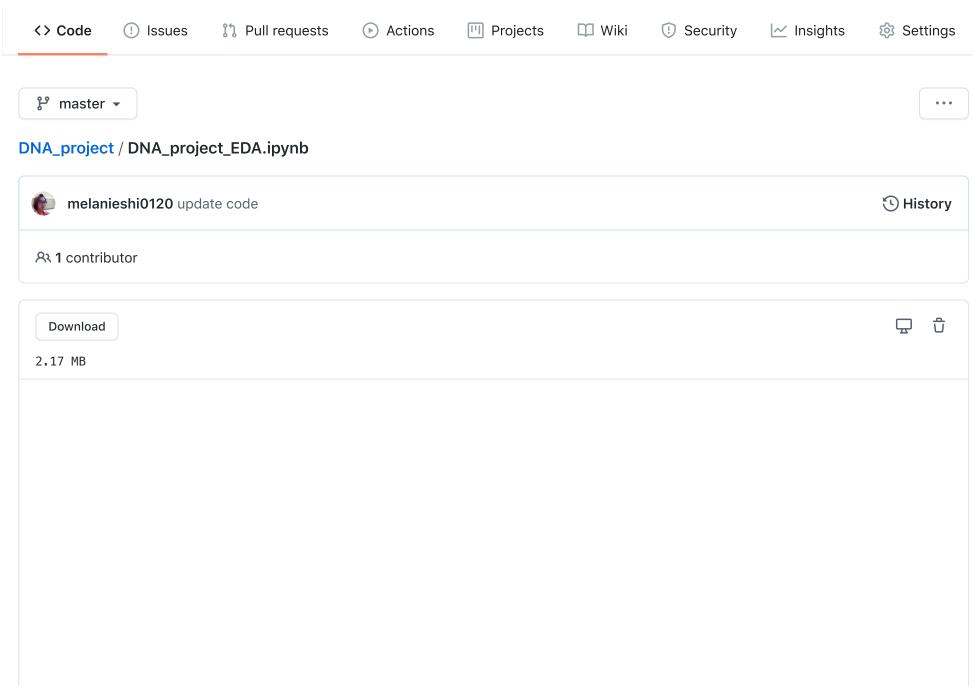
### melanieshi0120 / DNA\_project



```
In [1]: import pandas as pd
        import numpy as np
        import seaborn as sns
        sns.set()
        import matplotlib.pyplot as plt
        import os
        from keras.preprocessing.text import Tokenizer
        from keras.preprocessing.sequence import pad_sequences
        from keras.models import Sequential
        from keras.layers import Dense
        from keras.utils.np utils import to categorical
        from keras.optimizers import Adam
        Using TensorFlow backend.
In [2]: import warnings
        warnings.filterwarnings("ignore")
In [3]: # data source:https://www.kaggle.com/c/msk-redefining-cancer-treatment/data?select=stage1 solu
        tion filtered.csv.7z
In [4]: path='/Users/huashi/Downloads/msk-redefining-cancer-treatment/data/'
In [5]: # load the text train data and text data
        train text= pd.read csv(path+'training text', sep='\|\|', header=None, skiprows=1, names=["ID"
        , "Text"])
        train variants = pd.read csv(path+'training variants')
In [6]: # check the shape of each dataset
        train text.shape
Out[6]: (3321, 2)
In [7]: train_variants.shape
Out[7]: (3321, 4)
In [8]: # before we remove those missing
        #text data we need to merge variants data and text data
```

```
train = pd.merge(train_variants,train_text, how='left', on='ID')
 In [9]: train.isnull().sum() # there are five missing data in text column
 Out[9]: ID
                       0
                       0
         Gene
         Variation
                       0
         Class
                       0
         Text
         dtype: int64
In [10]: # remove missing values
         df_train=train.dropna(axis=0).copy()
         df_train.shape
Out[10]: (3316, 5)
In [11]: df_train.head()
```

Out[11]
---------

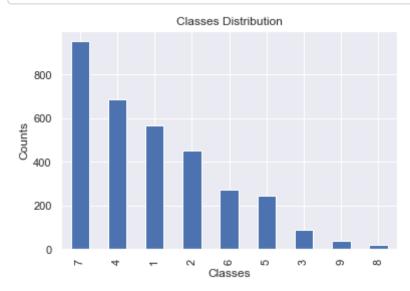
	ID	Gene	Variation	Class	Text
0	0	FAM58A	Truncating Mutations	1	Cyclin-dependent kinases (CDKs) regulate a var
1	1	CBL	W802*	2	Abstract Background Non-small cell lung canc
2	2	CBL	Q249E	2	Abstract Background Non-small cell lung canc
3	3	CBL	N454D	3	Recent evidence has demonstrated that acquired
4	4	CBL	L399V	4	Oncogenic mutations in the monomeric Casitas B

# **EDA**

- 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)

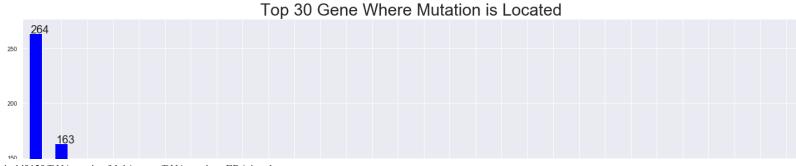
### **Class**

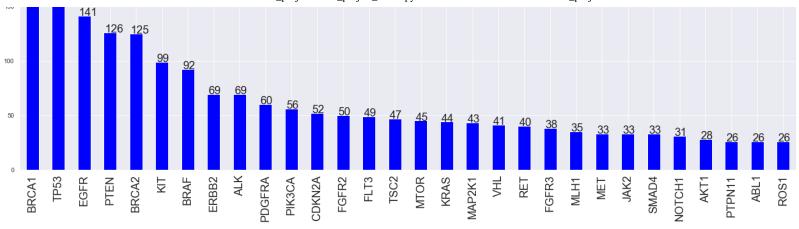
```
In [75]: df_train.Class.value_counts().plot(kind="bar",title='Classes Distribution')
    plt.xlabel('Classes')
    plt.ylabel('Counts')
    plt.show()
```

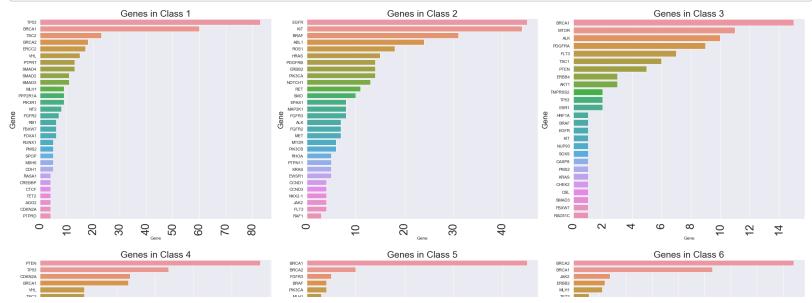


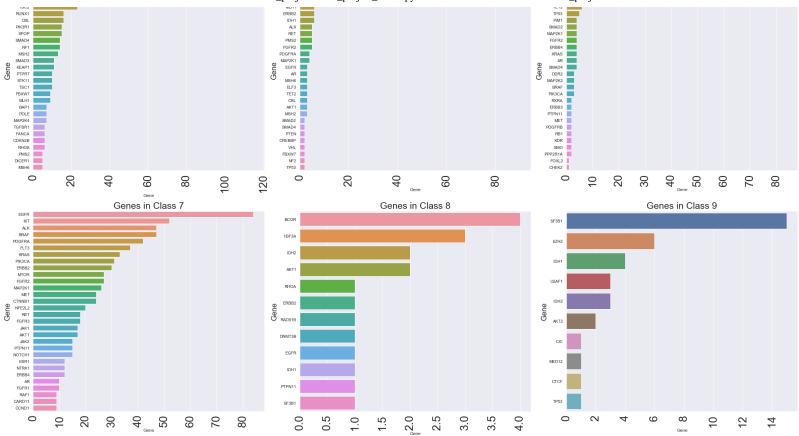
### Gene

```
In [80]: # Plot top 30 the frequency of the gene where this genetic mutation is located
    df_train.Gene.value_counts()[:30].plot(kind='bar',figsize=(25,10),color='blue')
    plt.xticks(fontsize=20)
    plt.title("Top 30 Genes Where Mutation is Located",fontsize=30)
    for i in range(0,30):
        plt.text(i-0.2,df_train.Gene.value_counts()[:30][i],"{}".format(df_train.Gene.value_counts()[:30][i]),fontsize=20)
```



