Cancer diagnosis

Description

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

Data: Memorial Sloan Kettering Cancer Center (MSKCC)

Problem statement :

Classify the provided genetic variations/mutations using data from text-based medical literature.

Exploratory Data Analysis

In [3]:
```
import pandas as pd
import matplotlib.pyplot as plt
import re
import time
from sklearn.metrics import accuracy_score, precision_score, recall

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.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.model_selection import cross_val_score
from sklearn.model_selection import cross_val_score

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")
import nltk
nltk.download("stopwords")
from mlxtend.classifier import StackingClassifier

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

```
[nltk_data] Downloading package stopwords to
[nltk_data]     /Users/ramkiranmeduri/nltk_data...
[nltk_data]   Package stopwords is already up-to-date!
```

Reading Data

Reading Gene and Variation Data

In [4]:
```
data = pd.read_csv('/Users/ramkiranmeduri/Desktop/training/training
print('Number of data points : ', data.shape[0])
print('Number of features : ', data.shape[1])
print('Features : ', data.columns.values)
data.head(10)
```

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

Out[4]:

	ID	Gene	Variation	Class
0	0	FAM58A	Truncating Mutations	1
1	1	CBL	W802*	2
2	2	CBL	Q249E	2
3	3	CBL	N454D	3
4	4	CBL	L399V	4
5	5	CBL	V391I	4
6	6	CBL	V430M	5
7	7	CBL	Deletion	1
8	8	CBL	Y371H	4
9	9	CBL	C384R	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

Reading Text Data

In [5]:
```
# note the seprator in this file
data_text =pd.read_csv("/Users/ramkiranmeduri/Desktop/training/trai
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(10)
```

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

Out[5]:

	ID	TEXT
0	0	Cyclin-dependent kinases (CDKs) regulate a var...
1	1	Abstract Background Non-small cell lung canc...
2	2	Abstract Background Non-small cell lung canc...
3	3	Recent evidence has demonstrated that acquired...
4	4	Oncogenic mutations in the monomeric Casitas B...
5	5	Oncogenic mutations in the monomeric Casitas B...
6	6	Oncogenic mutations in the monomeric Casitas B...
7	7	CBL is a negative regulator of activated recep...
8	8	Abstract Juvenile myelomonocytic leukemia (JM...
9	9	Abstract Juvenile myelomonocytic leukemia (JM...

Preprocessing of text

In [6]:
```
# loading stop words from nltk library
stop_words = set(stopwords.words('english'))


def nlp_pre_processing(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 fr
            if not word in stop_words:
                string += word + " "

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

In [7]:
```
#text processing stage.
start_time = time.perf_counter()
for index, row in data_text.iterrows():
    if type(row['TEXT']) is str:
        nlp_pre_processing(row['TEXT'], index, 'TEXT')
    else:
        print("there is no text description for id:",index)
print('Time took for preprocessing the text :',time.perf_counter()
```

```
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 : 20.339649166999152 seconds
```

In [8]:
```
#merging both gene_variations and text data based on ID
result = pd.merge(data, data_text,on='ID', how='left')
result.head()
```

Out[8]:

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

In [9]:
```
result[result.isnull().any(axis=1)]
```

Out[9]:

	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 [10]:
```
result.loc[result['TEXT'].isnull(),'TEXT'] = result['Gene'] +' '+re
```

In [11]:
```
result[result['ID']==1109]
```

Out[11]:

	ID	Gene	Variation	Class	TEXT
1109	1109	FANCA	S1088F	1	FANCA S1088F

Test, Train and Cross Validation Split

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

In [12]:
```
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 distributi
X_train, test_df, y_train, y_test = train_test_split(result, y_true
# split the train data into train and cross validation by maintaini
train_df, cv_df, y_train, y_cv = train_test_split(X_train, y_train,
```

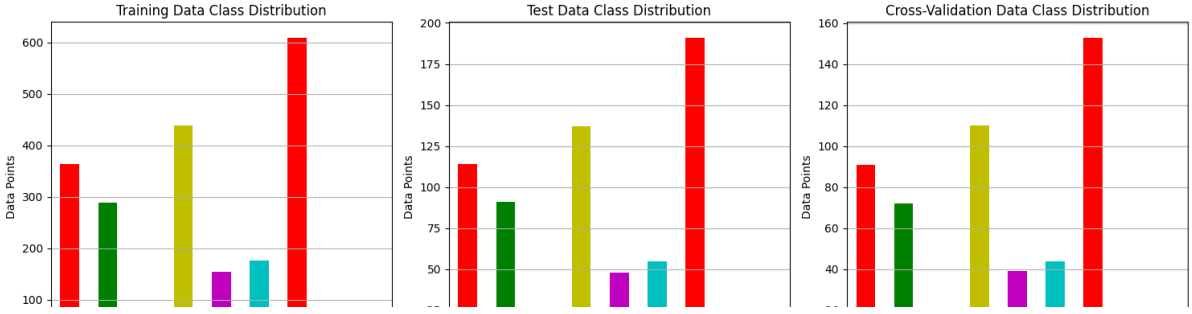
We split the data into train, test and cross validation data sets, preserving the ratio of class distribution in the original data set

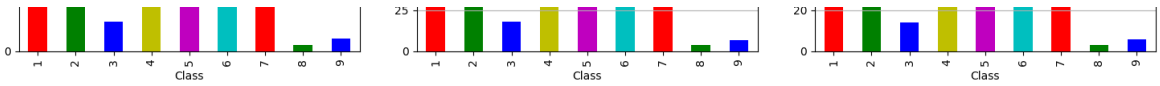
In [13]:
```
print('Number of data points in train data:', train_df.shape[0])
print('Number of data points in test data:', test_df.shape[0])
print('Number of data points in cross validation data:', cv_df.shap
```

```
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
```

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

In [14]:
```
# Calculate class distributions
train_class_distribution = train_df['Class'].value_counts().sort_in
test_class_distribution = test_df['Class'].value_counts().sort_inde
cv_class_distribution = cv_df['Class'].value_counts().sort_index()

# Plot class distributions
plt.figure(figsize=(15, 5))

plt.subplot(1, 3, 1)
train_class_distribution.plot(kind='bar', color=['r', 'g', 'b', 'y'
plt.xlabel('Class')
plt.ylabel('Data Points')
plt.title('Training Data Class Distribution')
plt.grid(axis='y')

plt.subplot(1, 3, 2)
test_class_distribution.plot(kind='bar', color=['r', 'g', 'b', 'y',
plt.xlabel('Class')
plt.ylabel('Data Points')
plt.title('Test Data Class Distribution')
plt.grid(axis='y')

plt.subplot(1, 3, 3)
cv_class_distribution.plot(kind='bar', color=['r', 'g', 'b', 'y', '
plt.xlabel('Class')
plt.ylabel('Data Points')
plt.title('Cross-Validation Data Class Distribution')
plt.grid(axis='y')

plt.tight_layout()
plt.show()

# Print class distribution details
def print_class_distribution(distribution, dataset_name):
    sorted_yi = np.argsort(-distribution.values)
    print(f"Class distribution in {dataset_name}:")
    for i in sorted_yi:
        print(f"Class {distribution.index[i]}: {distribution.values
              f"({np.round((distribution.values[i] / distribution.s
    print('-' * 80)

print_class_distribution(train_class_distribution, 'Training Set')
print_class_distribution(test_class_distribution, 'Test Set')
print_class_distribution(cv_class_distribution, 'Cross-Validation S
```






```
Class distribution in Training Set:
Class 7: 609 (28.672%)
Class 4: 439 (20.669%)
Class 1: 363 (17.09%)
Class 2: 289 (13.606%)
Class 6: 176 (8.286%)
Class 5: 155 (7.298%)
Class 3: 57 (2.684%)
Class 9: 24 (1.13%)
Class 8: 12 (0.565%)
------------------------------------------------------------------------
--------------
Class distribution in Test Set:
Class 7: 191 (28.722%)
Class 4: 137 (20.602%)
Class 1: 114 (17.143%)
Class 2: 91 (13.684%)
Class 6: 55 (8.271%)
Class 5: 48 (7.218%)
Class 3: 18 (2.707%)
Class 9: 7 (1.053%)
Class 8: 4 (0.602%)
------------------------------------------------------------------------
--------------
Class distribution in Cross-Validation Set:
Class 7: 153 (28.759%)
Class 4: 110 (20.677%)
Class 1: 91 (17.105%)
Class 2: 72 (13.534%)
Class 6: 44 (8.271%)
Class 5: 39 (7.331%)
Class 3: 14 (2.632%)
Class 9: 6 (1.128%)
Class 8: 3 (0.564%)
------------------------------------------------------------------------
--------------
```

Prediction using a 'Random' Model

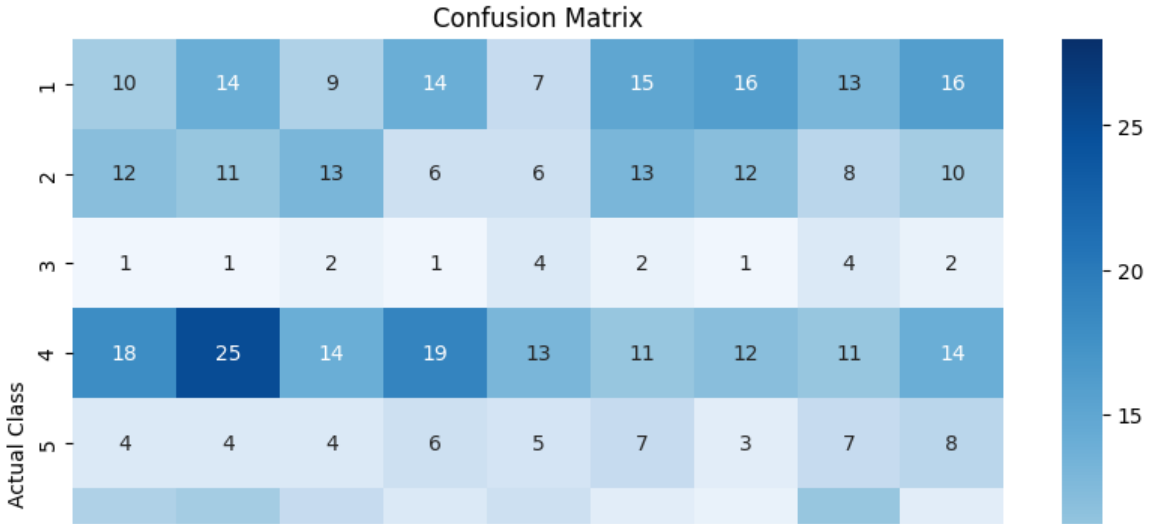
In a 'Random' Model, we generate the NINE class probabilites randomly such that they sum to 1.

