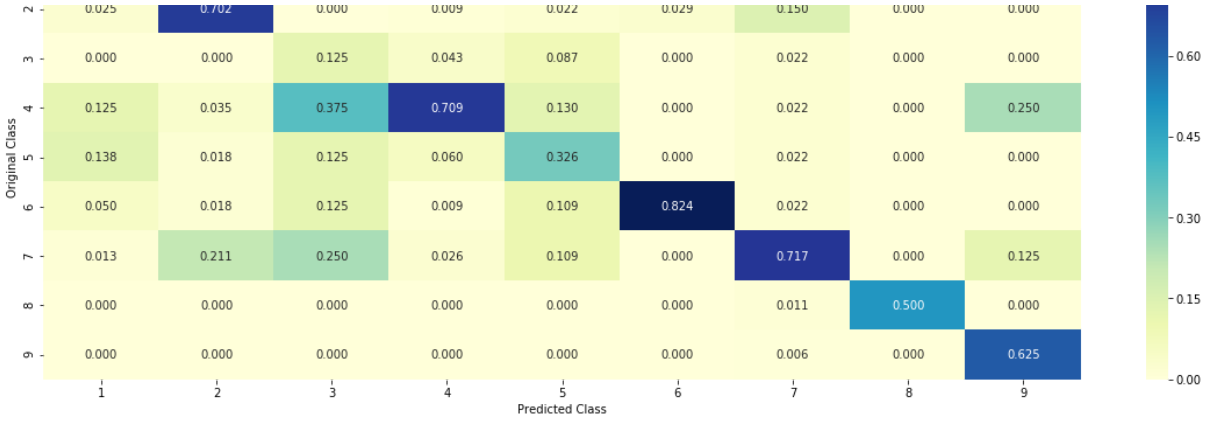
```
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/geometric-intuition-1/
#------------------------------
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_onehotCoding, cv_y, clf)
```

```
Log loss : 1.11521126992
Number of mis-classified points : 0.33458646616541354
-------------------- Confusion matrix --------------------
```

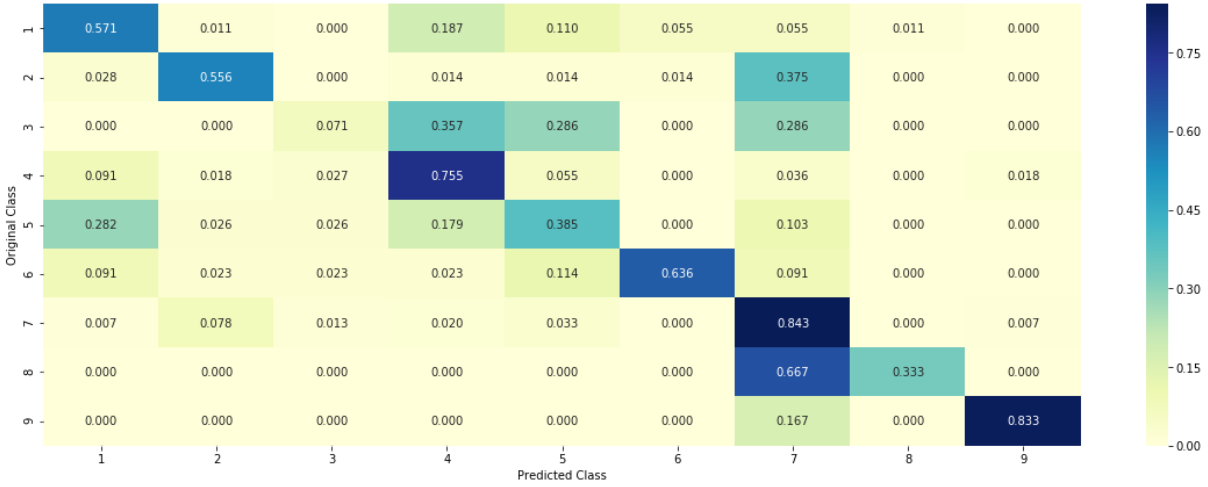



```
-------------------- Precision matrix (Columm Sum=1) --------------------
```






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



4.3.1.3. Feature Importance

In [64]:
```
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]:
```

```
            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 que
ry point")
    print("-"*50)
    print("The features that are most importent of the ",predicted_cls[
0]," class:")
    print (tabulate(tabulte_list, headers=["Index",'Feature name', 'Pre
sent or Not']))
```

4.3.1.3.1. Correctly Classified point

In [65]:
```
# from tabulate import tabulate
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], p
enalty='l2', loss='log', random_state=42)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.0337  0.0053  0.0018  0.7407  0.202
   0.0047  0.0012  0.0085  0.002 ]]
Actual Class : 5
--------------------------------------------------
148 Text feature [instability] present in test data point [True]
219 Text feature [strengthen] present in test data point [True]
229 Text feature [scandinavian] present in test data point [True]
244 Text feature [obligate] present in test data point [True]
282 Text feature [posing] present in test data point [True]
289 Text feature [homologues] present in test data point [True]
308 Text feature [suppressor] present in test data point [True]
366 Text feature [disperses] present in test data point [True]
367 Text feature [s1715] present in test data point [True]
368 Text feature [a1669] present in test data point [True]
369 Text feature [4729471] present in test data point [True]
370 Text feature [monteia] present in test data point [True]
371 Text feature [strang] present in test data point [True]
372 Text feature [scalia] present in test data point [True]
373 Text feature [rockvax] present in test data point [True]
374 Text feature [uncharacteristic] present in test data point [True]
375 Text feature [cterminus] present in test data point [True]
376 Text feature [d1692n] present in test data point [True]
377 Text feature [r1699] present in test data point [True]
378 Text feature [7340567] present in test data point [True]
379 Text feature [a1669s] present in test data point [True]
380 Text feature [bergthorsson] present in test data point [True]
381 Text feature [w1837x] present in test data point [True]
382 Text feature [v1668del] present in test data point [True]
383 Text feature [yeastbased] present in test data point [True]
415 Text feature [swedish] present in test data point [True]
435 Text feature [damage] present in test data point [True]
445 Text feature [satisfactorily] present in test data point [True]
448 Text feature [279] present in test data point [True]
451 Text feature [m1775k] present in test data point [True]
484 Text feature [grandmother] present in test data point [True]
Out of the top  500  features  31 are present in query point
```

4.3.1.3.2. Incorrectly Classified point

In [66]:
```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.6305  0.0134  0.002   0.3267  0.008
   0.0037  0.0049  0.0087  0.0021]]
Actual Class : 1
--------------------------------------------------
317 Text feature [stop] present in test data point [True]
Out of the top  500  features  1 are present in query point
```

