#### Introduction:

We have been entrusted with data from the Memorial Sloan Kettering Cancer Center (MSKCC) that revolves around cancer tumors and the multitude of genetic mutations associated with them. The challenge lies in distinguishing the driver mutations that have the most significant impact on tumor growth. Currently, pathologists manually sift through vast amounts of data, relying on text-based clinical literature to categorize each genetic mutation. This process is not only time-consuming but also resource-intensive. Our objective is to develop a Machine Learning model that streamlines the classification of genetic mutations, expediting the identification of crucial mutations for more prompt and accurate patient treatment.

It is imperative that our model is interpretable, aiding pathologists in making informed decisions. Given the high stakes involved, with potential life-threatening consequences for patients, precision is paramount. Therefore, the model we construct must demonstrate exceptional accuracy to minimize the risk of misinterpretations that could have severe implications for patient outcomes.

## **Importing Libraries**

```
In [46]:
```

```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import string
# Text Processing libraries
import re
from wordcloud import WordCloud
import nltk
from nltk.tokenize import word tokenize
from nltk.corpus import stopwords
from nltk.stem import WordNetLemmatizer
from sklearn.feature extraction.text import TfidfVectorizer
from sklearn.preprocessing import normalize
from sklearn.preprocessing import LabelEncoder
from imblearn.over sampling import SMOTE
# Metrices
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
from sklearn.metrics import log_loss
# Visualizer
import plotly.express as px
# Models
from sklearn.naive bayes import MultinomialNB
from sklearn.naive bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear model import SGDClassifier
from sklearn.svm import SVC
from sklearn.model selection import train test split
import plotly.offline as py
py.init_notebook mode(connected=True)
import warnings
warnings.filterwarnings('ignore')
```

## **Data Study**

```
In [2]:
```

```
df_variants = pd.read_csv('training_variants.csv')
```

```
df_variants.head(10)
Out[2]:
   ID
                         Variation Class
         Gene
                        Truncating
    0 FAM58A
                                      1
                        Mutations
    1
          CBL
                           W802*
                                      2
    2
          CBL
                           Q249E
3
    3
          CBL
                           N454D
                                      3
          CBL
                            L399V
                                      4
                            V391I
    5
          CBL
    6
          CBL
                           V430M
                                      5
          CBL
    7
                          Deletion
          CBL
8
    8
                           Y371H
    9
          CBL
                           C384R
                                      4
In [3]:
df_text = pd.read_csv("training_text", sep="\|\|", engine="python", names=["ID", "TEXT"], ski
prows=1)
df text.head(10)
Out[3]:
   ID
                                             TEXT
    0
        Cyclin-dependent kinases (CDKs) regulate a var...
0
1
   1
         Abstract Background Non-small cell lung canc...
```

2

4

2

5 5

6 6

7 7 8

8

In [4]:

Out[4]:

ID

Gene Variation

Class

In [5]:

Out[5]:

ID

dtype: int64

df variants.isnull().sum()

0 0

0

df text.isnull().sum()

0

Abstract Background Non-small cell lung canc...

Oncogenic mutations in the monomeric Casitas

**Oncogenic mutations in the monomeric Casitas** 

Oncogenic mutations in the monomeric Casitas

CBL is a negative regulator of activated recep...

Abstract Juvenile myelomonocytic leukemia (JM...

Abstract Juvenile myelomonocytic leukemia (JM...