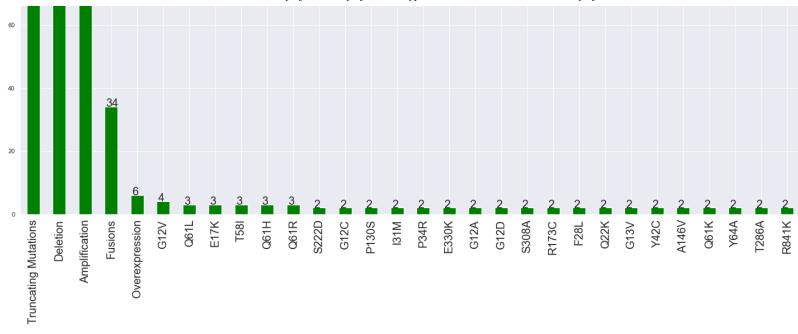






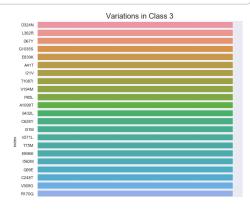
### **Variation**

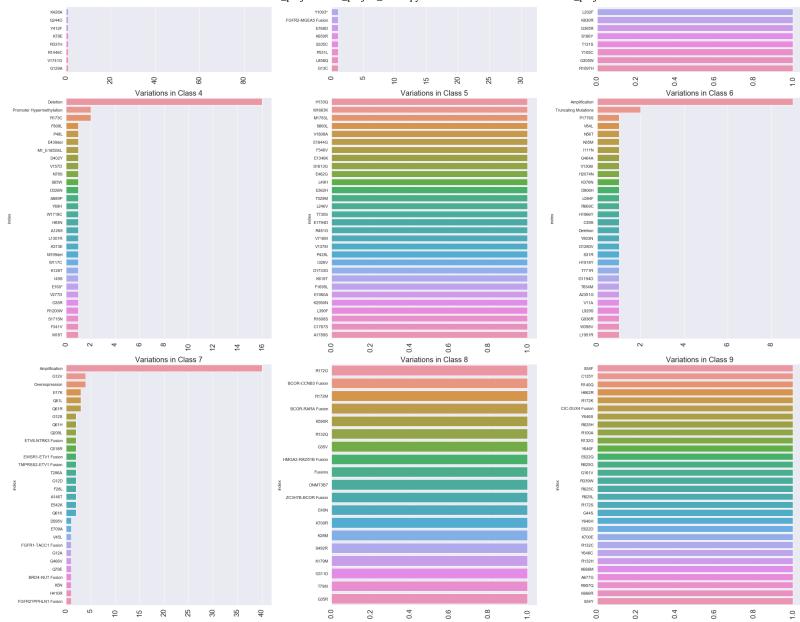
```
In [86]: df_train.Variation.value_counts()[:30].plot(kind='bar',figsize=(25,10),color='green')
    plt.xticks(fontsize=20)
    plt.title("Top 30 Variations",fontsize=30)
    for i in range(0,30):
        plt.text(i-0.2,df_train.Variation.value_counts()[:30][i],"{}".format(df_train.Variation.value_counts()[:30][i]),"{}".format(df_train.Variation.value_counts()[:30][i])
Top 30 Variations
```



# In [112]: # Gene & Class plt.figure(figsize=(30,30)) for i in range(0,9): class\_df=pd.DataFrame(df\_train[df\_train.Class==i+1].Variation.value\_counts()).reset\_index ()[:30] plt.subplot(3,3,i+1) sns.barplot(class\_df['Variation'],class\_df['index']) plt.xticks(rotation=90,size=19) plt.xlabel("") plt.title('Variations in Class {}'.format(list(set(df\_train.Class))[i]),fontsize=20) plt.tight\_layout(pad=0.4, w\_pad=0.5, h\_pad=1.0) plt.show()







# **Data Engineering**

In [198]: import re, string
 from nltk.corpus import stopwords
 import nltk

```
In [187]: # Create functions for tokenization, stemming, Lelemmatization and
          # finally combine all functions together to obtain cleaned text date for train and test data
          sw list = stopwords.words('english')
          sw list += list(string.punctuation)
          'said', "'s", "also", 'one', "n't", 'com', 'satirewire', '-', '-', "et al",
          '-', '_','et al ',"/"]
          sw set = set(sw list)
          # tokenization
          def process review(review):
             tokens = nltk.word tokenize(review) # tokenization
             stopwords_removed = [token.lower() for token in tokens if token.lower() not in sw_set]# st
          op workds removal
             return stopwords removed
          # Stemming
          from nltk.stem import PorterStemmer
          ps = PorterStemmer()
          # create a function stemming() and loop through each word in a review
          def stemming(review):
             stemmed review=[]
             for w in review:
                 stemmed review.append(ps.stem(w))
             return stemmed review
          # import libraries
          from nltk.stem.wordnet import WordNetLemmatizer
          lemmatizer = WordNetLemmatizer()
          # create a function and loop through each word in a review
          def lemmatization(review):
             lemma list=[]
             for word in review:
                 lemma word=lemmatizer.lemmatize(word, pos='v')
                 lemma list.append(lemma word)
             return lemma list
          # Conbime all functions above and obtian cleaned text data
          def data preprocessing(review):
```

```
#tokenization, stop words removal, punctuation marks removel
              processed review=list(map(process review,review))
              # stemming
              stemming reviews=list(map(stemming,processed_review))
              # lemmatization
              lemma reviews=list(map(lemmatization,stemming reviews))
              return lemma reviews
In [192]: cleaned train text=data preprocessing(df train['Text'])
In [157]: import pickle
          pickle_out1=open('cleaned_train_text', 'wb')
          pickle.dump(cleaned_train_text, pickle_out1)
          pickle_out1.close()
          pickle_out2.close()
In [12]: | import pickle
         pickle in train = open("cleaned train text", "rb")
         cleaned train text = pickle.load(pickle in train)
```

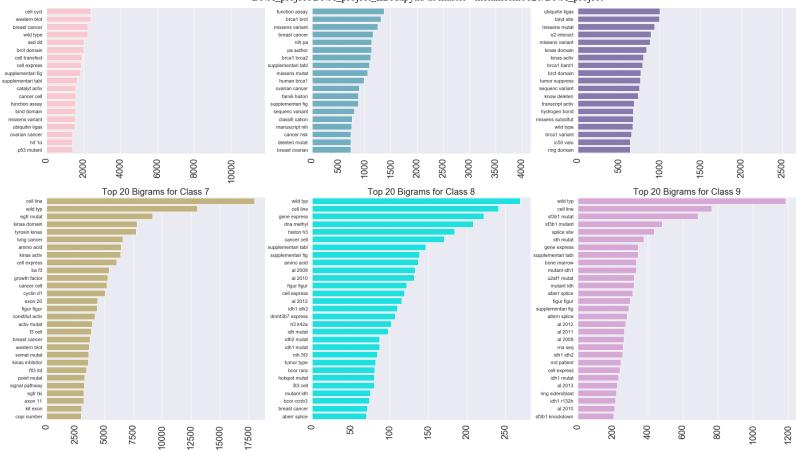
### **N**-grams

```
In [42]: df_train['cleaned_text']=[" ".join(i) for i in cleaned_train_text]

In [122]: from sklearn.feature_extraction.text import CountVectorizer
def get_top_n_bigram(corpus, n=None):
    vec = CountVectorizer(ngram_range=(2, 2), stop_words='english').fit(corpus)
    bag_of_words = vec.transform(corpus)
    sum_words = bag_of_words.sum(axis=0)
    words_freq = [(word, sum_words[0, idx]) for word, idx in vec.vocabulary_.items()]
    words_freq =sorted(words_freq, key = lambda x: x[1], reverse=True)
    return words_freq[:n]
    #source:https://towardsdatascience.com/a-complete-exploratory-data-analysis-and-visualization-for-text-data-29fblb96fb6a

In [124]: # Apply the function above foe each class
    class1 = get_top_n_bigram(df_train[df_train['class']==1]['cleaned_text'], 30)
    class2= get_top_n_bigram(df_train[df_train['class']==2]['cleaned_text'], 30)
    class3 = get top n bigram(df_train[df_train['class']==3]['cleaned_text'], 30)
```