4.3.2. Without Class balancing

4.3.2.1. Hyper paramter tuning

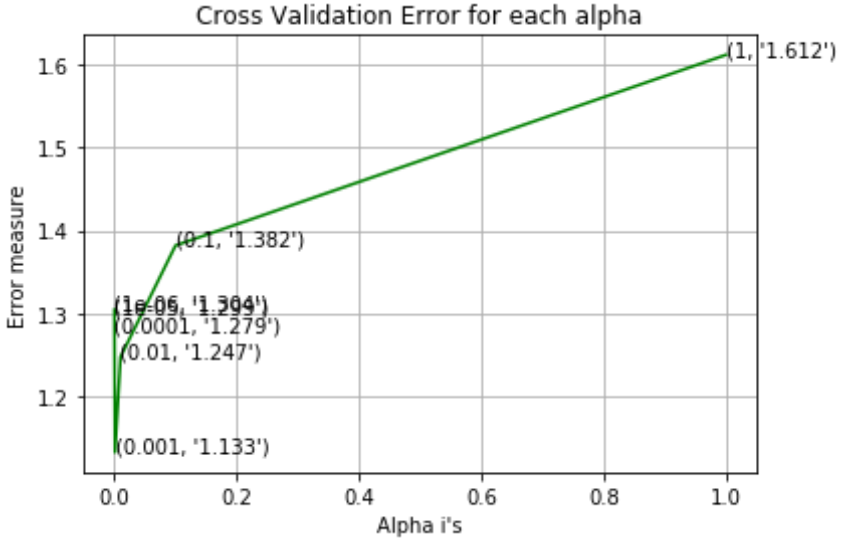
In [67]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/mod
ules/generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.1
5, fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, le
arning_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 S
tochastic Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#-------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/geometric-intuition-1/
#-------------------------------



# find more about CalibratedClassifierCV here at http://scikit-learn.or
g/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.h
tml
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, metho
d='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='l2', loss='log', random_state
=42)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
```

```
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.
classes_, eps=1e-15))
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()


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

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log
 loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=1e-15
))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross vali
dation log loss is:",log_loss(y_cv, predict_y, labels=clf.classes_, eps
=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log l
oss is:",log_loss(y_test, predict_y, labels=clf.classes_, eps=1e-15))
```

```
for alpha = 1e-06
Log Loss : 1.30436818439
for alpha = 1e-05
Log Loss : 1.29936164199
for alpha = 0.0001
```

```
Log Loss : 1.27905263975
for alpha = 0.001
Log Loss : 1.13263570348
for alpha = 0.01
Log Loss : 1.24746662278
for alpha = 0.1
Log Loss : 1.38189869892
for alpha = 1
Log Loss : 1.611617031
```



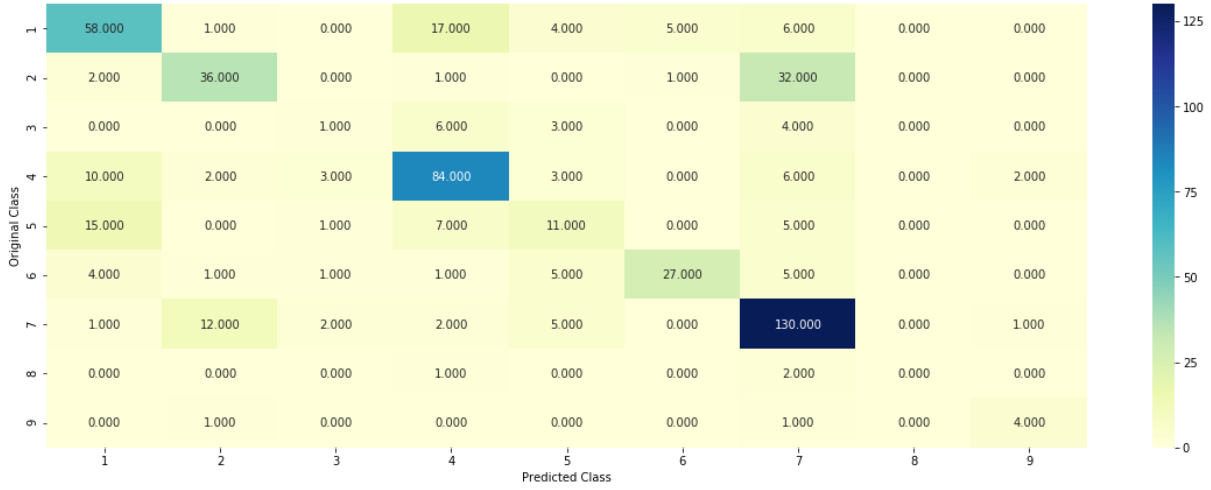

```
For values of best alpha =  0.001 The train log loss is: 0.580507591061
For values of best alpha =  0.001 The cross validation log loss is: 1.1
3263570348
For values of best alpha =  0.001 The test log loss is: 1.10327108332
```

4.3.2.2. Testing model with best hyper parameters

In [68]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/mod
ules/generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
```

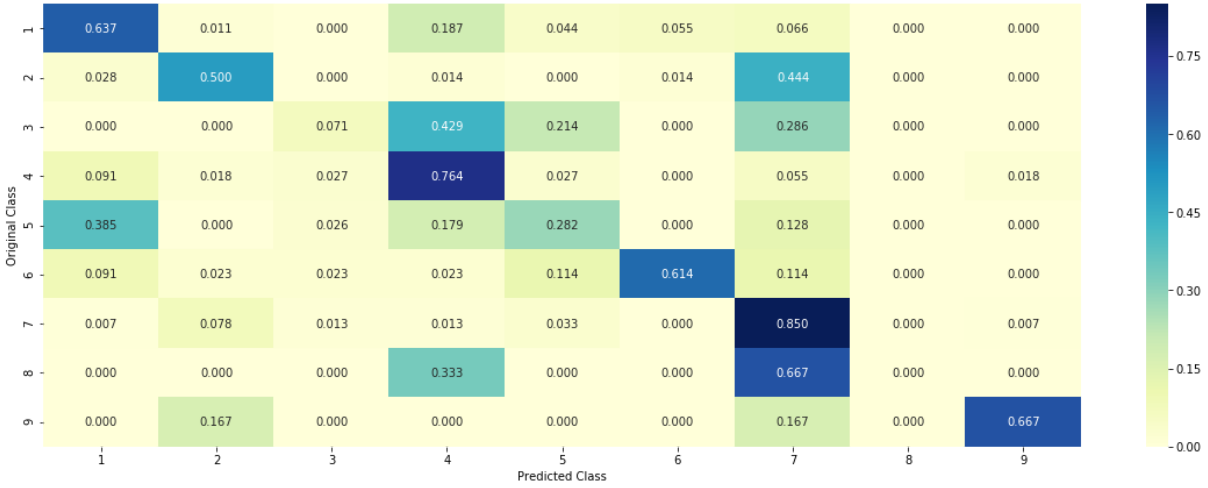
```
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.1
5, fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, le
arning_rate='optimal', eta0=0.0, power_t=0.5,
# class_weight=None, warm_start=False, average=False, n_iter=None)

# some of methods
# fit(X, y[, coef_init, intercept_init, …])     Fit linear model with S
tochastic Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#-------------------------------
# video link:
#-------------------------------

clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log',
random_state=42)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv_x_o
nehotCoding, cv_y, clf)
```

```
Log loss : 1.13263570348
Number of mis-classified points : 0.34022556390977443
-------------------- Confusion matrix --------------------
```