Recent evidence has demonstrated that acquired...

```
Э
TLYTL
dtype: int64
In [6]:
df text.shape
Out[6]:
(3321, 2)
In [7]:
df variants.shape
Out[7]:
(3321, 4)
In [8]:
df text = df text.sample(frac=0.33, replace=True, random state=42)
df variants = df variants.sample(frac=0.33, replace=True, random state=42)
print(df text.shape)
print(df_variants.shape)
(1096, 2)
(1096, 4)
Text Pre Process:
In [9]:
Stopwords = set(stopwords.words('english'))
lemmatizer = WordNetLemmatizer()
def pre process(text):
    text = str(text).lower()
    # remove HTML tags
   text = re.sub('<.*?>', ' ', text)
    # remove punctuations
   text = re.sub('[%s]' % re.escape(string.punctuation), ' ', text)
    # replace special characters with space
    text = re.sub('[^a-zA-Z0-9]', '', text)
    # remove multiple spaces
   text = re.sub(r'\s+', '', text)
    # tokenize text
    text_tokens = word_tokenize(text)
    # remove stopwords
    text tokens = [word for word in text tokens
                  if word not in Stopwords]
    # lemmatize the words
    text tokens = [lemmatizer.lemmatize(word)
                   for word in text_tokens]
```

```
In [10]:

df_text['TEXT'] = df_text['TEXT'].apply(pre_process)
df = pd.merge(df_variants, df_text, on='ID')
```

```
In [11]:
df.head()
Out[11]:
```

ID Gene Variation Class

return processed text

# Join them

processed\_text = ' '.join(text\_tokens)

```
ID
3174
          Gene Variation Class
RAB35 F161L 7
                                      Shrna screen gene affect akt phosphorylation i...
    860
           ABL1
                    F317L
                               2
                                    abstract mutation bcr abl kinase domain may ca...
1
                                      several group shown noonan syndrome n omim
2 1294
           HRAS
                     Q22K
                               2
3 1130
                  D1010H
                               2
                                    met proto oncogene receptor tyrosine kinase ge...
            MET
4 1095 MAP3K1
                   E1286V
                               5
                                      langerhans cell histiocytosis lch understood n...
In [12]:
df['TEXT'].isnull().sum()
Out[12]:
0
In [13]:
df.isnull().sum()
Out[13]:
ΙD
Gene
Variation
Class
                0
TEXT
dtype: int64
In [14]:
df['Class'].value counts()
Out[14]:
Class
7
      453
4
      303
1
      219
2
      191
6
      140
5
       98
3
       32
9
       24
8
       12
```

## **Visualizations**

Name: count, dtype: int64

```
In [15]:
```

```
plot_class = df['Class'].value_counts().sort_index()
fig = px.bar(plot_class, title='Frequency Distribution for all classes', text_auto=True)
fig.show()
```

# In [16]:

```
plot_gene = df['Gene'].value_counts()
fig = px.bar(plot_gene, title='Frequency Distribution for all genes')
fig.show()
```

# In [17]:

```
fig = px.ecdf(plot_gene)
fig.show()
```

## In [18]:

```
top_genes = df['Gene'].value_counts().head(10)
fig = px.bar(top_genes, title='''Frequency Distribution for most common genes''')
fig.show()
```

## **Observations:**

- 1. The dataset is imbalanced. Class 7 has most data-points and Class 8 has the least.
- 2. BRCA1, TP53, EGFR are the most common Genes

# **Feature Engineering**

```
df.head()
Out[19]:
     ID
            Gene Variation Class
                                                                            TFXT
0 3174
           RAB35
                     F161L
                               7
                                      shrna screen gene affect akt phosphorylation i...
    860
            ABL1
                     F317L
                                2
                                     abstract mutation bcr abl kinase domain may ca...
                                       several group shown noonan syndrome n omim
                     Q22K
           HRAS
2 1294
                                2
3 1130
            MET
                   D1010H
                                2
                                     met proto oncogene receptor tyrosine kinase ge...
  1095 MAP3K1
                                5
                   E1286V
                                       langerhans cell histiocytosis Ich understood n...
In [20]:
df['Text_Length'] = df['TEXT'].apply(lambda x: len(x))
df['Word Count'] = df['TEXT'].apply(lambda x: len(x.split()))
df['Gene Variation TEXT'] = df['Gene'] + ' ' + df['Variation'] + " " + df['TEXT']
df.head()
Out[20]:
     ID
            Gene Variation Class
                                                            TEXT Text_Length Word_Count
                                                                                                 Gene_Variation_TEXT
                                                                                                  RAB35_F161L shrna
                                        shrna screen gene affect akt
0 3174
           RAB35
                     F161L
                               7
                                                                         15268
                                                                                      2027
                                                                                                screen gene affect akt
                                                phosphorylation i...
                                                                                                             phosp...
                                                                                                 ABL1 F317L abstract
                                     abstract mutation bcr abl kinase
    860
            ABL1
                     F317L
                                2
                                                                         14285
                                                                                      1914
                                                                                               mutation bcr abl kinase
                                                  domain may ca...
                                                                                                                do...
                                                                                            HRAS_Q22K several group
                                        several group shown noonan
2 1294
           HRAS
                     Q22K
                               2
                                                                         8584
                                                                                      1111
                                                                                              shown noonan syndrome
                                            syndrome n omim 163...
                                                                                               MET_D1010H met proto
                                       met proto oncogene receptor
                   D1010H
                               2
3 1130
                                                                        187961
                                                                                     26599
            MFT
                                                                                                   oncogene receptor
                                                tyrosine kinase ge...
                                                                                                            tyrosin...
                                                                                                     MAP3K1_E1286V
                                     langerhans cell histiocytosis lch
   1095 MAP3K1
                   E1286V
                               5
                                                                         17879
                                                                                      2586
                                                                                                      langerhans cell
                                                    understood n...
                                                                                                     histiocytosis lc...
In [21]:
df_{copy} = df
```

