SOURCE CODE

from tkinter import messagebox from tkinter import * from tkinter import simpledialog import tkinter from tkinter import filedialog import matplotlib.pyplot as plt from tkinter.filedialog import askopenfilename from CustomButton import TkinterCustomButton from sklearn.model_selection import train_test_split from sklearn.metrics import precision_score from sklearn.metrics import recall_score from sklearn.metrics import fl_score from sklearn.metrics import accuracy_score import pandas as pd import numpy as np import pickle import os from string import punctuation from nltk.corpus import stopwords import nltk

from nltk.stem import WordNetLemmatizer

```
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.svm import LinearSVC
from sklearn.linear model import LogisticRegression
from sklearn.naive bayes import MultinomialNB
from sklearn.neural network import MLPClassifier
from sklearn.linear model import SGDClassifier
from sklearn.linear model import RidgeClassifier
from numpy import dot
from numpy.linalg import norm
main = Tk()
main.title("Integrated ML with NLP framework for Drug Recommendation System")
main.geometry("1300x1200")
global filename
global dataset
global X, Y
global X_train, X_test, y_train, y_test
accuracy = []
precision = []
recall = []
fscore = []
stop words = set(stopwords.words('english'))
```

```
lemmatizer = WordNetLemmatizer()
global drug name, condition, review, rating
global tfidf_vectorizer
global classifier
def cleanPost(doc):
  tokens = doc.split()
  table = str.maketrans(", ", punctuation)
  tokens = [w.translate(table) for w in tokens]
  tokens = [word for word in tokens if word.isalpha()]
  tokens = [w for w in tokens if not w in stop words]
  tokens = [word for word in tokens if len(word) > 1]
  tokens = [lemmatizer.lemmatize(token) for token in tokens]
  tokens = ' '.join(tokens)
  return tokens
def uploadDataset():
  global filename
  global dataset
  text.delete('1.0', END)
  filename = askopenfilename(initialdir = "Dataset")
  tfl.insert(END,str(filename))
  text.insert(END,"Dataset Loaded\n\n")
```

```
dataset = pd.read_csv(filename,sep="\t",nrows=5000)
  text.insert(END,str(dataset.head()))
  label = dataset.groupby('rating').size()
  label.plot(kind="bar")
  plt.title("Ratings Graph")
  plt.show()
def preprocessDataset():
  global X, Y
  global X train, X test, y train, y test
  global drug_name, condition, review, rating
  global dataset
  text.delete('1.0', END)
  if os.path.exists('model/data.npy'):
     data = np.load("model/data.npy")
    drug_name = data[0]
     condition = data[1]
    review = data[2]
    rating = data[3]
  else:
     for i in range(len(dataset)):
       dname = dataset.get value(i,"drugName")
       cond = dataset.get value(i,"condition")
```

```
reviewText = dataset.get_value(i,"review")
       ratings = dataset.get value(i,"rating")
       reviewText = str(reviewText)
       reviewText = reviewText.strip().lower()
       reviewText = cleanPost(reviewText)
       drug name.append(dname)
       condition.append(cond)
       review.append(reviewText)
       rating.append(ratings-1)
       print(i)
    data = [drug name,condition,review,rating]
    data = np.asarray(data)
    np.save("model/data",data)
  text.insert(END,"Reviews after cleaning and preprocessing\n\n")
  text.insert(END,str(review))
  label = dataset.groupby('drugName').size().head(20)
  label.plot(kind="bar")
  plt.title("Top 20 Drug Name Graph")
  plt.show()
def TFIDFExtraction():
  global drug_name, condition, review, rating
  global tfidf vectorizer
  text.delete('1.0', END)
```

```
global X, Y
  global X train, X test, y train, y test
  tfidf vectorizer = TfidfVectorizer(stop words=stop words, use idf=True,
smooth_idf=False, norm=None, decode_error='replace', max_features=700)
  tfidf = tfidf vectorizer.fit transform(review).toarray()
  df = pd.DataFrame(tfidf, columns=tfidf vectorizer.get feature names())
  text.insert(END,str(df)+"\n'")
  text.insert(END,str(df.values[0]))
  df = df.values
  X = df[:, 0:df.shape[1]]
  Y = rating
  indices = np.arange(X.shape[0])
  np.random.shuffle(indices)
  X = X[indices]
  Y = Y[indices]
  X train, X test, y train, y test = train test split(X, Y, test size=0.2)
def test(cls,name):
  predict = cls.predict(X_test)
  acc = accuracy_score(y_test,predict)*100
  p = precision score(y test,predict,average='macro') * 100
  r = recall score(y test,predict,average='macro') * 100
  f = f1 score(y test,predict,average='macro') * 100
  text.insert(END,name+" Precision : "+str(p)+"\n")
```

```
text.insert(END,name+" Recall : "+str(r)+"\n")
  text.insert(END,name+" F1-Score : "+str(f)+"\n")
  text.insert(END,name+" Accuracy : "+str(acc)+"\n\n")
  precision.append(p)
  accuracy.append(acc)
  recall.append(r)
  fscore.append(f)
def TrainML():
  global X, Y
  global X_train, X_test, y_train, y_test
  global classifier
  text.delete('1.0', END)
  if os.path.exists('model/lr.txt'):
     with open('model/lr.txt', 'rb') as file:
       lr cls = pickle.load(file)
     file.close()
     test(lr cls,"Logistic Regression")
  else:
     lr cls = LogisticRegression(max iter=500)
     lr cls.fit(X,Y)
     test(lr_cls,"Logistic Regression")
     with open('model/lr.txt', 'wb') as file:
       pickle.dump(lr cls, file)
```

```
if os.path.exists('model/svc.txt'):
  with open('model/svc.txt', 'rb') as file:
     svc_cls = pickle.load(file)
  file.close()
  test(svc cls,"Linear SVC")
else:
  svc_cls = LinearSVC()
  svc cls.fit(X,Y)
  test(svc cls,"Linear SVC")
  with open('model/svc.txt', 'wb') as file:
     pickle.dump(svc cls, file)
  file.close()
if os.path.exists('model/ridge.txt'):
  with open('model/ridge.txt', 'rb') as file:
     ridge_cls = pickle.load(file)
  file.close()
  test(ridge cls,"Ridge Classifier")
else:
  ridge_cls = RidgeClassifier()
  ridge cls.fit(X,Y)
  test(ridge cls,"Ridge Classifier")
```