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


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



4.3.2.3. Feature Importance, Correctly Classified point

In [69]:
```
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log',
```

```
random_state=42)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[  2.63000000e-02   6.10000000e-03   2.
00000000e-04   8.16800000e-01
    1.38000000e-01   4.20000000e-03   3.00000000e-03   5.50000000e-03
    0.00000000e+00]]
Actual Class : 5
--------------------------------------------------
173 Text feature [instability] present in test data point [True]
182 Text feature [obligate] present in test data point [True]
261 Text feature [strengthen] present in test data point [True]
300 Text feature [homologues] present in test data point [True]
305 Text feature [m1775k] present in test data point [True]
317 Text feature [scandinavian] present in test data point [True]
321 Text feature [suppressor] present in test data point [True]
364 Text feature [posing] present in test data point [True]
373 Text feature [pol] present in test data point [True]
463 Text feature [damage] present in test data point [True]
477 Text feature [mdc1] present in test data point [True]
486 Text feature [strang] present in test data point [True]
487 Text feature [rockvax] present in test data point [True]
488 Text feature [bergthorsson] present in test data point [True]
489 Text feature [s1715] present in test data point [True]
490 Text feature [d1692n] present in test data point [True]
491 Text feature [monteia] present in test data point [True]
```

```
492 Text feature [w1837x] present in test data point [True]
493 Text feature [7340567] present in test data point [True]
494 Text feature [4729471] present in test data point [True]
495 Text feature [cterminus] present in test data point [True]
496 Text feature [disperses] present in test data point [True]
497 Text feature [uncharacteristic] present in test data point [True]
498 Text feature [v1668del] present in test data point [True]
499 Text feature [r1699] present in test data point [True]
Out of the top  500  features  25 are present in query point
```

4.3.2.4. Feature Importance, Inorrectly Classified point

In [70]:
```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 1
Predicted Class Probabilities: [[  6.31900000e-01   1.37000000e-02   2.
00000000e-04   3.31900000e-01
    5.20000000e-03   2.40000000e-03   9.20000000e-03   5.40000000e-03
    1.00000000e-04]]
Actual Class : 1
--------------------------------------------------
272 Text feature [stop] present in test data point [True]
Out of the top  500  features  1 are present in query point
```

4.4. Linear Support Vector Machines

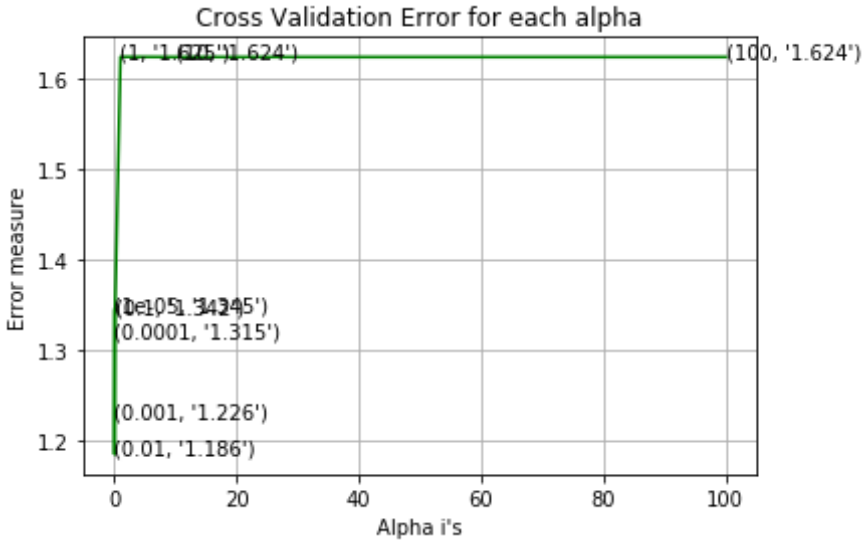
4.4.1. Hyper paramter tuning

In [71]:
```
# read more about support vector machines with linear kernals here htt
p://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, tol=0.001,
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decisi
on_function_shape='ovr', random_state=None)

# Some of methods of SVM()
# fit(X, y, [sample_weight])    Fit the SVM model according to the give
n 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.or
g/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.h
tml
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, metho
d='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='bal
anced')
    clf = SGDClassifier( class_weight='balanced', alpha=i, penalty='l2'
, loss='hinge', random_state=42)
    clf.fit(train_x_onehotCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_onehotCoding, train_y)
    sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
    cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.
classes_, eps=1e-15))
    print("Log Loss :",log_loss(cv_y, sig_clf_probs))

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()


best_alpha = np.argmin(cv_log_error_array)
# clf = SVC(C=i,kernel='linear',probability=True, class_weight='balance
d')
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], p
enalty='l2', loss='hinge', random_state=42)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
```

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

```
for C = 1e-05
Log Loss : 1.34485515995
for C = 0.0001
Log Loss : 1.31498107931
for C = 0.001
Log Loss : 1.22561628042
for C = 0.01
Log Loss : 1.18565126764
for C = 0.1
Log Loss : 1.34236274157
for C = 1
Log Loss : 1.6246498222
for C = 10
Log Loss : 1.62446130597
for C = 100
Log Loss : 1.62446133018
```



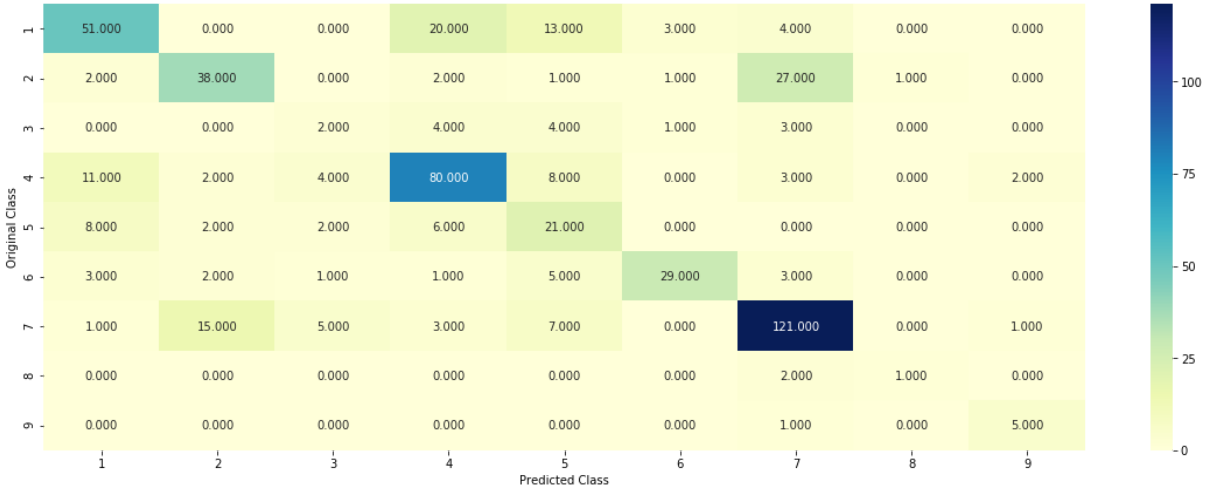

```
For values of best alpha =  0.01 The train log loss is: 0.69578176806
For values of best alpha =  0.01 The cross validation log loss is: 1.18
565126764
For values of best alpha =  0.01 The test log loss is: 1.16138576513
```