In [19]:

#### In [22]:

```
df.shape
```

Out[22]:

(1472, 8)

## Modelling

# Univariate analysis on TEXT columns

```
In [23]:
X = df['TEXT']
  = df['Class']
```

```
In [24]:
```

```
X.shape
Out[24]:
(1472,)
In [25]:
from sklearn.feature extraction.text import TfidfVectorizer
vectorizer = TfidfVectorizer(max features=100)
bow X = vectorizer.fit transform(X)
final X = bow X
#print(bow X[:1])
In [26]:
oversample = SMOTE()
X resampled, y resampled = oversample.fit resample(final X, y)
X resampled.shape
Out[26]:
(4077, 100)
In [27]:
y resampled.value counts()
Out[27]:
Class
7
    453
2
     453
5
    453
4
    453
9
    453
3
    453
6
    453
    453
1
8
    453
Name: count, dtype: int64
In [28]:
X_train, X_test, y_train, y_test = train_test_split(
    final_X, y, test_size=0.2, random_state=0)
In [29]:
X train.shape, X test.shape, y train.shape, y test.shape
Out[29]:
((1177, 100), (295, 100), (1177,), (295,))
RandomForest
In [30]:
from sklearn.metrics import accuracy score, f1 score
for i in range(50, 201, 50):
   print('n estimators: ', i)
    clf = RandomForestClassifier(n estimators=i, n jobs=-1)
    # Training
    clf.fit(X train, y train)
    # Test the training data
```

y pred train = clf.predict(X train)

accuracy train = accuracy score(y pred train, y train)

```
f1_train = f1_score(y_pred_train,y_train, average='weighted')
    # Test the test data
    y pred test = clf.predict(X test)
    accuracy test = accuracy score(y pred test, y test)
    f1_test = f1_score(y_pred_test, y_test, average='weighted')
    print('train accuracy: ',accuracy train,'test accuracy: ',accuracy test)
   print('train f1 score: ',f1 train,'test f1 score: ',f1 test)
n estimators: 50
train accuracy: 0.945624468988955 test accuracy: 0.7694915254237288
train f1 score: 0.9459047327079815 test f1 score: 0.773965906534416
```

```
n estimators: 100
train accuracy: 0.945624468988955 test accuracy: 0.7559322033898305
train f1 score: 0.9463514338208725 test f1 score: 0.7613635623208302
n estimators: 150
train accuracy: 0.945624468988955 test accuracy: 0.7661016949152543
train f1 score: 0.9464064737692404 test f1 score: 0.7711490072985043
n estimators: 200
train accuracy: 0.945624468988955 test accuracy: 0.7694915254237288
train fl score: 0.9465033606902027 test fl score: 0.7742145200331363
```

