Objective:-

1. Trying the feature engineering techniques to reduce the CV and test log-loss.

Personalized cancer diagnosis

1. Business Problem

1.1. Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Download training variants.zip and training text.zip from Kaggle.

Context:

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

Problem statement :

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

1.2. Source/Useful Links

Some articles and reference blogs about the problem statement

- https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almosteveryone-who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25
 (https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almosteveryone-who-took-it-almost-heres-what-it-teaches-us/#2a44ee2f6b25)
- https://www.youtube.com/watch?v=UwbuW7oK8rk (https://www.youtube.com/watch?v=UwbuW7oK8rk)
- 3. https://www.youtube.com/watch?v=qxXRKVompl8 (https://www.youtube.com/watch?v=qxXRKVompl8)

1.3. Real-world/Business objectives and constraints.

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

2. Machine Learning Problem Formulation

2.1. Data

2.1.1. Data Overview

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

2.1.2. Example Data Point

training_variants

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

• • •

training_text

ID,Text

0||Cyclin-dependent kinases (CDKs) regulate a variety of fundamental cellular processes. CDK10 stands out as one of the last orphan CDKs for which no activating cyclin has been identified and no kinase activity revealed. Previous work has shown that CDK10 silencing increases ETS2 (v-ets

erythroblastosis virus E26 oncogene homolog 2)-driven activation of the MAPK pathway, which confers tamoxifen resistance to breast cancer cells. The precise mechanisms by which CDK10 modulates ETS2 activity, and more generally the functions of CDK10, remain elusive. Here we demonstrate that CDK10 is a cyclin-dependent kinase by identifying cyclin M as an activating cyclin. Cyclin M, an orphan cyclin, is the product of FAM58A, whose mutations cause STAR syndrome, a human developmental anomaly whose features include toe syndactyly, telecanthus, and anogenital and renal malformations. We show that STAR syndrome-associated cyclin M mutants are unable to interact with CDK10. Cyclin M silencing phenocopies CDK10 silencing in increasing c-Raf and in conferring tamoxifen resistance to breast cancer cells. CDK10/cyclin M phosphorylates ETS2 in vitro, and in cells it positively controls ETS2 degradation by the proteasome. ETS2 protein levels are increased in cells derived from a STAR patient, and this increase is attributable to decreased cyclin M levels. Altogether, our results reveal an additional regulatory mechanism for ETS2, which plays key roles in cancer and development. They also shed light on the molecular mechanisms underlying STAR syndrome. Cyclin-dependent kinases (CDKs) play a pivotal role in the control of a number of fundamental cellular processes (1). The human genome contains 21 genes encoding proteins that can be considered as members of the CDK family owing to their sequence similarity with bona fide CDKs, those known to be activated by cyclins (2). Although discovered almost 20 y ago (3, 4), CDK10 remains one of the two CDKs without an identified cyclin partner. This knowledge gap has largely impeded the exploration of its biological functions. CDK10 can act as a positive cell cycle regulator in some cells (5, 6) or as a tumor suppressor in others (7, 8). CDK10 interacts with the ETS2 (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 [0]:
        import pandas as pd
        import matplotlib.pyplot as plt
        import re
        import time
        import warnings
        import numpy as np
        from nltk.corpus import stopwords
        from sklearn.decomposition import TruncatedSVD
        from sklearn.preprocessing import normalize
        from sklearn.feature extraction.text import TfidfVectorizer
        from sklearn.manifold import TSNE
        import seaborn as sns
        from sklearn.neighbors import KNeighborsClassifier
        from sklearn.metrics import confusion matrix
        from sklearn.metrics.classification import accuracy score, log loss
        from sklearn.feature extraction.text import TfidfVectorizer
        from sklearn.linear model import SGDClassifier
        from imblearn.over sampling import SMOTE
        from collections import Counter
        from scipy.sparse import hstack
        from sklearn.multiclass import OneVsRestClassifier
        from sklearn.svm import SVC
        from sklearn.model_selection import StratifiedKFold
        from collections import Counter, defaultdict
        from sklearn.calibration import CalibratedClassifierCV
        from sklearn.naive bayes import MultinomialNB
        from sklearn.naive bayes import GaussianNB
        from sklearn.model selection import train test split
        from sklearn.model selection import GridSearchCV
        import math
        from sklearn.metrics import normalized mutual info score
        from sklearn.ensemble import RandomForestClassifier
        warnings.filterwarnings("ignore")
        from mlxtend.classifier import StackingClassifier
        from sklearn import model selection
        from sklearn.linear model import LogisticRegression
```

In [2]: !pip install kaggle
 from google.colab import files
 files.upload()

Requirement already satisfied: kaggle in /usr/local/lib/python3.6/dist-packages (1.5.2)

Requirement already satisfied: urllib3<1.23.0,>=1.15 in /usr/local/lib/python3.6/dist-packages (from kaggle) (1.22)

Requirement already satisfied: six>=1.10 in /usr/local/lib/python3.6/dist-packa ges (from kaggle) (1.11.0)

Requirement already satisfied: certifi in /usr/local/lib/python3.6/dist-package s (from kaggle) (2018.11.29)

Requirement already satisfied: python-dateutil in /usr/local/lib/python3.6/dist-packages (from kaggle) (2.5.3)

Requirement already satisfied: requests in /usr/local/lib/python3.6/dist-packag es (from kaggle) (2.18.4)

Requirement already satisfied: tqdm in /usr/local/lib/python3.6/dist-packages (from kaggle) (4.28.1)

Requirement already satisfied: python-slugify in /usr/local/lib/python3.6/dist-packages (from kaggle) (2.0.1)

Requirement already satisfied: idna<2.7,>=2.5 in /usr/local/lib/python3.6/dist-packages (from requests->kaggle) (2.6)

Requirement already satisfied: chardet<3.1.0,>=3.0.2 in /usr/local/lib/python3. 6/dist-packages (from requests->kaggle) (3.0.4)

Requirement already satisfied: Unidecode>=0.04.16 in /usr/local/lib/python3.6/d ist-packages (from python-slugify->kaggle) (1.0.23)

Choose Files | No file chosen

Upload widget is only available when the cell has been executed in the current browser session. Please rerun this cell to enable.

Saving kaggle.json to kaggle.json

```
In [3]: !mkdir -p ~/.kaggle
!cp kaggle.json ~/.kaggle/

# This permissions change avoids a warning on Kaggle tool startup.
!chmod 600 ~/.kaggle/kaggle.json

!kaggle competitions download -c msk-redefining-cancer-treatment
!ls
```

```
Downloading training_variants.zip to /content
  0% 0.00/24.2k [00:00<?, ?B/s]
100% 24.2k/24.2k [00:00<00:00, 9.35MB/s]
Downloading test variants.zip to /content
  0% 0.00/47.5k [00:00<?, ?B/s]
100% 47.5k/47.5k [00:00<00:00, 51.7MB/s]
Downloading training text.zip to /content
 80% 49.0M/61.0M [00:01<00:00, 22.5MB/s]
100% 61.0M/61.0M [00:01<00:00, 39.4MB/s]
Downloading test text.zip to /content
92% 91.0M/99.0M [00:00<00:00, 81.3MB/s]
100% 99.0M/99.0M [00:00<00:00, 107MB/s]
Downloading stage2 sample submission.csv.7z to /content
  0% 0.00/765 [00:00<?, ?B/s]
100% 765/765 [00:00<00:00, 758kB/s]
Downloading stage2 test variants.csv.7z to /content
  0% 0.00/7.25k [00:00<?, ?B/s]
100% 7.25k/7.25k [00:00<00:00, 7.08MB/s]
Downloading stage2 test text.csv.7z to /content
  0% 0.00/8.88M [00:00<?, ?B/s]
100% 8.88M/8.88M [00:00<00:00, 81.2MB/s]
Downloading stage1 solution filtered.csv.7z to /content
 0% 0.00/1.28k [00:00<?, ?B/s]
100% 1.28k/1.28k [00:00<00:00, 1.32MB/s]
Downloading stage_2_private_solution.csv.7z to /content
 0% 0.00/592 [00:00<?, ?B/s]
100% 592/592 [00:00<00:00, 589kB/s]
kaggle.json
                                 stage2 test variants.csv.7z
sample data
                                 test text.zip
stage1_solution_filtered.csv.7z test_variants.zip
stage 2 private solution.csv.7z training text.zip
stage2_sample_submission.csv.7z training_variants.zip
stage2 test text.csv.7z
```

```
In [4]: !unzip test_text.zip
!unzip test_variants.zip
!unzip training_text.zip
!unzip training_variants.zip
```

```
Archive: test_text.zip
  inflating: test_text
Archive: test_variants.zip
  inflating: test_variants
Archive: training_text.zip
  inflating: training_text
Archive: training_variants.zip
  inflating: training_variants
```

3.1. Reading Data

3.1.1. Reading Gene and Variation Data

```
In [5]: 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[5]:	
---------	--

	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 [6]: # note the seprator in this file
          data_text =pd.read_csv("training_text",sep="\|\|",engine="python",names=["ID","TE
          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[6]:
             ID
                                                    TEXT
             0
                 Cyclin-dependent kinases (CDKs) regulate a var...
                   Abstract Background Non-small cell lung canc...
          1
             1
              2
          2
                   Abstract Background Non-small cell lung canc...
              3 Recent evidence has demonstrated that acquired...
          3
              4 Oncogenic mutations in the monomeric Casitas B...
```

3.1.3. Preprocessing of text

```
In [13]: import nltk
         nltk.download('stopwords')
         # loading stop words from nltk library
         stop words = set(stopwords.words('english'))
         def nlp preprocessing(total text, index, column):
             if type(total text) is not int:
                 string = ""
                 # replace every special char with space
                 total_text = re.sub('[^a-zA-Z0-9\n]', ' ', total_text)
                 # replace multiple spaces with single space
                 total_text = re.sub('\s+',' ', total_text)
                 # converting all the chars into lower-case.
                 total_text = total_text.lower()
                 for word in total text.split():
                 # if the word is a not a stop word then retain that word from the data
                     if not word in stop words:
                          string += word + " "
                 data text[column][index] = string
```

[nltk_data] Downloading package stopwords to /root/nltk_data...
[nltk data] Unzipping corpora/stopwords.zip.