In [15]:
```
# This function plots the confusion matrices given y_i, y_i_hat.
def plot_confusion_matrix(test_y, predict_y, labels):
    C = confusion_matrix(test_y, predict_y)
    # C = 9x9 matrix, each cell (i,j) represents the number of poin

    A = ((C.T) / C.sum(axis=1)).T
```

```
    # A is the recall matrix, where each element is divided by the
    B = C / C.sum(axis=0)
    # B is the precision matrix, where each element is divided by t

    # Plotting Confusion Matrix
    print("-" * 20, "Confusion Matrix", "-" * 20)
    plt.figure(figsize=(10, 7))
    sns.heatmap(C, annot=True, cmap="Blues", fmt="d", xticklabels=l
    plt.xlabel('Predicted Class')
    plt.ylabel('Actual Class')
    plt.title('Confusion Matrix')
    plt.show()

    # Plotting Precision Matrix
    print("-" * 20, "Precision Matrix (Column Sum = 1)", "-" * 20)
    plt.figure(figsize=(10, 7))
    sns.heatmap(B, annot=True, cmap="Oranges", fmt=".2f", xticklabe
    plt.xlabel('Predicted Class')
    plt.ylabel('Actual Class')
    plt.title('Precision Matrix')
    plt.show()

    # Plotting Recall Matrix
    print("-" * 20, "Recall Matrix (Row Sum = 1)", "-" * 20)
    plt.figure(figsize=(10, 7))
    sns.heatmap(A, annot=True, cmap="Greens", fmt=".2f", xticklabel
    plt.xlabel('Predicted Class')
    plt.ylabel('Actual Class')
    plt.title('Recall Matrix')
    plt.show()

# Assuming you have test_df, cv_df, y_test, y_cv
# Generate predictions with random probabilities
test_data_len = test_df.shape[0]
cv_data_len = cv_df.shape[0]

# Creating output arrays with random probabilities
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 / np.sum(rand_probs))

print("Log loss on Cross Validation Data using Random Model",
      log_loss(y_cv, cv_predicted_y))

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 / np.sum(rand_probs))

print("Log loss on Test Data using Random Model",
      log_loss(y_test, test_predicted_y))
```

```
# Convert probabilistic predictions to discrete class predictions
predicted_y = np.argmax(test_predicted_y, axis=1) + 1

# Define class labels
labels = [1, 2, 3, 4, 5, 6, 7, 8, 9]

# Plot confusion matrices
plot_confusion_matrix(y_test, predicted_y, labels)
```

```
Log loss on Cross Validation Data using Random Model 2.489578730
1536796
Log loss on Test Data using Random Model 2.4855642150194357
-------------------- Confusion Matrix --------------------
```



Univariate Analysis

In [16]:

```
def get_gv_fea_dict(alpha, feature, df):

    value_count = train_df[feature].value_counts()

    # gv_dict : Gene Variation Dict, which contains the probability
    gv_dict = dict()

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


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

            # cls_cnt.shape[0](numerator) will contain the number o
            vec.append((cls_cnt.shape[0] + alpha*10)/ (denominator

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

# Get Gene variation feature
def get_gv_feature(alpha, feature, df):

    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 f
    gv_fea = []
    # for every feature values in the given data frame we will chec
    # if not we will add [1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9,1/9] to g
    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
```

Univariate Analysis on Gene Feature

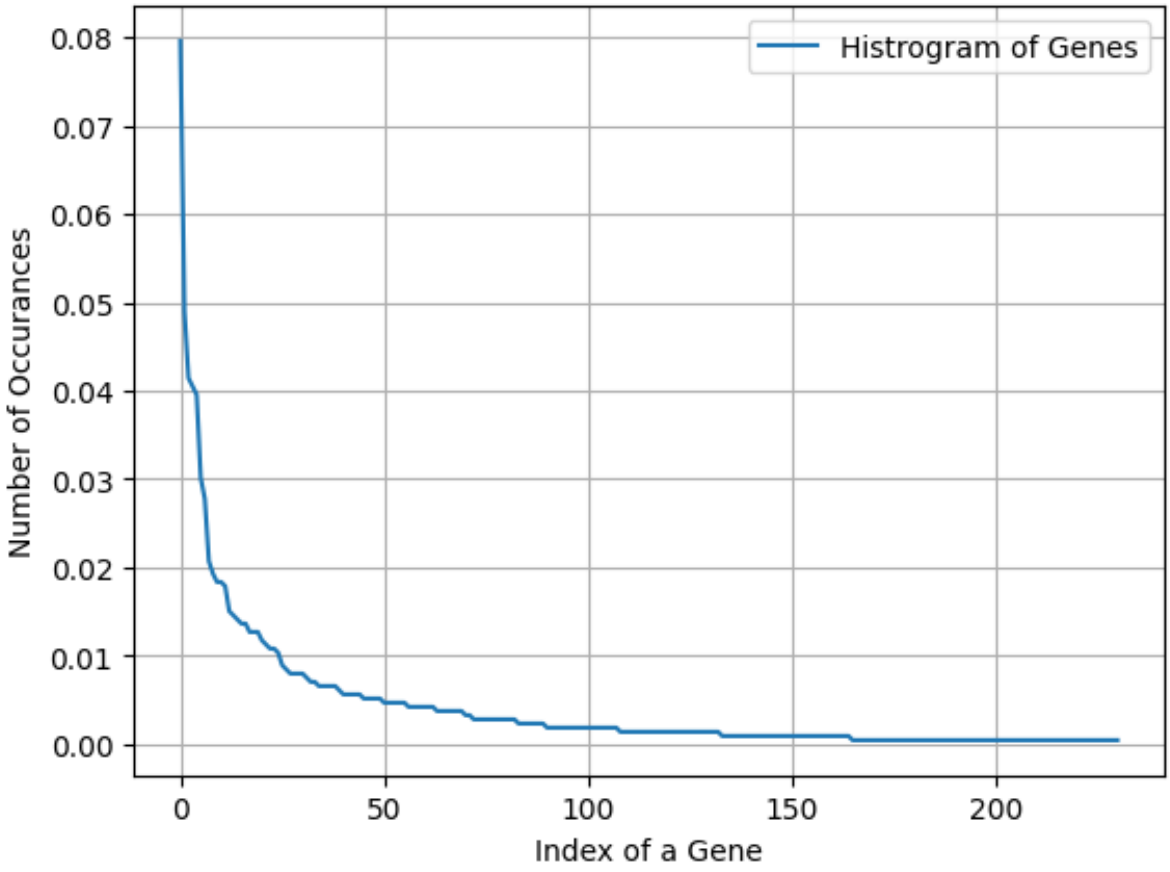
In [17]:
```
unique_genes = train_df['Gene'].value_counts()
print('Number of Unique Genes :', unique_genes.shape[0])
# the top 10 genes that occured most
print(unique_genes.head(10))
```

```
Number of Unique Genes : 231
Gene
BRCA1     169
TP53      104
EGFR       88
BRCA2      86
PTEN       84
BRAF       64
KIT        59
ERBB2      44
ALK        41
PDGFRA     39
Name: count, dtype: int64
```

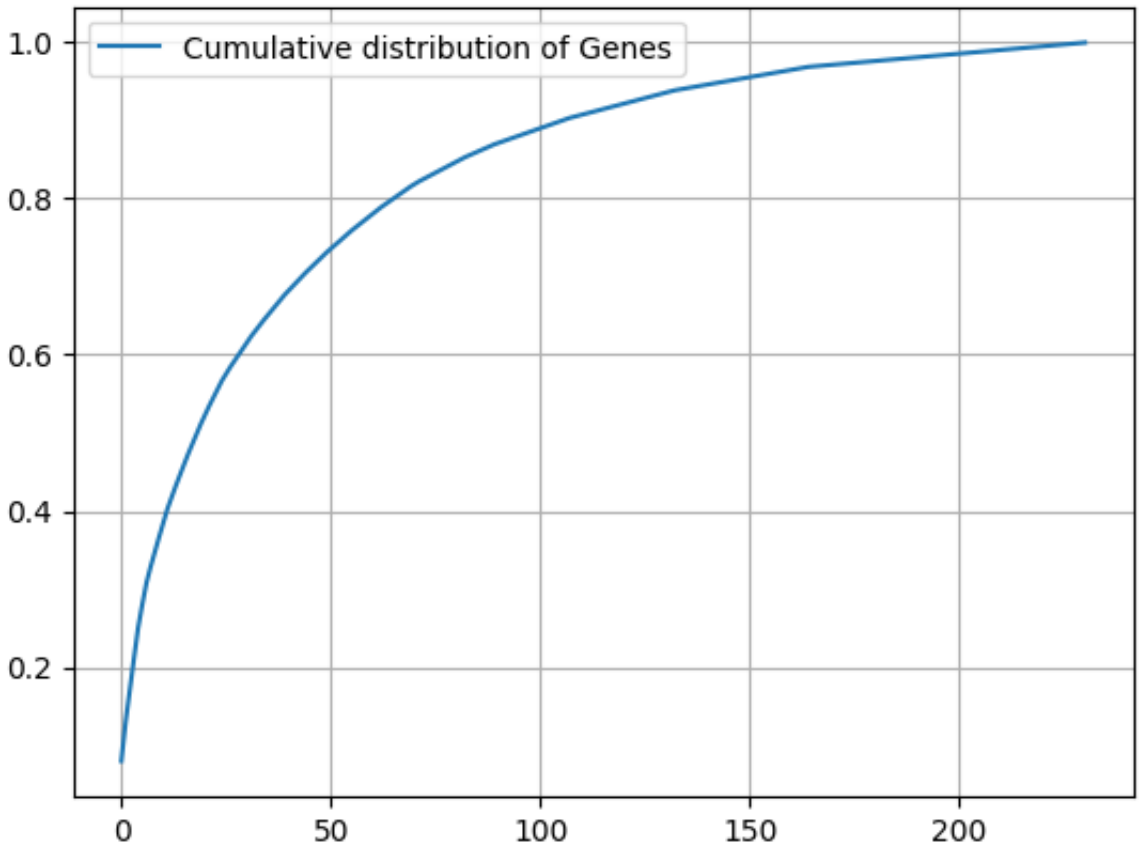
In [18]:
```
print("Ans: There are", unique_genes.shape[0] ,"different categorie
```

```
Ans: There are 231 different categories of genes in the train dat
a, and they are distibuted as follows
```

In [19]:
```
s = sum(unique_genes.values)
h = unique_genes.values/s
plt.plot(h, label="Histrogram of Genes")
plt.xlabel('Index of a Gene')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



In [20]:
```
c = np.cumsum(h)
plt.plot(c,label='Cumulative distribution of Genes')
plt.grid()
plt.legend()
plt.show()
```



In [21]:
```
#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,
# test gene feature
test_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "
# cross validation gene feature
cv_gene_feature_responseCoding = np.array(get_gv_feature(alpha, "Ge
```

In [22]:
```
# one-hot encoding of Gene feature.
gene_vectorizer = CountVectorizer()
train_gene_feature_onehotCoding = gene_vectorizer.fit_transform(tra
test_gene_feature_onehotCoding = gene_vectorizer.transform(test_df[
cv_gene_feature_onehotCoding = gene_vectorizer.transform(cv_df['Gen
```

In [ ]:
```

```

In [23]:
```
train_df['Gene'].head()
```

Out[23]:
```
2760      BRAF
1993    MAP2K1
2699      BRAF
2949       KDR
2960       KIT
Name: Gene, dtype: object
```

In [24]:
```
# Assuming gene_vectorizer is an instance of CountVectorizer
feature_names = gene_vectorizer.get_feature_names_out()
print(feature_names)
```