## **Univariate Analysis on Gene and Variation Columns**

```
In [31]:
```

```
from sklearn.preprocessing import OneHotEncoder
gene encoder = OneHotEncoder(sparse=False) # sparse=False to get a dense array
encoded gene = gene encoder.fit transform(df['Gene'].values.reshape(-1, 1))
gene_columns = [f"Gene_{gene}" for gene in gene_encoder.get_feature_names_out(['Gene'])]
encoded gene df = pd.DataFrame(encoded gene, columns=gene columns)
variation encoder = OneHotEncoder(sparse=False)
encoded variation = variation encoder.fit transform(df['Variation'].values.reshape(-1, 1
) )
variation columns = [f"Variation {variation}" for variation in variation encoder.get fea
ture names out(['Variation'])]
encoded variation df = pd.DataFrame(encoded variation, columns=variation columns)
```

# Gene

```
In [32]:
X = encoded gene df
y = df['Class']
In [33]:
X.shape, y.shape
Out[33]:
((1472, 177), (1472,))
In [34]:
oversample = SMOTE()
X resampled, y resampled = oversample.fit resample(X, y)
X resampled.shape
Out[34]:
(4077, 177)
```

```
In [35]:
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test size=0.2, random state=0)
In [36]:
from sklearn.metrics import accuracy score, f1 score
for i in range (50, 201, 50):
    print('n estimators: ', i)
    clf = RandomForestClassifier(n estimators=i, n jobs=-1)
    # Training
    clf.fit(X_train, y_train)
    # Test the training data
    y pred train = clf.predict(X_train)
    accuracy_train = accuracy_score(y_pred_train,y_train)
    f1 train = f1 score(y pred train, y train, average='weighted')
    # Test the test data
    y pred test = clf.predict(X test)
    accuracy test = accuracy score(y pred test,y test)
    f1_test = f1_score(y_pred_test, y_test, average='weighted')
    print('train accuracy: ',accuracy train,'test accuracy: ',accuracy test)
    print('train f1 score: ',f1 train,'test f1 score: ',f1 test)
n estimators: 50
train accuracy: 0.7051826677994902 test accuracy: 0.5796610169491525
train f1 score: 0.7271770209958094 test f1 score: 0.6177635720116642
n estimators: 100
train accuracy: 0.7051826677994902 test accuracy: 0.5694915254237288
train f1 score: 0.727197425832304 test f1 score: 0.6065014999670942
n estimators: 150
train accuracy: 0.7051826677994902 test accuracy: 0.5932203389830508
train f1 score: 0.7291296057147816 test f1 score: 0.6239726618297096
n estimators: 200
train accuracy: 0.7051826677994902 test accuracy: 0.5796610169491525
train f1 score: 0.7292696971684556 test f1 score: 0.6167789284616848
Variation
In [37]:
X = encoded variation df
y = df['Class']
In [38]:
oversample = SMOTE()
X resampled, y resampled = oversample.fit resample(X, y)
X resampled.shape
Out[38]:
(4077, 855)
In [39]:
X_train, X_test, y_train, y_test = train_test_split(
  X, y, test size=0.2, random state=0)
In [40]:
```

from sklearn.metrics import accuracy score, f1 score

for i in range (50, 201, 50):

```
print('n estimators: ', i)
    clf = RandomForestClassifier(n_estimators=i, n_jobs=-1)
    # Training
    clf.fit(X train, y train)
    # Test the training data
    y pred train = clf.predict(X train)
    accuracy train = accuracy score(y pred train, y train)
    f1 train = f1 score(y pred train, y train, average='weighted')
    # Test the test data
    y pred test = clf.predict(X test)
    accuracy test = accuracy score(y pred test,y test)
    f1 test = f1 score(y pred test, y test, average='weighted')
    print('train accuracy: ',accuracy_train,'test accuracy: ',accuracy_test)
    print('train f1 score: ',f1 train,'test f1 score: ',f1 test)
n estimators: 50
train accuracy: 0.9762107051826678 test accuracy: 0.6305084745762712
train f1 score: 0.9760875604284007 test f1 score: 0.6305115930404276
n estimators: 100
train accuracy: 0.9830076465590484 test accuracy: 0.6406779661016949
train f1 score: 0.9828604222947543 test f1 score: 0.64016663056344
n estimators: 150
train accuracy: 0.9830076465590484 test accuracy: 0.6576271186440678
train f1 score: 0.9830499998289368 test f1 score: 0.6596613789933343
n_estimators: 200
train accuracy: 0.9830076465590484 test accuracy: 0.6576271186440678
train f1 score: 0.9830499998289368 test f1 score: 0.6596613789933343
Multivariate Analysis
In [41]:
X = df['Gene Variation TEXT']
y = df['Class']
In [42]:
from sklearn.feature extraction.text import TfidfVectorizer
vectorizer = TfidfVectorizer(max features=100)
bow X = vectorizer.fit transform(X)
final X = bow X
In [43]:
oversample = SMOTE()
X resampled, y resampled = oversample.fit resample(final X, y)
X resampled.shape
Out[43]:
(4077, 100)
In [44]:
X train, X test, y train, y test = train test split(
   final_X, y, test_size=0.2, random_state=0)
In [45]:
```