4.4.2. Testing model with best hyper parameters

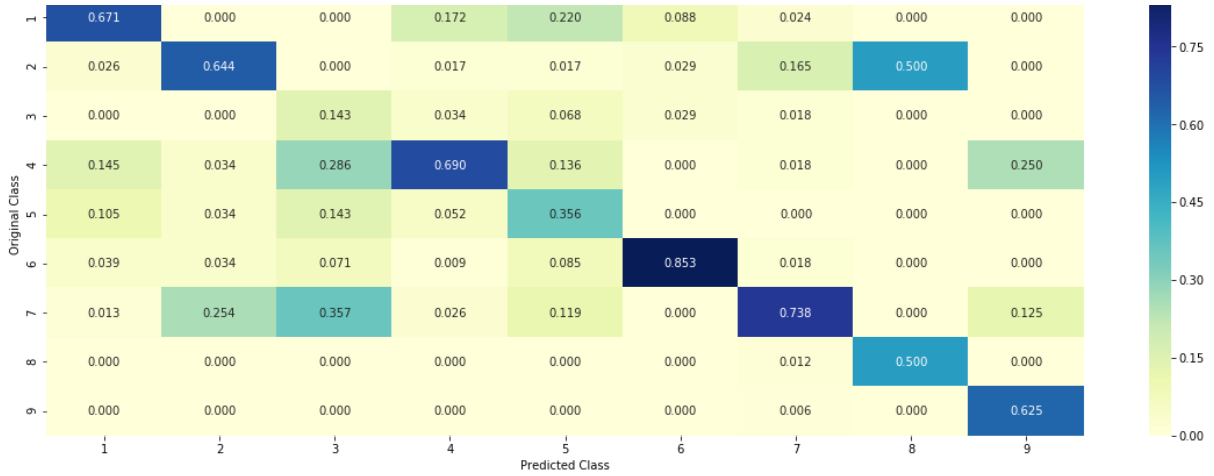
In [72]:
```
# read more about support vector machines with linear kernals here htt
p://scikit-learn.org/stable/modules/generated/sklearn.svm.SVC.html

# --------------------------------
# default parameters
# SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking
=True, probability=False, tol=0.001,
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decisi
on_function_shape='ovr', random_state=None)

# Some of methods of SVM()
# fit(X, y, [sample_weight])    Fit the SVM model according to the give
n 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='l2', loss='hinge', random_state=42,class_weight='balanced')
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding,cv_y, clf)
```

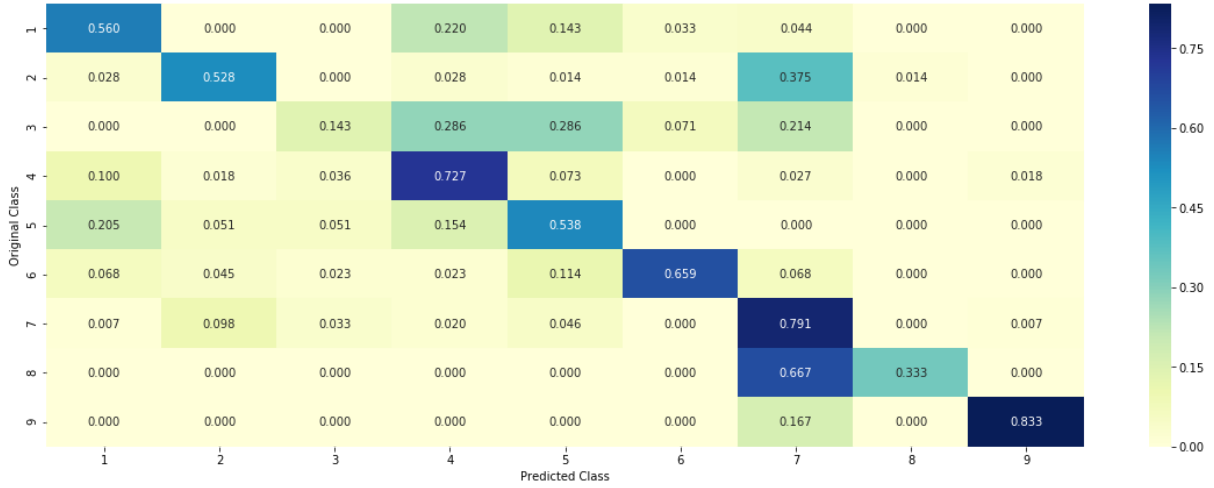
```
Log loss : 1.18565126764
Number of mis-classified points : 0.3458646616541353
-------------------- Confusion matrix --------------------
```




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



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



4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

In [73]:
```
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='hinge'
```

```
, random_state=42)
clf.fit(train_x_onehotCoding,train_y)
test_point_index = 1
# test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.0279  0.0362  0.0039  0.4694  0.414
9  0.0104  0.0248  0.0091  0.0034]]
Actual Class : 5
--------------------------------------------------
32 Text feature [instability] present in test data point [True]
51 Text feature [suppressor] present in test data point [True]
106 Text feature [strengthen] present in test data point [True]
118 Text feature [279] present in test data point [True]
130 Text feature [predisposing] present in test data point [True]
141 Text feature [swedish] present in test data point [True]
172 Text feature [nonsense] present in test data point [True]
216 Text feature [scandinavian] present in test data point [True]
262 Text feature [mismatch] present in test data point [True]
276 Text feature [damage] present in test data point [True]
368 Text feature [posing] present in test data point [True]
389 Text feature [homologues] present in test data point [True]
401 Text feature [grandmother] present in test data point [True]
437 Text feature [familial] present in test data point [True]
439 Text feature [idea] present in test data point [True]
Out of the top  500  features  15 are present in query point
```

4.3.3.2. For Incorrectly classified point

In [74]:
```
test_point_index = 100
no_feature = 500
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
print("-"*50)
get_impfeature_names(indices[0], test_df['TEXT'].iloc[test_point_index
],test_df['Gene'].iloc[test_point_index],test_df['Variation'].iloc[test
_point_index], no_feature)
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.5868  0.029   0.0022  0.3068  0.019
6  0.0114  0.0374  0.0053  0.0014]]
Actual Class : 1
--------------------------------------------------
222 Text feature [trimer] present in test data point [True]
420 Text feature [designations] present in test data point [True]
476 Text feature [stop] present in test data point [True]
Out of the top  500  features  3 are present in query point
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

In [75]:
```
# ------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='g
ini', max_depth=None, min_samples_split=2,
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='aut
o', max_leaf_nodes=None, min_impurity_decrease=0.0,
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, r
andom_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 give
n training data.
# predict(X)    Perform classification on samples in X.
# predict_proba (X)     Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/random-forest-and-their-construction-2/
# --------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.or
g/stable/modules/generated/sklearn.calibration.CalibratedClassifierCV.h
tml
# ----------------------------
# default paramters
# sklearn.calibration.CalibratedClassifierCV(base_estimator=None, metho
d='sigmoid', cv=3)
#
# some of the methods of CalibratedClassifierCV()
# fit(X, y[, sample_weight])    Fit the calibrated model
# get_params([deep])    Get parameters for this estimator.
# predict(X)    Predict the target of new samples.
# predict_proba(X)      Posterior probabilities of classification
#-------------------------------------
# video link:
#-------------------------------------

alpha = [100,200,500,1000,2000]
max_depth = [5, 10]
cv_log_error_array = []
for i in alpha:
```

```
    for j in max_depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gini',
max_depth=j, random_state=42, n_jobs=-1)
        clf.fit(train_x_onehotCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_onehotCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=
clf.classes_, eps=1e-15))
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))

'''fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ra
vel()
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)), (featur
es[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)], cri
terion='gini', max_depth=max_depth[int(best_alpha%2)], random_state=42,
 n_jobs=-1)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The
 train log loss is:",log_loss(y_train, predict_y, labels=clf.classes_,
eps=1e-15))
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
```