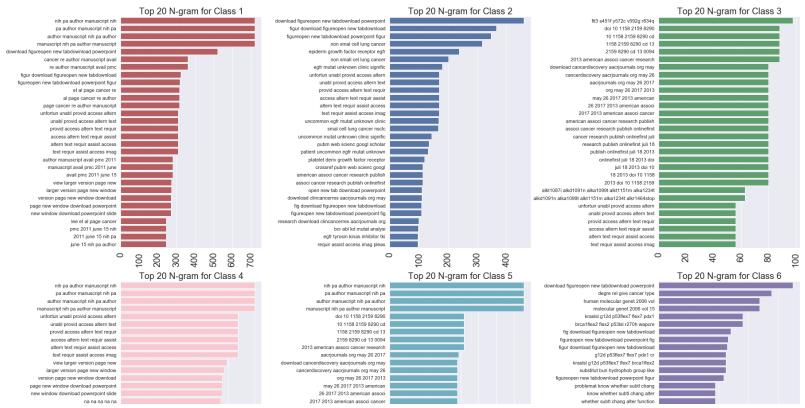
```
class4 = get top n bigram(df train[df train['Class']==4]['cleaned text'], 30)
                  class5 = get top n bigram(df train[df train['Class']==5]['cleaned text'], 30)
                  class6 = get_top_n bigram(df_train[df_train['Class']==6]['cleaned_text'], 30)
                  class7 = get_top_n_bigram(df_train[df_train['Class']==7]['cleaned_text'], 30)
                  class8 = get top n bigram(df_train[df_train['Class']==8]['cleaned_text'], 30)
                  class9 = get top n bigram(df_train[df_train['Class']==9]['cleaned_text'], 30)
In [179]: | classes data=[class1[1:],class2[1:],class3[1:],class4[1:],classfive,
                                          class6[1:],class7[1:],class8[1:],class9[1:]]
                  colors=['r','b','g','pink','c','m','y','aqua','plum']
In [180]: plt.figure(figsize=(25,25))
                  for i in range(0,9):
                        plt.subplot(3,3,i+1)
                        x=[x[0] for x in classes_data[i]]
                        y=[x[1] for x in classes data[i]]
                        sns.barplot(y,x,color=colors[i])
                        plt.xticks(rotation=90, fontsize=20)
                        plt.title("Top 20 Bigrams for Class {}".format(i+1),fontsize=20)
                  plt.tight_layout(pad=0.4, w_pad=0.5, h_pad=1.0)
                  plt.show()
                                     Top 20 Bigrams for Class 1
                                                                                            Top 20 Bigrams for Class 2
                                                                                                                                                  Top 20 Bigrams for Class 3
                                                                            cell line
                      wild typ
                                                                                                                                  wild typ
                     cell line
                                                                            wild tvp
                                                                                                                                 amino acid
                    amino acid
                                                                           eafr mutat
                                                                                                                                  cell line
                                                                                                                                brca1 variant
                  transcript activ
                                                                          kinas domain
                                                                           amino acid
                                                                                                                                breast cancer
                    mutant p53
                                                                           kinas activ
                                                                                                                                 cell express
                   missens mutat
                                                                          lung cancer
                                                                                                                                 alk mutat
                  supplementari fig
                                                                           cyclin d1
                                                                                                                                 vu neutral
                                                                           figur figur
                  tumor suppressor
                                                                                                                              homolog recombin
                                                                            exon 1
                                                                                                                                kinas domair
                  upplementari tabl
                                                                          cell express
                                                                                                                                brca1 protein
                    brct domain
                                                                        upplementari fig
                                                                                                                                   ha f3
                     cell cvcl
                                                                           cancer cell
                                                                                                                                 activ mutat
                   gene express
                                                                          copi number
                                                                                                                                  al 2008
                    cancer cell
                                                                            bcr abl
                                                                                                                               function assay
                                                                          growth factor
                     bind site
                                                                             ba f3
                                                                                                                                  al 2010
                   bind domain
                                                                         breast cancer
                                                                                                                                  stem cell
                  ovarian cancer
                                                                            kit exon
                                                                                                                                missens mutat
                      typ p53
                                                                            exon 20
                                                                                                                                 hdr assay
                 author manuscript
                                                                            egfr tki
                                                                                                                                 point mutat
                    brca1 brct
                    western blot
                                                                           activ mutat
                   cell transfect
                                                                           mentari tabl
                                                                                                                                western blot
                   missens variant
                                                                           kit mutat
                                                                                                                                 pten mutat
                   somat mutat
                                                                           tumor cell
                                                                                                                                 figur figur
                    cell express
                                                                         gene express
                                                                                                                               prostat cancer
                                                                                                                                                        400
                                                                                                                                                                300
                                                                                                                                                                         300
                                     Top 20 Bigrams for Class 4
                                                                                            Top 20 Bigrams for Class 5
                                                                                                                                                  Top 20 Bigrams for Class 6
                      wild typ
                                                                            wild typ
                                                                                                                                  wild typ
                    amino acid
                                                                           vu neutral
                                                                                                                                deleteri mutat
                     cell line
                                                                          brct domain
                                                                                                                                 brca1 brca2
                   missens muta
                                                                            cell line
                                                                                                                                 famili histori
                    pten muta
                                                                           amino acid
                                                                                                                                 amino acid
                  phosphatas activ
                                                                        author manuscript
                                                                                                                                breast cancer
                                                                         transcript activ
                                                                                                                                  cell line
                  tumor suppresso
                  transcript activ
                                                                         brca1 variant
                                                                                                                                 ligas activ
                     figur figu
                                                                         embryon stem
                                                                                                                               ovarian cancer
```

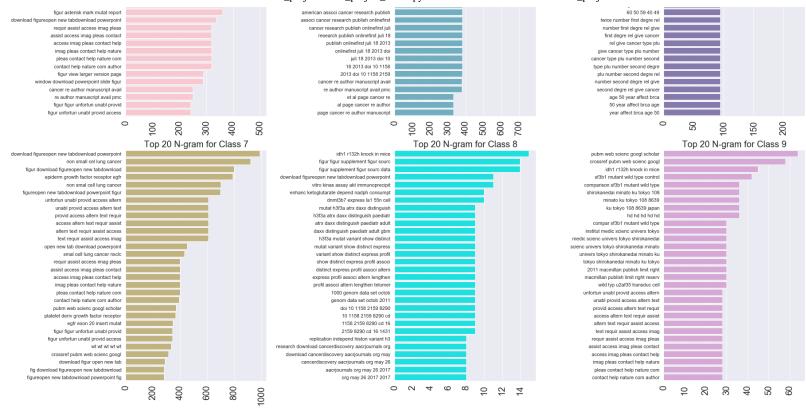


```
In [202]: # Trigrams
def get_top_n_ngram(corpus, n=None,k=None):
    vec = CountVectorizer(ngram_range=(k,k)).fit(corpus)
    bag_of_words = vec.transform(corpus)
    sum_words = bag_of_words.sum(axis=0)
    words_freq = [(word, sum_words[0, idx]) for word, idx in vec.vocabulary_.items()]
    words_freq =sorted(words_freq, key = lambda x: x[1], reverse=True)
    return words_freq[:n]
#source:https://towardsdatascience.com/a-complete-exploratory-data-analysis-and-visualization-for-text-data-29fblb96fb6a
```

```
In [203]: # Apply the function above foe each class
    class1t = get_top_n_ngram(df_train[df_train['Class']==1]['cleaned_text'], 30,5)
    class2t = get_top_n_ngram(df_train[df_train['Class']==2]['cleaned_text'], 30,5)
    class3t = get_top_n_ngram(df_train[df_train['Class']==3]['cleaned_text'], 30,5)
    class4t = get_top_n_ngram(df_train[df_train['Class']==4]['cleaned_text'], 30,5)
```

```
class5t = get_top_n_ngram(df_train[df_train['Class']==5]['cleaned_text'], 30,5)
class6t = get_top_n_ngram(df_train[df_train['Class']==6]['cleaned_text'], 30,5)
class7t = get_top_n_ngram(df_train[df_train['Class']==7]['cleaned_text'], 30,5)
class8t = get_top_n_ngram(df_train[df_train['Class']==8]['cleaned_text'], 30,5)
class9t = get_top_n_ngram(df_train[df_train['Class']==9]['cleaned_text'], 30,5)
```





In [43]: #declare inputs and target
 inputs=df\_train[['ID', 'Gene', 'Variation','cleaned\_text']]
 target=df\_train.Class

# Resampling

In [44]: from sklearn.utils import resample

In [45]: training = pd.DataFrame()
 training[list(inputs.columns)]=inputs
 training['target']=target
 training.head()

Out[45]: ID Gene Variation cleaned\_text target

Truncating Mutations | cyclin-depend kinas cdk regul varieti fundamen...