```
In [14]: | #text processing stage.
          start time = time.clock()
          for index, row in data text.iterrows():
               if type(row['TEXT']) is str:
                   nlp_preprocessing(row['TEXT'], index, 'TEXT')
               else:
                   print("there is no text description for id:",index)
          print('Time took for preprocessing the text :',time.clock() - start time, "second
          there is no text description for id: 1109
          there is no text description for id: 1277
          there is no text description for id: 1407
          there is no text description for id: 1639
          there is no text description for id: 2755
          Time took for preprocessing the text: 371.128525 seconds
In [52]: #merging both gene variations and text data based on ID
          result = pd.merge(data, data text,on='ID', how='left')
          result.head()
Out[52]:
              ID
                                                                                     TEXT
                    Gene
                                  Variation Class
                 FAM58A Truncating Mutations
           0
              0
                                               1
                                                    cyclin dependent kinases cdks regulate variety...
           1
              1
                    CBL
                                    W802*
                                               2
                                                    abstract background non small cell lung cancer...
                    CBL
                                    Q249E
                                                    abstract background non small cell lung cancer...
              3
                    CBL
                                    N454D
                                                  recent evidence demonstrated acquired uniparen...
           3
                    CBL
                                     L399V
                                                  oncogenic mutations monomeric casitas b lineag...
              4
          result[result.isnull().any(axis=1)]
Out[53]:
                   ID
                        Gene
                                       Variation Class TEXT
           1109
                1109
                      FANCA
                                        S1088F
                                                    1
                                                        NaN
                1277 ARID5B Truncating Mutations
           1277
                                                        NaN
           1407
                1407
                       FGFR3
                                         K508M
                                                       NaN
           1639 1639
                                    Amplification
                                                       NaN
                        FLT1
           2755 2755
                        BRAF
                                         G596C
                                                    7
                                                        NaN
          result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Variatio
 In [0]:
In [55]: result[result['ID']==1109]
Out[55]:
                        Gene Variation Class
                                                     TEXT
                                           1 FANCA S1088F
           1109 1109
                      FANCA
                               S1088F
```

Exploratory Data Analysis

```
In [57]: data = result
    print("For training data, there are a total of", len(data.ID.unique()), "IDs,")
    print(len(data.Gene.unique()), "unique genes,")
    print(len(data.Variation.unique()), "unique variations and ")
    print(len(data.Class.unique()), "classes")
```

For training data, there are a total of 3321 IDs, 264 unique genes, 2996 unique variations and 9 classes

```
In [58]: plt.figure(figsize=(8,6))
    sns.countplot(x="Class", data=data)
    plt.ylabel('Frequency', fontsize=14)
    plt.xlabel('Class', fontsize=14)
    plt.title("Distribution of genetic mutation classes", fontsize=18)
    plt.show()
```



```
In [59]: train genes = data.groupby("Gene")['Gene'].count()
         fewest genes = train genes.sort values(ascending=True)[:10]
         print("Genes with most occurences\n", train_genes.sort_values(ascending=False)[:1
         print("\nGenes with fewest occurences\n", fewest genes)
```

```
Genes with most occurences
Gene
BRCA1
          264
TP53
          163
EGFR
          141
PTEN
          126
BRCA2
          125
           99
KIT
BRAF
           93
ERBB2
           69
ALK
           69
PDGFRA
           60
Name: Gene, dtype: int64
Genes with fewest occurences
Gene
KLF4
          1
FGF19
          1
FANCC
          1
          1
FAM58A
PAK1
          1
ERRFI1
          1
PAX8
          1
PIK3R3
          1
PMS1
          1
PPM1D
          1
```

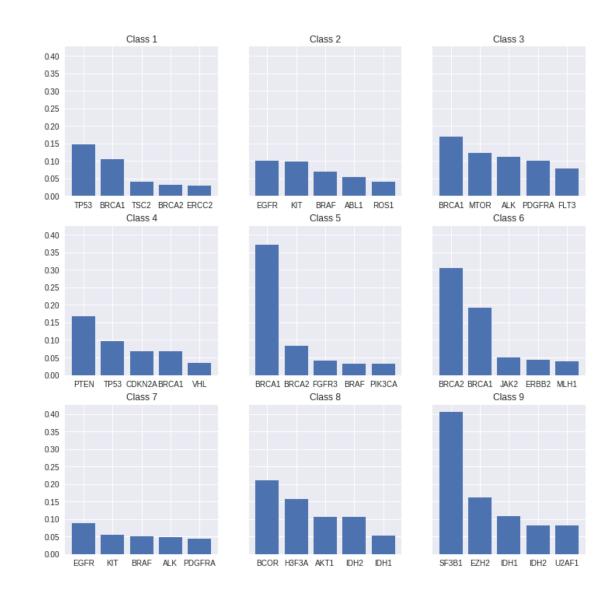
Name: Gene, dtype: int64

```
In [60]: # Genes with highest frequencies in each class
         fig, axes = plt.subplots(nrows=3, ncols=3, sharey=True, figsize=(12,12))
         # Normalize value counts for better comparison
         def normalize group(x):
             label, repetition = x.index, x
             t = sum(repetition)
             r = [n/t for n in repetition]
             return label, r
         for idx, g in enumerate(data.groupby('Class')):
             label, val = normalize_group(g[1]["Gene"].value_counts())
             ax = axes.flat[idx]
             ax.bar(np.arange(5), val[:5],
                    tick label=label[:5])
             ax.set_title("Class {}".format(g[0]))
         fig.text(0.5, 0.97, 'Top 5 Gene Frequency for each Class', ha='center', fontsize=
         fig.text(0.5, 0, 'Gene', ha='center', fontweight='bold')
         fig.text(0, 0.5, 'Frequency', va='center', rotation='vertical', fontweight='bold'
```

Out[60]: Text(0, 0.5, 'Frequency')

Frequency

Top 5 Gene Frequency for each Class

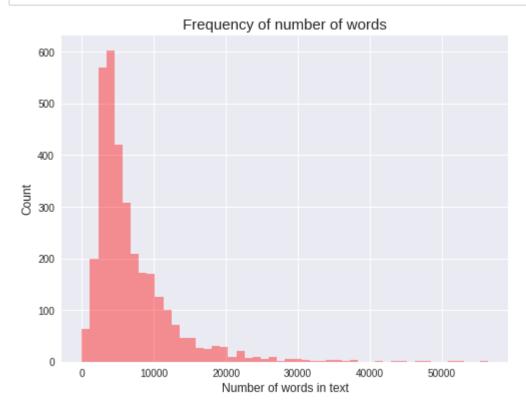


Gene

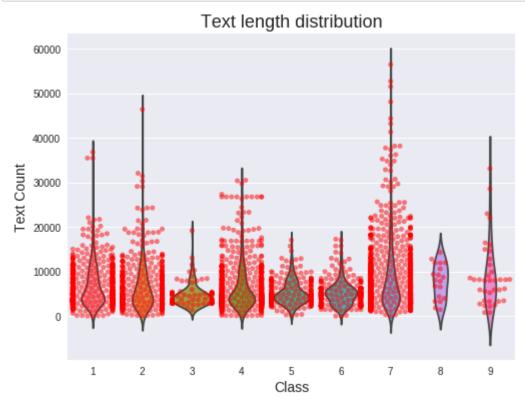
In [61]: data['Text_count'] = data["TEXT"].apply(lambda x: len(str(x).split()))
 data.head()

Out[61]:		ID	Gene	Variation	Class	TEXT	Text_count
	0	0	FAM58A	Truncating Mutations	1	cyclin dependent kinases cdks regulate variety	4370
	1	1	CBL	W802*	2	abstract background non small cell lung cancer	4139
	2	2	CBL	Q249E	2	abstract background non small cell lung cancer	4139
	3	3	CBL	N454D	3	recent evidence demonstrated acquired uniparen	3841
	4	4	CBL	L399V	4	oncogenic mutations monomeric casitas b lineag	4254

```
In [62]: #Frequency of no. of words in text
    plt.figure(figsize=(8, 6))
    sns.distplot(data.Text_count.values, bins=50, kde=False, color='r')
    plt.xlabel('Number of words in text', fontsize=12)
    plt.ylabel('Count', fontsize=12)
    plt.title("Frequency of number of words", fontsize=15)
    plt.show()
```



```
In [63]: # Distribution of text count for each class - violin plot
    plt.figure(figsize=(8,6))
    gene_count_grp = data.groupby('Gene')["Text_count"].sum().reset_index()
    sns.violinplot(x="Class", y="Text_count", data=data, inner=None)
    sns.swarmplot(x="Class", y="Text_count", data=data, color="r", alpha=.5);
    plt.ylabel('Text Count', fontsize=14)
    plt.xlabel('Class', fontsize=14)
    plt.title("Text length distribution", fontsize=18)
    plt.show()
```



Observation

- 1. In first plot, 3rd, 8th and 9th Class have very less datapoints because of which data is imbalanced.
- 2. In second plot, We can see that the most frequent genes in each classes are very different.
- 3. In third plot, We can see that all the classes have text counts between 0-20,000

3.1.4. Test, Train and Cross Validation Split

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

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

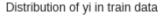
```
In [16]: print('Number of data points in train data:', train_df.shape[0])
    print('Number of data points in test data:', test_df.shape[0])
    print('Number of data points in cross validation data:', cv_df.shape[0])

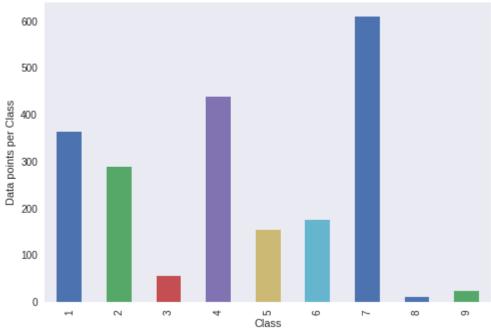
Number of data points in train data: 2124
    Number of data points in test data: 665
```

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

Number of data points in cross validation data: 532

```
In [17]: # it returns a dict, keys as class labels and values as the number of data points
         train_class_distribution = train_df['Class'].value_counts().sortlevel()
         test class distribution = test df['Class'].value counts().sortlevel()
         cv class distribution = cv df['Class'].value counts().sortlevel()
         my colors = 'rgbkymc'
         train class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in train data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort
         # -(train class distribution.values): the minus sign will give us in decreasing o
         sorted_yi = np.argsort(-train_class_distribution.values)
         for i in sorted vi:
             print('Number of data points in class', i+1, ':',train class distribution.val
         print('-'*80)
         my colors = 'rgbkymc'
         test class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in test data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort
         # -(train class distribution.values): the minus sign will give us in decreasing o
         sorted yi = np.argsort(-test class distribution.values)
         for i in sorted vi:
             print('Number of data points in class', i+1, ':',test_class_distribution.valu
         print('-'*80)
         my colors = 'rgbkymc'
         cv class distribution.plot(kind='bar')
         plt.xlabel('Class')
         plt.ylabel('Data points per Class')
         plt.title('Distribution of yi in cross validation data')
         plt.grid()
         plt.show()
         # ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort
         # -(train class distribution.values): the minus sign will give us in decreasing o
         sorted_yi = np.argsort(-train_class_distribution.values)
         for i in sorted yi:
             print('Number of data points in class', i+1, ':',cv class distribution.values
```





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 %)

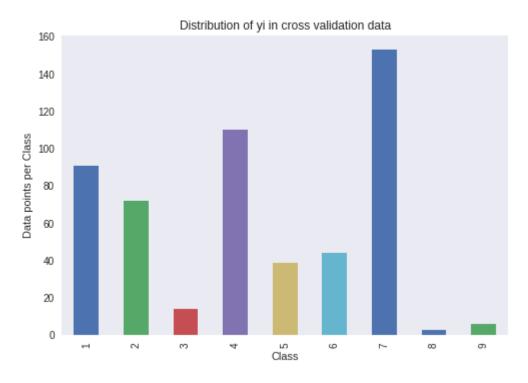
Number of data points in class 6 : 55 ( 8.271 %)

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 %)
```

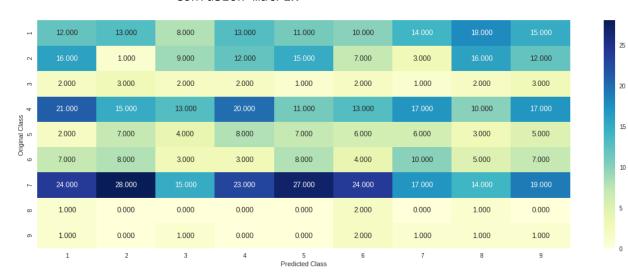
3.2 Prediction using a 'Random' Model

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

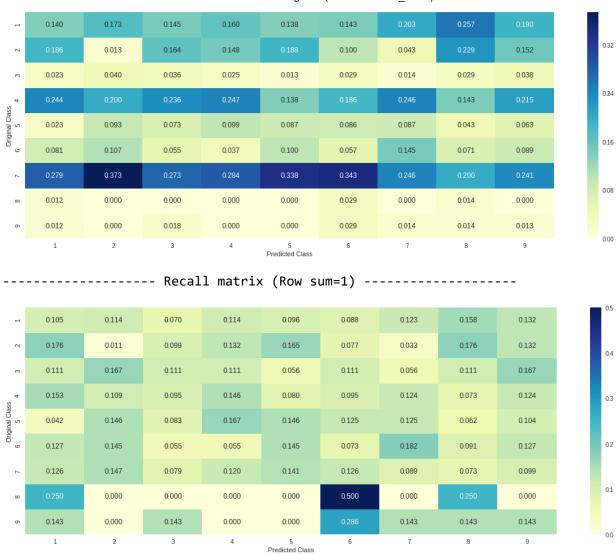
```
In [0]: # This function plots the confusion matrices given y_i, y_i_hat.
        def plot_confusion_matrix(test_y, predict_y):
            C = confusion matrix(test y, predict y)
            \# C = 9,9 \text{ matrix}, each cell (i,j) represents number of points of class i are
            A = (((C.T)/(C.sum(axis=1))).T)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