file.close()

```
with open('model/ridge.txt', 'wb') as file:
     pickle.dump(ridge_cls, file)
  file.close()
if os.path.exists('model/nb.txt'):
  with open('model/nb.txt', 'rb') as file:
     nb cls = pickle.load(file)
  file.close()
  test(nb_cls,"Multinomial Naive Bayes")
else:
  nb cls = MultinomialNB()
  nb_cls.fit(X,Y)
  test(nb cls,"Multinomial Naive Bayes")
  with open('model/nb.txt', 'wb') as file:
     pickle.dump(nb_cls, file)
  file.close()
if os.path.exists('model/sgd.txt'):
  with open('model/sgd.txt', 'rb') as file:
     sgd cls = pickle.load(file)
  file.close()
  test(sgd_cls,"SGDClassifier")
else:
  sgd cls = MultinomialNB()
```

```
sgd_cls.fit(X,Y)
  test(sgd_cls,"SGDClassifier")
  with open('model/sgd.txt', 'wb') as file:
    pickle.dump(sgd_cls, file)
  file.close()
if os.path.exists('model/mlp.txt'):
  with open('model/mlp.txt', 'rb') as file:
    mlp_cls = pickle.load(file)
  file.close()
  test(mlp cls,"Multilayer Perceptron Classifier")
  classifier = mlp_cls
else:
  mlp_cls = MLPClassifier()
  mlp_cls.fit(X,Y)
  test(mlp cls,"Multilayer Perceptron Classifier")
  with open('model/mlp.txt', 'wb') as file:
    pickle.dump(mlp_cls, file)
  file.close()
  classifier = mlp_cls
```