FAM58A

0

1	1	CBL	W802*	abstract background non-smal cell lung cancer	2
2	2	CBL	Q249E	abstract background non-smal cell lung cancer	2
3	3	CBL	N454D	recent evid demonstr acquir uniparent disomi a	3
4	4	CBL	L399V	oncogen mutat monomer casita b-lineag lymphoma	4

```
classes_list=[]
         for i in range(0,9):
             class_i= training[training.target==i+1]
             classes_list.append(class_i)
             print("Class {}: ".format(i+1)+str(len(class i)))
         # we can see class 7 is the majority class and class 3,8,9 contain very small size of samples
         Class 1: 566
         Class 2: 452
         Class 3: 89
         Class 4: 686
         Class 5: 242
         Class 6: 273
         Class 7: 952
         Class 8: 19
         Class 9: 37
In [47]: # upsample minority
         def oversampling(majority, minority):
             minority upsampled = resample(minority,
                                        replace=True, # sample with replacement
                                        n_samples=len(majority), # match number in majority class
                                        random_state=365) # reproducible results
             return minority upsampled
```

In [48]: # since class 7 is our majority group we need to remove it from our classes list classes\_list.pop(-3)# remove class 7 dataset

Out[48]:

	ID	Gene	Variation	cleaned_text	target
28	28	TERT	C228T	sequenc studi identifi mani recurr code mutat	7
31	31	TERT	Promoter Mutations	sequenc studi identifi mani recurr code mutat	7
34	34	TERT	C250T	sequenc studi identifi mani recurr code mutat	7

In [46]: # separate minority and majority classes

67	67	RHEB	Y35C	gene encod compon pi3k-akt-mtor signal axi fre	7	
68	68	RHEB	Y35N	gene encod compon pi3k-akt-mtor signal axi fre		
•••						
3292	3292	RET	C634Y	investigatedth transformingactivityofth ret pr	7	
3294	3294	RET	R886W	introduct inherit germ line activ mutat rearra	7	
3296	3296	RET	Y791F	ret proto-oncogen encod receptor tyrosin kinas	7	
3308	3308	RUNX1	R174*	famili platelet disord propens acut myeloid le	7	
3310	3310	RUNX1	Amplification	runx protein belong famili metazoan transcript	7	

```
952 rows × 5 columns
In [49]: len(classes_list)# now wen have 8 different classes
Out[49]: 8
In [50]: # now using the function above loop through all classes datasets
         upsampled_classes_list=[]
         for cla in classes_list:
             upsample_df=oversampling(training[training.target==7],cla)
             upsampled_classes_list.append(upsample_df)
In [51]: # and we also include class 7 data
         class_7df=training[training.target==7]
         upsampled_classes list.append(class 7df)
         # combine majority and upsampled minority
In [52]:
         upsampled=pd.concat(upsampled classes list)
         # check new class counts
         upsampled.target.value_counts(),len(upsampled_classes_list)
Out[52]: (7
               952
               952
               952
               952
               952
               952
               952
```

# **Vectorizing Text Data**

```
In [58]: from sklearn.feature_extraction.text import CountVectorizer
In [59]: def vectorizer(train,test):
    vectorizer=CountVectorizer()
    new_train=vectorizer.fit_transform(train)
    new_test=vectorizer.transform(test)
    return new_train,new_test

In [60]: # Vectorize each column for x_train and x_test
    gene_train,gene_test=vectorizer(x_train.Gene,x_test.Gene)
    variation_train,variation_test=vectorizer(x_train.Variation,x_test.Variation)
    cleaned_text_train,cleaned_text_test=vectorizer(x_train.cleaned_text,x_test.cleaned_text)
```

# **Naive Bayes**

```
In [74]: # Naive Bayes Classifier
         from sklearn.naive bayes import MultinomialNB
         from sklearn.metrics import mean squared error, accuracy score, f1 score, make scorer
         from sklearn.metrics import confusion matrix
         from sklearn.model selection import GridSearchCV
         f1 = make scorer(f1 score , average='weighted')
         def NB GridSearch(X train, y train):
             grid params = {'alpha':[0.1,0.2,0.3,0.4,0.5]},
                             'fit prior': [True, False], }
             gs = GridSearchCV( MultinomialNB(), grid params,scoring=f1, cv=10)
             gs.fit(X train, y train)
             print("Best Score: ", gs.best score )
             print("Best Alpha: ", qs.best params )
             return gs.best params .values()
In [78]: def NaiveBayes(X train, y train, X test, y test, alpha, fit prior):
             # fit the training dataset on the NB classifier
             Naive = MultinomialNB(alpha=0.1, fit prior= True)
             Naive.fit(X train,y train)
             #prediction
             nb_train_pre=Naive.predict(X_train)
             nb test pre=Naive.predict(X test)
             # Use accuracy score function to get the accuracy
             print("Naive Bayes Train Accuracy Score :",accuracy_score(nb_train pre, y train))
             print("Naive Bayes Test Accuracy Score : ",accuracy score(nb test pre, y test))
             # calculate f1 scores for test data and train data
             nb f1 score test=f1 score(y test,nb test pre,average='weighted')
             nb fl score train=fl score(y train,nb train pre,average='weighted')
             print("Train data f1 score:{}".format(nb_f1_score_train))
             print("Test data f1 score:{}".format(nb_f1_score_test ))
             print("confusion matrix:{}".format(confusion matrix(y test, nb test pre)))
             return nb train pre, nb test pre
In [79]: # to get best score and best alpha
         alpha1,fit prior1=NB GridSearch(gene train, y train)
         alpha2, fit prior2=NB GridSearch(variation train, y train)
```

```
alpha3, fit prior3=NB GridSearch(cleaned text train, y train)
         Best Score: 0.5970584437980415
         Best Alpha: {'alpha': 0.1, 'fit prior': True}
         Best Score: 0.7728241967182794
         Best Alpha: {'alpha': 0.1, 'fit prior': True}
         Best Score: 0.7511472104042424
         Best Alpha: {'alpha': 0.1, 'fit prior': True}
In [80]: # results
         nb train prel, nb test prel=NaiveBayes(gene train, y train, gene test, y test, alphal, fit prior1)
         nb train pre2, nb test pre2=NaiveBayes(variation train, y train, variation test, y test, alphal, fit
         prior1)
         nb train pre3,nb test pre3=NaiveBayes(cleaned text train,y train,cleaned text test,y test,alph
         al, fit prior1)
         Naive Bayes Train Accuracy Score: 0.6216807703530784
         Naive Bayes Test Accuracy Score: 0.6003500583430572
         Train data f1 score: 0.6157672054520656
         Test data f1 score:0.5930716695679839
         confusion matrix:[[ 93
                                                           2
                                                               41
                                  2
                                       7 28
                                             36
                                                 12
            3 115
                    5
                         1
                                  7 27
                                              21
          [ 7 10 118 13 31
                                  0
                                              01
                     6 118
                            22
                 4
                                 7
                                              01
                        11 101
          [ 12
                12
                     3
                                17
                                     7
                                              41
                 7
                            46
                                 99
                                    10 15
          [ 11
                                              01
                59 38
                           16
                                  8
                                     40 15
                                              41
                         0
             0
                10
                                  0
                                      0 166 211
                                      0 22 17911
         Naive Bayes Train Accuracy Score: 0.9772395681353954
         Naive Bayes Test Accuracy Score: 0.8191365227537923
         Train data f1 score: 0.9774319139048305
         Test data f1 score:0.8126132108732343
         confusion_matrix:[[156
                                           2
                                             34
                                                       0
                                                           0
                                                               0 1
             0 157
                     0
                            16
                                              01
                 0 189
                                  0
                                              0 ]
                 0
                     0 141 58
                                              0 ]
                         0 171
                 0
                                              0 ]
                            16 169
                                              0 ]
                18
                         0 141
                                  0
                                     22
                                              0 ]
                 6
                              0
                                  0
                                      0 191
                                              0 ]
                                  0
                                          0 20811
```

```
Naive Bayes Train Accuracy Score: 0.7993872191421068
Naive Bayes Test Accuracy Score: 0.7841306884480747
Train data f1 score: 0.798351080032705
Test data f1 score:0.7846091468870092
confusion_matrix:[[135
                      1
                                 24
                                             1
                                                  01
[ 2 153
           0 1 1
                      0 19
                                  01
             19
       1 146
                      0 13
                                  01
 [ 34
           3 143 17
           3
               5 117 10 14
 r 10
       8
               2 19 147 10
     38 12
                      0 129
                          0 176 21]
                      0
                          0 10 19811
```

In [65]: # thanks to :https://realpython.com/python-keras-text-classification/

### **Neural Network**

```
import keras
         # from keras.models import Sequential
         # from keras.layers import Dense, Dropout
         # from keras.optimizers import RMSprop
         from keras.optimizers import Adam, SGD
         from keras.utils import to categorical
In [70]: def history_model(X_train, y_train, X_test, y_test):
             #Before we build our model, we need to know the input dimension of our feature vectors.
             input dim = X train.shape[1]
             # Add layers one by one in order
             model = Sequential()
             model.add(keras.layers.Dense(60, input_dim=input_dim, activation='relu', kernel_initialize
         r='he_uniform'))
             model.add(keras.layers.Dense(10, activation='softmax'))
             opt = SGD(1r=0.01, momentum=0.9)
             #specify the optimizer and the loss function.
             model.compile(loss='categorical crossentropy',
                           optimizer='adam',
                           metrics=['accuracy'])
             #Give an overview of the model and the number of parameters available for training:
```

```
DNA_project/DNA_project_EDA.ipynb at master · melanieshi0120/DNA_project
             model.summary()
             # # fit the model
             history = model.fit(X_train, y_train,epochs=50, verbose=2,
                            validation data=(X test, y test),batch size=70)
             return history, model
In [67]: Y train=to categorical(y train)
         Y test=to categorical(y test)
In [71]: history1, model1=history_model(gene_train, Y_train,gene_test, Y_test)
         history2, model2=history model(variation train, Y train, variation test, Y test)
         history3, model3=history model(cleaned text train, Y train,cleaned text test, Y test)
         Model: "sequential 6"
                                     Output Shape
                                                              Param #
         Layer (type)
         ______
         dense 11 (Dense)
                                     (None, 60)
                                                              14520
```