```
In [19]: # 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 s
         # 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_pre
         # Test-Set error.
         #we create a output array that has exactly same as the test data
         test predicted y = np.zeros((test data len,9))
         for i in range(test data len):
             rand probs = np.random.rand(1,9)
             test predicted y[i] = ((rand probs/sum(sum(rand probs)))[0])
         print("Log loss on Test Data using Random Model",log loss(y test,test predicted y
         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 2.519642065472273 Log loss on Test Data using Random Model 2.4619529686123123



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



3.3 Univariate Analysis

```
In [0]: # code for response coding with Laplace smoothing.
        # alpha : used for laplace smoothing
        # feature: ['gene', 'variation']
        # df: ['train_df', 'test_df', 'cv_df']
        # algorithm
        # Consider all unique values and the number of occurances of given feature in tra
        # build a vector (1*9) , the first element = (number of times it occured in class
        # gv_dict is like a look up table, for every gene it store a (1*9) representation
        # for a value of feature in df:
        # if it is in train data:
        # we add the vector that was stored in 'gv_dict' look up table to 'gv_fea'
        # if it is not there is train:
        # we add [1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9, 1/9] to 'qv fea'
        # return 'qv 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
                                                        43
            # Deletion
                                                        43
            # Amplification
            # Fusions
                                                        22
            # Overexpression
                                                         3
            # E17K
                                                         3
                                                         3
            # 061L
                                                         2
            # S222D
            # P130S
                                                         2
            # ...
            # }
            value_count = train_df[feature].value_counts()
            #print(value count)
            # qv dict : Gene Variation Dict, which contains the probability array for each
            gv dict = dict()
            # denominator will contain the number of time that particular feature occured
            for i, denominator in value_count.items():
                # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to
                # vec is 9 diamensional vector
```

```
vec = []
        for k in range(1,10):
            # print(train_df.loc[(train_df['Class']==1) & (train_df['Gene']=='BRC
                                            Variation Class
                          Gene
            # 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
                                                           1
                                               E1660G
            # 2634 2634 BRCA1
                                               W1718L
                                                           1
            # cls_cnt.shape[0] will return the number of rows
            cls_cnt = train_df.loc[(train_df['Class']==k) & (train_df[feature]==i
            # cls cnt.shape[0](numerator) will contain the number of time that pa
            vec.append((cls cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))
       # we are adding the gene/variation to the dict as key and vec as value
        gv dict[i]=vec
        #print(qv dict)
   return gv dict
# Get Gene variation feature
def get_gv_feature(alpha, feature, df):
   # print(qv dict)
          { 'BRCA1': [0.20075757575757575, 0.037878787878788, 0.0681818181818181
           'TP53': [0.32142857142857145, 0.061224489795918366, 0.0612244897959183
           'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.06818181
           'BRCA2': [0.1333333333333333, 0.0606060606060608, 0.06060606060606
           'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106
           'KIT': [0.066225165562913912, 0.25165562913907286, 0.07284768211920529
           'BRAF': [0.0666666666666666666, 0.17999999999999, 0.07333333333333333
   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()
   # qv fea: Gene variation feature, it will contain the feature for each feature
   gv fea = []
   # for every feature values in the given data frame we will check if it is the
   # 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_fea
   for index, row in df.iterrows():
        if row[feature] in dict(value count).keys():
            gv fea.append(gv dict[row[feature]])
       else:
            gv fea.append([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
              gv_fea.append([-1,-1,-1,-1,-1,-1,-1,-1])
   return gv_fea
```

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?

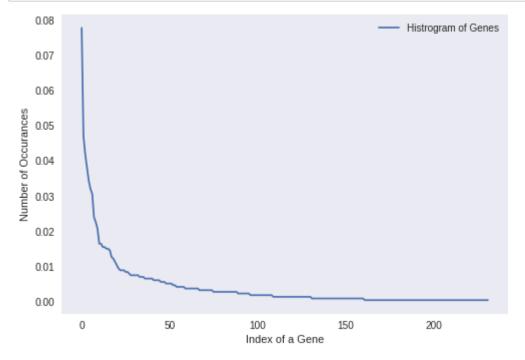
Ans. Gene is a categorical variable

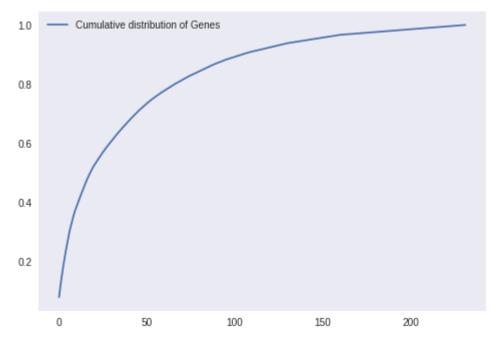
Q2. How many categories are there and How they are distributed?

```
In [21]:
         unique_genes = train_df['Gene'].value_counts()
         print('Number of Unique Genes :', unique_genes.shape[0])
         # the top 10 genes that occured most
         print(unique genes.head(10))
         Number of Unique Genes : 232
         BRCA1
                    165
         TP53
                    100
         EGFR
                     89
         PTEN
                     81
                     73
         BRCA2
         BRAF
                     68
         KIT
                     65
         ALK
                     51
         ERBB2
                     48
         PDGFRA
                     44
         Name: Gene, dtype: int64
         print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in
In [22]:
```

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

```
In [23]: s = sum(unique_genes.values);
h = unique_genes.values/s;
plt.plot(h, label="Histrogram of Genes")
plt.xlabel('Index of a Gene')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```





Q3. How to featurize this Gene feature?

Ans.there are two ways we can featurize this variable check out this video: https://www.appliedaicourse-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 [0]: #response-coding of the Gene feature
    # alpha is used for laplace smoothing
    alpha = 1
    # train gene feature
    train_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", train_
    # test gene feature
    test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", test_df
    # cross validation gene feature
    cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", cv_df))
```

```
In [0]: print("train gene feature responseCoding is converted feature using respone coding
          train gene feature responseCoding is converted feature using respone coding met
          hod. The shape of gene feature: (2124, 9)
  In [0]: # one-hot encoding of Gene feature.
           gene_vectorizer = TfidfVectorizer()
           train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(train_df['Gene'])
           test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df['Gene'])
           cv gene feature onehotCoding = gene vectorizer.transform(cv df['Gene'])
  In [0]: train df['Gene'].head()
Out[283]: 1412
                    FGFR3
           21
                      CBL
                     TP53
          504
          2126
                    CCND1
          884
                   PDGFRA
          Name: Gene, dtype: object
          gene vectorizer.get feature names()
  In [0]:
Out[284]: ['abl1',
            'acvr1',
            'ago2',
            'akt1',
            'akt2',
            'akt3',
            'alk',
            'apc',
            'ar',
            'araf',
            'arid1a',
            'arid1b',
            'arid2'
            'arid5b',
            'asxl1',
            'asx12',
            'atm',
            'atr',
            'atrx',
  In [0]: print("train gene feature onehotCoding is converted feature using one-hot encoding
```

train_gene_feature_onehotCoding is converted feature using one-hot encoding met hod. The shape of gene feature: (2124, 242)

Q4. How good is this gene feature in predicting y i?

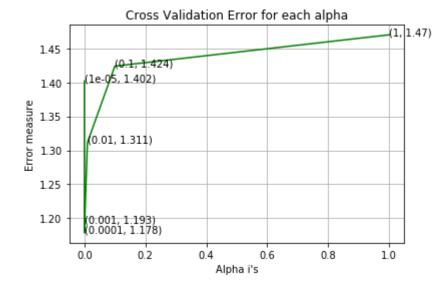
There are many ways to estimate how good a feature is, in predicting y_i. One of the good methods

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 [0]: | alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.
        # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gener
        # -----
        # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_inte
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate
        # class weight=None, warm start=False, average=False, n iter=None)
        # some of methods
        # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Grad
        \# predict(X) Predict class labels for samples in X.
        # video link:
        cv_log_error_array=[]
        for i in alpha:
            clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
            clf.fit(train gene feature onehotCoding, y train)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train gene feature onehotCoding, y train)
            predict y = sig clf.predict proba(cv gene feature onehotCoding)
            cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=
            print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict | )
        fig, ax = plt.subplots()
        ax.plot(alpha, cv log error array,c='g')
        for i, txt in enumerate(np.round(cv_log_error_array,3)):
            ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv log error array[i]))
        plt.grid()
        plt.title("Cross Validation Error for each alpha")
        plt.xlabel("Alpha i's")
        plt.ylabel("Error measure")
        plt.show()
        best alpha = np.argmin(cv log error array)
        clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_star
        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:",
        predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
        print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
        predict y = sig clf.predict proba(test gene feature onehotCoding)
        print('For values of best alpha = ', alpha[best alpha], "The test log loss is:",1
```

```
For values of alpha = 1e-05 The log loss is: 1.4019625605579298
For values of alpha = 0.0001 The log loss is: 1.178390947518176
```

For values of alpha = 0.001 The log loss is: 1.1932544784269383 For values of alpha = 0.01 The log loss is: 1.3114440889211676 For values of alpha = 0.1 The log loss is: 1.424005362413235 For values of alpha = 1 The log loss is: 1.4701532358158753



For values of best alpha = 0.0001 The train log loss is: 1.0604543628136502

For values of best alpha = 0.0001 The cross validation log loss is: 1.17839094

7518176

For values of best alpha = 0.0001 The test log loss is: 1.192214262109507

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.

Q6. How many data points in Test and CV datasets are covered by the 242 genes in train dataset?

Ans

- 1. In test data 655 out of 665 : 98.49624060150376
- 2. In cross validation data 518 out of 532 : 97.36842105263158

3.2.2 Univariate Analysis on Variation Feature

Q7. Variation, What type of feature is it?

Ans. Variation is a categorical variable

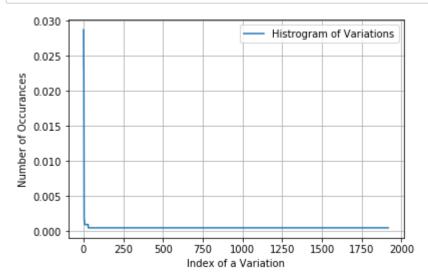
Q8. How many categories are there?

```
unique_variations = train_df['Variation'].value_counts()
In [0]:
         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: 1918
        Truncating_Mutations
                                 61
        Amplification
                                 50
        Deletion
                                 48
        Fusions
                                 21
                                  4
        Overexpression
        Q61H
                                  3
        Q61R
                                  3
                                  2
        G12V
                                  2
        G35R
                                  2
        E330K
        Name: Variation, dtype: int64
```

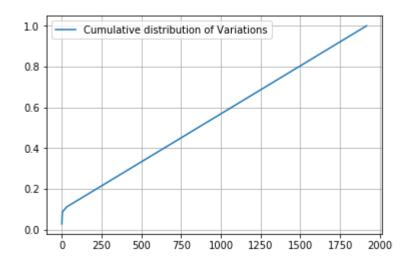
```
In [0]: print("Ans: There are", unique_variations.shape[0] ,"different categories of variations.shape[0]
```

Ans: There are 1918 different categories of variations in the train data, and they are distibuted as follows

```
In [0]: s = sum(unique_variations.values);
h = unique_variations.values/s;
plt.plot(h, label="Histrogram of Variations")
plt.xlabel('Index of a Variation')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



[0.0287194 0.05225989 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 [0]: # alpha is used for laplace smoothing
    alpha = 1
    # train gene feature
    train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variatio
    # test gene feature
    test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation
    # cross validation gene feature
    cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation",
```

```
In [0]: print("train_variation_feature_responseCoding is a converted feature using the re
```

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

1

- In [0]: # one-hot encoding of variation feature.
 variation_vectorizer = TfidfVectorizer()
 train_variation_feature_onehotCoding = variation_vectorizer.fit_transform(train_d
 test_variation_feature_onehotCoding = variation_vectorizer.transform(test_df['Var
 cv_variation_feature_onehotCoding = variation_vectorizer.transform(cv_df['Variation_vectorizer.tran
- In [0]: print("train_variation_feature_onehotEncoded is converted feature using the onne-

train_variation_feature_onehotEncoded is converted feature using the onne-hot e ncoding method. The shape of Variation feature: (2124, 1947)

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

Let's build a model just like the earlier!