def graph():

```
df = pd.DataFrame([['Logistic Regression','Accuracy',accuracy[0]],['Logistic
Regression', 'Precision', precision[0]], ['Logistic Regression', 'Recall', recall[0]], ['Logistic
Regression', 'FScore', fscore[0]],
                                          ['Linear SVC', 'Accuracy', accuracy[1]], ['Linear
SVC', 'Precision', precision[1]], ['Linear SVC', 'Recall', recall[1]], ['Linear SVC', 'Recall', recall', recall[1]], ['Linear SVC', 'Recall', recall', recall']
SVC','FScore',fscore[1]],
                                          ['Ridge Classifier','Accuracy',accuracy[2]],['Ridge
Classifier', 'Precision', precision[2]], ['Ridge Classifier', 'Recall', recall[2]], ['Ridge Classifier', 'Recall', recall[2]], ['Ridge Classifier', 'Recall', recall', recall']
Classifier', 'FScore', fscore[2]],
['MultinomialNB','Accuracy',accuracy[3]],['MultinomialNB','Precision',precision[3]],['Multin
omialNB', 'Recall', recall[3]], ['MultinomialNB', 'FScore', fscore[3]],
['SGDClassifier', 'Accuracy', accuracy[4]], ['SGDClassifier', 'Precision', precision[4]], ['SGDClassifier', precision', precision[4]], ['SGDClassifier', precision', precision[4]], ['SGDClassifier', precision[4]], ['SGDClassifier
sifier', 'Recall', recall[4]], ['SGDClassifier', 'FScore', fscore[4]],
                                          ['MLP Classifier', 'Accuracy', accuracy[5]], ['MLP
Classifier', 'Precision', precision[5]], ['MLP Classifier', 'Recall', recall[5]], ['MLP
Classifier', 'FScore', fscore[5]],
                                        ],columns=['Parameters','Algorithms','Value'])
       df.pivot("Parameters", "Algorithms", "Value").plot(kind='bar')
       plt.show()
def recommendDrug():
       text.delete('1.0', END)
       global X
       global drug name, condition, review, rating
       global classifier
```

```
global tfidf_vectorizer
  filename = askopenfilename(initialdir = "Dataset")
  testData = pd.read csv(filename)
  testData = testData.values
  for i in range(len(testData)):
    review = cleanPost(testData[i,0].strip().lower())
    array = tfidf vectorizer.transform([review]).toarray()
    predict = classifier.predict(array)[0]
    maxValue = 0
    dname = "none"
    print(str(array[0].shape)+" "+str(X.shape))
    for j in range(len(X)):
       score = dot(X[j], array[0])/(norm(X[j])*norm(array[0]))
       if score > maxValue:
         maxValue = score
         dname = drug name[j]
    text.insert(END,"Disease Name: "+str(testData[i,0])+"\n")
    text.insert(END,"Recommended Drug: "+str(dname)+"\n")
    text.insert(END,"Predicted Ratings: "+str(predict)+"\n\n")
font = ('times', 15, 'bold')
title = Label(main, text='Integrated ML with NLP framework for Drug Recommendation
System')
title.config(bg='HotPink4', fg='yellow2')
```

```
title.config(font=font)
title.config(height=3, width=120)
title.place(x=0,y=5)
font1 = ('times', 13, 'bold')
ff = ('times', 12, 'bold')
11 = Label(main, text='Dataset Location:')
11.config(font=font1)
11.place(x=50,y=100)
tf1 = Entry(main,width=60)
tfl.config(font=font1)
tfl.place(x=230,y=100)
uploadButton = TkinterCustomButton(text="Upload Drug Review Dataset", width=300,
corner radius=5, command=uploadDataset)
uploadButton.place(x=50,y=150)
preprocessButton = TkinterCustomButton(text="Read & Preprocess", width=300,
corner radius=5, command=preprocessDataset)
preprocessButton.place(x=400,y=150)
tfidfButton = TkinterCustomButton(text="TF-IDF Features Extraction", width=300,
corner radius=5, command=TFIDFExtraction)
```

```
trainMLButton = TkinterCustomButton(text="Train ML models", width=300,
corner_radius=5, command=TrainML)
trainMLButton.place(x=50,y=200)
graphButton = TkinterCustomButton(text="Performance Comparison", width=300,
corner radius=5, command=graph)
graphButton.place(x=400,y=200)
predictButton = TkinterCustomButton(text="Recommend Drug from Test Data", width=300,
corner radius=5, command=recommendDrug)
predictButton.place(x=790,y=200)
font1 = ('times', 13, 'bold')
text=Text(main,height=20,width=130)
scroll=Scrollbar(text)
text.configure(yscrollcommand=scroll.set)
text.place(x=10,y=250)
text.config(font=font1)
main.config(bg='plum2')
main.mainloop()
```

tfidfButton.place(x=790,y=150)

