Personalized Cancer Diagnosis With Top 1000 Words

November 3, 2018

1 Personalized cancer diagnosis

2 1. Business Problem

3 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.

4 1.2. Source/Useful Links

```
In [ ]: Some articles and reference blogs about the problem statement

        1.https://www.forbes.com/sites/matthewherper/2017/06/03/a-new-cancer-drug-helped-almos
        2.https://www.youtube.com/watch?v=UwbuW7oK8rk
        3.https://www.youtube.com/watch?v=qxXRKVompI8
```

5 2. Machine Learning Problem Formulation

6 2.1. Data

7 2.1.1. Data Overview

```
In [ ]: 1.Source: https://www.kaggle.com/c/msk-redefining-cancer-treatment/data
        2.We have two data files: one conatins the information about the genetic mutations and
        Both these data files are have a common column called ID
        3.Data file's information:

        1.training_variants (ID , Gene, Variations, Class)
        2.training_text (ID, Text)
```

8 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). ...

9 2.2. Mapping the real-world problem to an ML problem

10 2.2.1. Type of Machine Learning Problem

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

11 2.2.2. Performance Metric

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

    Metric(s):

    1.Multi class log-loss
    2.Confusion matrix
```

12 2.2.3. Machine Learing Objectives and Constraints

```
In [ ]: Objective: Predict the probability of each data-point belonging to each of the nine cla

        Constraints:

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

13 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

14 3. Exploratory Data Analysis

```
In [1]: import pandas as pd
        import matplotlib.pyplot as plt
        import re
        import time
        import warnings
        import numpy as np
        from nltk.corpus import stopwords
        from sklearn.decomposition import TruncatedSVD
        from sklearn.preprocessing import normalize
        from sklearn.feature_extraction.text import CountVectorizer
        from sklearn.manifold import TSNE
        import seaborn as sns
        from sklearn.neighbors import KNeighborsClassifier
        from sklearn.metrics import confusion_matrix
        from sklearn.metrics.classification import accuracy_score, log_loss
        from sklearn.feature_extraction.text import TfidfVectorizer
        from sklearn.linear_model import SGDClassifier
        from imblearn.over_sampling import SMOTE
        from collections import Counter
        from scipy.sparse import hstack
        from sklearn.multiclass import OneVsRestClassifier
        from sklearn.svm import SVC
        from sklearn.cross_validation import StratifiedKFold
        from collections import Counter, defaultdict
        from sklearn.calibration import CalibratedClassifierCV
        from sklearn.naive_bayes import MultinomialNB
        from sklearn.naive_bayes import GaussianNB
        from sklearn.model_selection import train_test_split
        from sklearn.model_selection import GridSearchCV
```

```
        import math
        from sklearn.metrics import normalized_mutual_info_score
        from sklearn.ensemble import RandomForestClassifier
        warnings.filterwarnings("ignore")

        from mlxtend.classifier import StackingClassifier

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

```
C:\Users\Saurabh\Anaconda3\lib\site-packages\sklearn\cross_validation.py:41: DeprecationWarning
  "This module will be removed in 0.20.", DeprecationWarning)
```

```
In [2]: data = pd.read_csv('training_variants')
        print('Number of data points : ', data.shape[0])
        print('Number of features : ', data.shape[1])
        print('Features : ', data.columns.values)
        data.head()
```

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

```
Out[2]:    ID    Gene             Variation  Class
        0   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

1.ID : the id of the row used to link the mutation to the clinical evidence 2.Gene : the gene where this genetic mutation is located 3.Variation : the aminoacid change for this mutations 4.Class : 1-9 the class this genetic mutation has been classified on

15 3.1.2. Reading Text Data

```
In [3]: # note the seprator in this file
        data_text =pd.read_csv("training_text",sep="\|\|",engine="python",names=["ID","TEXT"],s
        print('Number of data points : ', data_text.shape[0])
        print('Number of features : ', data_text.shape[1])
        print('Features : ', data_text.columns.values)
        data_text.head()
```

```
Number of data points :  3321
Number of features :  2
```

```
Features :  ['ID' 'TEXT']
```

Out[3]:

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

16 3.1.3. Preprocessing of text

In [4]:
```
# loading stop words from nltk library
stop_words = set(stopwords.words('english'))


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

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

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

In [5]:
```
#text processing stage.
start_time = time.clock()
for index, row in data_text.iterrows():
    if type(row['TEXT']) is str:
        nlp_preprocessing(row['TEXT'], index, 'TEXT')
    else:
        print("there is no text description for id:",index)
print('Time took for preprocessing the text :',time.clock() - start_time, "seconds")
```

```
there is no text description for id: 1109
there is no text description for id: 1277
there is no text description for id: 1407
there is no text description for id: 1639
there is no text description for id: 2755
Time took for preprocessing the text : 145.13455629318113 seconds
```

```
In [6]: #merging both gene_variations and text data based on ID
        result = pd.merge(data, data_text,on='ID', how='left')
        result.head()
```

```
Out[6]:    ID    Gene             Variation  Class  \
        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

                                                  TEXT
        0  cyclin dependent kinases cdks regulate variety...
        1  abstract background non small cell lung cancer...
        2  abstract background non small cell lung cancer...
        3  recent evidence demonstrated acquired uniparen...
        4  oncogenic mutations monomeric casitas b lineag...
```

```
In [7]: result[result.isnull().any(axis=1)]
```

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

```
In [8]: result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+result['Variation']
```

```
In [9]: result[result['ID']==1109]
```

```
Out[9]:         ID   Gene Variation  Class          TEXT
        1109  1109  FANCA    S1088F      1  FANCA S1088F
```

17 3.1.4. Test, Train and Cross Validation Split

18 3.1.4.1. Splitting data into train, test and cross validation (64:20:16)

```
In [10]: y_true = result['Class'].values
         result.Gene      = result.Gene.str.replace('\s+', '_')
         result.Variation = result.Variation.str.replace('\s+', '_')