```
In [0]: | alpha = [10 ** x for x in range(-5, 1)]
        # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gener
        # -----
        # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1_ratio=0.15, fit_inte
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate
        # class weight=None, warm start=False, average=False, n iter=None)
        # some of methods
        # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Grad
        \# predict(X) Predict class labels for samples in X.
        # video link:
        cv_log_error_array=[]
        for i in alpha:
            clf = SGDClassifier(alpha=i, penalty='12', loss='log', random state=42)
            clf.fit(train_variation_feature_onehotCoding, y_train)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train variation feature onehotCoding, y train)
            predict y = sig clf.predict proba(cv variation feature onehotCoding)
            cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=
            print('For values of alpha = ', i, "The log loss is:",log loss(y cv, predict | )
        fig, ax = plt.subplots()
        ax.plot(alpha, cv log error array,c='g')
        for i, txt in enumerate(np.round(cv log error array,3)):
            ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i]))
        plt.grid()
        plt.title("Cross Validation Error for each alpha")
        plt.xlabel("Alpha i's")
        plt.ylabel("Error measure")
        plt.show()
        best alpha = np.argmin(cv log error array)
        clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random sta
        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:",
        predict y = sig clf.predict proba(cv variation feature onehotCoding)
        print('For values of best alpha = ', alpha[best alpha], "The cross validation log
        predict y = sig clf.predict proba(test variation feature onehotCoding)
        print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",l
```

```
For values of alpha = 1e-05 The log loss is: 1.7061033297245032

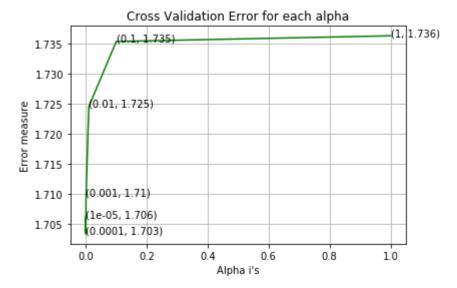
For values of alpha = 0.0001 The log loss is: 1.7033279641939136

For values of alpha = 0.001 The log loss is: 1.7096735602184494

For values of alpha = 0.01 The log loss is: 1.7245401724431388

For values of alpha = 0.1 The log loss is: 1.735425941378018

For values of alpha = 1 The log loss is: 1.7363709412512816
```



For values of best alpha = 0.0001 The train log loss is: 0.799892940719126
For values of best alpha = 0.0001 The cross validation log loss is: 1.70332796
41939136
For values of best alpha = 0.0001 The test log loss is: 1.7045757654046538

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 [0]: print("Q12. How many data points are covered by total ", unique_variations.shape[
    test_coverage=test_df[test_df['Variation'].isin(list(set(train_df['Variation'])))
    cv_coverage=cv_df[cv_df['Variation'].isin(list(set(train_df['Variation'])))].shap
    print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_
    print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":",(cov_df.shape[0])
```

Q12. How many data points are covered by total 1918 genes in test and cross v alidation data sets?

Ans

- 1. In test data 62 out of 665 : 9.323308270676693
- In cross validation data 54 out of 532 : 10.150375939849624

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 [35]: # building a TfidfVectorizer with all the words that occured minimum 3 times in to
    text_vectorizer = TfidfVectorizer(min_df=3,max_features=1000)
    train_text_feature_onehotCoding = text_vectorizer.fit_transform(train_df['TEXT'])
    # getting all the feature names (words)
    train_text_features= text_vectorizer.get_feature_names()

# train_text_feature_onehotCoding.sum(axis=0).A1 will sum every row and returns ()
    train_text_fea_counts = train_text_feature_onehotCoding.sum(axis=0).A1

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

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

Total number of unique words in train data: 1000

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

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

 # we use the same vectorizer that was trained on train data
 cv_text_feature_onehotCoding = text_vectorizer.transform(cv_df['TEXT'])
 # don't forget to normalize every feature
 cv_text_feature_onehotCoding = normalize(cv_text_feature_onehotCoding, axis=0)
- In [0]: #https://stackoverflow.com/a/2258273/4084039
 sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambda x: x[1] , resorted_text_occur = np.array(list(sorted_text_fea_dict.values()))

In [0]: # Number of words for a given frequency.
print(Counter(sorted_text_occur))

Counter({254.92485564185105: 1, 179.6743366077026: 1, 138.48643727952754: 1, 129.80535245216572: 1, 128.96575874866505: 1, 119.7414576102236: 1, 119.3522 720822652: 1, 115.01476649092555: 1, 111.76421625142224: 1, 109.561742518618 37: 1, 105.76516641704632: 1, 90.55426332692564: 1, 89.52704545646593: 1, 8 8.9021199890866: 1, 84.94280731801689: 1, 81.66471897938335: 1, 80.553541047 50046: 1, 80.18581330223554: 1, 79.45409353776236: 1, 75.39402760248896: 1, 75.11643642699688: 1, 75.08425737095087: 1, 71.05099875888212: 1, 68.8517708 320724: 1, 68.74832287501928: 1, 67.4351502441337: 1, 66.2649713448625: 1, 6 6.1604432175213: 1, 64.64542410454514: 1, 64.516623063368: 1, 64.43174995244 321: 1, 63.519629816470804: 1, 62.940623589195624: 1, 60.48918250791442: 1, 59.32698200783694: 1, 57.511612143086126: 1, 56.321345852853554: 1, 56.21697 3923270736: 1, 54.552294218017856: 1, 54.439117161411474: 1, 50.707308096549 46: 1, 49.557820346795154: 1, 49.383113608295645: 1, 49.001611717154674: 1, 48.42991228180798: 1, 48.23485103488938: 1, 48.226458726564466: 1, 46.346273 59000825: 1, 46.262150699962646: 1, 45.028466083698: 1, 44.50598663581978: 1, 43.57949679729767: 1, 43.52860726352477: 1, 43.47404694295213: 1, 43.4245 15813504996: 1, 43.17842428586127: 1, 42.76092293218395: 1, 42.6814979866371 4: 1, 42.33624327888522: 1, 42.17326616916091: 1, 42.124955794747514: 1, 41. 62745353422218: 1, 41.41720665335359: 1, 41.0906331938435: 1, 40.99655066806

```
In [0]: # Train a Logistic regression+Calibration model using text features whicha re on-
        alpha = [10 ** x for x in range(-5, 1)]
        # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gener
        # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit inte
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate
        # class weight=None, warm start=False, average=False, n iter=None)
        # some of methods
        # fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Grad
        \# predict(X) Predict class labels for samples in X.
        #-----
        # video link:
        #-----
        cv log error array=[]
        for i in alpha:
            clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
            clf.fit(train text feature onehotCoding, y train)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train text feature onehotCoding, y train)
            predict y = sig clf.predict proba(cv text feature onehotCoding)
            cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=
            print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_
        fig, ax = plt.subplots()
        ax.plot(alpha, cv_log_error_array,c='g')
        for i, txt in enumerate(np.round(cv log error array,3)):
            ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i]))
        plt.grid()
        plt.title("Cross Validation Error for each alpha")
        plt.xlabel("Alpha i's")
        plt.ylabel("Error measure")
        plt.show()
        best alpha = np.argmin(cv log error array)
        clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_sta
        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:",
        predict_y = sig_clf.predict_proba(cv_text_feature_onehotCoding)
        print('For values of best alpha = ', alpha[best alpha], "The cross validation log
        predict y = sig clf.predict proba(test text feature onehotCoding)
        print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",l
```

```
For values of alpha = 1e-05 The log loss is: 1.1417877137308243

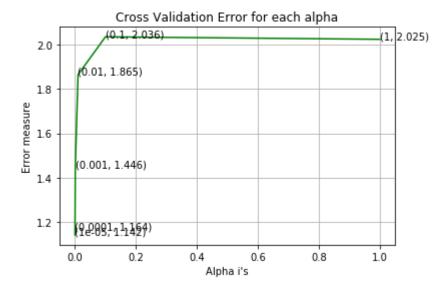
For values of alpha = 0.0001 The log loss is: 1.1637328605378794

For values of alpha = 0.001 The log loss is: 1.4457432306630014

For values of alpha = 0.01 The log loss is: 1.8651768087409692

For values of alpha = 0.1 The log loss is: 2.03622483427236

For values of alpha = 1 The log loss is: 2.024942550444193
```



For values of best alpha = 1e-05 The train log loss is: 0.8079914187375853

For values of best alpha = 1e-05 The cross validation log loss is: 1.141787713

7308243

For values of best alpha = 1e-05 The test log loss is: 1.1500729891599621

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

Ans. Yes, it seems like!

```
In [0]: def get_intersec_text(df):
    df_text_vec = TfidfVectorizer(min_df=3,max_features=1000)
    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_counts))
    len1 = len(set(df_text_features))
    len2 = len(set(train_text_features) & set(df_text_features))
    return len1,len2
```

```
In [0]: len1,len2 = get_intersec_text(test_df)
    print(np.round((len2/len1)*100, 3), "% of word of test data appeared in train data
    len1,len2 = get_intersec_text(cv_df)
    print(np.round((len2/len1)*100, 3), "% of word of Cross Validation appeared in train
```

94.7 % of word of test data appeared in train data 94.0 % of word of Cross Validation appeared in train data

4. Machine Learning Models

```
In [0]: #Data preparation for ML models.

#Misc. functionns for ML models

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

# for calculating log_loss we will provide the array of probabilities belong 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))
        plot_confusion_matrix(test_y, pred_y)
In [0]: def report_log_loss(train_x, train_y, test_x, test_y, clf):
        clf.fit(train_x, train_y)
```

```
In [0]: 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 [0]: # 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,max features=1000)
            gene vec = gene count vec.fit(train df['Gene'])
            var_vec = var_count_vec.fit(train_df['Variation'])
            text vec = text count vec.fit(train df['TEXT'])
            fea1_len = len(gene_vec.get_feature_names())
            fea2 len = len(var count vec.get feature names())
            word present = 0
            for i,v in enumerate(indices):
                 if (v < fea1 len):</pre>
                     word = gene_vec.get_feature_names()[v]
                     yes_no = True if word == gene else False
                     if yes no:
                         word_present += 1
                         print(i, "Gene feature [{}] present in test data point [{}]".form
                 elif (v < fea1 len+fea2 len):</pre>
                     word = var_vec.get_feature_names()[v-(fea1_len)]
                     yes no = True if word == var else False
                     if yes no:
                         word present += 1
                         print(i, "variation feature [{}] present in test data point [{}]"
                 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 [{}]".form
            print("Out of the top ",no_features," features ", word_present, "are present
```