```
['abl1' 'acvr1' 'ago2' 'akt1' 'akt2' 'akt3' 'alk' 'apc' 'ar' 'ara
f'
 'arid1b' 'arid5b' 'atm' 'atr' 'atrx' 'aurka' 'axl' 'b2m' 'bap1' '
bcl10'
 'bcl2' 'bcl2l11' 'bcor' 'braf' 'brca1' 'brca2' 'brip1' 'btk' 'car
d11'
 'carm1' 'casp8' 'cbl' 'ccnd1' 'ccnd2' 'ccnd3' 'ccne1' 'cdh1' 'cdk
12'
 'cdk6' 'cdkn1a' 'cdkn1b' 'cdkn2a' 'cdkn2b' 'cebpa' 'chek2' 'cic'
'crebbp'
 'ctcf' 'ctla4' 'ctnnb1' 'ddr2' 'dicer1' 'dnmt3a' 'dnmt3b' 'dusp4'
'egfr'
 'eif1ax' 'elf3' 'ep300' 'epas1' 'erbb2' 'erbb3' 'erbb4' 'ercc2' '
ercc3'
 'ercc4' 'erg' 'esr1' 'etv1' 'etv6' 'ewsr1' 'ezh2' 'fanca' 'fancc'
'fat1'
 'fbxw7' 'fgf19' 'fgf3' 'fgf4' 'fgfr1' 'fgfr2' 'fgfr3' 'fgfr4' 'fl
t1'
 'flt3' 'foxa1' 'foxl2' 'foxo1' 'foxp1' 'gata3' 'gli1' 'gna11' 'gn
aq'
 'gnas' 'h3f3a' 'hist1h1c' 'hla' 'hnf1a' 'hras' 'idh1' 'idh2' 'igf
1r'
 'ikzf1' 'il7r' 'jak1' 'jak2' 'kdm5a' 'kdm5c' 'kdm6a' 'kdr' 'keap
1' 'kit'
 'klf4' 'kmt2a' 'kmt2b' 'kmt2c' 'kmt2d' 'knstrn' 'kras' 'lats1' 'l
ats2'
 'map2k1' 'map2k2' 'map2k4' 'map3k1' 'mapk1' 'mdm2' 'mdm4' 'med12'
'mef2b'
 'met' 'mga' 'mlh1' 'mpl' 'msh2' 'msh6' 'mtor' 'myc' 'mycn' 'myd8
8'
 'myod1' 'ncor1' 'nf1' 'nf2' 'nfe2l2' 'nfkbia' 'nkx2' 'notch1' 'no
tch2'
 'npm1' 'nras' 'ntrk1' 'ntrk2' 'ntrk3' 'nup93' 'pak1' 'pax8' 'pbrm
1'
 'pdgfra' 'pdgfrb' 'pik3ca' 'pik3cb' 'pik3cd' 'pik3r1' 'pik3r2' 'p
ik3r3'
 'pim1' 'pms2' 'pole' 'ppp2r1a' 'ppp6c' 'prdm1' 'ptch1' 'pten' 'pt
pn11'
 'ptprd' 'ptprt' 'rab35' 'rac1' 'rad50' 'rad51c' 'rad51d' 'rad54l'
'raf1'
```

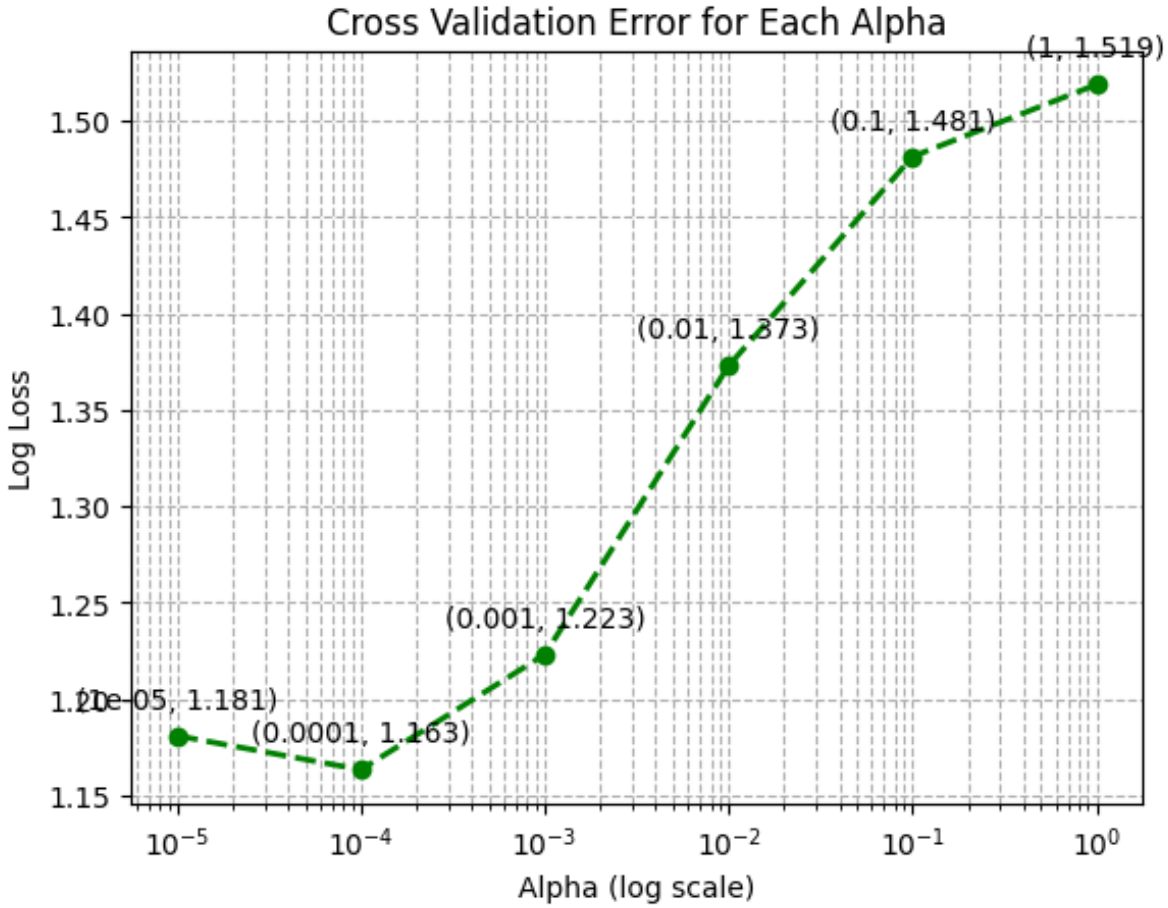
```
 'rasa1' 'rb1' 'rbm10' 'ret' 'rheb' 'rhoa' 'rit1' 'ros1' 'runx1' '
rxra'
 'rybp' 'sdhc' 'setd2' 'sf3b1' 'shoc2' 'smad2' 'smad3' 'smad4' 'sm
arca4'
 'smarcb1' 'smo' 'sos1' 'sox9' 'spop' 'src' 'stat3' 'stk11' 'tcf3'
 'tcf7l2' 'tert' 'tet1' 'tet2' 'tgfbr1' 'tgfbr2' 'tmprss2' 'tp53'
 'tp53bp1' 'tsc1' 'tsc2' 'u2af1' 'vegfa' 'vhl' 'whsc1l1' 'xpo1' 'x
rcc2'
 'yap1']
```

In [25]:

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.linear_model import SGDClassifier
from sklearn.calibration import CalibratedClassifierCV
from sklearn.metrics import log_loss

# Sample data: replace with your actual data
# train_gene_feature_onehotCoding, y_train, cv_gene_feature_onehotC

# Define alpha values to test
alpha = [10 ** x for x in range(-5, 1)]

cv_log_error_array = []
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log_loss', ran
    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.
    print('For alpha = ', i, "Log loss:", log_loss(y_cv, predict_y,

# Plotting the cross-validation log loss for each alpha
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array, color='green', marker='o', lines
for i, txt in enumerate(np.round(cv_log_error_array, 3)):
    ax.annotate((alpha[i], txt), (alpha[i], cv_log_error_array[i]),
ax.set_xscale('log')
ax.grid(True, which="both", ls="--")
plt.title("Cross Validation Error for Each Alpha")
plt.xlabel("Alpha (log scale)")
plt.ylabel("Log Loss")
plt.show()

# Finding the best alpha with the minimum log loss
best_alpha_index = np.argmin(cv_log_error_array)
best_alpha = alpha[best_alpha_index]

# Train the model with the best alpha
clf = SGDClassifier(alpha=best_alpha, penalty='l2', loss='log_loss'
clf.fit(train_gene_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_gene_feature_onehotCoding, y_train)
```

```
# Calculating and printing log loss for train, cross-validation, an
train_predict_y = sig_clf.predict_proba(train_gene_feature_onehotCo
print('Train Log Loss with best alpha =', best_alpha, ":", log_loss
cv_predict_y = sig_clf.predict_proba(cv_gene_feature_onehotCoding)
print('CV Log Loss with best alpha =', best_alpha, ":", log_loss(y_
test_predict_y = sig_clf.predict_proba(test_gene_feature_onehotCodi
print('Test Log Loss with best alpha =', best_alpha, ":", log_loss(
```

```
For alpha =  1e-05 Log loss: 1.1811096405085826
For alpha =  0.0001 Log loss: 1.1634949997146253
For alpha =  0.001 Log loss: 1.2232488719993015
For alpha =  0.01 Log loss: 1.3728589953944426
For alpha =  0.1 Log loss: 1.4812208267989928
For alpha =  1 Log loss: 1.518544938785446
```



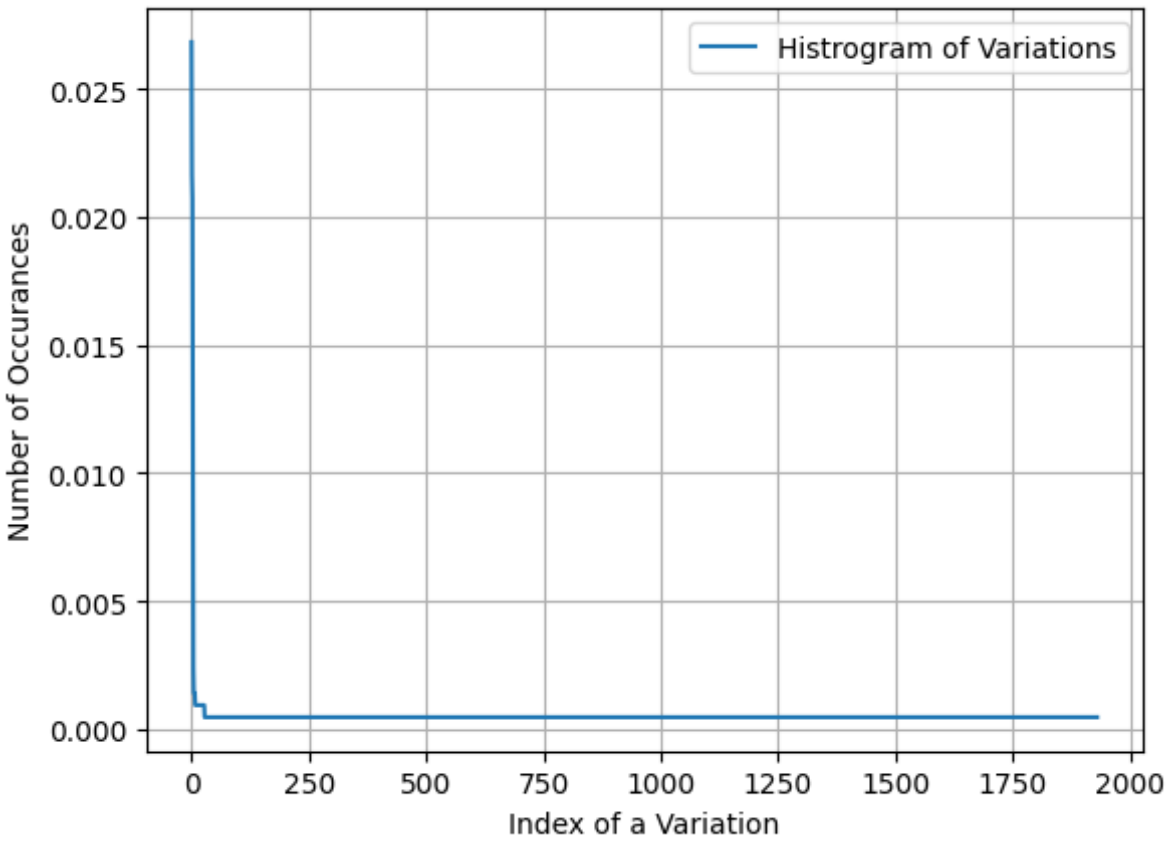

```
Train Log Loss with best alpha = 0.0001 : 0.9784652768675394
CV Log Loss with best alpha = 0.0001 : 1.1634949997146253
Test Log Loss with best alpha = 0.0001 : 1.249874682453196
```