         # split the data into test and train by maintaining same distribution of output varai
         X_train, test_df, y_train, y_test = train_test_split(result, y_true, stratify=y_true,
         # split the train data into train and cross validation by maintaining same distributi
         train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train, stratify=y_train,
```

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

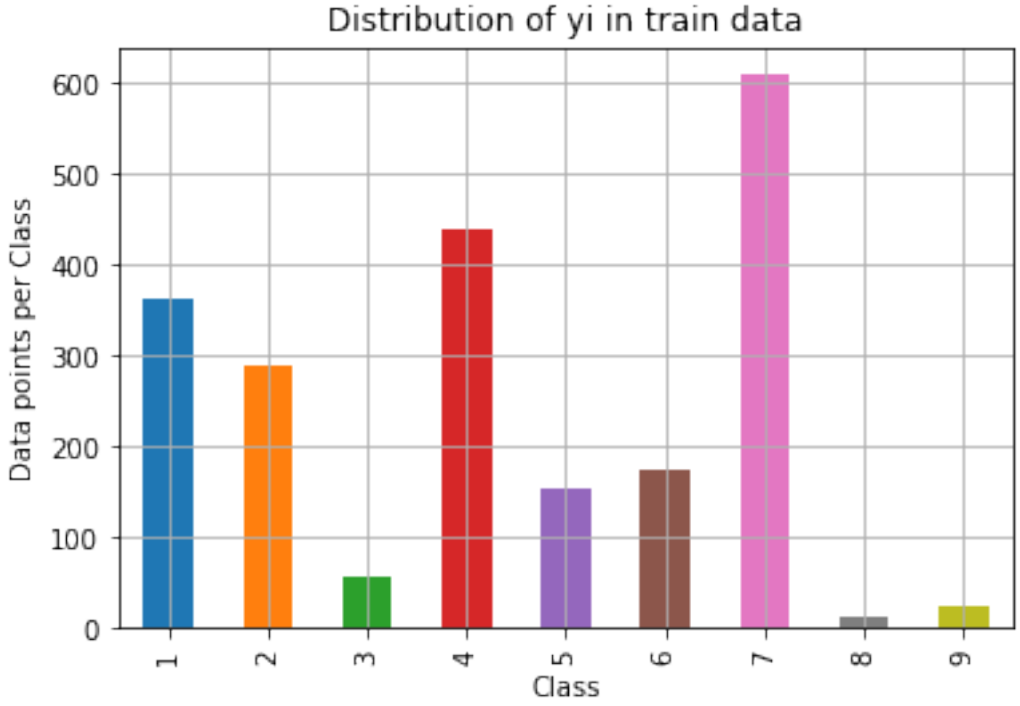
In [11]:
```
print('Number of data points in train data:', train_df.shape[0])
print('Number of data points in test data:', test_df.shape[0])
print('Number of data points in cross validation data:', cv_df.shape[0])
```

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

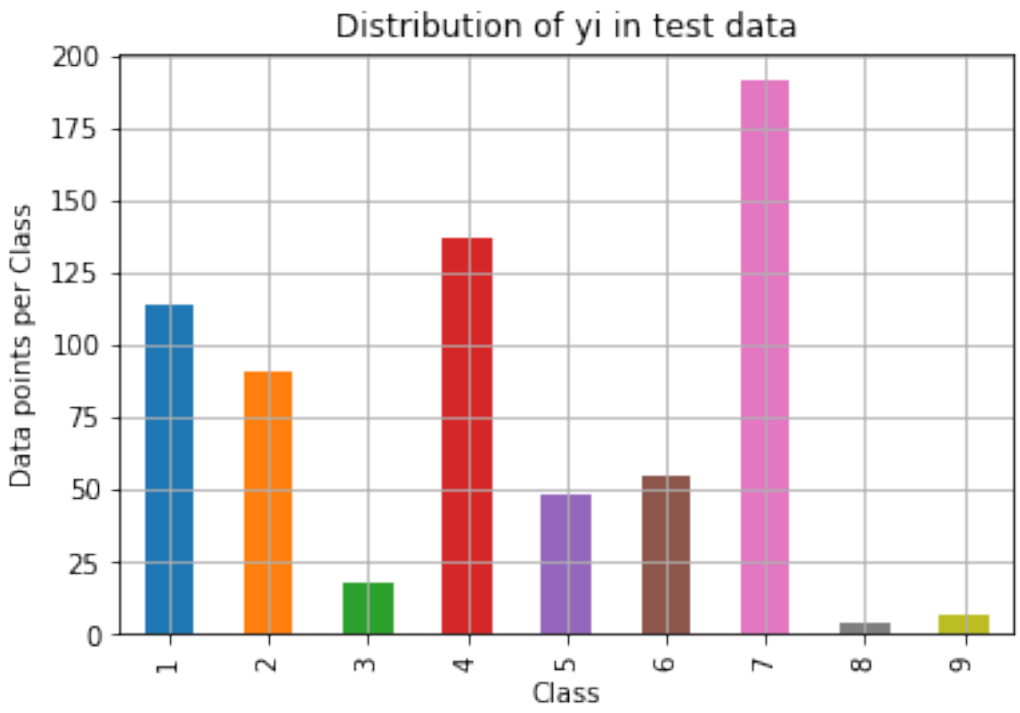
19 3.1.4.2. Distribution of y_i's in Train, Test and Cross Validation datasets

In [12]:
```
# it returns a dict, keys as class labels and values as the number of data points in
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.htm
# -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',train_class_distribution.values[


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.htm
# -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-test_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',test_class_distribution.values[i]
```

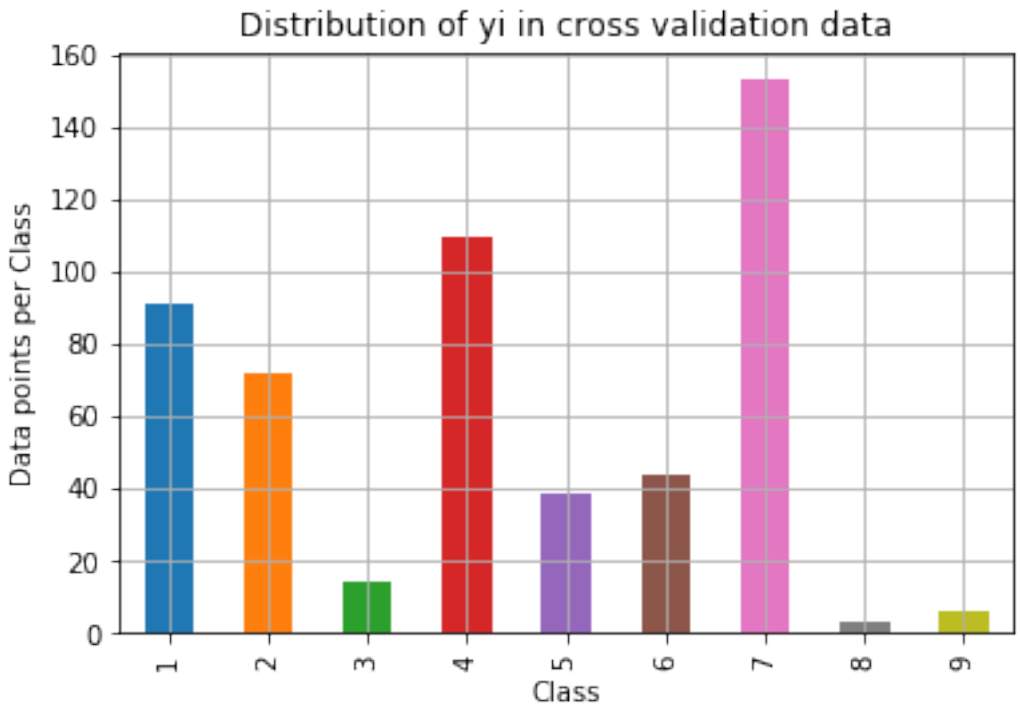
```
print('-'*80)
my_colors = 'rgbkymc'
cv_class_distribution.plot(kind='bar')
plt.xlabel('Class')
plt.ylabel('Data points per Class')
plt.title('Distribution of yi in cross validation data')
plt.grid()
plt.show()