Feature engineering

```
In [0]: # Combine Gene & Variation features
        Gene Var data=[]
        for i in data["Gene"].values:
            Gene Var data.append(i)
        for i in data["Variation"].values:
            Gene_Var_data.append(i)
        # Building TF-IDF vectorizer ontop of combined gene var data
        cnt vect=TfidfVectorizer()
        Fit_vect=cnt_vect.fit(Gene_Var_data)
        train text vect=cnt vect.transform(train df["TEXT"])
        cv_text_vect=cnt_vect.transform(cv_df["TEXT"])
        test_text_vect=cnt_vect.transform(test_df["TEXT"])
        # Normalization
        train_text_vect=normalize(train_text_vect,axis=0)
        cv text vect=normalize(cv text vect,axis=0)
        test_text_vect=normalize(test_text_vect,axis=0)
```

Stacking the three types of features

And also I stacking that with one hot encoding features

```
In [0]: # merging gene, variance and text features
        # building train, test and cross validation data sets
        \# a = [[1, 2],
               [3, 4]]
        #b = [[4, 5],
               [6, 7]]
        \# hstack(a, b) = [[1, 2, 4, 5],
                         [ 3, 4, 6, 7]]
        train gene var onehotCoding = hstack((train gene feature onehotCoding,train varia
        test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding,test_variatio)
        cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_variation_feat
        train gene var updt=hstack((train gene var onehotCoding,train text vect))
        train_x_onehotCoding = hstack((train_gene_var_updt, train_text_feature_onehotCodi
        train y = np.array(list(train df['Class']))
        test gene var updt=hstack((test gene var onehotCoding,test text vect))
        test x onehotCoding = hstack((test gene var updt, test text feature onehotCoding)
        test_y = np.array(list(test_df['Class']))
        cv gene var updt=hstack((cv gene var onehotCoding,cv text vect))
        cv x onehotCoding = hstack((cv gene var updt, cv text feature onehotCoding)).tocs
        cv y = np.array(list(cv df['Class']))
        train gene var responseCoding = np.hstack((train gene feature responseCoding,trai
        test gene var responseCoding = np.hstack((test gene feature responseCoding,test v
        cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCoding,cv_variati
        train_x_responseCoding = np.hstack((train_gene_var_responseCoding, train_text_fea
        test_x_responseCoding = np.hstack((test_gene_var_responseCoding, test_text_feature)
        cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_text_feature_resp
        print("One hot encoding features :")
In [0]:
        print("(number of data points * number of features) in train data = ", train x on
        print("(number of data points * number of features) in test data = ", test_x_oneh
        print("(number of data points * number of features) in cross validation data =",
        One hot encoding features :
```

(number of data points * number of features) in train data = (2124, 6427) (number of data points * number of features) in test data = (665, 6427)

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

```
http://localhost: 8888/notebooks/Desktop/case file/Personalized Cancer Diagnosis (ASSIGNMENT\_Part 4). ipynbulki (ASSIGNMEN
```

427)

(number of data points * number of features) in cross validation data = (532, 2

4.1. Base Line Model

4.1.1. Naive Bayes

7)

4.1.1.1. Hyper parameter tuning

```
In [0]: # find more about Multinomial Naive base function here http://scikit-learn.org/ste
        # -----
        # default paramters
        # sklearn.naive_bayes.MultinomialNB(alpha=1.0, fit_prior=True, class_prior=None)
        # some of methods of MultinomialNB()
        # fit(X, y[, sample_weight]) Fit Naive Bayes classifier according to X, y
        # predict(X) Perform classification on an array of test vectors X.
        # predict log proba(X) Return log-probability estimates for the test vector X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        # -----
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/m
        # ------
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
        # 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/les
        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 ,
            # to avoid rounding error while multiplying probabilites we use log-probabili
            print("Log Loss :",log_loss(cv_y, sig_clf_probs))
        fig, ax = plt.subplots()
        ax.plot(np.log10(alpha), cv log error array,c='g')
        for i, txt in enumerate(np.round(cv log error array,3)):
            ax.annotate((alpha[i],str(txt)), (np.log10(alpha[i]),cv_log_error_array[i]))
        plt.grid()
        plt.xticks(np.log10(alpha))
        plt.title("Cross Validation Error for each alpha")
        plt.xlabel("Alpha i's")
        plt.ylabel("Error measure")
        plt.show()
        best alpha = np.argmin(cv log error array)
        clf = MultinomialNB(alpha=alpha[best alpha])
```

```
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",legicle to the control of the control of the cross validation log
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",legicle to the control of th
```

```
for alpha = 1e-05
Log Loss: 1.1739581761584255
for alpha = 0.0001
Log Loss: 1.1728047951914005
for alpha = 0.001
Log Loss: 1.168864539462507
for alpha = 0.1
Log Loss: 1.158250468831457
for alpha = 1
Log Loss: 1.2577399951875554
for alpha = 10
Log Loss: 1.4134772942015252
for alpha = 100
Log Loss: 1.4109445895566923
for alpha = 1000
Log Loss: 1.4012076802171929
```

1.40 (10. '1 4180, '1 410') (1.401')

1.35 (1.401')

1.25 (1.401')

1.20 (1e.05. (0.000))(d.001, '1.169') (0.1, '1.158')

1.5 -4 -3 -1 0 1 2 3

Alpha i's

For values of best alpha = 0.1 The train log loss is: 0.7606205701319388

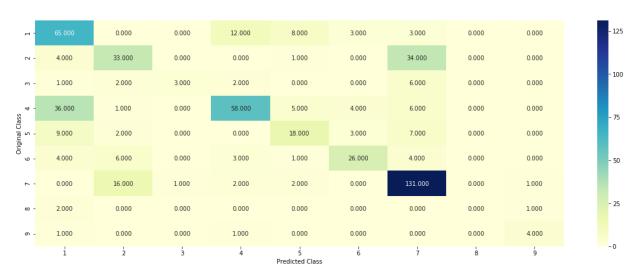
For values of best alpha = 0.1 The cross validation log loss is: 1.15825046883

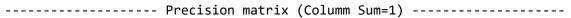
1457

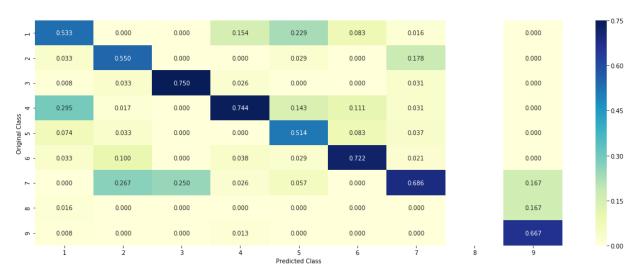
For values of best alpha = 0.1 The test log loss is: 1.1881531434320403

4.1.1.2. Testing the model with best hyper paramters

```
In [0]: # find more about Multinomial Naive base function here http://scikit-learn.org/st
        # default paramters
        # sklearn.naive bayes.MultinomialNB(alpha=1.0, fit prior=True, class prior=None)
        # some of methods of MultinomialNB()
        # fit(X, y[, sample weight]) Fit Naive Bayes classifier according to X, y
        # predict(X) Perform classification on an array of test vectors X.
        # predict log proba(X) Return log-probability estimates for the test vector X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/m
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample weight]) Fit the calibrated model
        # get_params([deep])
                               Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
        # predict proba(X) Posterior probabilities of classification
        clf = MultinomialNB(alpha=alpha[best alpha])
        clf.fit(train x onehotCoding, train y)
        sig clf = CalibratedClassifierCV(clf, method="sigmoid")
        sig clf.fit(train x onehotCoding, train y)
        sig_clf_probs = sig_clf.predict_proba(cv_x_onehotCoding)
        # to avoid rounding error while multiplying probabilites we use log-probability e
        print("Log Loss :",log_loss(cv_y, sig_clf_probs))
        print("Number of missclassified point :", np.count_nonzero((sig_clf.predict(cv_x_
        plot_confusion_matrix(cv_y, sig_clf.predict(cv_x_onehotCoding.toarray()))
```







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



4.1.1.3. Feature Importance, Correctly classified point

```
In [0]: 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_one print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
```

Predicted Class : 2

Predicted Class Probabilities: [[0.056 0.5863 0.0179 0.0976 0.052 0.0435 0.13

46 0.0064 0.0057]] Actual Class : 2

4.1.1.4. Feature Importance, Incorrectly classified point

```
In [0]: 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_one print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0472 0.0494 0.0151 0.0824 0.0439 0.0367 0.71 5 0.0054 0.0048]]
Actual Class : 7
```

4.2. K Nearest Neighbour Classification

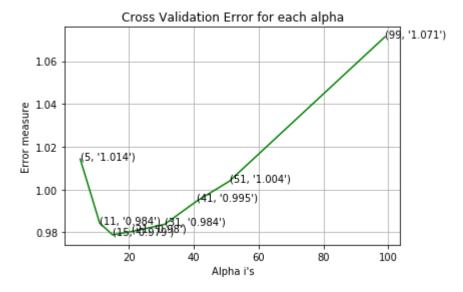
4.2.1. Hyper parameter tuning

```
In [0]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modu
        # -----
        # default parameter
        # KNeighborsClassifier(n neighbors=5, weights='uniform', algorithm='auto', leaf s
        # metric='minkowski', metric params=None, n jobs=1, **kwarqs)
        # methods of
        # fit(X, y): Fit the model using X as training data and y as target values
        # predict(X):Predict the class labels for the provided data
        # predict_proba(X):Return probability estimates for the test data X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/m
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
        # 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_,
            # to avoid rounding error while multiplying probabilites we use log-probabili
            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:",
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",lendict_proba(test_alpha), "The test log loss is:",lendi
```

```
for alpha = 5
Log Loss: 1.0142427410600647
for alpha = 11
Log Loss: 0.9843009431025068
for alpha = 15
Log Loss: 0.9788393451387649
for alpha = 21
Log Loss: 0.9804274194543124
for alpha = 31
Log Loss: 0.9837139436419055
for alpha = 41
Log Loss: 0.9946640234837321
for alpha = 51
Log Loss: 1.003891538065869
for alpha = 99
Log Loss: 1.071359160401408
```

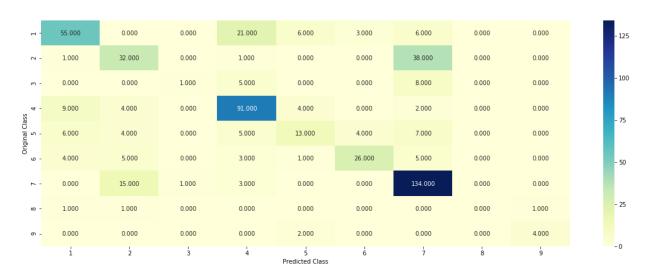


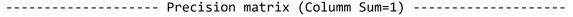
For values of best alpha = 15 The train log loss is: 0.7189457900171621
For values of best alpha = 15 The cross validation log loss is: 0.978839345138
7649
For values of best alpha = 15 The test log loss is: 1.055113934016944

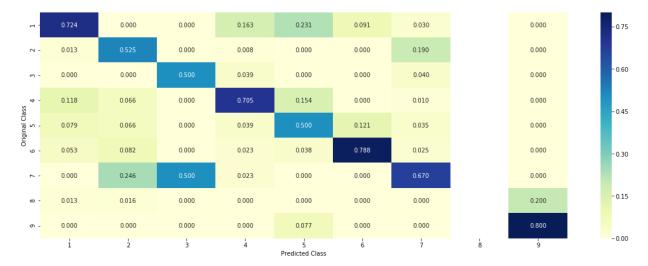
4.2.2. Testing the model with best hyper paramters

```
In [0]: # find more about KNeighborsClassifier() here http://scikit-learn.org/stable/modu
# ------
# default parameter
# KNeighborsClassifier(n_neighbors=5, weights='uniform', algorithm='auto', leaf_s
# 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/les.
# clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
predict_and_plot_confusion_matrix(train_x_responseCoding, train_y, cv_x_responseCoding)
```







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



4.2.3. Sample Query point -1

```
In [0]: clf = KNeighborsClassifier(n_neighbors=alpha[best_alpha])
    clf.fit(train_x_responseCoding, train_y)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_x_responseCoding, train_y)

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

Predicted Class: 4
Actual Class: 2
The 15 nearest neighbours of the test points belongs to classes [2 2 2 2 2 7 2 2 2 2 2 2 2 2]
Fequency of nearest points: Counter({2: 14, 7: 1})

4.2.4. Sample Query Point-2

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