```
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The
 cross validation log loss is:",log_loss(y_cv, predict_y, labels=clf.cl
asses_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The
 test log loss is:",log_loss(y_test, predict_y, labels=clf.classes_, ep
s=1e-15))
```

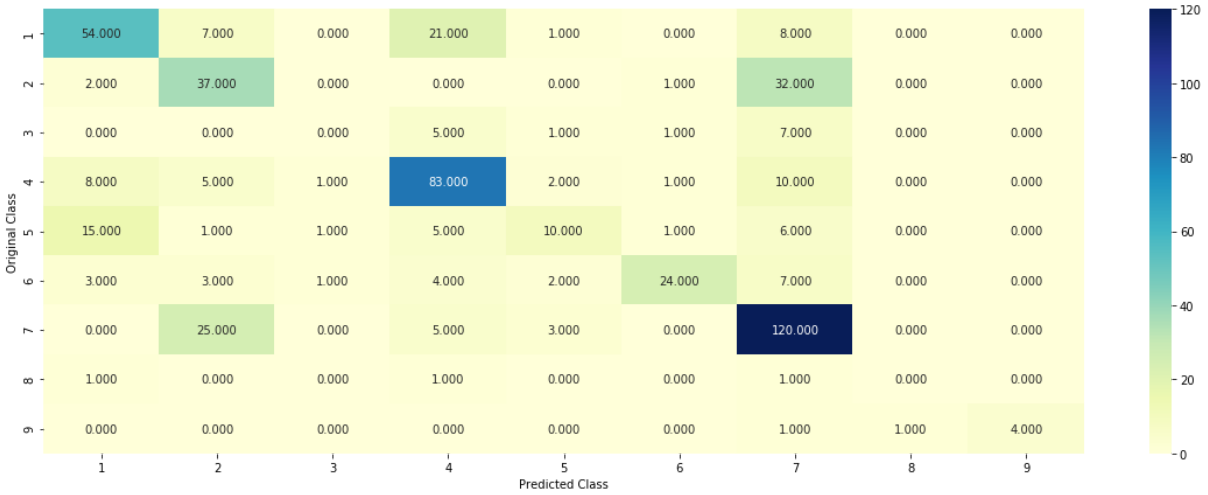
```
for n_estimators = 100 and max depth =  5
Log Loss : 1.23551544133
for n_estimators = 100 and max depth =  10
Log Loss : 1.1852253013
for n_estimators = 200 and max depth =  5
Log Loss : 1.23389536818
for n_estimators = 200 and max depth =  10
Log Loss : 1.1772807339
for n_estimators = 500 and max depth =  5
Log Loss : 1.2280773188
for n_estimators = 500 and max depth =  10
Log Loss : 1.16640691223
for n_estimators = 1000 and max depth =  5
Log Loss : 1.22099825388
for n_estimators = 1000 and max depth =  10
Log Loss : 1.16529675815
for n_estimators = 2000 and max depth =  5
Log Loss : 1.2168350629
for n_estimators = 2000 and max depth =  10
Log Loss : 1.16386262213
For values of best estimator =  2000 The train log loss is: 0.638979166
279
For values of best estimator =  2000 The cross validation log loss is:
1.16386308695
For values of best estimator =  2000 The test log loss is: 1.1632333289
1
```

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

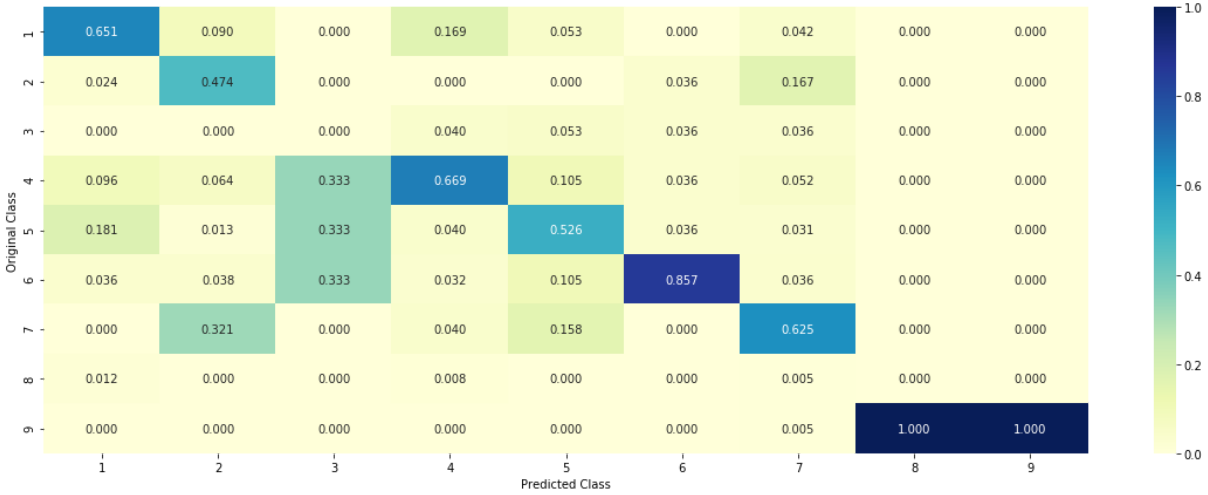
In [76]:
```
# -------------------------------
```

```
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='g
ini', max_depth=None, min_samples_split=2,
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='aut
o', max_leaf_nodes=None, min_impurity_decrease=0.0,
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, r
andom_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 give
n training data.
# predict(X)    Perform classification on samples in X.
# predict_proba (X)     Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/random-forest-and-their-construction-2/
# --------------------------------

clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], cri
terion='gini', max_depth=max_depth[int(best_alpha%2)], random_state=42,
 n_jobs=-1)
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_on
ehotCoding,cv_y, clf)
```

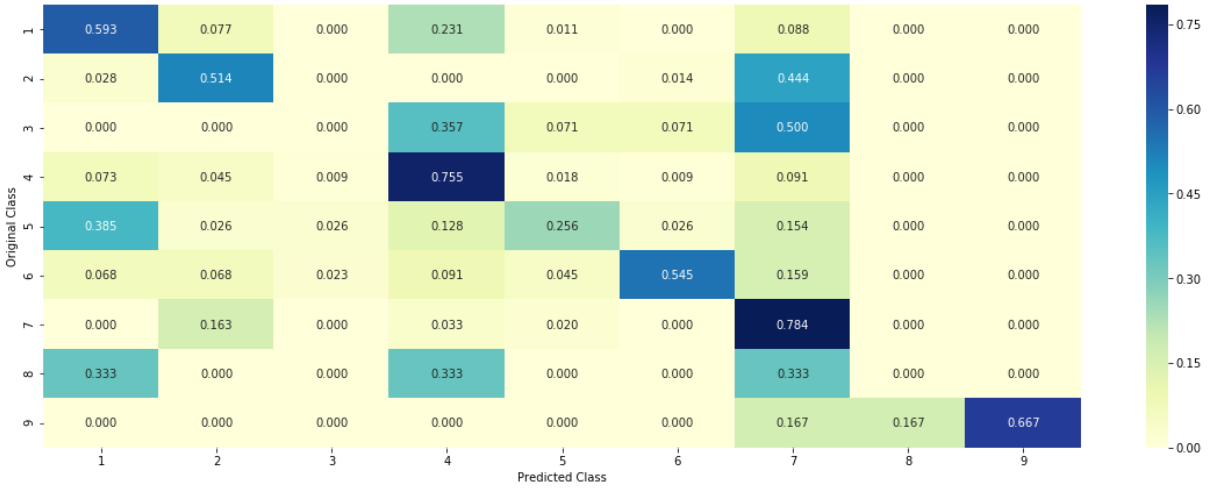
```
Log loss : 1.16386220191
Number of mis-classified points : 0.37593984962406013
-------------------- Confusion matrix --------------------
```



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



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



4.5.3. Feature Importance

4.5.3.1. Correctly Classified point

In [77]:
```
# test_point_index = 10
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], cri
terion='gini', max_depth=max_depth[int(best_alpha%2)], random_state=42,
 n_jobs=-1)
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

test_point_index = 1
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
```

```
get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_po
int_index],test_df['Gene'].iloc[test_point_index],test_df['Variation'].
iloc[test_point_index], no_feature)
```