# ref: argsort https://docs.scipy.org/doc/numpy/reference/generated/numpy.argsort.htm
# -(train_class_distribution.values): the minus sign will give us in decreasing order
sorted_yi = np.argsort(-train_class_distribution.values)
for i in sorted_yi:
    print('Number of data points in class', i+1, ':',cv_class_distribution.values[i],
```




```
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 %)
```

20 3.2 Prediction using a 'Random' Model

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

```
In [13]: # This function plots the confusion matrices given y_i, y_i_hat.
         def plot_confusion_matrix(test_y, predict_y):
             C = confusion_matrix(test_y, predict_y)
             # C = 9,9 matrix, each cell (i,j) represents number of points of class i are pred

             A =(((C.T)/(C.sum(axis=1))).T)
             #divid each element of the confusion matrix with the sum of elements in that colu
```

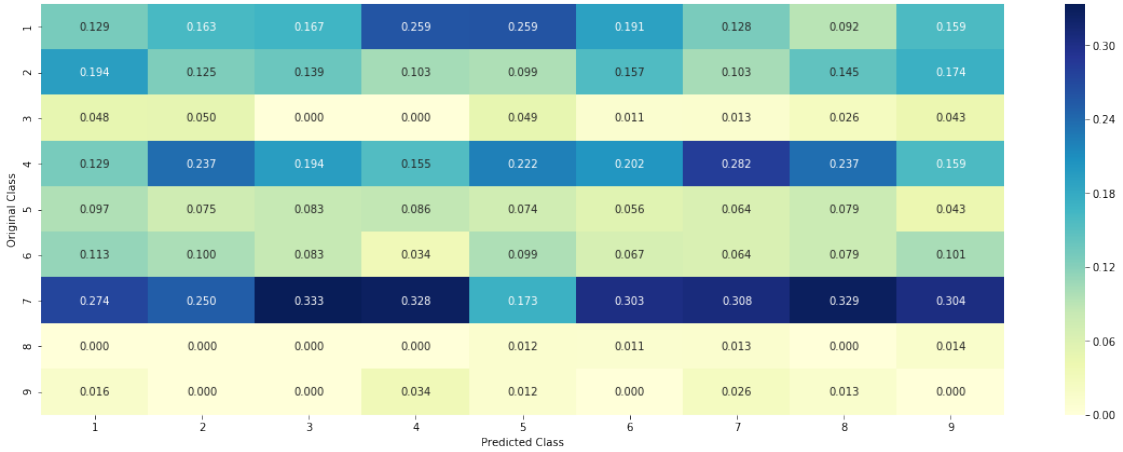
```
        # C = [[1, 2],
        #     [3, 4]]
        # C.T = [[1, 3],
        #        [2, 4]]
        # C.sum(axis = 1)  axis=0 corresonds to columns and axis=1 corresponds to rows in
        # C.sum(axix =1) = [[3, 7]]
        # ((C.T)/(C.sum(axis=1))) = [[1/3, 3/7]
        #                            [2/3, 4/7]]

        # ((C.T)/(C.sum(axis=1))).T = [[1/3, 2/3]
        #                            [3/7, 4/7]]
        # sum of row elements = 1
        B =(C/C.sum(axis=0))
        #divid each element of the confusion matrix with the sum of elements in that row
        # C = [[1, 2],
        #     [3, 4]]
        # C.sum(axis = 0)  axis=0 corresonds to columns and axis=1 corresponds to rows in
        # 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, yticklabe
        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, yticklabe
        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, yticklabe
        plt.xlabel('Predicted Class')
        plt.ylabel('Original Class')
        plt.show()
```

```
In [14]: # we need to generate 9 numbers and the sum of numbers should be 1
         # one solution is to genarate 9 numbers and divide each of the numbers by their sum
         # ref: https://stackoverflow.com/a/18662466/4084039
```

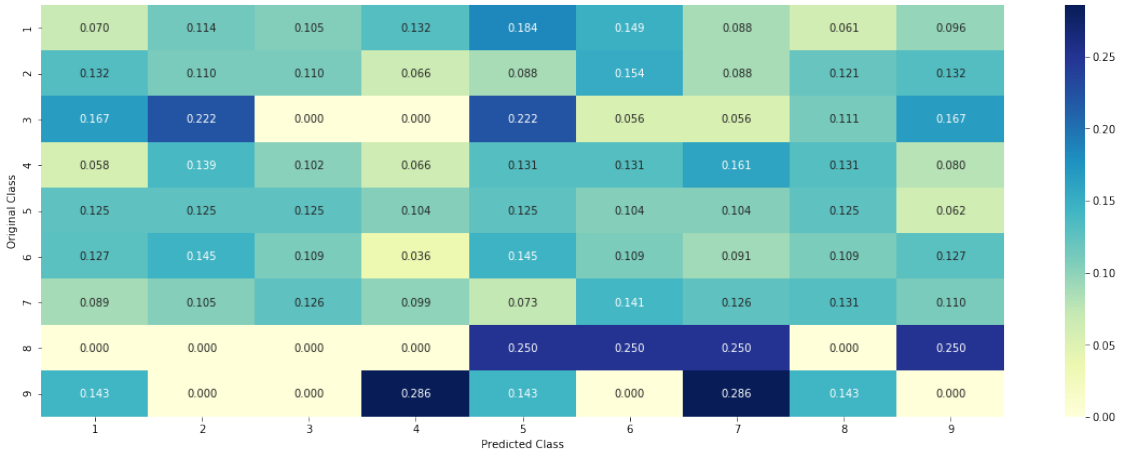
```
test_data_len = test_df.shape[0]
cv_data_len = cv_df.shape[0]

# 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_predicte


# Test-Set error.
#we create a output array that has exactly same as the test data
test_predicted_y = np.zeros((test_data_len,9))
for i in range(test_data_len):
    rand_probs = np.random.rand(1,9)
    test_predicted_y[i] = ((rand_probs/sum(sum(rand_probs)))[0])
print("Log loss on Test Data using Random Model",log_loss(y_test,test_predicted_y, eps

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 2.4707739436850926
Log loss on Test Data using Random Model 2.526548611006996
-------------------- Confusion matrix --------------------
```


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



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



21 3.3 Univariate Analysis

In [15]:
```
# code for response coding with Laplace smoothing.
# alpha : used for laplace smoothing
# feature: ['gene', 'variation']
# df: ['train_df', 'test_df', 'cv_df']
# algorithm
# ----------
# Consider all unique values and the number of occurances of given feature in train d
# build a vector (1*9) , the first element = (number of times it occured in class1 +
# gv_dict is like a look up table, for every gene it store a (1*9) representation of
```