```
Predicted Class : 7
Actual Class : 7
the k value for knn is 15 and the nearest neighbours of the test points belongs
to classes [7 7 7 7 7 3 7 7 7 7 7 7 7]
Fequency of nearest points : Counter({7: 14, 3: 1})
```

4.3. Logistic Regression

4.3.1. With Class balancing

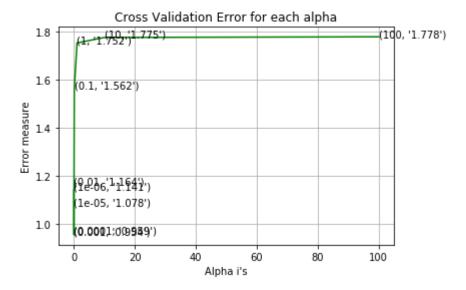
4.3.1.1. Hyper paramter tuning

```
In [0]:
        # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gener
        # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intel
        # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rat
        # class weight=None, warm start=False, average=False, n iter=None)
        # some of methods
        # fit(X, y[, coef_init, intercept_init, ...]) Fit linear model with Stochastic Grad
        \# predict(X) Predict class labels for samples in X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        #-----
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/m
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample_weight]) Fit the calibrated model
        # get_params([deep]) Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
        # predict proba(X) Posterior probabilities of classification
        # video link:
        alpha = [10 ** x for x in range(-6, 3)]
        cv log error array = []
        for i in alpha:
            print("for alpha =", i)
            clf = SGDClassifier(class weight='balanced', alpha=i, penalty='12', loss='log
            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_,
            # to avoid rounding error while multiplying probabilites we use log-probabili
            print("Log Loss :",log_loss(cv_y, sig_clf_probs))
        fig, ax = plt.subplots()
        ax.plot(alpha, cv log error array,c='g')
        for i, txt in enumerate(np.round(cv_log_error_array,3)):
            ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
        plt.grid()
        plt.title("Cross Validation Error for each alpha")
        plt.xlabel("Alpha i's")
        plt.ylabel("Error measure")
        plt.show()
        best alpha = np.argmin(cv log error array)
```

```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12
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:",
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best
```

```
for alpha = 1e-06
Log Loss: 1.1413576067484803
for alpha = 1e-05
Log Loss: 1.0777443009202097
for alpha = 0.0001
Log Loss: 0.9593629043270478
for alpha = 0.001
Log Loss: 0.9541478702481345
for alpha = 0.01
Log Loss: 1.1642179922517195
for alpha = 0.1
Log Loss: 1.5618342052704404
for alpha = 1
Log Loss: 1.752104678422237
for alpha = 10
Log Loss: 1.7749643040101175
for alpha = 100
Log Loss: 1.7777065191600168
```



For values of best alpha = 0.001 The train log loss is: 0.6483218400933497

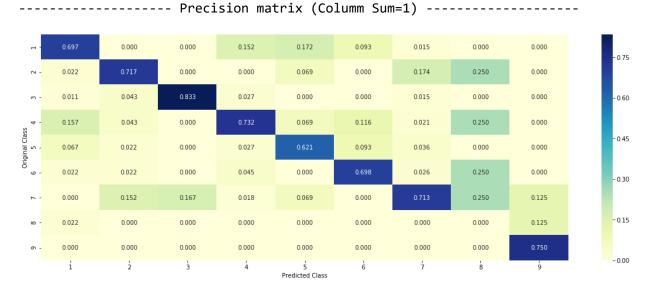
For values of best alpha = 0.001 The cross validation log loss is: 0.954147870

2481345

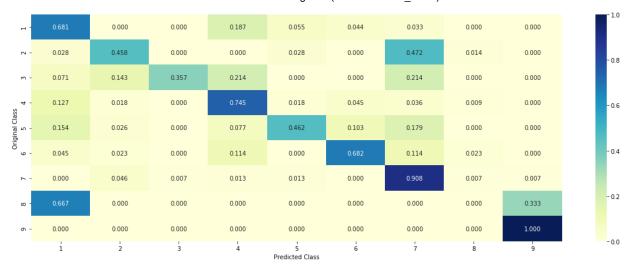
For values of best alpha = 0.001 The test log loss is: 0.9771034733314872

4.3.1.2. Testing the model with best hyper paramters





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



4.3.1.3. Feature Importance

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

4.3.1.3.1. Correctly Classified point

```
In [0]: # from tabulate import tabulate
    clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12
    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_one
    print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
```

```
Predicted Class: 2
Predicted Class Probabilities: [[0.0063 0.5497 0.0033 0.0078 0.0302 0.0092 0.38 48 0.0081 0.0006]]
Actual Class: 2
```

4.3.1.3.2. Incorrectly Classified point

```
In [0]: 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_one print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0404 0.0621 0.0108 0.0391 0.0281 0.0169 0.79
39 0.0048 0.004 ]]
Actual Class : 7
```

4.3.2. Without Class balancing

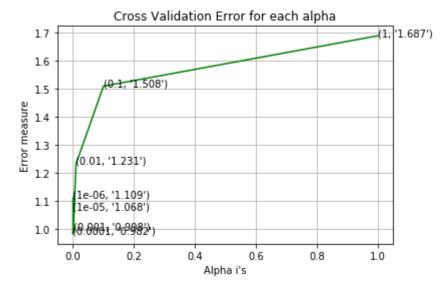
4.3.2.1. Hyper paramter tuning

```
In [0]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gener
        # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intel
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate
        # class weight=None, warm start=False, average=False, n iter=None)
        # some of methods
        # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Grad
        \# predict(X) Predict class labels for samples in X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/m
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample_weight]) Fit the calibrated model
        # get_params([deep]) Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
        # predict proba(X) Posterior probabilities of classification
        # video link:
        alpha = [10 ** x for x in range(-6, 1)]
        cv log error array = []
        for i in alpha:
            print("for alpha =", i)
            clf = SGDClassifier(alpha=i, penalty='12', loss='log', random_state=42)
            clf.fit(train x onehotCoding, train y)
            sig clf = CalibratedClassifierCV(clf, method="sigmoid")
            sig clf.fit(train x onehotCoding, train y)
            sig clf probs = sig clf.predict proba(cv x onehotCoding)
            cv_log_error_array.append(log_loss(cv_y, sig_clf_probs, labels=clf.classes_,
            print("Log Loss :",log loss(cv y, sig clf probs))
        fig, ax = plt.subplots()
        ax.plot(alpha, cv log error array,c='g')
        for i, txt in enumerate(np.round(cv_log_error_array,3)):
            ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
        plt.grid()
        plt.title("Cross Validation Error for each alpha")
        plt.xlabel("Alpha i's")
        plt.ylabel("Error measure")
        plt.show()
        best alpha = np.argmin(cv log error array)
        clf = SGDClassifier(alpha=alpha[best alpha], penalty='12', loss='log', random sta
```

```
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:",
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",lenter the company of th
```

for alpha = 1e-06 Log Loss : 1.109469275804417 for alpha = 1e-05 Log Loss : 1.0683437405676588 for alpha = 0.0001 Log Loss : 0.981756287843249 for alpha = 0.001 Log Loss : 0.9976035090112372 for alpha = 0.01 Log Loss : 1.231375738984243 for alpha = 0.1 Log Loss : 1.5078919931015102 for alpha = 1 Log Loss : 1.6872906162760626



For values of best alpha = 0.0001 The train log loss is: 0.456388293599789

For values of best alpha = 0.0001 The cross validation log loss is: 0.98175628

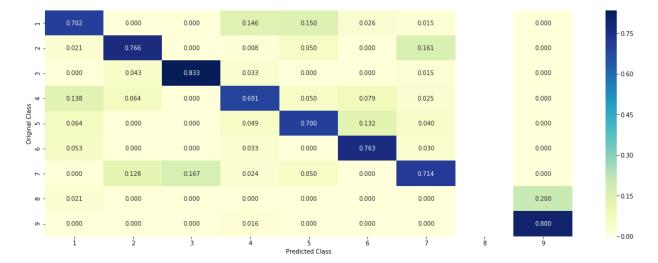
7843249

For values of best alpha = 0.0001 The test log loss is: 0.9866424801154886

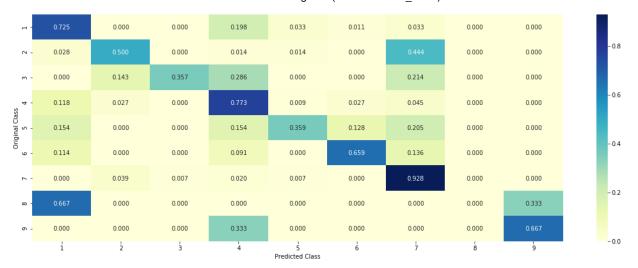
4.3.2.2. Testing model with best hyper parameters







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



4.3.2.3. Feature Importance, Correctly Classified point

```
In [0]: clf = SGDClassifier(alpha=alpha[best_alpha], penalty='12', loss='log', random_staclf.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_one print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
Predicted Class : 2
```

```
Predicted Class: 2
Predicted Class Probabilities: [[1.270e-02 7.029e-01 2.800e-03 8.600e-03 2.940e
-02 6.400e-03 2.286e-01
8.300e-03 3.000e-04]]
Actual Class: 2
```

4.3.2.4. Feature Importance, Inorrectly Classified point

```
In [0]: 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_one print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0371 0.0424 0.012 0.0197 0.0343 0.0165 0.82 93 0.0047 0.0039]]
Actual Class : 7
```

4.4. Linear Support Vector Machines

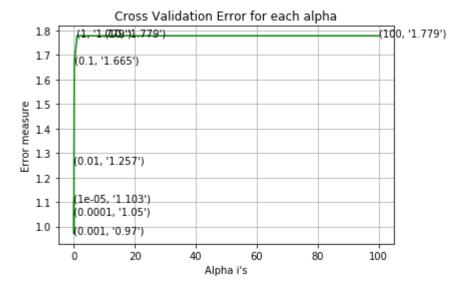
4.4.1. Hyper paramter tuning

```
In [0]: # read more about support vector machines with linear kernals here http://scikit-
        # -----
        # default parameters
        # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, prol
        # cache size=200, class weight=None, verbose=False, max iter=-1, decision function
        # Some of methods of SVM()
        # fit(X, y, [sample weight]) Fit the SVM model according to the given training
        \# predict(X) Perform classification on samples in X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/m
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base_estimator=None, method='sigmoid
        # some of the methods of CalibratedClassifierCV()
        # fit(X, y[, sample weight]) Fit the calibrated model
        # get params([deep]) Get parameters for this estimator.
        # predict(X) Predict the target of new samples.
        # predict_proba(X) Posterior probabilities of classification
        # video link:
        alpha = [10 ** x for x in range(-5, 3)]
        cv_log_error_array = []
        for i in alpha:
            print("for C =", i)
             clf = SVC(C=i,kernel='linear',probability=True, class_weight='balanced')
            clf = SGDClassifier( class_weight='balanced', alpha=i, penalty='12', loss='hi
            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_,
            print("Log Loss :",log loss(cv y, sig clf probs))
        fig, ax = plt.subplots()
        ax.plot(alpha, cv log error array,c='g')
        for i, txt in enumerate(np.round(cv_log_error_array,3)):
            ax.annotate((alpha[i],str(txt)), (alpha[i],cv_log_error_array[i]))
        plt.grid()
        plt.title("Cross Validation Error for each alpha")
        plt.xlabel("Alpha i's")
        plt.ylabel("Error measure")
        plt.show()
        best alpha = np.argmin(cv log error array)
        # clf = SVC(C=i,kernel='linear',probability=True, class_weight='balanced')
```