Train on 6854 samples, validate on 1714 samples Epoch 1/50 - 1s - loss: 2.2053 - accuracy: 0.2733 - val loss: 2.0776 - val accuracy: 0.4825 Epoch 2/50 - 1s - loss: 1.8962 - accuracy: 0.5474 - val loss: 1.6911 - val accuracy: 0.5741 Epoch 3/50 - 1s - loss: 1.4966 - accuracy: 0.5940 - val loss: 1.3390 - val accuracy: 0.5998 Epoch 4/50 - 1s - loss: 1.2364 - accuracy: 0.6112 - val loss: 1.1728 - val accuracy: 0.5992 Epoch 5/50 - 1s - loss: 1.1157 - accuracy: 0.6157 - val loss: 1.0968 - val accuracy: 0.5986 Epoch 6/50 - 1s - loss: 1.0543 - accuracy: 0.6176 - val loss: 1.0532 - val accuracy: 0.6021 Epoch 7/50 - 1s - loss: 1.0185 - accuracy: 0.6186 - val loss: 1.0292 - val accuracy: 0.6015 - 1s - loss: 0.9946 - accuracy: 0.6176 - val loss: 1.0155 - val accuracy: 0.5998 Epoch 9/50

```
- 1s - 1oss: 0.9/92 - accuracy: 0.6185 - val loss: 1.0033 - val accuracy: 0.6039
Epoch 10/50
- 1s - loss: 0.9679 - accuracy: 0.6176 - val loss: 0.9954 - val accuracy: 0.6021
Epoch 11/50
- 1s - loss: 0.9603 - accuracy: 0.6172 - val loss: 0.9915 - val accuracy: 0.5980
Epoch 12/50
- 1s - loss: 0.9528 - accuracy: 0.6188 - val loss: 0.9855 - val accuracy: 0.5992
Epoch 13/50
- 1s - loss: 0.9484 - accuracy: 0.6174 - val loss: 0.9852 - val accuracy: 0.5986
Epoch 14/50
- 1s - loss: 0.9445 - accuracy: 0.6172 - val loss: 0.9796 - val accuracy: 0.6021
Epoch 15/50
- 1s - loss: 0.9411 - accuracy: 0.6182 - val loss: 0.9794 - val accuracy: 0.5998
Epoch 16/50
- 1s - loss: 0.9386 - accuracy: 0.6186 - val loss: 0.9748 - val accuracy: 0.6009
Epoch 17/50
- 1s - loss: 0.9356 - accuracy: 0.6195 - val loss: 0.9723 - val accuracy: 0.6004
Epoch 18/50
- 1s - loss: 0.9340 - accuracy: 0.6204 - val loss: 0.9726 - val accuracy: 0.5980
Epoch 19/50
- 1s - loss: 0.9324 - accuracy: 0.6182 - val loss: 0.9725 - val accuracy: 0.6039
Epoch 20/50
- 1s - loss: 0.9309 - accuracy: 0.6188 - val loss: 0.9707 - val accuracy: 0.6015
Epoch 21/50
- 1s - loss: 0.9297 - accuracy: 0.6183 - val loss: 0.9730 - val accuracy: 0.5986
Epoch 22/50
- 1s - loss: 0.9281 - accuracy: 0.6195 - val loss: 0.9687 - val_accuracy: 0.6009
Epoch 23/50
- 1s - loss: 0.9273 - accuracy: 0.6205 - val loss: 0.9673 - val accuracy: 0.6009
Epoch 24/50
- 1s - loss: 0.9268 - accuracy: 0.6176 - val loss: 0.9683 - val accuracy: 0.5992
Epoch 25/50
- 1s - loss: 0.9258 - accuracy: 0.6164 - val loss: 0.9729 - val accuracy: 0.5928
Epoch 26/50
- 1s - loss: 0.9261 - accuracy: 0.6183 - val loss: 0.9710 - val accuracy: 0.6015
Epoch 27/50
- 1s - loss: 0.9243 - accuracy: 0.6188 - val loss: 0.9675 - val accuracy: 0.6015
Epoch 28/50
- 1s - loss: 0.9244 - accuracy: 0.6188 - val loss: 0.9647 - val accuracy: 0.6021
Epoch 29/50
- 1s - loss: 0.9233 - accuracy: 0.6182 - val loss: 0.9682 - val accuracy: 0.6027
Epoch 30/50
- 1s - loss: 0.9231 - accuracy: 0.6199 - val loss: 0.9670 - val accuracy: 0.5998
Epoch 31/50
```

```
- 1s - loss: 0.9234 - accuracy: 0.6183 - val loss: 0.9696 - val accuracy: 0.5998
Epoch 32/50
- 1s - loss: 0.9219 - accuracy: 0.6208 - val_loss: 0.9678 - val_accuracy: 0.5974
Epoch 33/50
- 1s - loss: 0.9227 - accuracy: 0.6188 - val loss: 0.9667 - val accuracy: 0.6039
Epoch 34/50
- 1s - loss: 0.9220 - accuracy: 0.6185 - val loss: 0.9653 - val accuracy: 0.5963
Epoch 35/50
- 1s - loss: 0.9218 - accuracy: 0.6193 - val loss: 0.9659 - val accuracy: 0.5992
Epoch 36/50
- 1s - loss: 0.9206 - accuracy: 0.6167 - val loss: 0.9660 - val accuracy: 0.5992
Epoch 37/50
- 1s - loss: 0.9210 - accuracy: 0.6176 - val loss: 0.9666 - val accuracy: 0.5980
Epoch 38/50
- 1s - loss: 0.9208 - accuracy: 0.6186 - val loss: 0.9669 - val accuracy: 0.5980
Epoch 39/50
- 1s - loss: 0.9203 - accuracy: 0.6185 - val loss: 0.9668 - val accuracy: 0.5992
Epoch 40/50
- 1s - loss: 0.9203 - accuracy: 0.6195 - val_loss: 0.9670 - val_accuracy: 0.6004
Epoch 41/50
- 0s - loss: 0.9198 - accuracy: 0.6186 - val loss: 0.9687 - val accuracy: 0.5974
Epoch 42/50
- 0s - loss: 0.9186 - accuracy: 0.6172 - val loss: 0.9701 - val accuracy: 0.5957
Epoch 43/50
- 1s - loss: 0.9194 - accuracy: 0.6170 - val loss: 0.9687 - val accuracy: 0.6009
Epoch 44/50
- 0s - loss: 0.9191 - accuracy: 0.6189 - val loss: 0.9701 - val accuracy: 0.6009
Epoch 45/50
- 1s - loss: 0.9190 - accuracy: 0.6170 - val loss: 0.9711 - val accuracy: 0.6015
Epoch 46/50
- 1s - loss: 0.9190 - accuracy: 0.6169 - val loss: 0.9667 - val accuracy: 0.6033
Epoch 47/50
- 1s - loss: 0.9184 - accuracy: 0.6191 - val loss: 0.9686 - val accuracy: 0.6015
Epoch 48/50
- 1s - loss: 0.9194 - accuracy: 0.6202 - val loss: 0.9686 - val accuracy: 0.6009
Epoch 49/50
- 1s - loss: 0.9186 - accuracy: 0.6161 - val loss: 0.9658 - val accuracy: 0.6009
Epoch 50/50
- 1s - loss: 0.9190 - accuracy: 0.6191 - val loss: 0.9659 - val accuracy: 0.5974
Model: "sequential 7"
```