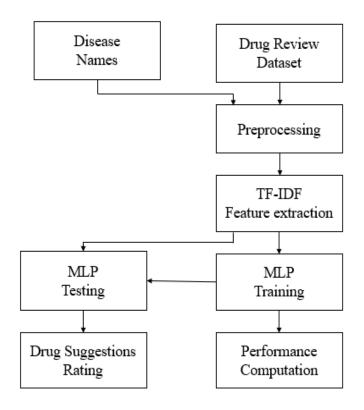
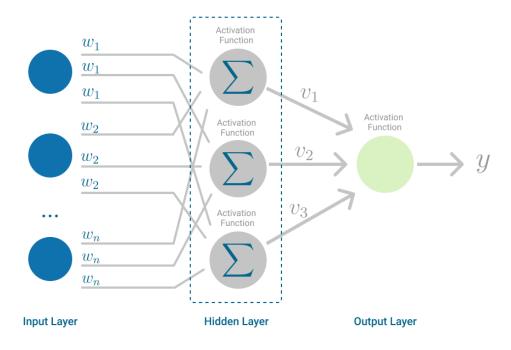


Fig. 1: Block Diagram of Proposed System.



Architecture of MLP.

RESULTS AND DISCUSSION

DRUGREVIEW Dataset

Data Set Information

The dataset provides patient reviews on specific drugs along with related conditions and a 10-star patient rating reflecting overall patient satisfaction. The data was obtained by crawling online pharmaceutical review sites. The intention was to study.

- 1. Sentiment analysis of drug experience over multiple facets, i.e., sentiments learned on specific aspects such as effectiveness and side effects,
- 2. The transferability of models among domains, i.e., conditions, and
- 3. The transferability of models among different data sources (see 'Drug Review Dataset (Druglib.com)').

The data is split into a train (75%) and a test (25%) partition (see publication) and stored in two.tsv (tab-separated-values) files, respectively.

Attribute Information

- drugName (categorical): name of drug.
- condition (categorical): name of condition.
- review (text): patient review.
- rating (numerical): 10-star patient rating.
- date (date): date of review entry.
- usefulCount (numerical): number of users who found review useful.

```
drugName conditionreview rating date usefulCount

206461 ValsartanLeft Ventricular Dysfunction """It has no side effect, I take it in combination of Bystolic 5 Mg and Fish Oil"""

3 95260 Guanfacine ADHD """My son is halfway through his fourth week of Intuniv. We became concerned when he began this 1
We have tried many different medications and so far this is the most effective.""" 8.0 April 27, 2010 192

92703 Lybrel Birth Control """I used to take another oral contraceptive, which had 21 pill cycle, and was very happy- very light p
The positive side is that I didn&#039:t have any other side effects. The idea of being period free was so tempting... Alas.""" 5.0 Dec
138000 Ortho Evra Birth Control """This is my first time using any form of birth control. L&#039:m glad. I went with the patch, 11
8 35696 Buprenorphine / naloxone Opiate Dependence """Suboxone has completely turned my life around. I feel healthier, L&#
1 15963 Cialis Benign Prostatic Hyperplasia """2nd day on Sing started to work with rock hard erections however experianced
10 165907 Levonorgestrel Emergency Contraception """He pulled out, but he cummed a bit in me. I took the Plan B 26 hours late
10 12654 Aripiprazole Bipolar Disorde """Abilify changed my life. There is hope. I was on Zoloft and Clonidine when I first started
10 12654 Aripiprazole Bipolar Disorde """Abilify changed my life. There is hope. I was on Zoloft and Clonidine when I first started
11 248228
12 24907 Topiramate Migraine Prevention """I have been on this medication almost two weeks, started out on 25 mg and working
13 Topic L-methylfolate Depression """I have taken anti-depressants for years, with some improvement but mostly moderate to
14 I long take Cymbalta now mostly for pain.

18 When I began Deplin, I noticed a major improvement overnight. More energy, better disposition, and no sinking to the low lows of maj
191290 Pentasa Crohn's Disease """I have been on this medication almost two weeks, started out on 25 mg and working
19 29404 Nexplanon Birth Control """I have a l
```