```
clf = SGDClassifier(class_weight='balanced', alpha=alpha[best_alpha], penalty='12
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

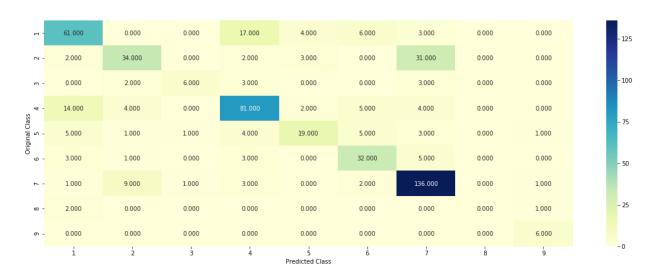
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
proba('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",left
print('For values of best alpha = ', alpha[best
```

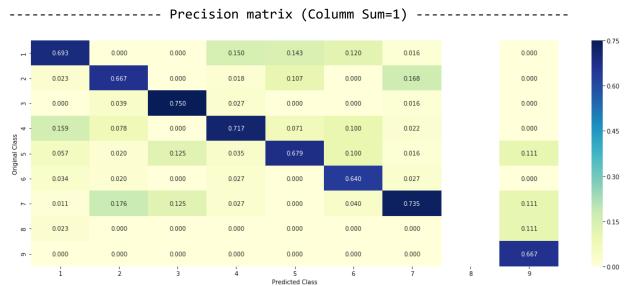
```
for C = 1e-05
Log Loss: 1.1030285478134367
for C = 0.0001
Log Loss: 1.0501924182104416
for C = 0.001
Log Loss: 0.9702112724497592
for C = 0.01
Log Loss: 1.2574780041704086
for C = 0.1
Log Loss: 1.664590275567539
for C = 1
Log Loss: 1.7785275815700619
for C = 10
Log Loss: 1.7785275064282509
for C = 100
Log Loss: 1.7785275973570276
```

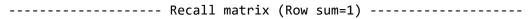


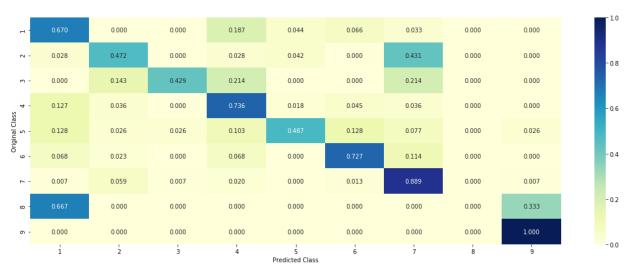
```
For values of best alpha = 0.001 The train log loss is: 0.5562551362875902
For values of best alpha = 0.001 The cross validation log loss is: 0.970211272
4497592
For values of best alpha = 0.001 The test log loss is: 1.0399317714748202
```

4.4.2. Testing model with best hyper parameters









4.3.3. Feature Importance

4.3.3.1. For Correctly classified point

```
Predicted Class : 2
Predicted Class Probabilities: [[0.0477 0.7184 0.0098 0.0286 0.0356 0.0136 0.13
54 0.0079 0.003 ]]
Actual Class : 2
```

4.3.3.2. For Incorrectly classified point

```
In [0]: 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_one print("Actual Class :", test_y[test_point_index])
    indices = np.argsort(-clf.coef_)[predicted_cls-1][:,:no_feature]
    print("-"*50)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.066 0.037 0.0123 0.0246 0.0371 0.0196 0.79 52 0.0047 0.0035]]
Actual Class : 7
```

4.5 Random Forest Classifier

4.5.1. Hyper paramter tuning (With One hot Encoding)

```
In [0]: # -----
        # default parameters
        # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
        # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf
        # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state
        # class weight=None)
        # Some of methods of RandomForestClassifier()
        # fit(X, y, [sample weight]) Fit the SVM model according to the given training
        \# 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/les
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/m
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
        # 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=
                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.classe
                print("Log Loss :",log_loss(cv_y, sig_clf_probs))
        '''fig, ax = plt.subplots()
        features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel()
        ax.plot(features, cv log error array,c='g')
        for i, txt in enumerate(np.round(cv_log_error_array,3)):
            ax.annotate((alpha[int(i/2)],max_depth[int(i%2)],str(txt)), (features[i],cv_l
        plt.title("Cross Validation Error for each alpha")
```

```
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()

'''

best_alpha = np.argmin(cv_log_error_array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)], criterion='gi
clf.fit(train_x_onehotCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_onehotCoding, train_y)

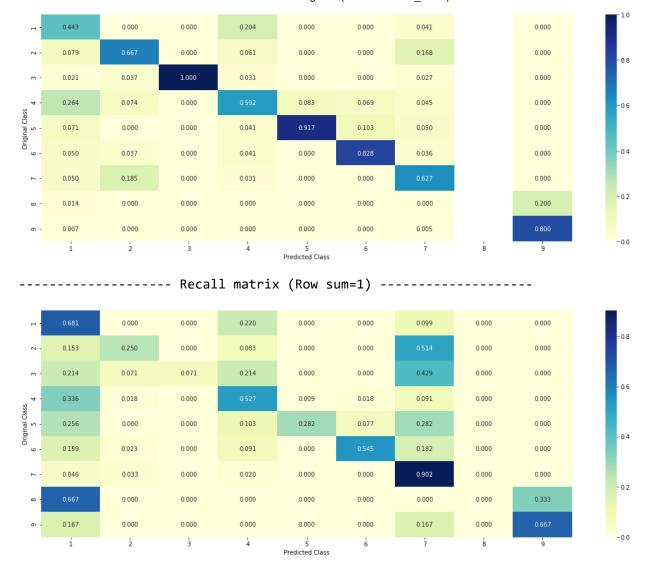
predict_y = sig_clf.predict_proba(train_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The train log
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The cross val
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best estimator = ', alpha[int(best_alpha/2)], "The test log
```

```
for n_estimators = 100 and max depth =
Log Loss: 1.1957565414748372
for n estimators = 100 and max depth =
Log Loss: 1.1922923251796937
for n estimators = 200 and max depth =
Log Loss: 1.1833444907195354
for n_estimators = 200 and max depth =
                                       10
Log Loss: 1.1848133910918428
for n estimators = 500 and max depth =
Log Loss: 1.1751897894382282
for n estimators = 500 and max depth = 10
Log Loss: 1.1775093298275472
for n_estimators = 1000 and max depth =
Log Loss: 1.175324285771641
for n estimators = 1000 and max depth =
Log Loss: 1.1759318447074925
for n estimators = 2000 and max depth =
Log Loss: 1.1746573512695804
for n estimators = 2000 and max depth =
Log Loss: 1.1750976400837914
For values of best estimator = 2000 The train log loss is: 0.9133225437684408
For values of best estimator = 2000 The cross validation log loss is: 1.174657
3512695804
For values of best estimator = 2000 The test log loss is: 1.1843228074266527
```

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

```
In [0]:
        # default parameters
        # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
        # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf
        # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state
        # class weight=None)
        # Some of methods of RandomForestClassifier()
        # fit(X, y, [sample weight]) Fit the SVM model according to the given training
                        Perform classification on samples in X.
        # predict(X)
        \# predict proba (X) Perform classification on samples in X.
        # some of attributes of RandomForestClassifier()
        # feature importances : array of shape = [n features]
        # The feature importances (the higher, the more important the feature).
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        clf = RandomForestClassifier(n estimators=alpha[int(best alpha/2)], criterion='gi
        predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y,cv_x_onehotCoding
```





4.5.3. Feature Importance

4.5.3.1. Correctly Classified point

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0321 0.3367 0.0178 0.0319 0.0469 0.037 0.48 84 0.0068 0.0024]]
Actual Class : 2
```

4.5.3.2. Inorrectly Classified point

```
In [0]: 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_one print("Actuall Class :", test_y[test_point_index])
    indices = np.argsort(-clf.feature_importances_)
    print("-"*50)
```

```
Predicted Class : 7
Predicted Class Probabilities: [[0.0506 0.174 0.0193 0.0494 0.0519 0.0435 0.60 19 0.0066 0.0029]]
Actuall Class : 7
```

4.5.3. Hyper paramter tuning (With Response Coding)

```
In [0]: # -----
        # default parameters
        # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
        # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf
        # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state
        # class weight=None)
        # Some of methods of RandomForestClassifier()
        # fit(X, y, [sample weight]) Fit the SVM model according to the given training
        \# 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/les
        # find more about CalibratedClassifierCV here at http://scikit-learn.org/stable/m
        # default paramters
        # sklearn.calibration.CalibratedClassifierCV(base estimator=None, method='sigmoid
        # 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=
                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.classe
                print("Log Loss :",log_loss(cv_y, sig_clf_probs))
        fig, ax = plt.subplots()
        features = np.dot(np.array(alpha)[:,None],np.array(max depth)[None]).ravel()
        ax.plot(features, cv log error array,c='g')
        for i, txt in enumerate(np.round(cv_log_error_array,3)):
            ax.annotate((alpha[int(i/4)],max_depth[int(i%4)],str(txt)), (features[i],cv_l
        plt.title("Cross Validation Error for each alpha")
```

```
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()

'''

best_alpha = np.argmin(cv_log_error_array)
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gi
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The train log los
predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The cross validat
predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best alpha = ', alpha[int(best_alpha/4)], "The test log loss
```

```
for n_estimators = 10 and max depth =
Log Loss: 2.252395114049456
for n estimators = 10 and max depth =
Log Loss: 1.731497744533845
for n estimators = 10 and max depth =
Log Loss: 1.3226414368397983
for n_estimators = 10 and max depth =
Log Loss: 2.0136420928338534
for n estimators = 50 and max depth =
Log Loss: 1.752653605603669
for n_estimators = 50 and max depth =
Log Loss: 1.4520872336624988
for n_estimators = 50 and max depth =
Log Loss: 1.2873101045833217
for n estimators = 50 and max depth =
Log Loss: 1.7841439204453657
for n estimators = 100 and max depth =
Log Loss: 1.5728644081443437
for n_estimators = 100 and max depth =
Log Loss: 1.5258605820806055
for n estimators = 100 and max depth =
Log Loss: 1.2615756094201513
for n_estimators = 100 and max depth =
                                        10
Log Loss: 1.7541425342240604
for n estimators = 200 and max depth =
Log Loss: 1.6622199505325508
for n estimators = 200 and max depth =
Log Loss: 1.5578686388512741
for n_estimators = 200 and max depth =
Log Loss: 1.3670922590377885
for n estimators = 200 and max depth =
                                        10
Log Loss: 1.7883157999609138
for n estimators = 500 and max depth =
Log Loss: 1.7500832413184833
for n estimators = 500 and max depth =
Log Loss: 1.6102893559095166
for n estimators = 500 and max depth =
Log Loss: 1.3780588483750758
```

```
for n_estimators = 500 and max depth = 10
Log Loss : 1.8537106360768496
for n_estimators = 1000 and max depth = 2
Log Loss : 1.711888119815348
for n_estimators = 1000 and max depth = 3
Log Loss : 1.6059204768943431
for n_estimators = 1000 and max depth = 5
Log Loss : 1.3557250699593748
for n_estimators = 1000 and max depth = 10
Log Loss : 1.8467500422905054
For values of best alpha = 100 The train log loss is: 0.062364610913203444
For values of best alpha = 100 The cross validation log loss is: 1.26157560942
01513
For values of best alpha = 100 The test log loss is: 1.2463169929506979
```

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

In [0]: # default parameters # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max # min samples leaf=1, min weight fraction leaf=0.0, max features='auto', max leaf # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state # class weight=None) # Some of methods of RandomForestClassifier() # fit(X, y, [sample weight]) Fit the SVM model according to the given training Perform classification on samples in X. # predict(X) # predict proba (X) Perform classification on samples in X. # some of attributes of RandomForestClassifier() # feature importances : array of shape = [n features] # The feature importances (the higher, the more important the feature). # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les clf = RandomForestClassifier(max depth=max depth[int(best alpha%4)], n estimators predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,cv_x_responseCo