Univariate Analysis on Variation Feature

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

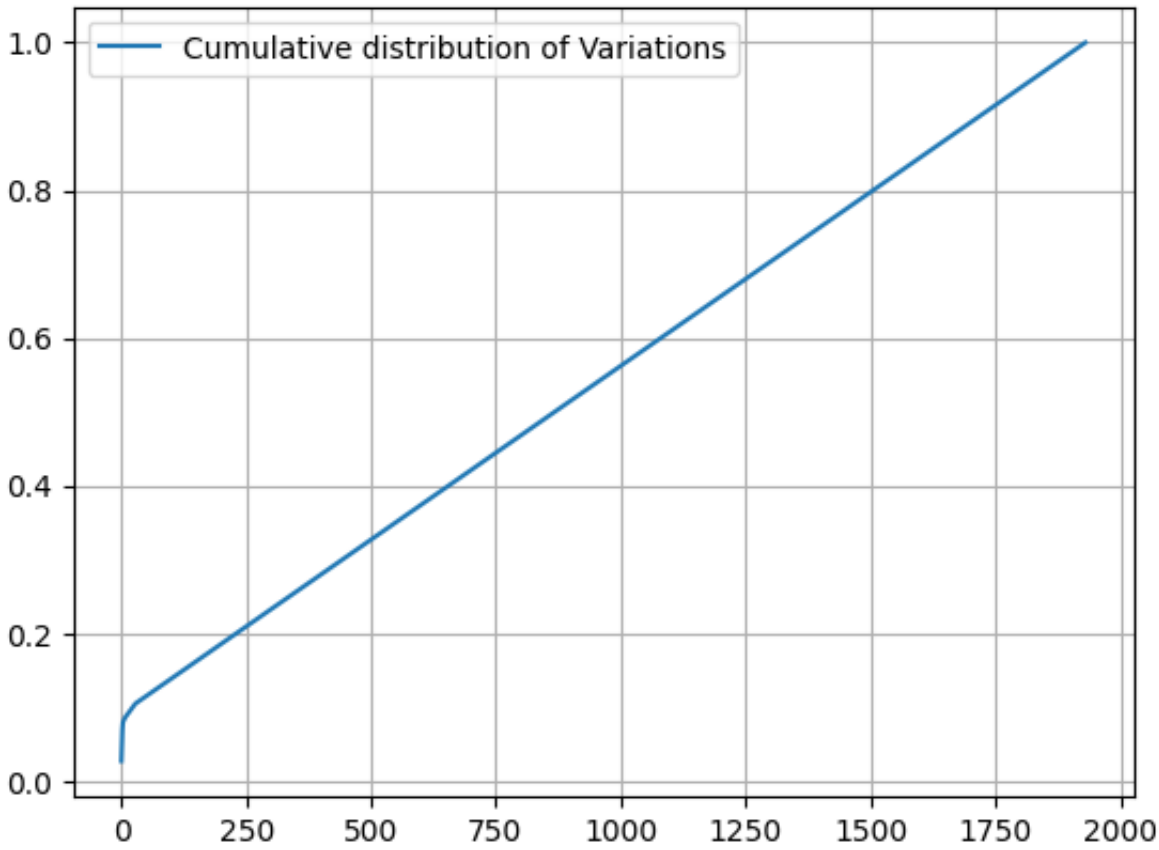
```
Number of Unique Variations : 1931
Variation
Truncating Mutations    57
Deletion                46
Amplification           44
Fusions                 20
Overexpression           5
Q61R                     3
T58I                     3
E17K                     3
Q22K                     2
I31M                     2
Name: count, dtype: int64
```

In [27]:
```
s = sum(unique_variations.values);
h = unique_variations.values/s;
plt.plot(h, label="Histrogram of Variations")
plt.xlabel('Index of a Variation')
plt.ylabel('Number of Occurances')
plt.legend()
plt.grid()
plt.show()
```



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

```
[0.02683616 0.04849341 0.06920904 ... 0.99905838 0.99952919 1.
]
```



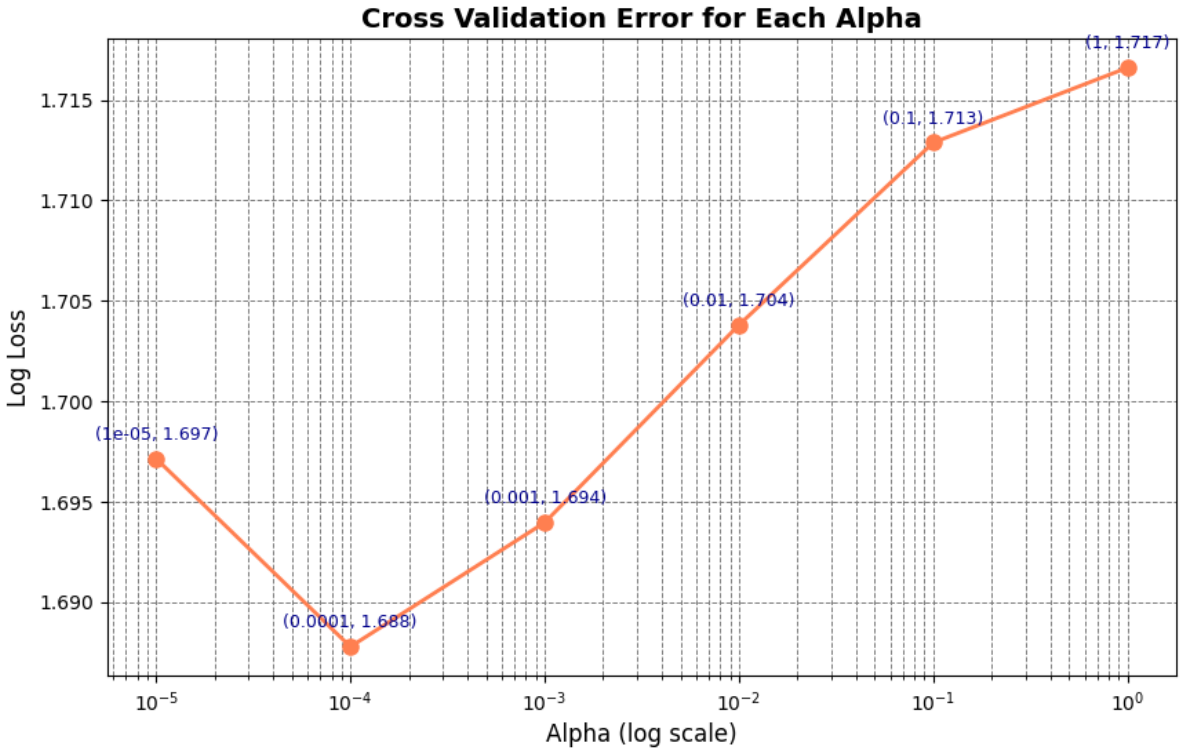
In [29]:
```
# alpha is used for laplace smoothing
alpha = 1
# train gene feature
train_variation_feature_responseCoding = np.array(get_gv_feature(al
# test gene feature
test_variation_feature_responseCoding = np.array(get_gv_feature(alp
# cross validation gene feature
cv_variation_feature_responseCoding = np.array(get_gv_feature(alpha
```

In [30]:
```
# one-hot encoding of variation feature.
variation_vectorizer = CountVectorizer()
train_variation_feature_onehotCoding = variation_vectorizer.fit_tra
test_variation_feature_onehotCoding = variation_vectorizer.transfor
cv_variation_feature_onehotCoding = variation_vectorizer.transform(
```

In [ ]:
```
```

In [31]:
```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.linear_model import SGDClassifier
from sklearn.calibration import CalibratedClassifierCV
from sklearn.metrics import log_loss

# Define alpha values to test
alpha = [10 ** x for x in range(-5, 1)]

cv_log_error_array = []
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log_loss', ran
    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_onehotCo

    cv_log_error_array.append(log_loss(y_cv, predict_y, labels=clf.
    print('For alpha =', i, "Log loss:", log_loss(y_cv, predict_y,

# Plotting the cross-validation log loss for each alpha
fig, ax = plt.subplots(figsize=(10, 6))
ax.plot(alpha, cv_log_error_array, color='coral', marker='o', lines
for i, txt in enumerate(np.round(cv_log_error_array, 3)):
    ax.annotate(f'({alpha[i]}, {txt:.3f})', (alpha[i], cv_log_error

ax.set_xscale('log')
ax.grid(True, which="both", linestyle='--', linewidth=0.7, color='g
plt.title("Cross Validation Error for Each Alpha", fontsize=14, fon
plt.xlabel("Alpha (log scale)", fontsize=12)
plt.ylabel("Log Loss", fontsize=12)
plt.xticks(fontsize=10)
plt.yticks(fontsize=10)
plt.show()

# Find the best alpha
best_alpha_index = np.argmin(cv_log_error_array)
best_alpha = alpha[best_alpha_index]

# Train the model with the best alpha
clf = SGDClassifier(alpha=best_alpha, penalty='l2', loss='log_loss'
clf.fit(train_variation_feature_onehotCoding, y_train)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_variation_feature_onehotCoding, y_train)

# Calculate and print log loss for train, cross-validation, and tes
train_predict_y = sig_clf.predict_proba(train_variation_feature_one
print('Train Log Loss with best alpha =', best_alpha, ":", log_loss
cv_predict_y = sig_clf.predict_proba(cv_variation_feature_onehotCod
print('CV Log Loss with best alpha =', best_alpha, ":", log_loss(y_
test_predict_y = sig_clf.predict_proba(test_variation_feature_oneho
print('Test Log Loss with best alpha =', best_alpha, ":", log_loss(
```

```
For alpha = 1e-05 Log loss: 1.6971429487691596
For alpha = 0.0001 Log loss: 1.6877686417744924
For alpha = 0.001 Log loss: 1.6939576229795312
For alpha = 0.01 Log loss: 1.7038010749066912
For alpha = 0.1 Log loss: 1.7128818951442064
For alpha = 1 Log loss: 1.7166158914062493
```




```
Train Log Loss with best alpha = 0.0001 : 0.7462077295180893
CV Log Loss with best alpha = 0.0001 : 1.6877686417744924
Test Log Loss with best alpha = 0.0001 : 1.6813151789885856
```

Univariate Analysis on Text Feature

In [32]:
```
# 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 [33]:
```
import math
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
            text_feature_responseCoding[row_index][i] = math.exp(su
            row_index += 1
    return text_feature_responseCoding
```

In [34]:
```
from sklearn.feature_extraction.text import CountVectorizer

# Building a CountVectorizer with all the words that occurred a min
text_vectorizer = CountVectorizer(min_df=3)
train_text_feature_onehotCoding = text_vectorizer.fit_transform(tra

# Getting all the feature names (words)
train_text_features = text_vectorizer.get_feature_names_out()

# Summing up occurrences of each word
train_text_fea_counts = train_text_feature_onehotCoding.sum(axis=0)

# Creating a dictionary with words and their counts
text_fea_dict = dict(zip(train_text_features, train_text_fea_counts

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

```
Total number of unique words in train data: 52322
```

In [35]:
```
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 [36]:
```
#response coding of text features
train_text_feature_responseCoding  = get_text_responsecoding(train_
test_text_feature_responseCoding  = get_text_responsecoding(test_df
cv_text_feature_responseCoding  = get_text_responsecoding(cv_df)
```

In [37]:
```
# we convert each row values such that they sum to 1
train_text_feature_responseCoding = (train_text_feature_responseCod
test_text_feature_responseCoding = (test_text_feature_responseCodin
cv_text_feature_responseCoding = (cv_text_feature_responseCoding.T/
```

In [38]:
```
# don't forget to normalize every feature
train_text_feature_onehotCoding = normalize(train_text_feature_oneh