```
# 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, 1/9] to 'gv_fea'
# return 'gv_fea'
# ----------------------

# get_gv_fea_dict: Get Gene varaition Feature Dict
def get_gv_fea_dict(alpha, feature, df):
    # value_count: it contains a dict like
    # print(train_df['Gene'].value_counts())
    # output:
    #        {BRCA1      174
    #         TP53       106
    #         EGFR        86
    #         BRCA2       75
    #         PTEN        69
    #         KIT         61
    #         BRAF        60
    #         ERBB2       47
    #         PDGFRA      46
    #         ...}
    # print(train_df['Variation'].value_counts())
    # output:
    # {
    # Truncating_Mutations                     63
    # Deletion                                 43
    # Amplification                            43
    # Fusions                                  22
    # Overexpression                            3
    # E17K                                      3
    # Q61L                                      3
    # S222D                                     2
    # P130S                                     2
    # ...
    # }
    value_count = train_df[feature].value_counts()

    # gv_dict : Gene Variation Dict, which contains the probability array for each ge
    gv_dict = dict()

    # denominator will contain the number of time that particular feature occured in
    for i, denominator in value_count.items():
        # vec will contain (p(yi==1/Gi) probability of gene/variation belongs to pert
        # vec is 9 diamensional vector
        vec = []
        for k in range(1,10):
```

```
                # print(train_df.loc[(train_df['Class']==1) & (train_df['Gene']=='BRCA1')]
                #         ID   Gene             Variation  Class
                # 2470  2470  BRCA1                S1715C      1
                # 2486  2486  BRCA1                S1841R      1
                # 2614  2614  BRCA1                   M1R      1
                # 2432  2432  BRCA1                L1657P      1
                # 2567  2567  BRCA1                T1685A      1
                # 2583  2583  BRCA1                E1660G      1
                # 2634  2634  BRCA1                W1718L      1
                # cls_cnt.shape[0] will return the number of rows

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

                # cls_cnt.shape[0](numerator) will contain the number of time that partic
                vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator + 90*alpha))

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

    # Get Gene variation feature
    def get_gv_feature(alpha, feature, df):
        # print(gv_dict)
        #     {'BRCA1': [0.200757575757575, 0.037878787878788, 0.068181818181818177, (
        #      'TP53': [0.32142857142857145, 0.061224489795918366, 0.061224489795918366, (
        #      'EGFR': [0.056818181818181816, 0.21590909090909091, 0.0625, 0.068181818181(
        #      'BRCA2': [0.13333333333333333, 0.060606060606060608, 0.060606060606060608,
        #      'PTEN': [0.069182389937106917, 0.062893081761006289, 0.069182389937106917,
        #      'KIT': [0.066225165562913912, 0.25165562913907286, 0.072847682119205295, 0
        #      'BRAF': [0.066666666666666666, 0.17999999999999999, 0.073333333333333334, (
        #      ...
        #     }
        gv_dict = get_gv_fea_dict(alpha, feature, df)
        # value_count is similar in get_gv_fea_dict
        value_count = train_df[feature].value_counts()

        # gv_fea: Gene_variation feature, it will contain the feature for each feature va
        gv_fea = []
        # for every feature values in the given data frame we will check if it is there i
        # 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([1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9])
    #             gv_fea.append([-1,-1,-1,-1,-1,-1,-1,-1,-1])
        return gv_fea
```

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

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

22 3.2.1 Univariate Analysis on Gene Feature

Q1. Gene, What type of feature it is ?

Ans. Gene is a categorical variable

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

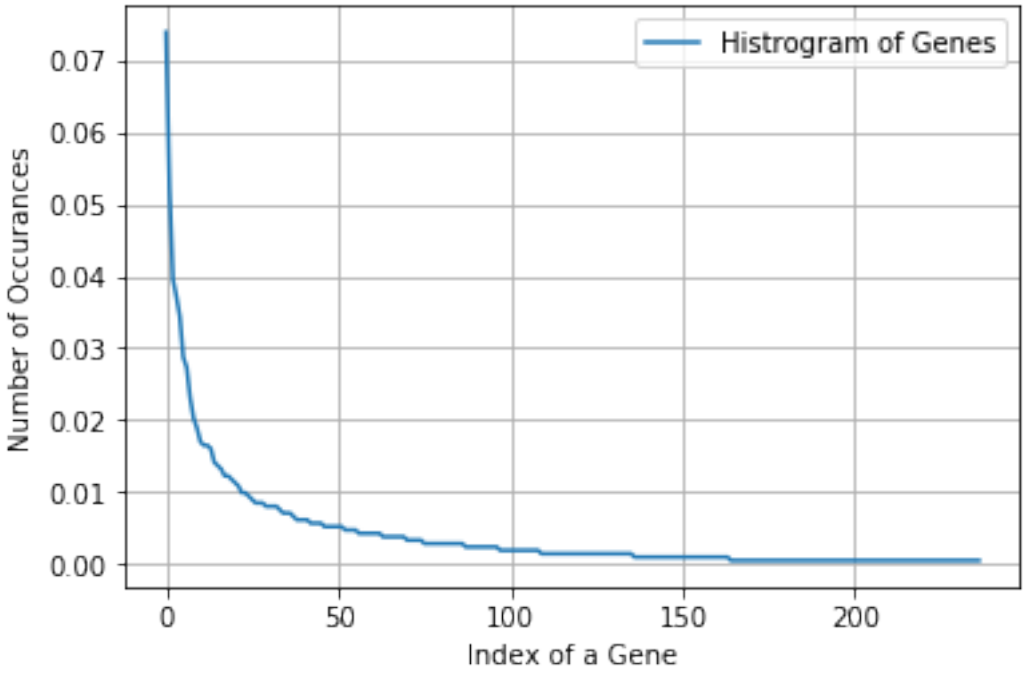
```
In [16]: unique_genes = train_df['Gene'].value_counts()
         print('Number of Unique Genes :', unique_genes.shape[0])
         # the top 10 genes that occured most
         print(unique_genes.head(10))
```

```
Number of Unique Genes : 237
BRCA1     157
TP53      111
EGFR       84
BRCA2      79
PTEN       73
BRAF       61
KIT        58
ALK        49
ERBB2      43
PDGFRA     40
Name: Gene, dtype: int64
```

```
In [17]: print("Ans: There are", unique_genes.shape[0] ,"different categories of genes in the t
```

```
Ans: There are 237 different categories of genes in the train data, and they are distibuted as
```