from sklearn.metrics import accuracy score, f1 score

for i in range(50, 201, 50):
 print('n estimators: ', i)

```
clf = RandomForestClassifier(n_estimators=i, n_jobs=-1)
    # Training
    clf.fit(X_train, y_train)
    # Test the training data
    y pred train = clf.predict(X train)
    accuracy train = accuracy score(y pred train, y train)
    f1 train = f1 score(y pred train, y train, average='weighted')
    # Test the test data
    y pred test = clf.predict(X test)
    accuracy test = accuracy score(y pred test, y test)
    f1 test = f1 score(y pred test, y test, average='weighted')
    print('train accuracy: ',accuracy_train,'test accuracy: ',accuracy_test)
    print('train f1 score: ',f1 train,'test f1 score: ',f1 test)
n estimators: 50
train accuracy: 0.945624468988955 test accuracy: 0.7694915254237288
train f1 score: 0.946049067442206 test f1 score: 0.7733850482836372
n estimators: 100
train accuracy: 0.945624468988955 test accuracy: 0.7627118644067796
train f1 score: 0.9459337923154081 test f1 score: 0.7662846043173872
n estimators: 150
train accuracy: 0.945624468988955 test accuracy: 0.7694915254237288
train f1 score: 0.9462667300548241 test f1 score: 0.7751412018217388
n estimators: 200
train accuracy: 0.945624468988955 test accuracy: 0.7661016949152543
train f1 score: 0.9464538481606171 test f1 score: 0.771101867774866
In [60]:
X = df['Gene Variation TEXT']  # Assuming 'TEXT' is the column containing text data
y = df['Class']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=0)
In [61]:
X train.shape, y train.shape
Out[61]:
((1177,),(1177,))
In [62]:
tfidf vectorizer = TfidfVectorizer(max features=500)
X train tfidf = tfidf vectorizer.fit transform(X train)
X test tfidf = tfidf vectorizer.transform(X test)
In [63]:
svm model = SVC(kernel='linear', C=1.0)
svm_model.fit(X_train_tfidf, y_train)
Out[63]:
         SVC
SVC(kernel='linear')
In [64]:
y pred train = svm model.predict(X train tfidf)
y pred test = svm model.predict(X test tfidf)
In [65]:
from sklearn metrics import accuracy score classification report confusion matrix
```

```
TIOM UNITED THEORY ACCOURAGE OF CHARLEST CONTINUE OF CONTROL OF CO
# Training Set
print("Training Set Accuracy:", accuracy_score(y_train, y_pred_train))
print("Classification Report (Training Set):\n", classification report(y train, y pred t
rain))
print("Confusion Matrix (Training Set):\n", confusion matrix(y train, y pred train))
# Test Set
print("\nTest Set Accuracy:", accuracy score(y test, y pred test))
print("Classification Report (Test Set):\n", classification report(y test, y pred test))
print("Confusion Matrix (Test Set):\n", confusion matrix(y test, y pred test))
Training Set Accuracy: 0.7434154630416313
Classification Report (Training Set):
                           precision recall f1-score support
                                  0.69 0.73 0.71
                     1
                                                                                              171
                                                                        0.54
                                                                                              148
                                  0.79
                                                     0.41
                                                                        0.29
                     3
                                  0.83
                                                     0.18
                                                                                                28
                     4
                                  0.79
                                                     0.80
                                                                        0.80
                                                                                              243
                     5
                                  0.59
                                                     0.53
                                                                        0.56
                                                                                                 74
                     6
                                  0.95
                                                     0.73