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

# we use the same vectorizer that was trained on train data
cv_text_feature_onehotCoding = text_vectorizer.transform(cv_df['TEX
# don't forget to normalize every feature
cv_text_feature_onehotCoding = normalize(cv_text_feature_onehotCodi
```

In [39]:
```
sorted_text_fea_dict = dict(sorted(text_fea_dict.items(), key=lambd
sorted_text_occur = np.array(list(sorted_text_fea_dict.values()))
```

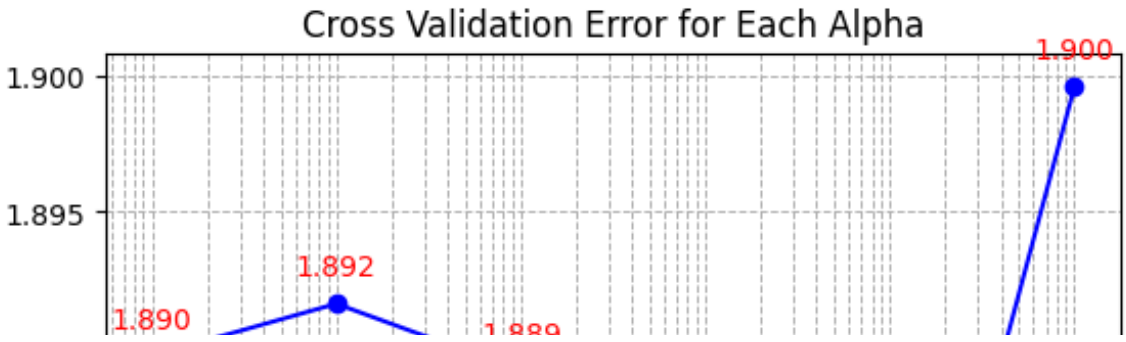
In [40]:
```
# Number of words for a given frequency.
print(Counter(sorted_text_occur))
```

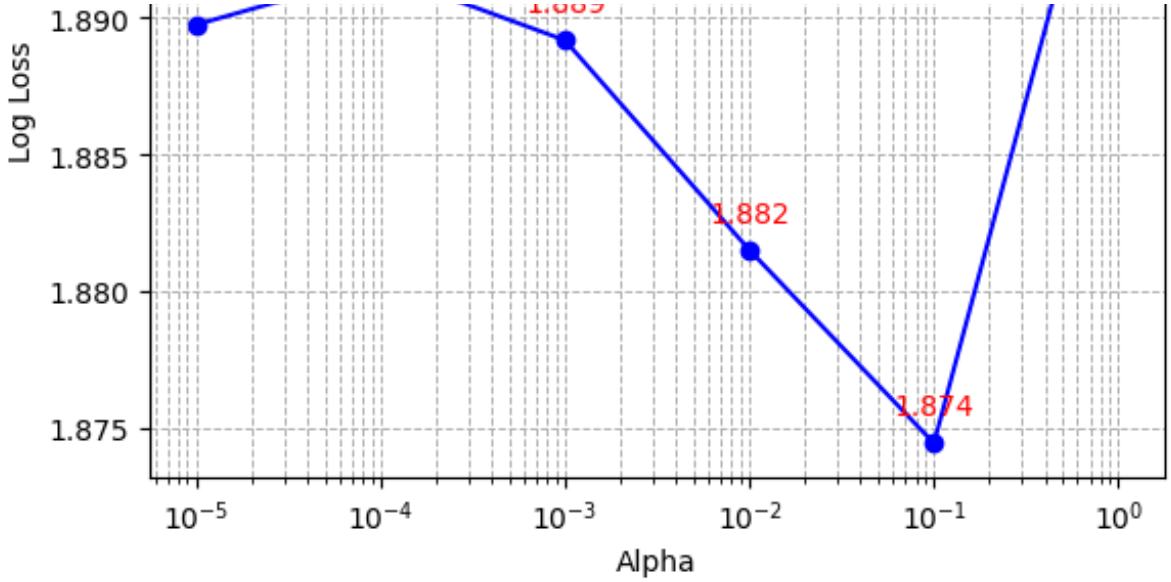
```
Counter({3: 4466, 4: 3929, 5: 3105, 6: 2835, 9: 1798, 8: 1686,
7: 1594, 12: 1563, 11: 1346, 10: 1330, 13: 1125, 14: 942, 16: 77
1, 18: 753, 15: 706, 20: 615, 21: 595, 17: 560, 24: 494, 22: 46
6, 28: 455, 19: 449, 27: 403, 26: 401, 32: 351, 23: 346, 30: 33
5, 48: 320, 45: 320, 25: 316, 33: 304, 36: 286, 29: 279, 31: 26
1, 40: 237, 41: 226, 39: 220, 42: 217, 34: 210, 35: 193, 44: 18
7, 51: 185, 52: 181, 37: 176, 38: 167, 46: 166, 50: 164, 54: 15
6, 55: 146, 56: 145, 43: 143, 49: 141, 53: 138, 60: 127, 47: 12
6, 57: 123, 66: 121, 72: 117, 67: 115, 59: 114, 70: 112, 64: 10
8, 63: 106, 61: 105, 65: 103, 62: 103, 58: 103, 82: 96, 96: 93,
69: 92, 81: 90, 73: 85, 68: 83, 100: 82, 71: 81, 83: 79, 80: 77,
74: 77, 90: 76, 84: 76, 87: 74, 75: 72, 91: 68, 77: 68, 85: 67,
92: 66, 88: 66, 86: 64, 78: 64, 76: 64, 95: 63, 79: 62, 104: 60,
89: 60, 108: 59, 97: 58, 93: 58, 110: 54, 101: 54, 126: 52, 105:
52, 109: 51, 94: 51, 144: 50, 107: 49, 119: 48, 118: 48, 114: 4
8, 129: 47, 98: 47, 132: 46, 106: 46, 102: 46, 128: 45, 120: 45,
123: 44, 99: 44, 115: 43, 117: 42, 146: 41, 141: 40, 139: 40, 13
6: 40, 113: 40, 111: 40, 116: 38, 103: 38, 137: 37, 125: 37, 12
1: 37, 168: 36, 140: 36, 134: 36, 130: 36, 142: 35, 124: 35, 15
```

In [41]:
```
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.linear_model import SGDClassifier
from sklearn.calibration import CalibratedClassifierCV
from sklearn.metrics import log_loss
import matplotlib.pyplot as plt
import numpy as np

# Building a CountVectorizer with all the words that occurred a min
text_vectorizer = CountVectorizer(min_df=3)
train_text_feature_onehotCoding = text_vectorizer.fit_transform(tra

# Getting all the feature names (words)
train_text_features = text_vectorizer.get_feature_names_out()

# Summing up occurrences of each word
train_text_fea_counts = train_text_feature_onehotCoding.sum(axis=0)

# Creating a dictionary with words and their counts
text_fea_dict = dict(zip(train_text_features, train_text_fea_counts

print("Total number of unique words in train data:", len(train_text

# Hyperparameter tuning for SGDClassifier
alpha = [10 ** x for x in range(-5, 1)]

cv_log_error_array = []
for i in alpha:
    clf = SGDClassifier(alpha=i, penalty='l2', loss='log_loss', ran
    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.
    print('For values of alpha =', i, "The log loss is:", log_loss(

# Plotting the results
fig, ax = plt.subplots()
ax.plot(alpha, cv_log_error_array, marker='o', linestyle='-', color
for i, txt in enumerate(np.round(cv_log_error_array, 3)):
    ax.annotate(f'{txt:.3f}', (alpha[i], cv_log_error_array[i]), te
plt.xscale('log')
plt.grid(True, which='both', linestyle='--', linewidth=0.7)
plt.title("Cross Validation Error for Each Alpha")
plt.xlabel("Alpha")
plt.ylabel("Log Loss")
plt.show()

# Fit the best model
best_alpha = alpha[np.argmin(cv_log_error_array)]
clf = SGDClassifier(alpha=best_alpha, penalty='l2', loss='log_loss'
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_train = sig_clf.predict_proba(train_text_feature_onehotCo
predict_y_cv = sig_clf.predict_proba(cv_text_feature_onehotCoding)
predict_y_test = sig_clf.predict_proba(test_text_feature_onehotCodi

print('For values of best alpha =', best_alpha, "The train log loss
print('For values of best alpha =', best_alpha, "The cross validati
print('For values of best alpha =', best_alpha, "The test log loss
```

```
Total number of unique words in train data: 52322
For values of alpha = 1e-05 The log loss is: 1.889744416152233
For values of alpha = 0.0001 The log loss is: 1.891646338956518
For values of alpha = 0.001 The log loss is: 1.8891800402874848
For values of alpha = 0.01 The log loss is: 1.881517872471457
For values of alpha = 0.1 The log loss is: 1.8744585145396429
For values of alpha = 1 The log loss is: 1.8995687103052101
```






```
For values of best alpha = 0.1 The train log loss is: 0.8820627828
6325
For values of best alpha = 0.1 The cross validation log loss is:
1.8744585145396429
For values of best alpha = 0.1 The test log loss is: 1.87723491069
13782
```

In [42]:
```
def get_intersec_text(df):
    df_text_vec = CountVectorizer(min_df=3)
    df_text_fea = df_text_vec.fit_transform(df['TEXT'])
    df_text_features = df_text_vec.get_feature_names()

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

In [43]:
```
from sklearn.feature_extraction.text import CountVectorizer

def get_intersec_text(df):
    # Vectorize text data with minimum document frequency of 3
    text_vectorizer = CountVectorizer(min_df=3)
    df_text_fea = text_vectorizer.fit_transform(df['TEXT'])

    # Getting all the feature names (words)
    df_text_features = text_vectorizer.get_feature_names_out()

    # Summing up occurrences of each word
    df_text_fea_counts = df_text_fea.sum(axis=0).A1

    # Creating a dictionary with words and their counts
    df_text_fea_dict = dict(zip(df_text_features, df_text_fea_count

    # Find intersection with train text features
    train_text_features = text_vectorizer.get_feature_names_out()

    # Calculate intersection
    intersect_words = set(df_text_features).intersection(set(train_

    len1 = len(df_text_features)
    len2 = len(intersect_words)

    return len1, len2

# Apply function and print results
len1, len2 = get_intersec_text(test_df)
print(np.round((len2 / len1) * 100, 3), "% of words in test data ap

len1, len2 = get_intersec_text(cv_df)
print(np.round((len2 / len1) * 100, 3), "% of words in cross-valida
```

```
100.0 % of words in test data appeared in train data
100.0 % of words in cross-validation data appeared in train data
```

Ensemble Models

In [44]:
```
#Data preparation for ML models.

#Misc. functionns for ML models


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

    # for calculating log_loss we willl provide the array of probab
    print("Log loss :",log_loss(test_y, sig_clf.predict_proba(test_
    # calculating the number of data points that are misclassified
    print("Number of mis-classified points :", np.count_nonzero((pr
    plot_confusion_matrix(test_y, pred_y)
```

In [45]:
```
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 [46]:
```
# 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 t
def get_impfeature_names(indices, text, gene, var, no_features):
    gene_count_vec = CountVectorizer()
    var_count_vec = CountVectorizer()
    text_count_vec = CountVectorizer(min_df=3)

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

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

    word_present = 0
    for i,v in enumerate(indices):
        if (v < fea1_len):
            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 po
        elif (v < fea1_len+fea2_len):
            word = var_vec.get_feature_names()[v-(fea1_len)]
            yes_no = True if word == var else False
            if yes_no:
                word_present += 1
                print(i, "variation feature [{}] present in test da
        else:
            word = text_vec.get_feature_names()[v-(fea1_len+fea2_le
            yes_no = True if word in text.split() else False
            if yes_no:
                word_present += 1
                print(i, "Text feature [{}] present in test data po

    print("Out of the top ",no_features," features ", word_present,
```

In [47]:
```
train_gene_var_onehotCoding = hstack((train_gene_feature_onehotCodi
test_gene_var_onehotCoding = hstack((test_gene_feature_onehotCoding
cv_gene_var_onehotCoding = hstack((cv_gene_feature_onehotCoding,cv_

train_x_onehotCoding = hstack((train_gene_var_onehotCoding, train_t
train_y = np.array(list(train_df['Class']))

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

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


train_gene_var_responseCoding = np.hstack((train_gene_feature_respo
test_gene_var_responseCoding = np.hstack((test_gene_feature_respons
cv_gene_var_responseCoding = np.hstack((cv_gene_feature_responseCod

train_x_responseCoding = np.hstack((train_gene_var_responseCoding,
test_x_responseCoding = np.hstack((test_gene_var_responseCoding, te
cv_x_responseCoding = np.hstack((cv_gene_var_responseCoding, cv_tex
```

In [48]:
```
print("One hot encoding features :")
print("(number of data points * number of features) in train data =
print("(number of data points * number of features) in test data =
print("(number of data points * number of features) in cross valida
```