```
Predicted Class : 5
Predicted Class Probabilities: [[ 0.2839  0.0196  0.0136  0.242   0.326
8  0.0917  0.0152  0.0036  0.0036]]
Actual Class : 5
--------------------------------------------------
0 Text feature [kinase] present in test data point [True]
2 Text feature [activating] present in test data point [True]
3 Text feature [activation] present in test data point [True]
4 Text feature [phosphorylation] present in test data point [True]
9 Text feature [missense] present in test data point [True]
10 Text feature [constitutive] present in test data point [True]
12 Text feature [suppressor] present in test data point [True]
13 Text feature [signaling] present in test data point [True]
18 Text feature [nonsense] present in test data point [True]
20 Text feature [function] present in test data point [True]
21 Text feature [activate] present in test data point [True]
22 Text feature [stability] present in test data point [True]
25 Text feature [loss] present in test data point [True]
31 Text feature [variants] present in test data point [True]
33 Text feature [protein] present in test data point [True]
35 Text feature [unstable] present in test data point [True]
38 Text feature [downstream] present in test data point [True]
41 Text feature [pathogenic] present in test data point [True]
44 Text feature [cells] present in test data point [True]
46 Text feature [patients] present in test data point [True]
50 Text feature [defective] present in test data point [True]
51 Text feature [functional] present in test data point [True]
61 Text feature [variant] present in test data point [True]
63 Text feature [sensitivity] present in test data point [True]
64 Text feature [deleterious] present in test data point [True]
66 Text feature [yeast] present in test data point [True]
67 Text feature [brca1] present in test data point [True]
68 Text feature [proteins] present in test data point [True]
71 Text feature [cell] present in test data point [True]
72 Text feature [phosphorylated] present in test data point [True]
75 Text feature [ligand] present in test data point [True]
```

```
76 Text feature [neutral] present in test data point [True]
78 Text feature [active] present in test data point [True]
80 Text feature [dna] present in test data point [True]
83 Text feature [functions] present in test data point [True]
84 Text feature [unclassified] present in test data point [True]
86 Text feature [response] present in test data point [True]
88 Text feature [expression] present in test data point [True]
90 Text feature [brca2] present in test data point [True]
91 Text feature [sensitive] present in test data point [True]
92 Text feature [clinical] present in test data point [True]
94 Text feature [splice] present in test data point [True]
96 Text feature [predicted] present in test data point [True]
97 Text feature [affect] present in test data point [True]
Out of the top  100  features  44 are present in query point
```

4.5.3.2. Inorrectly Classified point

In [78]:
```
test_point_index = 100
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_index])
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_onehotCoding[test_point_index]),4))
print("Actuall Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[test_po
int_index],test_df['Gene'].iloc[test_point_index],test_df['Variation'].
iloc[test_point_index], no_feature)
```

```
Predicted Class : 1
Predicted Class Probabilities: [[ 0.4371  0.0502  0.0134  0.3566  0.044
   0.0429  0.0421  0.0055  0.0082]]
Actuall Class : 1
--------------------------------------------------
12 Text feature [suppressor] present in test data point [True]
20 Text feature [function] present in test data point [True]
25 Text feature [loss] present in test data point [True]
```

```
31 Text feature [variants] present in test data point [True]
33 Text feature [protein] present in test data point [True]
44 Text feature [cells] present in test data point [True]
47 Text feature [growth] present in test data point [True]
48 Text feature [amplification] present in test data point [True]
61 Text feature [variant] present in test data point [True]
62 Text feature [transformation] present in test data point [True]
66 Text feature [yeast] present in test data point [True]
68 Text feature [proteins] present in test data point [True]
71 Text feature [cell] present in test data point [True]
80 Text feature [dna] present in test data point [True]
82 Text feature [pathway] present in test data point [True]
86 Text feature [response] present in test data point [True]
87 Text feature [serum] present in test data point [True]
88 Text feature [expression] present in test data point [True]
93 Text feature [kit] present in test data point [True]
97 Text feature [affect] present in test data point [True]
Out of the top  100  features  20 are present in query point
```

4.5.3. Hyper paramter tuning (With Response Coding)

In [79]:

```
# ---------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='g
ini', max_depth=None, min_samples_split=2,
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='aut
o', max_leaf_nodes=None, min_impurity_decrease=0.0,
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, r
andom_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 give
n training data.
# predict(X)    Perform classification on samples in X.
# predict_proba (X)     Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
```

```
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# ----------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-online/lessons/random-forest-and-their-construction-2/
# ----------------------------------


# find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/modules/generated/sklearn.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 = [10,50,100,200,500,1000]
max_depth = [2,3,5,10]
cv_log_error_array = []
for i in alpha:
    for j in max_depth:
        print("for n_estimators =", i,"and max depth = ", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gini', max_depth=j, random_state=42, n_jobs=-1)
        clf.fit(train_x_responseCoding, train_y)
        sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig_clf.fit(train_x_responseCoding, train_y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_responseCoding)
        cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=
```

```
clf.classes_, eps=1e-15))
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))
'''
fig, ax = plt.subplots()
features = np.dot(np.array(alpha)[:,None],np.array(max_depth)[None]).ra
vel()
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)), (featur
es[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)], cri
terion='gini', max_depth=max_depth[int(best_alpha%4)], random_state=42,
 n_jobs=-1)
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The tra
in log loss is:",log_loss(y_train, predict_y, labels=clf.classes_, eps=
1e-15))
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The cro
ss validation log loss is:",log_loss(y_cv, predict_y, labels=clf.classe
s_, eps=1e-15))
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The tes
t 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 : 2.1585243448
```

```
for n_estimators = 10 and max depth =  3
Log Loss : 1.68817432309
for n_estimators = 10 and max depth =  5
Log Loss : 1.36134498969
for n_estimators = 10 and max depth =  10
Log Loss : 1.76699310114
for n_estimators = 50 and max depth =  2
Log Loss : 1.65620880265
for n_estimators = 50 and max depth =  3
Log Loss : 1.45789420294
for n_estimators = 50 and max depth =  5
Log Loss : 1.33255865481
for n_estimators = 50 and max depth =  10
Log Loss : 1.84294556746
for n_estimators = 100 and max depth =  2
Log Loss : 1.50959546016
for n_estimators = 100 and max depth =  3
Log Loss : 1.46633410139
for n_estimators = 100 and max depth =  5
Log Loss : 1.32238982026
for n_estimators = 100 and max depth =  10
Log Loss : 1.7996104245
for n_estimators = 200 and max depth =  2
Log Loss : 1.61067360638
for n_estimators = 200 and max depth =  3
Log Loss : 1.46885260599
for n_estimators = 200 and max depth =  5
Log Loss : 1.39369233845
for n_estimators = 200 and max depth =  10
Log Loss : 1.86124485666
for n_estimators = 500 and max depth =  2
Log Loss : 1.6939258919
for n_estimators = 500 and max depth =  3
Log Loss : 1.54644197113
for n_estimators = 500 and max depth =  5
Log Loss : 1.38919648516
for n_estimators = 500 and max depth =  10
Log Loss : 1.86995317047
for n_estimators = 1000 and max depth =  2
```