Layer	(type)	Output	Shape	Param #
	:=============			

610

dense 14 (Dense)

```
______
Total params: 147,490
Trainable params: 147,490
Non-trainable params: 0
Train on 6854 samples, validate on 1714 samples
Epoch 1/50
- 1s - loss: 2.2117 - accuracy: 0.4056 - val loss: 2.0611 - val accuracy: 0.7089
Epoch 2/50
- 1s - loss: 1.7969 - accuracy: 0.8297 - val loss: 1.5322 - val accuracy: 0.7795
Epoch 3/50
- 1s - loss: 1.2291 - accuracy: 0.9472 - val loss: 1.0709 - val accuracy: 0.8891
Epoch 4/50
- 1s - loss: 0.7919 - accuracy: 0.9745 - val loss: 0.7719 - val accuracy: 0.8938
Epoch 5/50
- 1s - loss: 0.5054 - accuracy: 0.9746 - val loss: 0.5878 - val accuracy: 0.8996
Epoch 6/50
- 1s - loss: 0.3286 - accuracy: 0.9756 - val loss: 0.4797 - val accuracy: 0.8973
Epoch 7/50
- 1s - loss: 0.2233 - accuracy: 0.9755 - val loss: 0.4153 - val accuracy: 0.8985
Epoch 8/50
- 1s - loss: 0.1626 - accuracy: 0.9772 - val loss: 0.3779 - val accuracy: 0.8961
Epoch 9/50
- 1s - loss: 0.1269 - accuracy: 0.9755 - val loss: 0.3549 - val accuracy: 0.8996
Epoch 10/50
- 1s - loss: 0.1047 - accuracy: 0.9762 - val loss: 0.3403 - val accuracy: 0.8938
Epoch 11/50
- 1s - loss: 0.0905 - accuracy: 0.9765 - val loss: 0.3314 - val accuracy: 0.8961
Epoch 12/50
- 1s - loss: 0.0814 - accuracy: 0.9759 - val loss: 0.3257 - val accuracy: 0.8973
Epoch 13/50
- 1s - loss: 0.0745 - accuracy: 0.9768 - val loss: 0.3201 - val accuracy: 0.8961
Epoch 14/50
- 1s - loss: 0.0700 - accuracy: 0.9752 - val loss: 0.3201 - val accuracy: 0.8973
Epoch 15/50
- 1s - loss: 0.0662 - accuracy: 0.9765 - val loss: 0.3127 - val accuracy: 0.8961
Epoch 16/50
- 1s - loss: 0.0634 - accuracy: 0.9767 - val loss: 0.3134 - val accuracy: 0.8973
Epoch 17/50
- 1s - loss: 0.0613 - accuracy: 0.9764 - val loss: 0.3110 - val accuracy: 0.8973
Epoch 18/50
```

(None, 10)

```
- 1s - loss: 0.0603 - accuracy: 0.9761 - val loss: 0.3097 - val accuracy: 0.8973
Epoch 19/50
- 1s - loss: 0.0581 - accuracy: 0.9764 - val loss: 0.3118 - val accuracy: 0.8973
Epoch 20/50
- 1s - loss: 0.0576 - accuracy: 0.9767 - val loss: 0.3107 - val accuracy: 0.8973
Epoch 21/50
- 1s - loss: 0.0564 - accuracy: 0.9768 - val loss: 0.3046 - val accuracy: 0.8996
Epoch 22/50
- 1s - loss: 0.0552 - accuracy: 0.9768 - val loss: 0.3131 - val accuracy: 0.8967
Epoch 23/50
- 1s - loss: 0.0551 - accuracy: 0.9751 - val loss: 0.3073 - val accuracy: 0.8973
Epoch 24/50
- 1s - loss: 0.0539 - accuracy: 0.9774 - val loss: 0.3048 - val accuracy: 0.8961
Epoch 25/50
- 1s - loss: 0.0534 - accuracy: 0.9769 - val loss: 0.3041 - val accuracy: 0.8973
Epoch 26/50
- 1s - loss: 0.0535 - accuracy: 0.9769 - val loss: 0.3032 - val accuracy: 0.8973
Epoch 27/50
- 1s - loss: 0.0529 - accuracy: 0.9765 - val loss: 0.3025 - val accuracy: 0.8973
Epoch 28/50
- 1s - loss: 0.0526 - accuracy: 0.9759 - val loss: 0.3079 - val accuracy: 0.8961
Epoch 29/50
- 1s - loss: 0.0523 - accuracy: 0.9752 - val loss: 0.3037 - val accuracy: 0.8961
Epoch 30/50
- 1s - loss: 0.0519 - accuracy: 0.9755 - val loss: 0.3026 - val accuracy: 0.8996
Epoch 31/50
- 1s - loss: 0.0520 - accuracy: 0.9758 - val loss: 0.3043 - val accuracy: 0.8973
Epoch 32/50
- 1s - loss: 0.0517 - accuracy: 0.9767 - val loss: 0.3073 - val accuracy: 0.8950
Epoch 33/50
- 1s - loss: 0.0514 - accuracy: 0.9748 - val loss: 0.3088 - val accuracy: 0.8973
Epoch 34/50
- 1s - loss: 0.0512 - accuracy: 0.9769 - val loss: 0.2999 - val accuracy: 0.8996
Epoch 35/50
- 1s - loss: 0.0509 - accuracy: 0.9767 - val loss: 0.2999 - val accuracy: 0.8996
Epoch 36/50
- 1s - loss: 0.0509 - accuracy: 0.9759 - val loss: 0.3024 - val accuracy: 0.8996
Epoch 37/50
- 1s - loss: 0.0508 - accuracy: 0.9772 - val loss: 0.3046 - val accuracy: 0.8973
Epoch 38/50
- 1s - loss: 0.0509 - accuracy: 0.9765 - val loss: 0.3097 - val accuracy: 0.8950
Epoch 39/50
- 1s - loss: 0.0504 - accuracy: 0.9759 - val loss: 0.3018 - val accuracy: 0.8996
Epoch 40/50
```

```
- 1s - loss: 0.0506 - accuracy: 0.9755 - val loss: 0.2980 - val accuracy: 0.8996
Epoch 41/50
- 1s - loss: 0.0501 - accuracy: 0.9767 - val loss: 0.3014 - val accuracy: 0.8996
Epoch 42/50
- 1s - loss: 0.0502 - accuracy: 0.9762 - val loss: 0.3017 - val_accuracy: 0.8938
Epoch 43/50
- 1s - loss: 0.0500 - accuracy: 0.9755 - val loss: 0.3043 - val accuracy: 0.8961
Epoch 44/50
- 1s - loss: 0.0497 - accuracy: 0.9769 - val loss: 0.2981 - val accuracy: 0.8996
Epoch 45/50
- 1s - loss: 0.0504 - accuracy: 0.9753 - val loss: 0.3022 - val accuracy: 0.8961
Epoch 46/50
- 1s - loss: 0.0496 - accuracy: 0.9772 - val loss: 0.3020 - val accuracy: 0.8973
Epoch 47/50
- 1s - loss: 0.0504 - accuracy: 0.9742 - val loss: 0.3066 - val accuracy: 0.8973
Epoch 48/50
- 1s - loss: 0.0499 - accuracy: 0.9772 - val loss: 0.3020 - val accuracy: 0.8961
Epoch 49/50
- 1s - loss: 0.0501 - accuracy: 0.9758 - val loss: 0.3011 - val accuracy: 0.8973
Epoch 50/50
- 1s - loss: 0.0498 - accuracy: 0.9767 - val loss: 0.3061 - val accuracy: 0.8973
Model: "sequential 8"
Layer (type)
                           Output Shape
                                                   Param #
______
dense 15 (Dense)
                           (None, 60)
                                                   7647120
                                                   610
dense 16 (Dense)
                           (None, 10)
______
Total params: 7,647,730
Trainable params: 7,647,730
Non-trainable params: 0
Train on 6854 samples, validate on 1714 samples
Epoch 1/50
- 27s - loss: 1.1684 - accuracy: 0.6570 - val loss: 0.6470 - val accuracy: 0.7993
Epoch 2/50
```

Epoch 3/50
 - 26s - loss: 0.4335 - accuracy: 0.8496 - val\_loss: 0.4699 - val\_accuracy: 0.8518
Epoch 4/50
 - 25s - loss: 0.3750 - accuracy: 0.8653 - val\_loss: 0.4928 - val\_accuracy: 0.8471
Epoch 5/50

\_ 25c \_ loce. 0 3608 \_ accuracy. 0 8677 \_ val loce. 0 4879 \_ val accuracy. 0 8431

- 27s - loss: 0.5375 - accuracy: 0.8216 - val loss: 0.5605 - val accuracy: 0.8186