```
One hot encoding features :
(number of data points * number of features) in train data =  (212
4, 54516)
(number of data points * number of features) in test data =  (665,
54516)
(number of data points * number of features) in cross validation d
ata = (532, 54516)
```

In [49]:
```
print(" Response encoding features :")
print("(number of data points * number of features) in train data =
print("(number of data points * number of features) in test data =
print("(number of data points * number of features) in cross valida
```

```
 Response encoding features :
(number of data points * number of features) in train data =  (212
4, 27)
(number of data points * number of features) in test data =  (665,
27)
(number of data points * number of features) in cross validation d
ata = (532, 27)
```

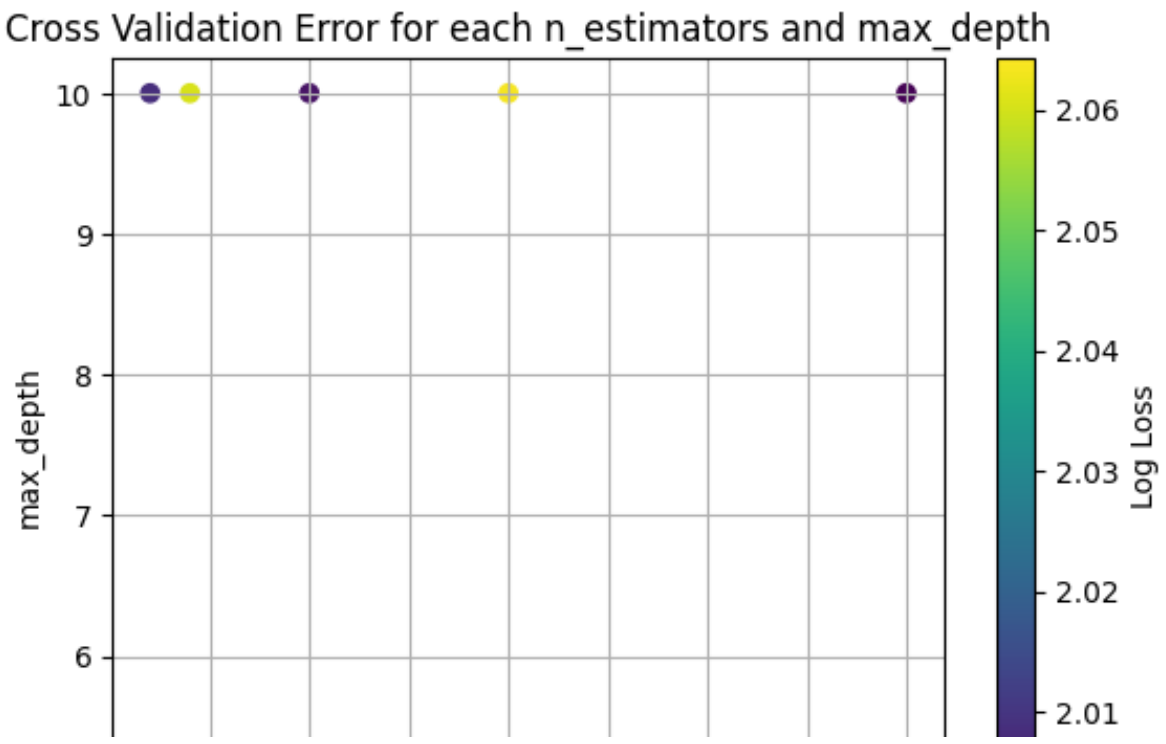
Random Forest Classifier

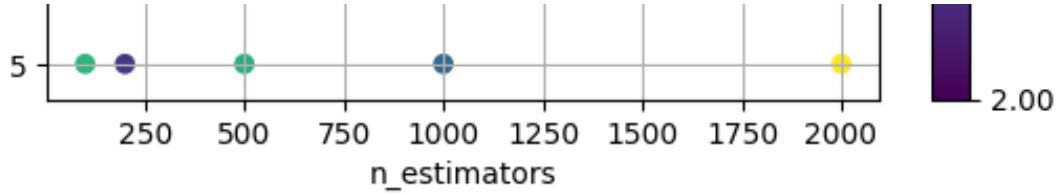
Hyper paramter tuning (With One hot Encoding)

In [50]:
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.calibration import CalibratedClassifierCV
from sklearn.metrics import log_loss
import matplotlib.pyplot as plt
import numpy as np

alpha = [100, 200, 500, 1000, 2000]
max_depth = [5, 10]
cv_log_error_array = []

# Iterate over hyperparameters
for i in alpha:
    for j in max_depth:
        print("For n_estimators =", i, "and max_depth =", j)
        clf = RandomForestClassifier(n_estimators=i, criterion='gin
        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))
        print("Log Loss:", log_loss(cv_y, sig_clf_probs))

# Plotting
fig, ax = plt.subplots()
# Create a grid for plotting
alpha_grid, max_depth_grid = np.meshgrid(alpha, max_depth)
alpha_flat = alpha_grid.ravel()
max_depth_flat = max_depth_grid.ravel()
cv_log_error_array = np.array(cv_log_error_array)

# Scatter plot of log loss with hyperparameters
sc = ax.scatter(alpha_flat, max_depth_flat, c=cv_log_error_array, c
plt.colorbar(sc, ax=ax, label='Log Loss')
plt.grid()
plt.title("Cross Validation Error for each n_estimators and max_dep
plt.xlabel("n_estimators")
plt.ylabel("max_depth")
plt.show()

# Finding the best parameters
best_index = np.argmin(cv_log_error_array)
best_n_estimators = alpha_flat[best_index]
best_max_depth = max_depth_flat[best_index]

# Train and evaluate with best parameters
clf = RandomForestClassifier(n_estimators=best_n_estimators, criter
```

```
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 n_estimators =', best_n_estimators, "The
predict_y = sig_clf.predict_proba(cv_x_onehotCoding)
print('For values of best n_estimators =', best_n_estimators, "The
predict_y = sig_clf.predict_proba(test_x_onehotCoding)
print('For values of best n_estimators =', best_n_estimators, "The
```

```
For n_estimators = 100 and max_depth = 5
Log Loss: 2.042136334013561
For n_estimators = 100 and max_depth = 10
Log Loss: 2.010300030629125
For n_estimators = 200 and max_depth = 5
Log Loss: 2.0402525846953927
For n_estimators = 200 and max_depth = 10
Log Loss: 2.0215751100607307
For n_estimators = 500 and max_depth = 5
Log Loss: 2.0642905061644985
For n_estimators = 500 and max_depth = 10
Log Loss: 2.008527366117461
For n_estimators = 1000 and max_depth = 5
Log Loss: 2.0604096745159985
For n_estimators = 1000 and max_depth = 10
Log Loss: 2.003132704952187
For n_estimators = 2000 and max_depth = 5
Log Loss: 2.063386046704813
For n_estimators = 2000 and max_depth = 10
Log Loss: 1.9999875830233729
```

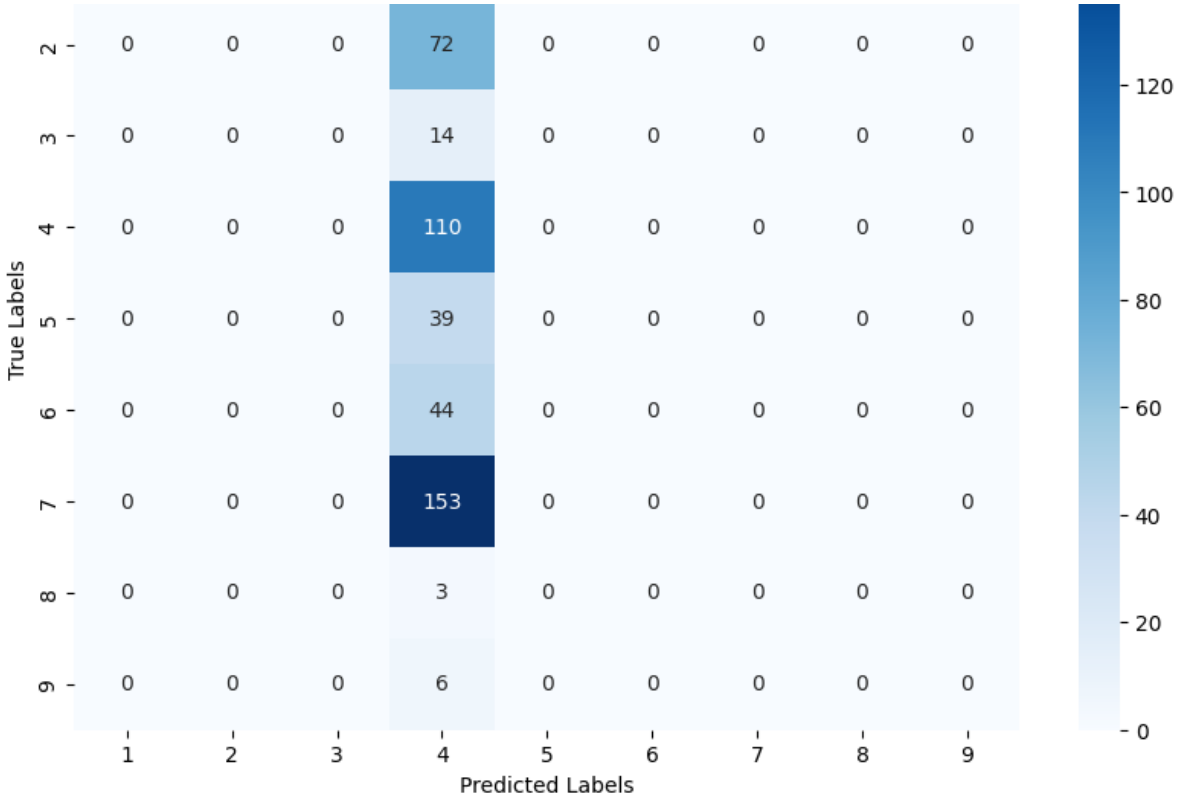





```
For values of best n_estimators = 2000 The train log loss is: 0.67
92338171533059
For values of best n_estimators = 2000 The cross validation log lo
ss is: 1.9999875830233729
For values of best n_estimators = 2000 The test log loss is: 2.003
9483873293813
```

Testing model with best hyper parameters (One Hot Encoding)

In [51]:
```
from sklearn.metrics import confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt

def plot_confusion_matrix(cm, labels):
    plt.figure(figsize=(10, 7))
    sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=
    plt.xlabel('Predicted Labels')
    plt.ylabel('True Labels')
    plt.title('Confusion Matrix')
    plt.show()

def predict_and_plot_confusion_matrix(train_x, train_y, test_x, tes
    clf.fit(train_x, train_y)
    pred_y = clf.predict(test_x)

    # Compute confusion matrix
    cm = confusion_matrix(test_y, pred_y, labels=clf.classes_)

    # Plot confusion matrix
    plot_confusion_matrix(cm, labels=clf.classes_)

    # Calculate the number of misclassified points
    misclassified_count = np.count_nonzero(pred_y != test_y) / test
    print("Number of misclassified points:", misclassified_count)

# Usage
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/2)],
predict_and_plot_confusion_matrix(train_x_onehotCoding, train_y, cv
```




```
Number of misclassified points: 0.7612781954887218
```