```
Log Loss : 1.67397461604
for n_estimators = 1000 and max depth =  3
Log Loss : 1.5567764057
for n_estimators = 1000 and max depth =  5
Log Loss : 1.40458056228
for n_estimators = 1000 and max depth =  10
Log Loss : 1.84821733628
For values of best alpha =  100 The train log loss is: 0.0572493014874
For values of best alpha =  100 The cross validation log loss is: 1.322
38982026
For values of best alpha =  100 The test log loss is: 1.34476982137
```

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

In [80]:

```
# --------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='g
ini', max_depth=None, min_samples_split=2,
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='aut
o', max_leaf_nodes=None, min_impurity_decrease=0.0,
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, r
andom_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 give
n training data.
# predict(X)    Perform classification on samples in X.
# predict_proba (X)     Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# --------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/random-forest-and-their-construction-2/
# --------------------------------
```

```
clf = RandomForestClassifier(max_depth=max_depth[int(best_alpha%4)], n_
estimators=alpha[int(best_alpha/4)], criterion='gini', max_features='au
to',random_state=42)
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_
responseCoding,cv_y, clf)
```

```
Log loss : 1.32238982026
Number of mis-classified points : 0.41353383458646614
-------------------- Confusion matrix --------------------
```


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

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

4.5.5. Feature Importance

4.5.5.1. Correctly Classified point

In [81]:
```
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], cri
terion='gini', max_depth=max_depth[int(best_alpha%4)], random_state=42,
 n_jobs=-1)
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)


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 :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:
        print("Text is important feature")
```

```
Predicted Class : 5
Predicted Class Probabilities: [[ 0.046   0.005   0.0884  0.1147  0.589
6  0.1428  0.0025  0.0048  0.0062]]
Actual Class : 5
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text 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
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Gene is important feature
```

4.5.5.2. Incorrectly Classified point

In [82]:

```
test_point_index = 100
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_index]
.reshape(1,-1))
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(
test_x_responseCoding[test_point_index].reshape(1,-1)),4))
print("Actual Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
for i in indices:
    if i<9:
        print("Gene is important feature")
    elif i<18:
        print("Variation is important feature")
    else:
        print("Text is important feature")
```

```
Predicted Class : 4
Predicted Class Probabilities: [[ 0.3283  0.0163  0.1076  0.4229  0.027
7  0.061   0.0055  0.0129  0.0178]]
Actual Class : 1
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Text 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
Text is important feature
Gene is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Gene is important feature
```

4.7 Stack the models

4.7.1 testing with hyper parameter tuning

In [83]:
```
# read more about SGDClassifier() at http://scikit-learn.org/stable/mod
ules/generated/sklearn.linear_model.SGDClassifier.html
# ------------------------------
# default parameters
# SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.1
5, fit_intercept=True, max_iter=None, tol=None,
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, le
arning_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 S
tochastic Gradient Descent.
# predict(X)    Predict class labels for samples in X.

#------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/geometric-intuition-1/
#------------------------------


# read more about support vector machines with linear kernals here htt
p://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, tol=0.001,
# cache_size=200, class_weight=None, verbose=False, max_iter=-1, decisi
on_function_shape='ovr', random_state=None)

# Some of methods of SVM()
# fit(X, y, [sample_weight])    Fit the SVM model according to the give
n 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 htt
p://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomFo
restClassifier.html
# ---------------------------------
# default parameters
# sklearn.ensemble.RandomForestClassifier(n_estimators=10, criterion='g
ini', max_depth=None, min_samples_split=2,
# min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='aut
o', max_leaf_nodes=None, min_impurity_decrease=0.0,
# min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=1, r
andom_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 give
n training data.
# predict(X)    Perform classification on samples in X.
# predict_proba (X)     Perform classification on samples in X.

# some of attributes of  RandomForestClassifier()
# feature_importances_ : array of shape = [n_features]
# The feature importances (the higher, the more important the feature).

# ---------------------------------
# video link: https://www.appliedaicourse.com/course/applied-ai-course-
online/lessons/random-forest-and-their-construction-2/
# ---------------------------------


clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log', class_weigh
t='balanced', random_state=0)
clf1.fit(train_x_onehotCoding, train_y)
sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")

clf2 = SGDClassifier(alpha=1, penalty='l2', loss='hinge', class_weight=
'balanced', random_state=0)
clf2.fit(train_x_onehotCoding, train_y)
sig_clf2 = CalibratedClassifierCV(clf2, method="sigmoid")
```

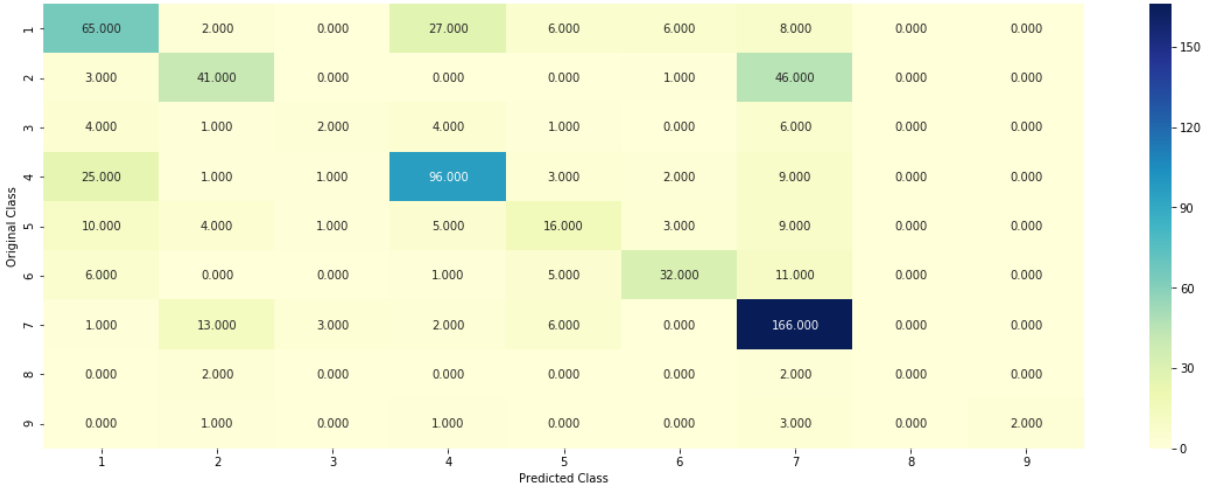
```
clf3 = MultinomialNB(alpha=0.001)
clf3.fit(train_x_onehotCoding, train_y)
sig_clf3 = CalibratedClassifierCV(clf3, method="sigmoid")

sig_clf1.fit(train_x_onehotCoding, train_y)
print("Logistic Regression :  Log Loss: %0.2f" % (log_loss(cv_y, sig_cl
f1.predict_proba(cv_x_onehotCoding))))
sig_clf2.fit(train_x_onehotCoding, train_y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y, sig
_clf2.predict_proba(cv_x_onehotCoding))))
sig_clf3.fit(train_x_onehotCoding, train_y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predic
t_proba(cv_x_onehotCoding))))
print("-"*50)
alpha = [0.0001,0.001,0.01,0.1,1,10]
best_alpha = 999
for i in alpha:
    lr = LogisticRegression(C=i)
    sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3
], meta_classifier=lr, use_probas=True)
    sclf.fit(train_x_onehotCoding, train_y)
    print("Stacking Classifer : for the value of alpha: %f Log Loss: %
0.3f" % (i, log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))))
    log_error =log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    if best_alpha > log_error:
        best_alpha = log_error
```