https://github.com/melanieshi0120/DNA\_project/blob/master/DNA\_project\_EDA.ipynb

```
- 235 - 1055. V.3000 - accuracy. V.00// - Var_1055. V.40/3 - Var_accuracy. V.0431
Epoch 6/50
- 26s - loss: 0.3518 - accuracy: 0.8726 - val loss: 0.4457 - val accuracy: 0.8495
Epoch 7/50
- 30s - loss: 0.3348 - accuracy: 0.8793 - val loss: 0.4756 - val accuracy: 0.8559
Epoch 8/50
- 38s - loss: 0.3156 - accuracy: 0.8761 - val loss: 0.4620 - val accuracy: 0.8553
Epoch 9/50
- 51s - loss: 0.3096 - accuracy: 0.8802 - val loss: 0.4638 - val accuracy: 0.8448
Epoch 10/50
- 32s - loss: 0.3121 - accuracy: 0.8821 - val loss: 0.4943 - val accuracy: 0.8384
Epoch 11/50
- 30s - loss: 0.3038 - accuracy: 0.8808 - val loss: 0.4697 - val accuracy: 0.8524
Epoch 12/50
- 27s - loss: 0.2952 - accuracy: 0.8837 - val loss: 0.5020 - val accuracy: 0.8489
Epoch 13/50
- 28s - loss: 0.2845 - accuracy: 0.8865 - val loss: 0.4479 - val accuracy: 0.8565
Epoch 14/50
- 27s - loss: 0.2838 - accuracy: 0.8879 - val loss: 0.4757 - val accuracy: 0.8635
Epoch 15/50
- 49s - loss: 0.2903 - accuracy: 0.8869 - val loss: 0.4753 - val accuracy: 0.8541
Epoch 16/50
- 28s - loss: 0.2719 - accuracy: 0.8913 - val loss: 0.4635 - val accuracy: 0.8606
Epoch 17/50
- 31s - loss: 0.2729 - accuracy: 0.8901 - val loss: 0.4451 - val accuracy: 0.8670
Epoch 18/50
- 28s - loss: 0.2737 - accuracy: 0.8884 - val loss: 0.4392 - val accuracy: 0.8594
Epoch 19/50
- 33s - loss: 0.2650 - accuracy: 0.8923 - val loss: 0.4662 - val accuracy: 0.8652
Epoch 20/50
- 31s - loss: 0.2721 - accuracy: 0.8906 - val loss: 0.5097 - val accuracy: 0.8466
Epoch 21/50
- 31s - loss: 0.2710 - accuracy: 0.8887 - val loss: 0.4537 - val accuracy: 0.8617
Epoch 22/50
- 30s - loss: 0.2610 - accuracy: 0.8910 - val loss: 0.4620 - val accuracy: 0.8419
Epoch 23/50
- 27s - loss: 0.2666 - accuracy: 0.8910 - val loss: 0.4564 - val accuracy: 0.8565
Epoch 24/50
- 28s - loss: 0.2566 - accuracy: 0.8947 - val loss: 0.4734 - val accuracy: 0.8652
Epoch 25/50
- 27s - loss: 0.2569 - accuracy: 0.8926 - val loss: 0.4762 - val accuracy: 0.8536
Epoch 26/50
- 27s - loss: 0.2626 - accuracy: 0.8944 - val loss: 0.4713 - val accuracy: 0.8705
Epoch 27/50
```

```
- 27s - loss: 0.2604 - accuracy: 0.8929 - val loss: 0.4359 - val accuracy: 0.8629
Epoch 28/50
- 28s - loss: 0.2614 - accuracy: 0.8919 - val loss: 0.4347 - val accuracy: 0.8681
Epoch 29/50
- 27s - loss: 0.2577 - accuracy: 0.8923 - val loss: 0.4543 - val accuracy: 0.8594
Epoch 30/50
- 28s - loss: 0.2540 - accuracy: 0.8947 - val loss: 0.4673 - val accuracy: 0.8588
Epoch 31/50
- 29s - loss: 0.2593 - accuracy: 0.8938 - val loss: 0.4529 - val accuracy: 0.8547
Epoch 32/50
- 28s - loss: 0.2523 - accuracy: 0.8954 - val loss: 0.4746 - val accuracy: 0.8536
Epoch 33/50
- 28s - loss: 0.2544 - accuracy: 0.8958 - val loss: 0.4812 - val accuracy: 0.8606
Epoch 34/50
- 26s - loss: 0.2511 - accuracy: 0.8933 - val loss: 0.4650 - val accuracy: 0.8629
Epoch 35/50
- 28s - loss: 0.2434 - accuracy: 0.8974 - val_loss: 0.4677 - val_accuracy: 0.8693
Epoch 36/50
- 27s - loss: 0.2493 - accuracy: 0.8945 - val loss: 0.5142 - val accuracy: 0.8588
Epoch 37/50
- 27s - loss: 0.2489 - accuracy: 0.8961 - val loss: 0.4614 - val accuracy: 0.8606
Epoch 38/50
- 27s - loss: 0.2511 - accuracy: 0.8950 - val loss: 0.4824 - val accuracy: 0.8699
Epoch 39/50
- 28s - loss: 0.2532 - accuracy: 0.8929 - val_loss: 0.4608 - val_accuracy: 0.8611
Epoch 40/50
- 27s - loss: 0.2498 - accuracy: 0.8952 - val loss: 0.4679 - val accuracy: 0.8746
Epoch 41/50
- 26s - loss: 0.2507 - accuracy: 0.8957 - val_loss: 0.4813 - val_accuracy: 0.8641
Epoch 42/50
- 29s - loss: 0.2522 - accuracy: 0.8936 - val loss: 0.4689 - val accuracy: 0.8699
Epoch 43/50
- 28s - loss: 0.2441 - accuracy: 0.8987 - val loss: 0.4864 - val accuracy: 0.8699
Epoch 44/50
- 26s - loss: 0.2391 - accuracy: 0.8974 - val loss: 0.4942 - val accuracy: 0.8623
Epoch 45/50
- 26s - loss: 0.2410 - accuracy: 0.8986 - val loss: 0.4780 - val accuracy: 0.8763
Epoch 46/50
- 27s - loss: 0.2442 - accuracy: 0.8942 - val loss: 0.4952 - val accuracy: 0.8571
Epoch 47/50
- 27s - loss: 0.2392 - accuracy: 0.8977 - val loss: 0.5171 - val accuracy: 0.8600
Epoch 48/50
- 26s - loss: 0.2377 - accuracy: 0.8990 - val loss: 0.4981 - val accuracy: 0.8676
Epoch 49/50
```

```
- 27s - loss: 0.2392 - accuracy: 0.8961 - val_loss: 0.4993 - val_accuracy: 0.8763
         Epoch 50/50
         - 27s - loss: 0.2401 - accuracy: 0.8993 - val_loss: 0.5078 - val_accuracy: 0.8611
In [75]: def NN results(history, model, x train, x test):
             #prediction
             nn train pre=model.predict classes(x train)
             nn test pre=model.predict classes(x test)
             #calculate f1 scores for test data and train data
             nn f1 score test=f1 score([int(i) for i in y test],nn test pre,average='weighted')
             nn f1 score train=f1 score(y train,nn train pre,average='weighted')
            print("Train data f1 score:{}".format(nn f1 score train))
             print("Test data f1 score:{}".format(nn f1 score test ))
             print(confusion matrix(y test, nn test pre))
             return nn train pre, nn test pre
In [76]: # apply funtion above to obtian the results
         nn train prel,nn test prel=NN results(history1,model1,gene train,gene test)
         nn train pre2, nn test pre2=NN results(history2, model2, variation train, variation test)
         nn_train_pre3,nn_test_pre3=NN_results(history3,model3,cleaned_text_train,cleaned_text_test)
         Train data f1 score: 0.6143893769581936
         Test data f1 score: 0.5884727438700839
                           30
         [[ 82
            4 115
                    5
                                            2]
               10 118 13
                          31
                                            0]
                7
                    6 128
                          19
                                7
                                            0]
          [ 11
               12
                    3 13
                           97
                               20
                           46
                               99 10 15
               62 38
                        0 13
                                   40 15
                                            4]
               10
                            0
                                0
                                    0 166 21]
                                    0 22 17911
         Train data f1 score: 0.9780175131194836
         Test data f1 score: 0.9038712574030837
                                   34
         [[156
                0
            0 157
                                  19
                                            01
                    0
                0 189
                                            01
                        0
                0
                    0 141
                            1
                                  57
                                           0]
                        0 160
                                  11
                                            0 ]
                8
                            0 169
                                  16
                                            0 ]
               15
                    0
                                0 167
                                            0 ]
```

# **Logistic regression**

```
In [87]: #import Logistic Regression
        from sklearn.linear model import LogisticRegression
        def Logistic Regression(X train, y train, X test, y test):
            log re = LogisticRegression(max_iter=1000)
            log_re.fit(X_train, y_train)
            #calculate scores for test data and train data
            test_data_score = log_re.score(X_test, y_test)
            train_data_score = log_re.score(X_train, y_train)
            print("Train data score:{}".format(train_data_score ))
            print("Test data score:{}".format(test_data_score ))
            # predict values for test data and train data
            log y test pre=log re.predict(X_test)
            log y train pre=log re.predict(X train)
            # calculate f1 scores for test data and train data
            log f1_score test=f1_score(y test,log y test pre,average="weighted")
            log f1 score train=f1 score(y train,log y train pre,average="weighted")
            print("Train data f1 score:{}".format(log f1 score train))
            print("Test data f1 score:{}".format(log_f1_score_test ))
            return log y train_pre,log_y_test_pre
```

```
In [88]: | log y train prel, log y test prel=Logistic Regression(gene train, y train, gene test, y test)
        log y train pre2, log y test pr2=Logistic Regression(variation train, y train, variation test, y
        test)
        log y train pre3,log y test pre3=Logistic Regression(cleaned text train, y train,cleaned text
        test, y test)
        Train data score: 0.621388969944558
        Test data score: 0.603267211201867
        Train data f1 score: 0.615936855192663
        Test data f1 score: 0.5957018668273237
        Train data score: 0.9768018675226146
        Test data score: 0.8961493582263711
        Train data f1 score: 0.9769987251836152
        Test data f1 score: 0.9029228363338574
        ______
        Train data score: 0.9034140647796907
        Test data score: 0.8640606767794633
        Train data f1 score: 0.9039234128069726
        Test data f1 score: 0.8628257154404384
        ______
```