```
In [18]: s = sum(unique_genes.values);
         h = unique_genes.values/s;
         plt.plot(h, label="Histrogram of Genes")
         plt.xlabel('Index of a Gene')
         plt.ylabel('Number of Occurances')
         plt.legend()
         plt.grid()
         plt.show()
```



Q3. How to featurize this Gene feature ?

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

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

```
In [20]: #response-coding of the Gene feature
         # alpha is used for laplace smoothing
         alpha = 1
         # train gene feature
         train_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", train_df))
         # test gene feature
         test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", test_df))
         # cross validation gene feature
         cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Gene", cv_df))

In [21]: print("train_gene_feature_responseCoding is converted feature using respone coding me

train_gene_feature_responseCoding is converted feature using respone coding method. The shape

In [32]: # TF-IDF encoding of Gene feature.
         gene_vectorizer = TfidfVectorizer()
         train_gene_feature_tfidfcoding = gene_vectorizer.fit_transform(train_df['Gene'])
```

```
test_gene_feature_tfidfcoding = gene_vectorizer.transform(test_df['Gene'])
cv_gene_feature_tfidfcoding = gene_vectorizer.transform(cv_df['Gene'])
```

In [33]:
```
train_df['Gene'].head()
```

Out[33]:
```
1187    PIK3CA
2488     BRCA1
1326      MLH1
404       TP53
102       MSH6
Name: Gene, dtype: object
```

In [34]:
```
gene_vectorizer.get_feature_names()
```

Out[34]:
```
['abl1',
 'acvr1',
 'ago2',
 'akt1',
 'akt2',
 'akt3',
 'alk',
 'apc',
 'ar',
 'araf',
 'arid1a',
 'arid1b',
 'arid2',
 'atm',
 'atr',
 'aurka',
 'aurkb',
 'axin1',
 'b2m',
 'bap1',
 'bard1',
 'bcl10',
 'bcl2',
 'bcl2l11',
 'bcor',
 'braf',
 'brca1',
 'brca2',
 'brd4',
 'brip1',
 'btk',
 'card11',
 'carm1',
 'casp8',
 'cbl',
```

```
'ccnd1',
'ccnd3',
'ccne1',
'cdh1',
'cdk12',
'cdk4',
'cdk6',
'cdk8',
'cdkn1a',
'cdkn1b',
'cdkn2a',
'cdkn2b',
'cdkn2c',
'cebpa',
'chek2',
'cic',
'crebbp',
'ctcf',
'ctnnb1',
'ddr2',
'dicer1',
'dnmt3a',
'dnmt3b',
'dusp4',
'egfr',
'eif1ax',
'elf3',
'ep300',
'epas1',
'erbb2',
'erbb3',
'erbb4',
'ercc2',
'ercc4',
'erg',
'errfi1',
'esr1',
'etv1',
'etv6',
'ewsr1',
'ezh2',
'fam58a',
'fanca',
'fancc',
'fat1',
'fbxw7',
'fgf19',
'fgf3',
```

```
'fgf4',
'fgfr1',
'fgfr2',
'fgfr3',
'fgfr4',
'flt3',
'foxa1',
'foxl2',
'foxo1',
'foxp1',
'fubp1',
'gata3',
'gli1',
'gnas',
'h3f3a',
'hist1h1c',
'hla',
'hnf1a',
'hras',
'idh1',
'idh2',
'igf1r',
'ikbke',
'il7r',
'inpp4b',
'jak1',
'jak2',
'kdm5a',
'kdm5c',
'kdm6a',
'kdr',
'keap1',
'kit',
'klf4',
'kmt2a',
'kmt2b',
'kmt2c',
'kmt2d',
'knstrn',
'kras',
'lats1',
'lats2',
'map2k1',
'map2k2',
'map2k4',
'map3k1',
'mapk1',
'mdm4',
```

```
'med12',
'mef2b',
'men1',
'met',
'mga',
'mlh1',
'mpl',
'msh2',
'msh6',
'mtor',
'myc',
'mycn',
'myd88',
'ncor1',
'nf1',
'nf2',
'nfe2l2',
'nfkbia',
'nkx2',
'notch1',
'notch2',
'npm1',
'nras',
'ntrk1',
'ntrk2',
'ntrk3',
'pbrm1',
'pdgfra',
'pdgfrb',
'pik3ca',
'pik3cb',
'pik3cd',
'pik3r1',
'pik3r2',
'pik3r3',
'pim1',
'pms1',
'pms2',
'pole',
'ppm1d',
'ppp2r1a',
'ppp6c',
'prdm1',
'ptch1',
'pten',
'ptpn11',
'ptprd',
'ptprt',
```

```
'rab35',
'rac1',
'rad21',
'rad50',
'rad51c',
'rad51d',
'rad54l',
'raf1',
'rasa1',
'rb1',
'rbm10',
'ret',
'rheb',
'rhoa',
'rictor',
'rit1',
'rnf43',
'ros1',
'rras2',
'runx1',
'rxra',
'setd2',
'sf3b1',
'shq1',
'smad2',
'smad3',
'smad4',
'smarca4',
'smarcb1',
'smo',
'sos1',
'sox9',
'spop',
'src',
'srsf2',
'stat3',
'stk11',
'tcf3',
'tcf7l2',
'tert',
'tet1',
'tet2',
'tgfbr1',
'tgfbr2',
'tmprss2',
'tp53',
'tp53bp1',
'tsc1',
```

```
 'tsc2',
 'u2af1',
 'vegfa',
 'vhl',
 'whsc1',
 'whsc1l1',
 'xpo1',
 'xrcc2',
 'yap1']
```

```
In [35]: print("train_gene_feature_tfidfcoding is converted feature using tfidf-coding method.
```