```
Logistic Regression :  Log Loss: 1.11
Support vector machines : Log Loss: 1.62
Naive Bayes : Log Loss: 1.30
--------------------------------------------------
Stacking Classifer : for the value of alpha: 0.000100 Log Loss: 2.178
Stacking Classifer : for the value of alpha: 0.001000 Log Loss: 2.037
Stacking Classifer : for the value of alpha: 0.010000 Log Loss: 1.507
Stacking Classifer : for the value of alpha: 0.100000 Log Loss: 1.115
Stacking Classifer : for the value of alpha: 1.000000 Log Loss: 1.221
Stacking Classifer : for the value of alpha: 10.000000 Log Loss: 1.465
```

4.7.2 testing the model with the best hyper parameters

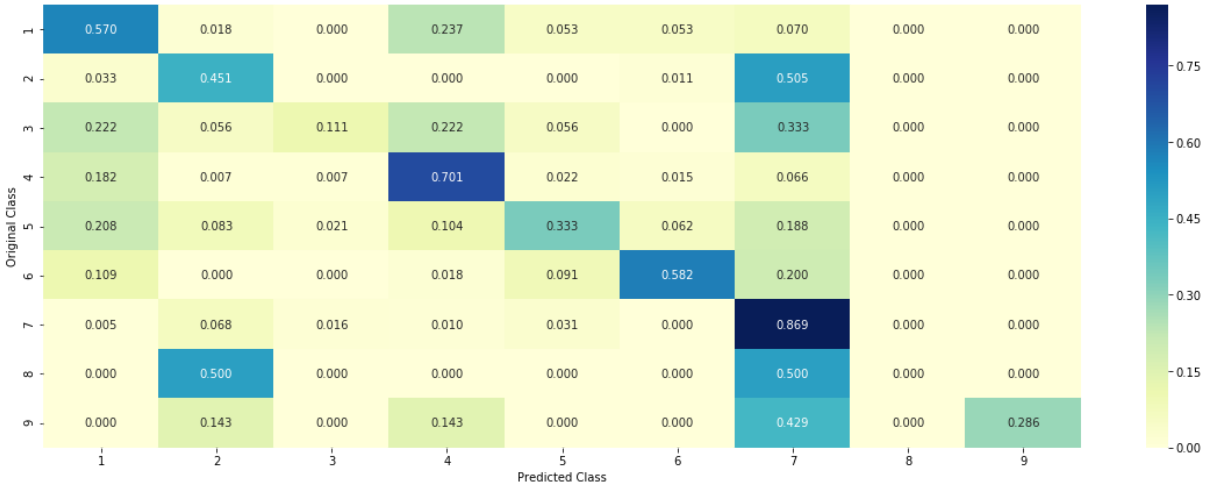
In [84]:
```
lr = LogisticRegression(C=0.1)
sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], m
eta_classifier=lr, use_probas=True)
sclf.fit(train_x_onehotCoding, train_y)

log_error = log_loss(train_y, sclf.predict_proba(train_x_onehotCoding))
print("Log loss (train) on the stacking classifier :",log_error)

log_error = log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
print("Log loss (CV) on the stacking classifier :",log_error)

log_error = log_loss(test_y, sclf.predict_proba(test_x_onehotCoding))
print("Log loss (test) on the stacking classifier :",log_error)

print("Number of missclassified point :", np.count_nonzero((sclf.predic
t(test_x_onehotCoding)- test_y))/test_y.shape[0])
plot_confusion_matrix(test_y=test_y, predict_y=sclf.predict(test_x_oneh
otCoding))
```

```
Log loss (train) on the stacking classifier : 0.636375151566
Log loss (CV) on the stacking classifier : 1.11533810879
Log loss (test) on the stacking classifier : 1.13571187405
Number of missclassified point : 0.3684210526315789
-------------------- Confusion matrix --------------------
```



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

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



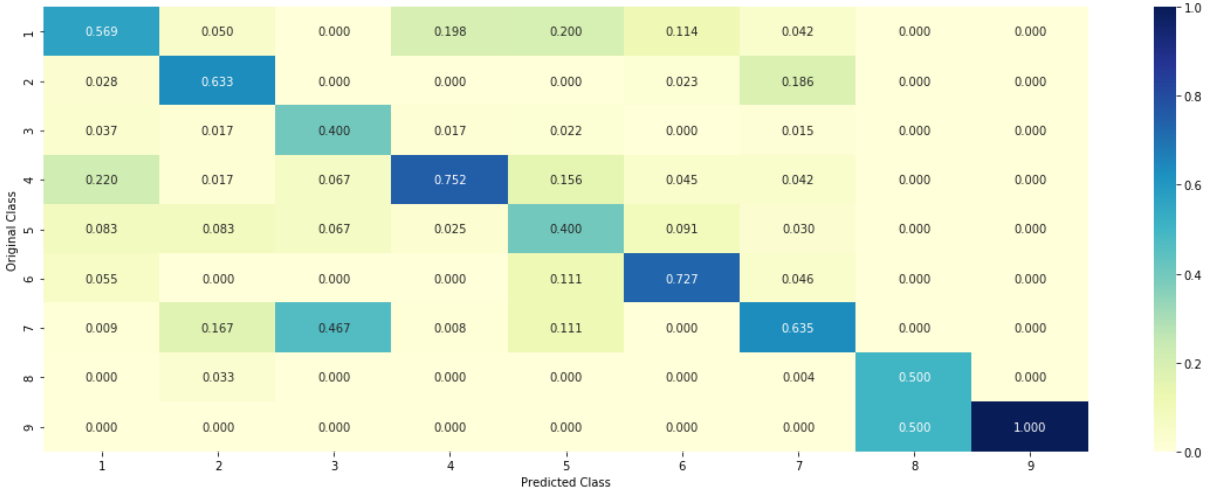
4.7.3 Maximum Voting classifier

In [85]:
```
#Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassifier.html
from sklearn.ensemble import VotingClassifier
vclf = VotingClassifier(estimators=[('lr', sig_clf1), ('svc', sig_clf2), ('rf', sig_clf3)], voting='soft')
vclf.fit(train_x_onehotCoding, train_y)
print("Log loss (train) on the VotingClassifier :", log_loss(train_y, vclf.predict_proba(train_x_onehotCoding)))
print("Log loss (CV) on the VotingClassifier :", log_loss(cv_y, vclf.predict_proba(cv_x_onehotCoding)))
print("Log loss (test) on the VotingClassifier :", log_loss(test_y, vclf.predict_proba(test_x_onehotCoding)))
```

```
print("Number of missclassified point :", np.count_nonzero((vclf.predic
t(test_x_onehotCoding)- test_y))/test_y.shape[0])
plot_confusion_matrix(test_y=test_y, predict_y=vclf.predict(test_x_oneh
otCoding))
```

```
Log loss (train) on the VotingClassifier : 0.862977104222
Log loss (CV) on the VotingClassifier : 1.18350039919
Log loss (test) on the VotingClassifier : 1.18185290919
Number of missclassified point : 0.3669172932330827
-------------------- Confusion matrix --------------------
```


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



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