Feature Importance

Correctly Classified point

In [52]:
```python
from sklearn.feature_extraction.text import CountVectorizer

def get_impfeature_names(indices, text, gene, var, no_features):
    # Vectorize features
    text_count_vec = CountVectorizer(min_df=3)
    text_vec = text_count_vec.fit_transform(train_df['TEXT'])

    gene_vec = CountVectorizer(min_df=3)
    gene_vec.fit(train_df['Gene'])

    var_count_vec = CountVectorizer(min_df=3)
    var_vec = var_count_vec.fit(train_df['Variation'])

    # Get feature names
    text_features = text_count_vec.get_feature_names_out()
    gene_features = gene_vec.get_feature_names_out()
    var_features = var_count_vec.get_feature_names_out()

    print(f"Text Features Length: {len(text_features)}")
    print(f"Gene Features Length: {len(gene_features)}")
    print(f"Variation Features Length: {len(var_features)}")
```

```
    # Display important features
    print("Top Features:")
    for i in indices:
        if i < len(text_features):
            print(f"Text Feature: {text_features[i]}")
        elif i < len(text_features) + len(gene_features):
            print(f"Gene Feature: {gene_features[i - len(text_featu
        elif i < len(text_features) + len(gene_features) + len(var_
            print(f"Variation Feature: {var_features[i - len(text_f

# Example Usage
test_point_index = 1
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_inde
print("Predicted Class:", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_pr
print("Actual Class:", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-" * 50)
get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[tes
```

```
Predicted Class: 4
Predicted Class Probabilities: [[0.2785 0.1313 0.0276 0.3341 0.073
6 0.0522 0.0881 0.007  0.0076]]
Actual Class: 7
--------------------------------------------------
Text Features Length: 52322
Gene Features Length: 134
Variation Features Length: 26
Top Features:
Text Feature: m135t
Text Feature: phenylmethylsulphonylfluoride
Text Feature: synthetase
Text Feature: functioning
Text Feature: e7x
Text Feature: noncanccrous
Text Feature: mg132
Text Feature: h3k36me3
Text Feature: l118
Text Feature: thymocytes21
Text Feature: snapfrozen
Text Feature: hypotension
Text Feature: k23
Text Feature: deregulation
Text Feature: cysteinyl
Text Feature: therapy3
Text Feature: vivo44
Text Feature: gau
Text Feature: gfpt2
Text Feature: upgrading
Text Feature: 1n8z
```

```
Text Feature: cova
Text Feature: ser98
Text Feature: transported
Text Feature: preliminary
Text Feature: m1411t
Text Feature: ibaraki
Text Feature: gelatin
Text Feature: y780
Text Feature: ssgsea
Text Feature: bellomo
Text Feature: pbmcs
Text Feature: ei
Text Feature: asp450glu
Text Feature: prep4
Text Feature: e79q
Text Feature: tyr67
Text Feature: l110f
Text Feature: treats
Text Feature: l112p
Text Feature: endoplasmatic
Text Feature: deletions34
Text Feature: functioned
Text Feature: d297
Text Feature: preleukemic
Text Feature: exclusion
Text Feature: v730d
Text Feature: m2m3
Text Feature: korinek
Text Feature: dysplasia
Text Feature: coupling
Text Feature: vice
Text Feature: r420l
Text Feature: setup
Text Feature: recruits
Text Feature: bai3
Text Feature: reasoning
Text Feature: leucocyte
Text Feature: asp450glu12
Text Feature: purities
Text Feature: w80a
Text Feature: identity
Text Feature: novelties
Text Feature: ming
Text Feature: iodoacetamide
Text Feature: l1854
Text Feature: korn
Text Feature: rsbweb
Text Feature: c3h
Text Feature: detections
Text Feature: asp537
Text Feature: chiron
Text Feature: understand
Text Feature: fibrodysplasia
```

```
Text Feature: v599e
Text Feature: chitin
Text Feature: explanation
Text Feature: v714m
Text Feature: interactions43
Text Feature: subfamilies
Text Feature: radisky
Text Feature: fibroxanthoma
Text Feature: lmnb2
Text Feature: palb2
Text Feature: pierre
Text Feature: pupupuc
Text Feature: segregate
Text Feature: mimicry
Text Feature: immunochemical
Text Feature: 455
Text Feature: vi
Text Feature: 753
Text Feature: peptidylprolyl
Text Feature: deregulation191
```

Inorrectly Classified point

In [53]:
```
test_point_index = 100
no_feature = 100
predicted_cls = sig_clf.predict(test_x_onehotCoding[test_point_inde
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_pr
print("Actuall Class :", test_y[test_point_index])
indices = np.argsort(-clf.feature_importances_)
print("-"*50)
get_impfeature_names(indices[:no_feature], test_df['TEXT'].iloc[tes
```

```
Predicted Class : 4
Predicted Class Probabilities: [[0.2785 0.1313 0.0275 0.3342 0.073
6 0.0522 0.0881 0.007  0.0076]]
Actuall Class : 1
--------------------------------------------------
Text Features Length: 52322
Gene Features Length: 134
Variation Features Length: 26
Top Features:
Text Feature: m135t
Text Feature: phenylmethylsulphonylfluoride
Text Feature: synthetase
Text Feature: functioning
Text Feature: e7x
Text Feature: noncanccrous
Text Feature: mg132
Text Feature: h3k36me3
Text Feature: l118
```

```
Text Feature: thymocytes21
Text Feature: snapfrozen
Text Feature: hypotension
Text Feature: k23
Text Feature: deregulation
Text Feature: cysteinyl
Text Feature: therapy3
Text Feature: vivo44
Text Feature: gau
Text Feature: gfpt2
Text Feature: upgrading
Text Feature: 1n8z
Text Feature: cova
Text Feature: ser98
Text Feature: transported
Text Feature: preliminary
Text Feature: m1411t
Text Feature: ibaraki
Text Feature: gelatin
Text Feature: y780
Text Feature: ssgsea
Text Feature: bellomo
Text Feature: pbmcs
Text Feature: ei
Text Feature: asp450glu
Text Feature: prep4
Text Feature: e79q
Text Feature: tyr67
Text Feature: l110f
Text Feature: treats
Text Feature: l112p
Text Feature: endoplasmatic
Text Feature: deletions34
Text Feature: functioned
Text Feature: d297
Text Feature: preleukemic
Text Feature: exclusion
Text Feature: v730d
Text Feature: m2m3
Text Feature: korinek
Text Feature: dysplasia
Text Feature: coupling
Text Feature: vice
Text Feature: r420l
Text Feature: setup
Text Feature: recruits
Text Feature: bai3
Text Feature: reasoning
Text Feature: leucocyte
Text Feature: asp450glu12
Text Feature: purities
Text Feature: w80a
Text Feature: identity
```

```
Text Feature: novelties
Text Feature: ming
Text Feature: iodoacetamide
Text Feature: l1854
Text Feature: korn
Text Feature: rsbweb
Text Feature: c3h
Text Feature: detections
Text Feature: asp537
Text Feature: chiron
Text Feature: understand
Text Feature: fibrodysplasia
Text Feature: v599e
Text Feature: chitin
Text Feature: explanation
Text Feature: v714m
Text Feature: interactions43
Text Feature: subfamilies
Text Feature: radisky
Text Feature: fibroxanthoma
Text Feature: lmnb2
Text Feature: palb2
Text Feature: pierre
Text Feature: pupupuc
Text Feature: segregate
Text Feature: mimicry
Text Feature: immunochemical
Text Feature: 455
Text Feature: vi
Text Feature: 753
Text Feature: peptidylprolyl
Text Feature: deregulation191
```

Hyper paramter tuning (With Response Coding)

In [54]:

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.calibration import CalibratedClassifierCV
from sklearn.metrics import log_loss
import numpy as np

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='gin
        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, lab
        print("Log Loss:", log_loss(cv_y, sig_clf_probs))

# Identify the best parameters
best_alpha = np.argmin(cv_log_error_array)
best_n_estimators = alpha[int(best_alpha / len(max_depth))]
best_max_depth = max_depth[int(best_alpha % len(max_depth))]

clf = RandomForestClassifier(n_estimators=best_n_estimators, criter
clf.fit(train_x_responseCoding, train_y)
sig_clf = CalibratedClassifierCV(clf, method="sigmoid")
sig_clf.fit(train_x_responseCoding, train_y)

# Evaluate performance
predict_y = sig_clf.predict_proba(train_x_responseCoding)
print('For values of best n_estimators =', best_n_estimators, "The

predict_y = sig_clf.predict_proba(cv_x_responseCoding)
print('For values of best n_estimators =', best_n_estimators, "The

predict_y = sig_clf.predict_proba(test_x_responseCoding)
print('For values of best n_estimators =', best_n_estimators, "The
```

```
for n_estimators = 10 and max depth = 2
Log Loss: 2.1344425557831674
for n_estimators = 10 and max depth = 3
Log Loss: 1.7025021817189092
for n_estimators = 10 and max depth = 5
Log Loss: 1.4443603666260367
for n_estimators = 10 and max depth = 10
Log Loss: 1.8228558274065016
for n_estimators = 50 and max depth = 2
Log Loss: 1.6582066412353447
for n_estimators = 50 and max depth = 3
Log Loss: 1.4229400272223622
for n_estimators = 50 and max depth = 5
Log Loss: 1.3712900648288773
for n_estimators = 50 and max depth = 10
Log Loss: 1.6482932192704394
for n_estimators = 100 and max depth = 2
Log Loss: 1.5292782295858809
for n_estimators = 100 and max depth = 3
Log Loss: 1.4350748296215818
for n_estimators = 100 and max depth = 5
Log Loss: 1.3277646617357146
for n_estimators = 100 and max depth = 10
Log Loss: 1.637376198684531
for n_estimators = 200 and max depth = 2
Log Loss: 1.5490830441375891
for n_estimators = 200 and max depth = 3
Log Loss: 1.4537690814348134
for n_estimators = 200 and max depth = 5
```

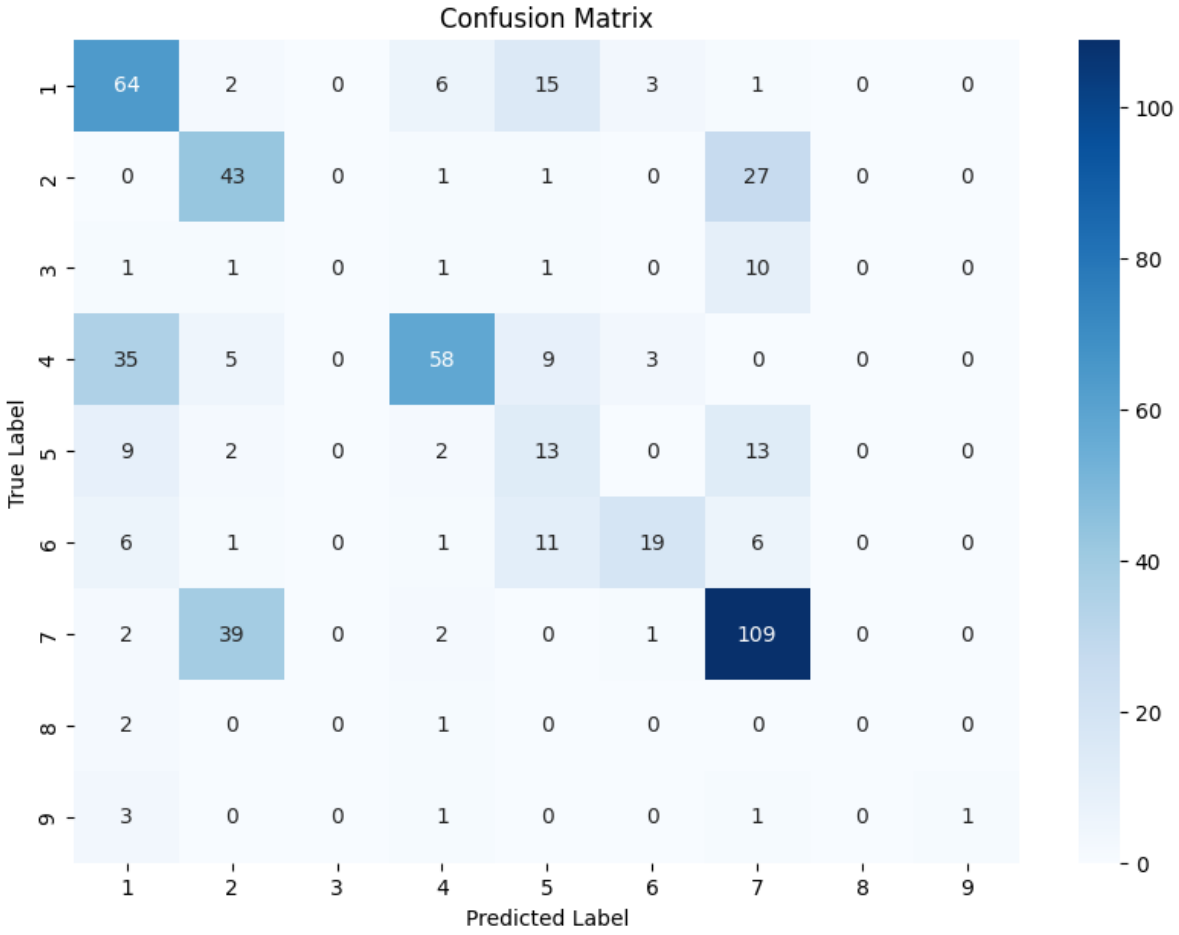
```
Log Loss: 1.3537040987115632
for n_estimators = 200 and max depth = 10
Log Loss: 1.6515700974437848
for n_estimators = 500 and max depth = 2
Log Loss: 1.5698558311721738
for n_estimators = 500 and max depth = 3
Log Loss: 1.457322269832948
for n_estimators = 500 and max depth = 5
Log Loss: 1.3500774399472621
for n_estimators = 500 and max depth = 10
Log Loss: 1.700940330599249
for n_estimators = 1000 and max depth = 2
Log Loss: 1.5685923540718476
for n_estimators = 1000 and max depth = 3
Log Loss: 1.4702092920085046
for n_estimators = 1000 and max depth = 5
Log Loss: 1.3427022066827794
for n_estimators = 1000 and max depth = 10
Log Loss: 1.692646077529831
For values of best n_estimators = 100 The train log loss is: 0.064
53714752762901
For values of best n_estimators = 100 The cross validation log los
s is: 1.3277646617357148
For values of best n_estimators = 100 The test log loss is: 1.3098
29648051413
```

Testing model with best hyper parameters (Response Coding)

In [55]:

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np

def predict_and_plot_confusion_matrix(train_x, train_y, test_x, tes
    clf.fit(train_x, train_y)
    pred_y = clf.predict(test_x)

    # Compute confusion matrix
    cm = confusion_matrix(test_y, pred_y)

    # Plot confusion matrix
    fig, ax = plt.subplots(figsize=(10, 7))
    sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=
    ax.set_xlabel('Predicted Label')
    ax.set_ylabel('True Label')
    ax.set_title('Confusion Matrix')
    plt.show()

# Use 'sqrt' for max_features
```

```
clf = RandomForestClassifier(max_depth=max_depth[int(best_alpha % l
                             n_estimators=alpha[int(best_alpha / le
                             criterion='gini',
                             max_features='sqrt',  # Updated parame
                             random_state=42)

predict_and_plot_confusion_matrix(train_x_responseCoding, train_y,
```