4.5.5. Feature Importance

4.5.5.1. Correctly Classified point

```
In [0]: | clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)], criterion='gi
        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
        print("Predicted Class :", predicted_cls[0])
        print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_res
        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: 2
        Predicted Class Probabilities: [[0.0106 0.7461 0.0425 0.0136 0.0127 0.0277 0.11
        46 0.0242 0.0081]]
        Actual Class : 2
        Variation is important feature
        Gene is important feature
        Text is important feature
        Variation is important feature
        Text is important feature
        Gene is important feature
        Text is important feature
        Text is important feature
        Text is important feature
        Gene is important feature
        Variation is important feature
        Gene is important feature
        Gene is important feature
        Text is important feature
        Gene is important feature
        Variation is important feature
        Text is important feature
        Text is important feature
        Gene is important feature
        Variation is important feature
        Text is important feature
```

Gene is important feature Gene is important feature

4.5.5.2. Incorrectly Classified point

```
In [0]: test point index = 100
        predicted cls = sig clf.predict(test x responseCoding[test point index].reshape(1
        print("Predicted Class :", predicted_cls[0])
        print("Predicted Class Probabilities:", np.round(sig_clf.predict_proba(test_x_res
        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: 7
        Predicted Class Probabilities: [[0.0237 0.195 0.2041 0.0223 0.0324 0.0451 0.40
        41 0.0489 0.0243]]
        Actual Class: 7
        Variation is important feature
        Gene is important feature
        Text is important feature
        Variation is important feature
        Text is important feature
        Gene is important feature
        Text is important feature
        Text is important feature
        Text is important feature
        Gene is important feature
        Variation is important feature
        Gene is important feature
        Gene is important feature
        Text is important feature
        Gene is important feature
        Variation is important feature
        Text is important feature
        Text is important feature
        Gene is important feature
        Variation is important feature
        Text 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 [0]: # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/gener
        # -----
        # default parameters
        # SGDClassifier(loss='hinge', penalty='l2', alpha=0.0001, l1 ratio=0.15, fit intel
        # shuffle=True, verbose=0, epsilon=0.1, n jobs=1, random state=None, learning rate
        # class weight=None, warm start=False, average=False, n iter=None)
        # some of methods
        # fit(X, y[, coef init, intercept init, ...]) Fit linear model with Stochastic Grad
        \# predict(X) Predict class labels for samples in X.
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        # read more about support vector machines with linear kernals here http://scikit-
        # default parameters
        # SVC(C=1.0, kernel='rbf', degree=3, gamma='auto', coef0=0.0, shrinking=True, prol
        # cache size=200, class weight=None, verbose=False, max iter=-1, decision function
        # Some of methods of SVM()
        # fit(X, y, [sample weight]) Fit the SVM model according to the given training
        \# predict(X) Perform classification on samples in X.
        # ------
        # video link: https://www.appliedaicourse.com/course/applied-ai-course-online/les
        # read more about support vector machines with linear kernals here http://scikit-
        # default parameters
        # sklearn.ensemble.RandomForestClassifier(n estimators=10, criterion='qini', max
        # min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf
        # min impurity split=None, bootstrap=True, oob score=False, n jobs=1, random state
        # class weight=None)
        # Some of methods of RandomForestClassifier()
        # fit(X, y, [sample weight]) Fit the SVM model according to the given training
        \# 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/les
        # _____
        clf1 = SGDClassifier(alpha=0.001, penalty='12', loss='log', class_weight='balance
        clf1.fit(train_x_onehotCoding, train_y)
        sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")
```

```
clf2 = SGDClassifier(alpha=1, penalty='l2', loss='hinge', class weight='balanced'
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 v)
print("Logistic Regression : Log Loss: %0.2f" % (log loss(cv y, sig clf1.predict
sig_clf2.fit(train_x_onehotCoding, train_y)
print("Support vector machines : Log Loss: %0.2f" % (log loss(cv y, sig clf2.pred
sig clf3.fit(train x onehotCoding, train y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.predict_proba(cv]
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_cl
    sclf.fit(train x onehotCoding, train y)
    print("Stacking Classifer : for the value of alpha: %f Log Loss: %0.3f" % (i,
    log_error =log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    if best_alpha > log_error:
        best alpha = log error
Logistic Regression : Log Loss: 0.96
Support vector machines : Log Loss: 1.78
Naive Bayes : Log Loss: 1.17
```

```
Support vector machines: Log Loss: 1.78

Naive Bayes: Log Loss: 1.17

Stacking Classifer: for the value of alpha: 0.000100 Log Loss: 2.178

Stacking Classifer: for the value of alpha: 0.001000 Log Loss: 2.033

Stacking Classifer: for the value of alpha: 0.010000 Log Loss: 1.485

Stacking Classifer: for the value of alpha: 0.100000 Log Loss: 1.063

Stacking Classifer: for the value of alpha: 1.000000 Log Loss: 1.180

Stacking Classifer: for the value of alpha: 10.000000 Log Loss: 1.521
```

4.7.2 testing the model with the best hyper parameters

```
In [0]: lr = LogisticRegression(C=0.1)
    sclf = StackingClassifier(classifiers=[sig_clf1, sig_clf2, sig_clf3], meta_classis.
    sclf.fit(train_x_onehotCoding, train_y)

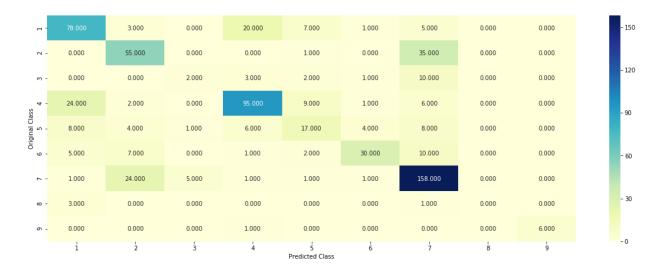
log_error = log_loss(train_y, sclf.predict_proba(train_x_onehotCoding))
    print("Log loss (train) on the stacking classifier :",log_error)

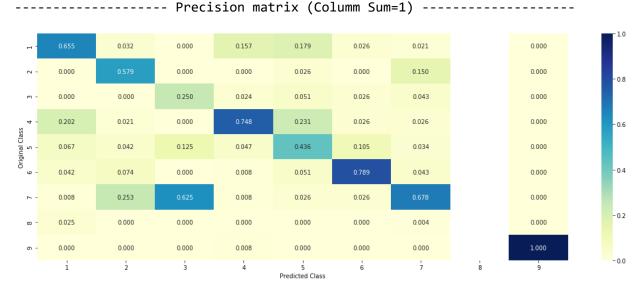
log_error = log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding))
    print("Log loss (CV) on the stacking classifier :",log_error)

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

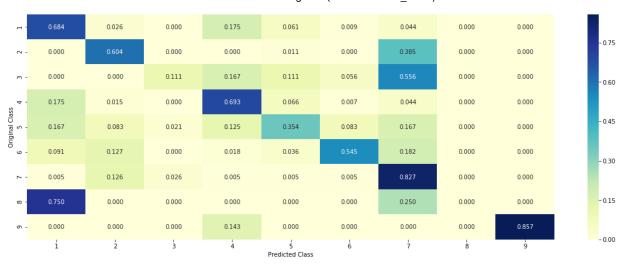
print("Number of missclassified point :", np.count_nonzero((sclf.predict(test_x_onehotCoding)))

print("Number of missclassified point :", np.count_nonzero((sclf.predict(test_x_onehotCoding)))
```





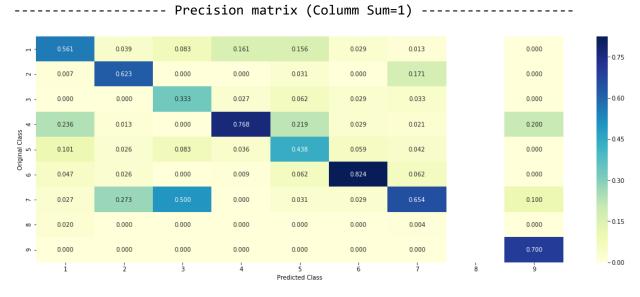
----- Recall matrix (Row sum=1)

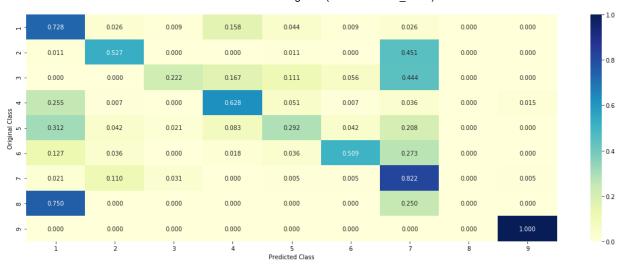


4.7.3 Maximum Voting classifier

In [0]: #Refer:http://scikit-learn.org/stable/modules/generated/sklearn.ensemble.VotingClassifier vclf = VotingClassifier(estimators=[('lr', sig_clf1), ('svc', sig_clf2), ('rf', s vclf.fit(train_x_onehotCoding, train_y) print("Log loss (train) on the VotingClassifier :", log_loss(train_y, vclf.predict print("Log loss (CV) on the VotingClassifier :", log_loss(cv_y, vclf.predict_prob print("Log loss (test) on the VotingClassifier :", log_loss(test_y, vclf.predict_ print("Number of missclassified point :", np.count_nonzero((vclf.predict(test_x_o plot_confusion_matrix(test_y=test_y, predict_y=vclf.predict(test_x_onehotCoding))







```
In [2]: from prettytable import PrettyTable
        x = PrettyTable()
        x.field names = ["S.No", "Model", "Train logloss", "Cv logloss", "Test logloss", "Mis
        x.add row(["1","Naive Bayes","0.760","1.158","1.188","0.36"])
        x.add_row(["2","KNN","0.718","0.978","1.055","0.33"])
        x.add_row(["3","Logistic regression with class balancing","0.648","0.95","0.977",
x.add_row(["4","Logistic regression without class balancing","0.456","0.981","0.9
        x.add row(["5","Linear svm(with one hot encoding)","0.55","0.97","1.03","0.30"])
        x.add_row(["6","Random Forest(with one hot encoding)","0.97","1.17","1.18","0.40"
        x.add_row(["7","Random Forest(with response coding)","0.062","1.26","1.24","0.41"
        x.add_row(["8","Stacking classifier","0.61","1.06","1.08","0.33"])
        x.add row(["9","Maximum voting classifier","0.86","1.138","1.33","0.35"])
        print(x)
        | S.No |
                                   Model
                                                            | Train logloss | Cv loglo
        ss | Test_logloss | Misclassified_error |
                                Naive Bayes
                                                                  0.760
                                                                                1.158
             1.188
                                0.36
                                                                  0.718
                                                                                0.978
           2
             KNN
             1.055
                                0.33
           3 | Logistic regression with class balancing |
                                                                  0.648
                                                                                0.95
                                0.30
             0.977
             | Logistic regression without class balancing |
                                                                                0.981
                                                                  0.456
             0.986
                                0.28
                      Linear svm(with one hot encoding)
           5
             0.55
                                                                                 0.97
              1.03
                                0.30
```

Random Forest(with one hot encoding)

0.41

Stacking classifier

Maximum voting classifier

Random Forest(with response coding)

0.40

0.33

0.35

+----+

Conclusion:

1.18

1.24

1.08

1.33

7

Feature enginnering steps:

1. At first we are taking the Gene & Variation features and combine both in Gene_Var_data corpus.

0.97

0.062

0.61

0.86

1.17

1.26

1.06

1.138

- 2. Then build TF_IDF veactorizer on top of Gene_Var_data fit that by using TFIDF transform into Train, Test, cv.
- 3. By doing the above feature engineering steps we can have some more information to train our model.
- 4. After Feature engineering misclassified errors are quite low when compared to without feature engineered models.