```
train_gene_feature_tfidfcoding is converted feature using tfidf-coding method. The shape of ge
```

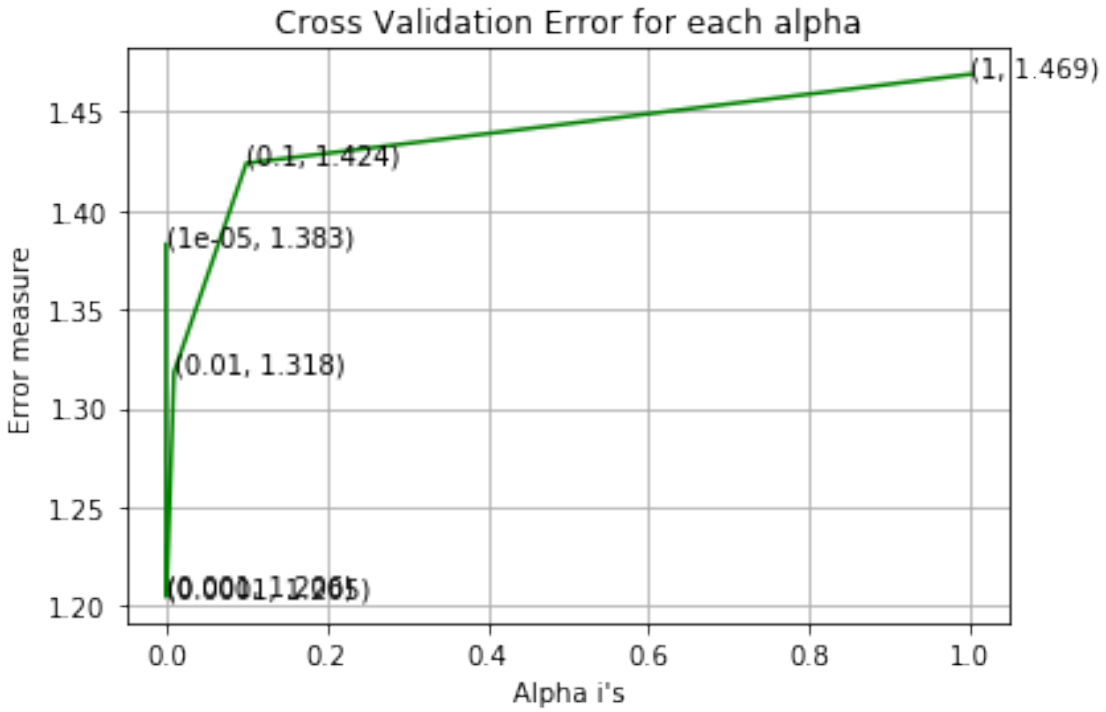
Q4. How good is this gene feature in predicting y_i?

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 [36]: alpha = [10 ** x for x in range(-5, 1)] # hyperparam for SGD classifier.

         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # 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 Gr
         # predict(X)        Predict class labels for samples in X.

         #-------------------------------
         # video link:
         #-------------------------------
         cv_log_error_array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
             clf.fit(train_gene_feature_tfidfcoding, y_train)
             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_gene_feature_tfidfcoding, y_train)
             predict_y = sig_clf.predict_proba(cv_gene_feature_tfidfcoding)
             cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, la

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

```
        ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i]))
    plt.grid()
    plt.title("Cross Validation Error for each alpha")
    plt.xlabel("Alpha i's")
    plt.ylabel("Error measure")
    plt.show()
    best_alpha = np.argmin(cv_log_error_array)
    clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42
    clf.fit(train_gene_feature_tfidfcoding, y_train)
    sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
    sig_clf.fit(train_gene_feature_tfidfcoding, y_train)

    predict_y = sig_clf.predict_proba(train_gene_feature_tfidfcoding)
    print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_l
    predict_y = sig_clf.predict_proba(cv_gene_feature_tfidfcoding)
    print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
    predict_y = sig_clf.predict_proba(test_gene_feature_tfidfcoding)
    print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_lo
```

```
For values of alpha =  1e-05 The log loss is: 1.3827940815435866
For values of alpha =  0.0001 The log loss is: 1.2045841169436815
For values of alpha =  0.001 The log loss is: 1.20579205292768
For values of alpha =  0.01 The log loss is: 1.3180120098392534
For values of alpha =  0.1 The log loss is: 1.423790019653204
For values of alpha =  1 The log loss is: 1.4687740443632886
```



```
For values of best alpha =  0.0001 The train log loss is: 1.0493777784454428
For values of best alpha =  0.0001 The cross validation log loss is: 1.2045841169436815
For values of best alpha =  0.0001 The test log loss is: 1.2044631218454251
```

Q5. Is the Gene feature stable across all the data sets (Test, Train, Cross validation)?
Ans. Yes, it is. Otherwise, the CV and Test errors would be significantly more than train error.

```
In [37]: print("Q6. How many data points in Test and CV datasets are covered by the ", unique_g

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

         print('Ans\n1. In test data',test_coverage, 'out of',test_df.shape[0], ":",(test_cover
         print('2. In cross validation data',cv_coverage, 'out of ',cv_df.shape[0],":" ,(cv_cov
```

```
Q6. How many data points in Test and CV datasets are covered by the  237  genes in train datase
Ans
1. In test data 644 out of 665 : 96.84210526315789
2. In cross validation data 521 out of  532 : 97.93233082706767
```

23 3.2.2 Univariate Analysis on Variation Feature

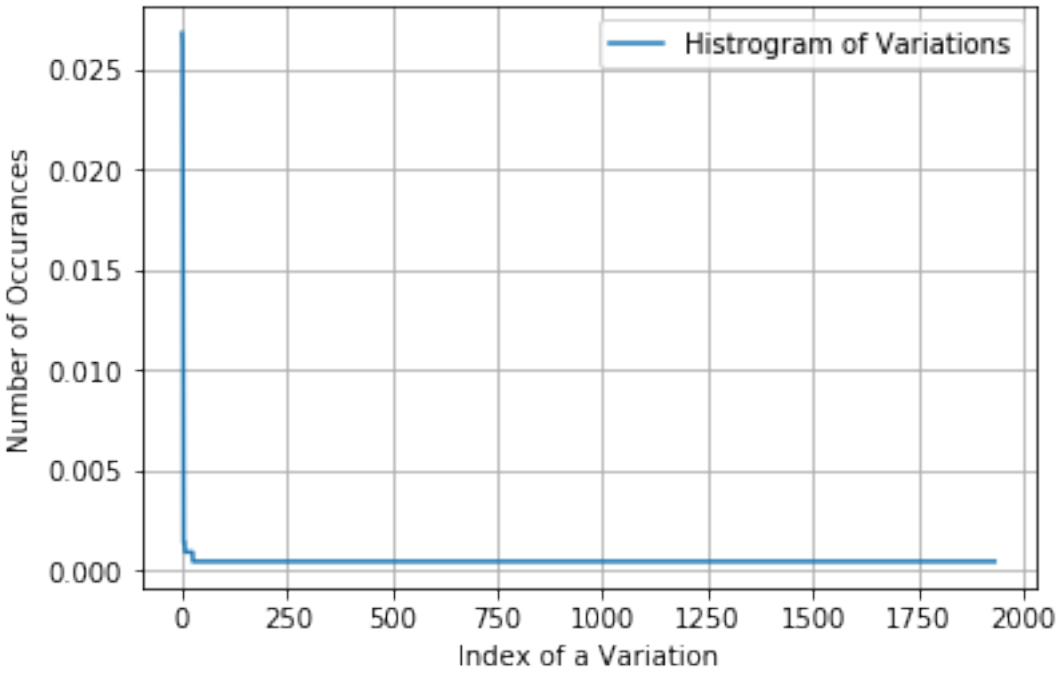
Q7. Variation, What type of feature is it ?
Ans. Variation is a categorical variable
Q8. How many categories are there?