# **Model Stacking**

```
In [89]: X train = pd.DataFrame( {
              'nb gene':nb train pre1,
              'nb variation':nb train pre2,
              'nb text':nb train pre3,
              'nn gene':nn train prel,
              'nn variation':nn train pre2,
              'nn text':nn train pre3,
              'log gene':log y train prel,
              'log variation':log y train pre2,
             'log_text':log_y_train_pre3
             })
         X test = pd.DataFrame( {
              'nb gene':nb test pre1,
              'nb variation':nb test pre2,
              'nb text':nb_test_pre3,
              'nn gene':nn test prel,
              'nn variation':nn test pre2,
```

```
'nn_text':nn_test_pre3,
'log_gene':log_y_test_pre1,
'log_variation':log_y_test_pr2,
'log_text':log_y_test_pre3
})
```

In [90]: X\_train.head()

Out[90]:

	nb_gene	nb_variation	nb_text	nn_gene	nn_variation	nn_text	log_gene	log_variation	log_text
0	5	1	5	5	1	5	5	1	5
1	7	7	7	7	7	7	7	7	7
2	9	9	9	9	9	9	9	9	9
3	3	3	3	3	3	3	3	3	3
4	7	2	2	7	2	2	7	2	2

In [91]: X\_test.head()

Out[91]:

	nb_gene	nb_variation	nb_text	nn_gene	nn_variation	nn_text	log_gene	log_variation	log_text
0	5	5	5	5	5	5	5	5	5
1	1	1	1	1	1	1	1	1	1
2	3	3	3	3	3	3	3	3	3
3	4	4	4	4	4	4	4	4	4
4	2	2	2	2	2	2	2	2	2

# **XGboost**

```
'max features':[1,2,3],
                       'min samples leaf':[13,14,15,16,17,18],
                        'min_samples_split':[5,6,7,8,9,10]
         gbm=xgb.XGBClassifier(
                                  n jobs=-1,
                                  random state=0)
         # randommized searchCV
         rs=RandomizedSearchCV(gbm,RS,cv=5,scoring=f1,verbose=0)
In [93]: # fit the train data
         rs.fit(X_train,y_train)
Out[93]: RandomizedSearchCV(cv=5, error score=nan,
                             estimator=XGBClassifier(base score=0.5, booster='gbtree',
                                                     colsample_bylevel=1,
                                                     colsample bynode=1,
                                                     colsample bytree=1, gamma=0,
                                                     learning rate=0.1, max delta step=0,
                                                     max_depth=3, min_child_weight=1,
                                                     missing=None, n_estimators=100,
                                                     n jobs=-1, nthread=None,
                                                     objective='binary:logistic',
                                                     random state=0, reg alpha=0,
                                                     reg lambda=1, s...
                                                   'max_features': [1, 2, 3],
                                                  'min samples_leaf': [13, 14, 15, 16, 17,
                                                                        18],
                                                  'min_samples_split': [5, 6, 7, 8, 9,
                                                                         10],
                                                   'n estimators': [260, 261, 262, 263,
                                                                    264, 265, 266, 267,
                                                                    268, 269, 270, 271,
                                                                    272, 273, 274, 275,
                                                                    276, 277, 278, 279,
                                                                    280, 281, 282, 283,
                                                                    284, 285, 286, 287,
                                                                    288, 289]},
                             pre dispatch='2*n jobs', random state=None, refit=True,
                             return train score=False,
                             scoring=make scorer(f1 score, average=weighted), verbose=0)
In [95]: # obtian best parameters best score
         re hoet coord re hoet narame
```

```
ra.near_acore_'ra.near_harama_
Out[95]: (0.9948908366372446,
          {'n estimators': 280,
            'min samples split': 5,
            'min samples leaf': 14,
            'max features': 1,
            'max depth': 13})
In [96]: GBM = xgb.XGBClassifier(
                                  n estimators=280,
                                  min samples split=5,
                                  min samples leaf=14,
                                  max features= 1,
                                  max depth=13,
                                  n jobs=-1,
                                  random state=0)
         # fit the model
         GBM.fit(X train, y train)
Out[96]: XGBClassifier(base score=0.5, booster='gbtree', colsample bylevel=1,
                       colsample bynode=1, colsample bytree=1, gamma=0,
                       learning rate=0.1, max delta step=0, max depth=13, max features=1,
                       min child weight=1, min samples leaf=14, min samples split=5,
                       missing=None, n estimators=280, n jobs=-1, nthread=None,
                       objective='multi:softprob', random state=0, reg alpha=0,
                       reg lambda=1, scale pos weight=1, seed=None, silent=None,
                       subsample=1, verbosity=1)
In [97]: train_pre=GBM.predict(X_train)
         test_pre=GBM.predict(X_test)
         # obtian f1 score
         f1_score_train=f1_score(list(y_train),train_pre,average="weighted")
         f1_score_test=f1_score(list(y_test),test_pre,average="weighted")
         # Score for train and test data
         print("F1 Score of train data :" , f1_score_train)
         print("F1 Score of test data : " ,f1_score_test)
         F1 Score of train data: 0.9969347300484679
         F1 Score of test data: 0.920427735492214
In [98]: | accuracy train=accuracy score(list(y train), train pre)
         accuracy test=accuracy score(list(y test), test pre)
         print("Accuracy of train data :" , accuracy train)
         print("Accuracy of test data :" ,accuracy test)
```

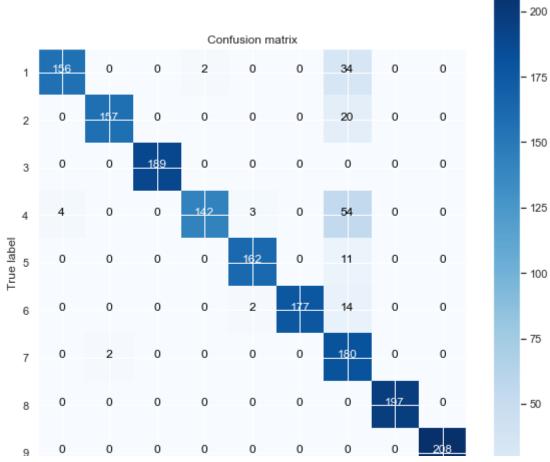
```
Accuracy of train data: 0.996936095710534
         Accuracy of test data: 0.9148191365227538
In [101]: import itertools
          def plot_confusion_matrix(cm, classes,
                                   normalize=False,
                                     title='Confusion matrix',
                                     cmap=plt.cm.Blues):
               ......
               This function prints and plots the confusion matrix.
              Normalization can be applied by setting `normalize=True`.
              if normalize:
                  cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
                  print("Normalized confusion matrix")
              else:
                  print('Confusion Matrix, without normalization')
              print(cm)
              plt.imshow(cm, interpolation='nearest', cmap=cmap)
              plt.title(title)
              plt.colorbar()
              tick marks = np.arange(len(classes))
              plt.xticks(tick marks, classes, rotation=45)
              plt.yticks(tick_marks, classes)
              fmt = '.2f' if normalize else 'd'
              thresh = cm.max() / 2.
              for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
                  plt.text(j, i, format(cm[i, j], fmt),
                           horizontalalignment="center",
                           color="white" if cm[i, j] > thresh else "black")
              plt.tight layout()
              plt.ylabel('True label')
              plt.xlabel('Predicted label')
```

```
https://github.com/melanieshi0120/DNA_project/blob/master/DNA_project_EDA.ipynb
```

plt.figure(figsize=(8,8))

In [102]: classes=[1,2,3,4,5,6,7,8,9]

Confusion			Matı	cix,	with	nout	normalization		
[[1	56	0	0	2	0	0	34	0	0]
[	0	157	0	0	0	0	20	0	0]
[	0	0	189	0	0	0	0	0	0]
[	4	0	0	142	3	0	54	0	0]
[	0	0	0	0	162	0	11	0	0]
[	0	0	0	0	2	177	14	0	0]
[	0	2	0	0	0	0	180	0	0]
[	0	0	0	0	0	0	0	197	0]
[	0	0	0	0	0	0	0	0	208]]





```
In [104]: # Prediction vs Actual Values
    y_test.value_counts().sort_index().plot(kind='bar',label='Actual Values',color='blue')
    pd.Series(test_pre).value_counts().sort_index().plot(kind='bar',label='Predicted Values',color
    ='r',alpha=0.7)
    plt.title('Actual Values VS Predictied Values')
    plt.xlabel('Classes')
    plt.ylabel("Counts")
    plt.legend()
    plt.show()
```