                                                                        0.82
                                                                                              124
                                                    0.73
0.97
0.00
0.64
                                                                        0.81
                     7
                                  0.70
                                                                                              359
                     8
                                  0.00
                                                                        0.00
                                                                                                  8
                                                                        0.76
                                   0.93
                                                                                                 22
                                                                         0.74
                                                                                             1177
       accuracy
                                                                                           1177
                                  0.70 0.55
     macro avg
                                                                        0.59
                                                                         0.73
weighted avg
                                   0.75
                                                      0.74
                                                                                              1177
Confusion Matrix (Training Set):
 [[125  2  0  19  8  3  14  0  0]
 [ 6 61 0 3 0 0 78 0 0]
[ 0 0 5 9 4 1 9 0 0]
 [ 25  1  1 194  8  0 13  0  1]
  [ 11  2  0  6  39  1  15  0  0]
  [ 4 3 0 8 7 90 12 0 0]
  [ 6 5 0 1 0 0 347 0 0]
  [ 0 3 0 4 0 0 1 0 0 ]
  [ 3 0 0 1 0 0 4 0 14]]
Test Set Accuracy: 0.6813559322033899
Classification Report (Test Set):
                            precision recall f1-score support
                                                 0.62 0.63

0.28 0.40

0.25 0.40

0.70 0.72

0.50 0.59

0.75 0.75

0.96 0.78

0.00 0.00

1.00 1.00
                                   0.64 0.62
0.71 0.28
                     1
                                                                                                  48
                     2
                                                                                                  43
                     3
                                    1.00
                     4
                                   0.74
                                                                                                  60
                     5
                                  0.71
                                                                                                 24
                                                                                                 16
                     6
                                 0.75
                                                                                                 94
                     7
                                  0.65
                                                                                                 4
                     8
                                  0.00
                     9
                                  1.00
                                                                        0.68 295
       accuracy
                                  0.69 0.56
                                                                       0.58
                                                                                              295
     macro avg
weighted avg
                                  0.68
                                                     0.68
                                                                        0.65
                                                                                              295
Confusion Matrix (Test Set):
  [[30 0 0 9 1 2 6 0 0]
  [ 1 12 0 0 0 0 30 0 0]
  [001110100]
  [8 1 0 42 2 1 6 0 0]
 [ 5 0 0 3 12 1 3 0 0]
[ 0 0 0 1 1 12 2 0 0]
[ 3 1 0 0 0 0 90 0 0]
[ 0 3 0 1 0 0 0 0 0 0
```