```
In [38]: unique_variations = train_df['Variation'].value_counts()
         print('Number of Unique Variations :', unique_variations.shape[0])
         # the top 10 variations that occured most
         print(unique_variations.head(10))
```

```
Number of Unique Variations : 1933
Truncating_Mutations    57
Deletion                56
Amplification           43
Fusions                 14
G12V                     3
Q61H                     3
Overexpression           3
G13V                     2
S222D                    2
Q61L                     2
Name: Variation, dtype: int64
```

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

```
In [39]: 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()
```



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

```
In [31]: # alpha is used for laplace smoothing
         alpha = 1
         # train gene feature
         train_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", t
         # test gene feature
         test_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", te
         # cross validation gene feature
         cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha, "Variation", cv_
```

```
In [40]: print("train_variation_feature_responseCoding is a converted feature using the respons

train_variation_feature_responseCoding is a converted feature using the response coding method
```

```
In [41]: # TFIDF encoding of variation feature.
         variation_vectorizer = TfidfVectorizer()
         train_variation_feature_tfidfcoding = variation_vectorizer.fit_transform(train_df['Va
         test_variation_feature_tfidfcoding = variation_vectorizer.transform(test_df['Variatio
         cv_variation_feature_tfidfcoding = variation_vectorizer.transform(cv_df['Variation'])
```

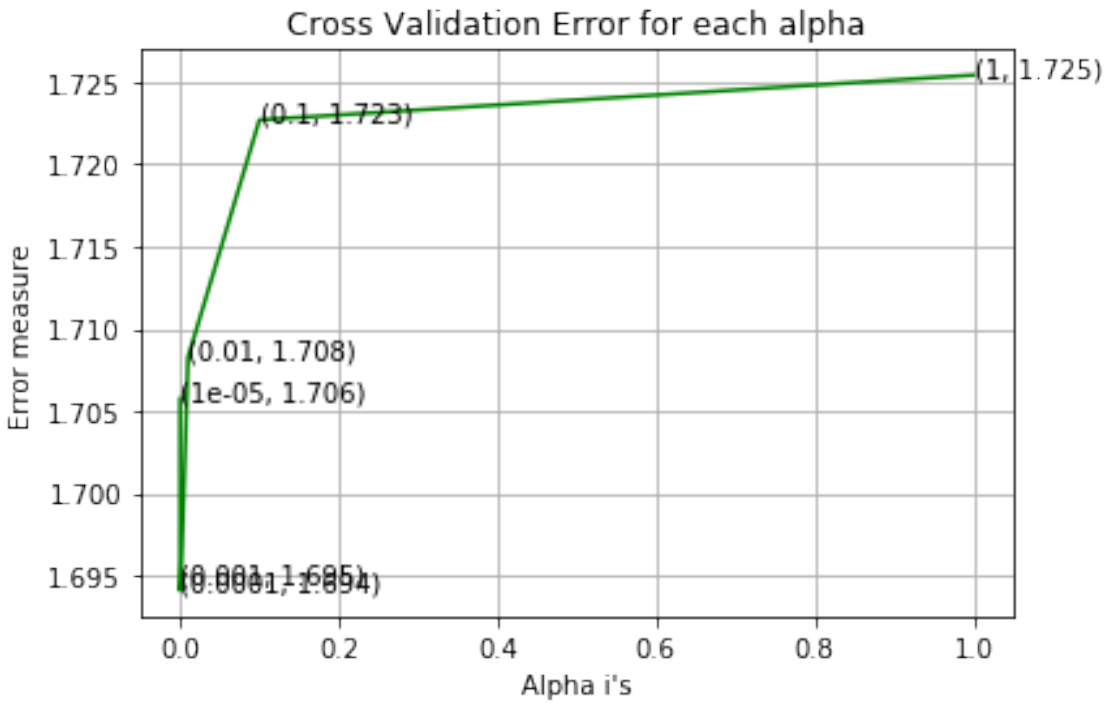
```
In [42]: print("train_variation_feature_TFIDF coded is converted feature using the tfidfcoding

train_variation_feature_TFIDF coded is converted feature using the tfidfcoding encoding method
```

Q10. How good is this Variation feature in predicting y_i?
Let's build a model just like the earlier!

```
In [43]: alpha = [10 ** x for x in range(-5, 1)]

         # read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated
         # ------------------------------
         # default parameters
         # SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
         # shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
         # 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 Gr
         # predict(X)        Predict class labels for samples in X.

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

         cv_log_error_array=[]
         for i in alpha:
             clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
             clf.fit(train_variation_feature_tfidfcoding, y_train)

             sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
             sig_clf.fit(train_variation_feature_tfidfcoding, y_train)
             predict_y = sig_clf.predict_proba(cv_variation_feature_tfidfcoding)

             cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.classes_, eps=1e-15
             print('For values of alpha = ', i, "The log loss is:",log_loss(y_cv, predict_y, la

         fig, ax = plt.subplots()
```

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

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

        predict_y = sig_clf.predict_proba(train_variation_feature_tfidfcoding)
        print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_l
        predict_y = sig_clf.predict_proba(cv_variation_feature_tfidfcoding)
        print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
        predict_y = sig_clf.predict_proba(test_variation_feature_tfidfcoding)
        print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_lo
```

```
For values of alpha =  1e-05 The log loss is: 1.705744778024589
For values of alpha =  0.0001 The log loss is: 1.6940793338459674
For values of alpha =  0.001 The log loss is: 1.6945750576684664
For values of alpha =  0.01 The log loss is: 1.7082631286892376
For values of alpha =  0.1 The log loss is: 1.7227058641925947
For values of alpha =  1 The log loss is: 1.725433492230424
```




```
For values of best alpha =  0.0001 The train log loss is: 0.8030908462044387
For values of best alpha =  0.0001 The cross validation log loss is: 1.6940793338459674
For values of best alpha =  0.0001 The test log loss is: 1.699100043646769
```

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

```
Q12. How many data points are covered by total  1933  genes in test and cross validation data s
Ans
1. In test data 68 out of 665 : 10.225563909774436
2. In cross validation data 57 out of  532 : 10.714285714285714
```

24 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 [45]: # cls_text is a data frame
         # for every row in data fram consider the 'TEXT'
         # split the words by space
         # make a dict with those words
         # increment its count whenever we see that word