Figure 1. Sample dataset

In above screen first row represents dataset column names such as drug name, condition, review and rating and remaining rows contains dataset values and we will used above REVIEWS and RATINGS to trained machine learning models. Below is the test data which contains only disease name and machine learning will predict Drug name and ratings.

- 1 Disease_name
- 2 Rheumatoid Arthritis
- 3 Panic Disorde
- 4 Depression
- 5 Underactive Thyroid
- 6 Constipation
- 7 Urinary Tract Infection 8 High Blood Pressure

Figure 2. Dataset properties

In above test data we have only disease name and machine learning will predict ratings and drug names.

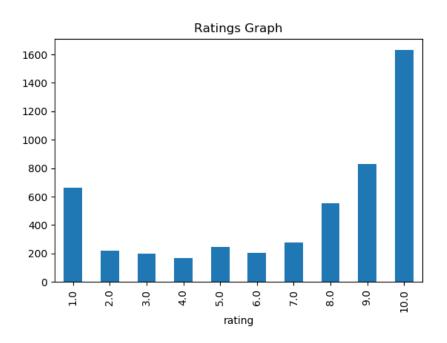


Figure 3. Drugs ratings graph

In above graph we can see dataset loaded and in graph x-axis represents ratings and y-axis represents total number of records which got that rating. Now close above graph and then click on 'Read & Pre-process Dataset' button to read all dataset values and then pre-process to remove stop words and special symbols and then form a features array.

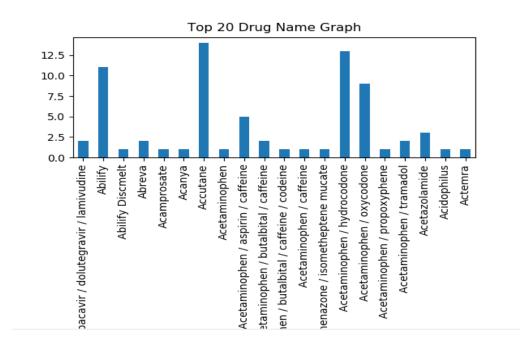


Figure 5. Drug names dataset

In above screen we can see from all reviews stop words and special symbols are removed and in graph I am displaying TOP 20 medicines exist in dataset. In above graph x-axis represents drug name and y-axis represents its count.

Table 1. Performance comparison

Method	Precision	Recall	F1-Score	Accuracy
Existing Logistic regression	80.54	79.30	79.27	76
Existing SVC	70.51	71.18	70,46	67.80
Existing Ridge classifier	66.786	37.72	42.78	55.1
Existing Multimodal navie bayes	41.32	47.98	43.14	47.19
Existing SGDC	41.324	47.18	43.44	47.49
Proposed MLP	99.96	99.72	99.84	99.9

In above table for each algorithm we calculate accuracy, precision, recall and FSCORE and in all algorithms MLP has got high performance.

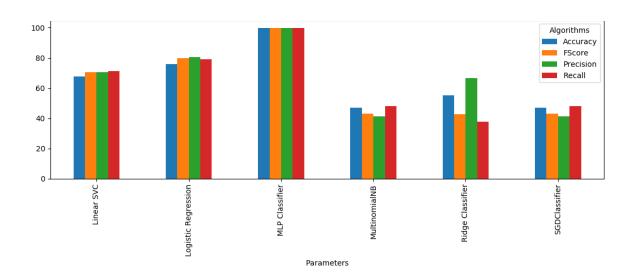


Figure 6. Performance comparison graph

In above graph x-axis represents algorithm name and y-axis represents accuracy, precision recall and FSCORE where each different colour bar will represent one metric and in above graph we can see MLP got high performance.



Figure 7. Drug recommendations from test data.

In above screen for each disease name application has predicted recommended drug name and ratings.