In [66]:

[0000000002]]

```
UM DETUGEN: MOUCH DETUCETON IMPORT OFFICE CHECKETON
param grid = {'kernel': ['linear', 'rbf'], 'C': [0.1, 1, 10, 100]}
grid search = GridSearchCV(SVC(), param_grid, cv=5)
grid search.fit(X train tfidf, y train)
best svm model = grid search.best estimator
In [67]:
grid search.best params
Out [67]:
{'C': 10, 'kernel': 'rbf'}
In [71]:
svm model = SVC(kernel='rbf', C=10)
svm model.fit(X train tfidf, y train)
Out[71]:
▼ SVC
SVC(C=10)
In [72]:
y pred train = svm model.predict(X train tfidf)
y pred test = svm model.predict(X test tfidf)
In [73]:
from sklearn.metrics import accuracy score, classification report, confusion matrix
# Training Set
print("Training Set Accuracy:", accuracy_score(y_train, y_pred_train))
print("Classification Report (Training Set):\n", classification report(y train, y pred t
print("Confusion Matrix (Training Set):\n", confusion matrix(y train, y pred train))
# Test Set
print("\nTest Set Accuracy:", accuracy score(y test, y pred test))
print("Classification Report (Test Set):\n", classification_report(y_test, y_pred_test))
print("Confusion Matrix (Test Set):\n", confusion matrix(y test, y pred test))
Training Set Accuracy: 0.9320305862361937
Classification Report (Training Set):
                          recall f1-score support
              precision
                          0.93
                                     0.91
          1
                  0.88
                                                171
          2
                  0.93
                           0.93
                                     0.93
                                                148
          3
                  0.94
                           0.54
                                     0.68
                                                 28
                           0.93
                                     0.95
          4
                  0.96
                                                243
                                                 74
          5
                  0.78
                           0.82
                                     0.80
                                     0.94
                                                124
          6
                  0.95
                           0.94
          7
                  0.96
                            0.98
                                     0.97
                                                359
          8
                  1.00
                            1.00
                                     1.00
                                                  8
                  1.00
                            1.00
                                     1.00
                                                 22
                                     0.93
                                               1177
   accuracy
  macro avg
                  0.93
                            0.90
                                     0.91
                                               1177
weighted avg
                  0.93
                           0.93
                                     0.93
                                               1177
Confusion Matrix (Training Set):
 [[159 1 0 1 7 3 0
                                0
                                  0]
 [ 0 137  0  0  1  1  9
                               0
                                 0 ]
 0 ]
      0 15 7
                 1 1 4
                               0
      1 0 226
                 2 0 0
 [ 14
                                 0 ]
       3
          1 0 61 0 3
 Γ
  6
                               0
                                 0.1
   1
       2
          0
                  4 116 0
 Γ
              1
                               0
                                   0.1
   0
       3
          0 0
                  2 1 353
                                   01
 Γ
                               0
```

 $\cap$ 

 $\cap$ 

 $\cap$ 

 $\cap$ 

 $\cap$ 

 $\cap$   $\cap$ 

 $\cap$  1

```
Test Set Accuracy: 0.7694915254237288
Classification Report (Test Set):
             precision recall f1-score support
                         0.69
                                    0.69
                                                48
          1
                  0.69
                                                43
          2
                 0.77
                          0.70
                                    0.73
          3
                 0.75
                          0.75
                                   0.75
                                                4
                          0.75
                                                60
          4
                 0.79
                                   0.77
          5
                 0.77
                          0.71
                                   0.74
                                                24
                0.86
                          0.75
                                   0.80
                                               16
          7
                          0.88
                                   0.83
                                               94
                 0.78
          8
                 1.00
                          0.75
                                   0.86
                                                4
                 0.50
                          0.50
                                   0.50
                                                2
                                    0.77
                                               295
   accuracy
                  0.77
                           0.72
                                    0.74
                                               295
  macro avg
                                    0.77
weighted avg
                 0.77
                           0.77
                                               295
Confusion Matrix (Test Set):
 [[33 0 1 10 1 0 3 0 0]
 [ 1 30 0 0 0 12 0 0]
 [ 0 0 3 1 0 0 0 0 0 ]
 [8 0 0 45 1 1 5 0 0]
 [ 4 0 0 0 17 1 2 0 0]
 [ 0 1 0 1 1 12 1 0 0]
 [ 1 7 0 0 2 0 83 0 1]
 [0 1 0 0 0 0 0 3 0]
 [1 0 0 0 0 0 0 0 1]]
In [74]:
from sklearn.linear model import LogisticRegression
logreg model = LogisticRegression(max iter=1000)
logreg model.fit(X train tfidf, y train)
Out[74]:
       LogisticRegression
LogisticRegression(max iter=1000)
In [75]:
y pred train = logreg model.predict(X train tfidf)
y pred test = logreg model.predict(X test tfidf)
In [76]:
print("Training Set Accuracy:", accuracy_score(y_train, y_pred_train))
print("Test Set Accuracy:", accuracy score(y test, y pred test))
Training Set Accuracy: 0.7187765505522515
Test Set Accuracy: 0.6610169491525424
In [79]:
print("Training Set F1_score:", f1_score(y_train, y_pred_train, average='weighted'))
print("Test Set F1 score:", f1 score(y test, y pred test, average='weighted'))
Training Set F1 score: 0.6944706612130505
Test Set F1 score: 0.6304002073396894
In [ ]:
```

0

0

0