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

```
In [46]: import math
         #https://stackoverflow.com/a/1602964
         def get_text_responsecoding(df):
             text_feature_responseCoding = np.zeros((df.shape[0],9))
             for i in range(0,9):
                 row_index = 0
                 for index, row in df.iterrows():
                     sum_prob = 0
                     for word in row['TEXT'].split():
                         sum_prob += math.log(((dict_list[i].get(word,0)+10 )/(total_dict.get(w
                     text_feature_responseCoding[row_index][i] = math.exp(sum_prob/len(row['TE
                     row_index += 1
             return text_feature_responseCoding
```

```
In [49]: text_vectorizer = TfidfVectorizer(ngram_range=(1,1), max_features=1000)
         train_text_feature_tfidfcoding = text_vectorizer.fit_transform(train_df['TEXT'])
         # getting all the feature names (words)
         train_text_features= text_vectorizer.get_feature_names()

         # train_text_feature_tfidfcoding.sum(axis=0).A1 will sum every row and returns (1*num
         train_text_fea_counts = train_text_feature_tfidfcoding.sum(axis=0).A1

         # zip(list(text_features),text_fea_counts) will zip a word with its number of times i
         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 [50]: 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 [51]:
```
#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 [52]:
```
# https://stackoverflow.com/a/16202486
# we convert each row values such that they sum to 1
train_text_feature_responseCoding = (train_text_feature_responseCoding.T/train_text_fe
test_text_feature_responseCoding = (test_text_feature_responseCoding.T/test_text_featu
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/cv_text_feature_res
```

In [53]:
```
# don't forget to normalize every feature
train_text_feature_tfidfcoding = normalize(train_text_feature_tfidfcoding, axis=0)

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

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

In [54]:
```
#https://stackoverflow.com/a/2258273/4084039
sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambda x: x[1] , reverse
sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))
```

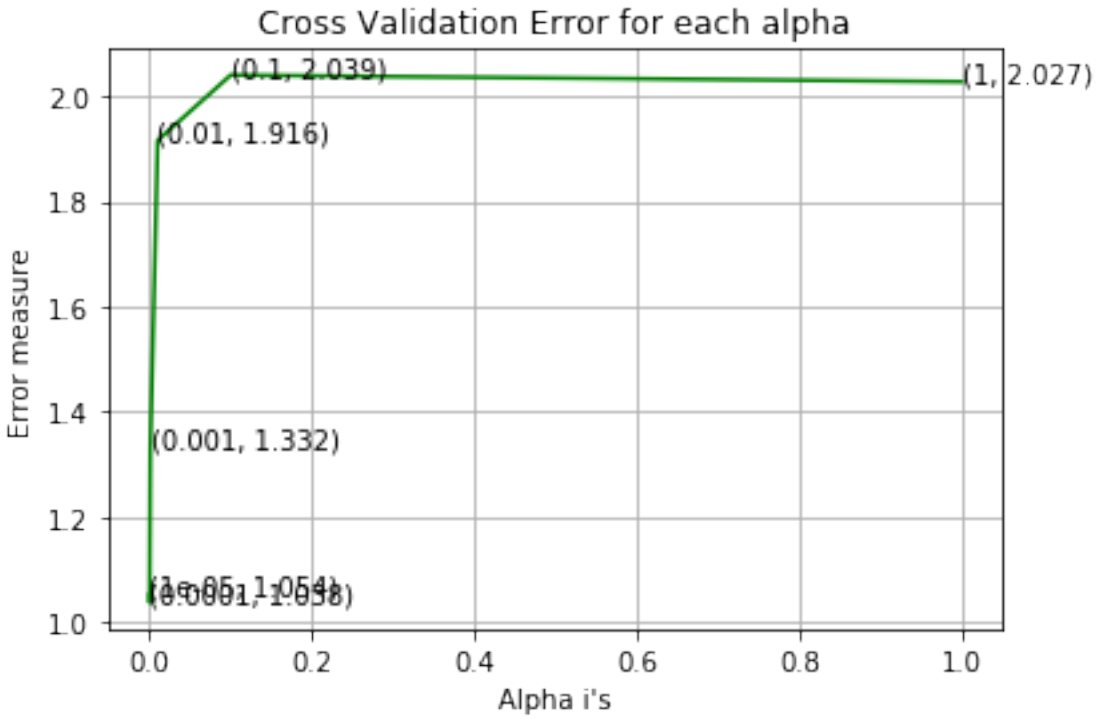
In [55]:
```
# Number of words for a given frequency.
print(Counter(sorted_text_occur))
```

```
Counter({248.77269232657878: 1, 184.1013561433984: 1, 132.66004697768378: 1, 131.1389786402285
```

In [57]:
```
# Train a Logistic regression+Calibration model using text features which are TFIDF e
alpha = [10 ** x for x in range(-5, 1)]

# read more about SGDClassifier() at http://scikit-learn.org/stable/modules/generated/
# ------------------------------
# default parameters
# SGDClassifier(loss=hinge, penalty=l2, alpha=0.0001, l1_ratio=0.15, fit_intercept=Tr
# shuffle=True, verbose=0, epsilon=0.1, n_jobs=1, random_state=None, learning_rate=op
# 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 Gr
# predict(X)        Predict class labels for samples in X.

#-------------------------------
# video link:
#-------------------------------
cv_log_error_array=[]
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log', random_state=42)
    clf.fit(train_text_feature_tfidfcoding, y_train)

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

fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array,c='g')
for i, txt in enumerate(np.round(cv_log_error_array,3)):
    ax.annotate((alpha[i],np.round(txt,3)), (alpha[i],cv_log_error_array[i]))
plt.grid()
plt.title("Cross Validation Error for each alpha")
plt.xlabel("Alpha i's")
plt.ylabel("Error measure")
plt.show()
best_alpha = np.argmin(cv_log_error_array)
clf = SGDClassifier(alpha=alpha[best_alpha], penalty='l2', loss='log', random_state=42
clf.fit(train_text_feature_tfidfcoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_text_feature_tfidfcoding, y_train)

predict_y = sig_clf.predict_proba(train_text_feature_tfidfcoding)
print('For values of best alpha = ', alpha[best_alpha], "The train log loss is:",log_l
predict_y = sig_clf.predict_proba(cv_text_feature_tfidfcoding)
print('For values of best alpha = ', alpha[best_alpha], "The cross validation log loss
predict_y = sig_clf.predict_proba(test_text_feature_tfidfcoding)
```

```
        print('For values of best alpha = ', alpha[best_alpha], "The test log loss is:",log_l
```

```
For values of alpha =  1e-05 The log loss is: 1.0535542571954777
For values of alpha =  0.0001 The log loss is: 1.0382579407634964
For values of alpha =  0.001 The log loss is: 1.3318572522723997
For values of alpha =  0.01 The log loss is: 1.915509710874571
For values of alpha =  0.1 The log loss is: 2.0394875914178248
For values of alpha =  1 The log loss is: 2.026921250219763
```




```
For values of best alpha =  0.0001 The train log loss is: 0.8505183897726535
For values of best alpha =  0.0001 The cross validation log loss is: 1.0382579407634964
For values of best alpha =  0.0001 The test log loss is: 1.1125400718790734
```

Q. Is the Text feature stable across all the data sets (Test, Train, Cross validation)?
Ans. Yes, it seems like!

```
In [58]: def get_intersec_text(df):
             df_text_vec = TfidfVectorizer()
             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 [59]: 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 d
```

```
1.328 % of word of test data appeared in train data
1.545 % of word of Cross Validation appeared in train data
```