Feature Importance

Correctly Classified point

In [56]:
```
clf = RandomForestClassifier(n_estimators=alpha[int(best_alpha/4)],
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_in
print("Predicted Class :", predicted_cls[0])
```

```
print("Predicted Class Probabilities:", np.round(sig_clf.predict_pr
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 : 3
Predicted Class Probabilities: [[0.0398 0.1581 0.2636 0.0488 0.047
8 0.0622 0.1079 0.1535 0.1182]]
Actual Class : 7
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Text is important feature
Gene 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
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Text is important feature
Gene is important feature
```

4.5.5.2. Incorrectly Classified point

In [57]:
```
test_point_index = 100
predicted_cls = sig_clf.predict(test_x_responseCoding[test_point_in
print("Predicted Class :", predicted_cls[0])
print("Predicted Class Probabilities:", np.round(sig_clf.predict_pr
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 : 1
Predicted Class Probabilities: [[0.205  0.1234 0.1795 0.1916 0.034
9 0.0542 0.0172 0.1276 0.0667]]
Actual Class : 1
--------------------------------------------------
Variation is important feature
Variation is important feature
Variation is important feature
Variation is important feature
Gene is important feature
Variation is important feature
Variation is important feature
Text is important feature
Text is important feature
Text is important feature
Text is important feature
Gene 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
Variation is important feature
Text is important feature
Text is important feature
Gene is important feature
Gene is important feature
Text is important feature
Gene is important feature
```

Stack the models

testing with hyper parameter tuning

In [58]:
```
from sklearn.linear_model import SGDClassifier, LogisticRegression
from sklearn.naive_bayes import MultinomialNB
from sklearn.calibration import CalibratedClassifierCV
from sklearn.ensemble import StackingClassifier
from sklearn.metrics import log_loss

# Initialize classifiers with corrected parameters
clf1 = SGDClassifier(alpha=0.001, penalty='l2', loss='log_loss', cl
clf1.fit(train_x_onehotCoding, train_y)
sig_clf1 = CalibratedClassifierCV(clf1, method="sigmoid")

clf2 = SGDClassifier(alpha=1, penalty='l2', loss='hinge', class_wei
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")

# Print log loss for each classifier
sig_clf1.fit(train_x_onehotCoding, train_y)
print("Logistic Regression :  Log Loss: %0.2f" % (log_loss(cv_y, si
sig_clf2.fit(train_x_onehotCoding, train_y)
print("Support vector machines : Log Loss: %0.2f" % (log_loss(cv_y,
sig_clf3.fit(train_x_onehotCoding, train_y)
print("Naive Bayes : Log Loss: %0.2f" % (log_loss(cv_y, sig_clf3.pr
print("-"*50)

# Perform stacking with logistic regression as meta-classifier
alpha = [0.0001, 0.001, 0.01, 0.1, 1, 10]
best_alpha = 999
for i in alpha:
    lr = LogisticRegression(C=i)
    sclf = StackingClassifier(estimators=[('sgd_log', sig_clf1), ('
    sclf.fit(train_x_onehotCoding, train_y)
    log_error = log_loss(cv_y, sclf.predict_proba(cv_x_onehotCoding
    print("Stacking Classifier : for the value of alpha: %f Log Los
    if best_alpha > log_error:
        best_alpha = log_error
```

```
Logistic Regression :  Log Loss: 1.87
Support vector machines : Log Loss: 1.85
Naive Bayes : Log Loss: 1.32
--------------------------------------------------
Stacking Classifier : for the value of alpha: 0.000100 Log Loss:
2.174
Stacking Classifier : for the value of alpha: 0.001000 Log Loss:
2.155
```

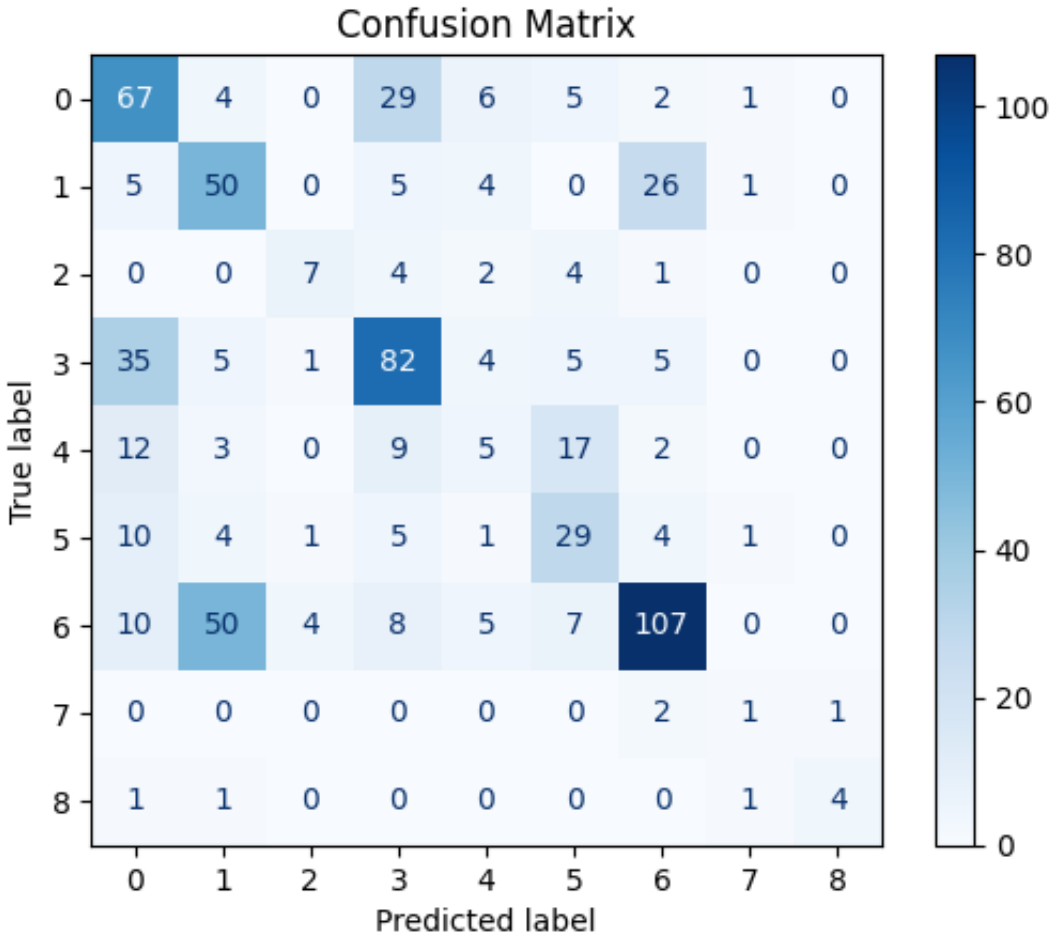
```
Stacking Classifier : for the value of alpha: 0.010000 Log Loss:
2.107
Stacking Classifier : for the value of alpha: 0.100000 Log Loss:
2.051
Stacking Classifier : for the value of alpha: 1.000000 Log Loss:
2.048
Stacking Classifier : for the value of alpha: 10.000000 Log Loss:
2.028
```

testing the model with the best hyper parameters

In [59]:

```
from sklearn.ensemble import StackingClassifier
from sklearn.metrics import log_loss, confusion_matrix, ConfusionMa
import matplotlib.pyplot as plt
import numpy as np

# Initialize the Logistic Regression for the meta-classifier
lr = LogisticRegression(C=0.1)

# Initialize the Stacking Classifier with the correct parameters
sclf = StackingClassifier(
    estimators=[('log_reg', sig_clf1), ('svm', sig_clf2), ('nb', si
    final_estimator=lr,
    passthrough=True
)
sclf.fit(train_x_onehotCoding, train_y)

# Evaluate the performance
log_error = log_loss(train_y, sclf.predict_proba(train_x_onehotCodi
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 the number of misclassified points
misclassified_points = np.count_nonzero(sclf.predict(test_x_onehotC
print("Number of misclassified points:", misclassified_points)

# Plot confusion matrix
def plot_confusion_matrix(y_true, y_pred):
    cm = confusion_matrix(y_true, y_pred)
    disp = ConfusionMatrixDisplay(confusion_matrix=cm)
    disp.plot(cmap=plt.cm.Blues)
    plt.title('Confusion Matrix')
    plt.show()

plot_confusion_matrix(test_y, sclf.predict(test_x_onehotCoding))
```

```
Log loss (train) on the stacking classifier : 0.24907505838543788
Log loss (CV) on the stacking classifier : 2.051036360121043
Log loss (test) on the stacking classifier : 2.0783792348534624
Number of misclassified points: 313
```



Maximum Voting classifier

In [67]:
```
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.metrics import confusion_matrix

def plot_confusion_matrix_static(y_true, y_pred, class_names):
    cm = confusion_matrix(y_true, y_pred, labels=class_names)
    plt.figure(figsize=(10, 7))
    sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
                xticklabels=class_names, yticklabels=class_names)
    plt.xlabel('Predicted label')
    plt.ylabel('True label')
    plt.title('Confusion Matrix')
    plt.show()

# Example usage
plot_confusion_matrix_static(test_y, y_pred, class_names)
```