Compiled Report for Disease Prediction using Symptoms

By-

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```
#Importing Libraries
from mpl_toolkits.mplot3d import Axes3D
from sklearn.preprocessing import StandardScaler
import matplotlib.pyplot as plt
from tkinter import *
import numpy as np
import pandas as pd
import os
```

These are the imported libraries that are utilized to use various tools that are available in that specific library. Tkinter is used to build a Graphical User Interface in Python.

```
#List of the symptoms is listed here in list l1.

l1=['back_pain','constipation','abdominal_pain','diarrhoea','mild_fever','yellow_urine',
    'yellowing_of_eyes','acute_liver_failure','fluid_overload','swelling_of_stomach',
    'swelled_lymph_nodes','malaise','blurred_and_distorted_vision','phlegm','throat_irritation',
    'redness_of_eyes','sinus_pressure','runny_nose','congestion','chest_pain','weakness_in_limbs',
    'fast_heart_rate','pain_during_bowel_movements','pain_in_anal_region','bloody_stool',
    'irritation_in_anus','neck_pain','dizziness','cramps','bruising','obesity','swollen_legs',
    'swollen_blood_vessels','puffy_face_and_eyes','enlarged_thyroid','brittle_nails',
    'swollen_extremeties','excessive_hunger','extra_marital_contacts','drying_and_tingling_lips',
    'slurred_speech','knee_pain','hip_joint_pain','muscle_weakness','stiff_neck','swelling_joints',
    'movement_stiffness','spinning_movements','loss_of_balance','unsteadiness',
    'weakness_of_one_body_side','loss_of_smell','bladder_discomfort','foul_smell_of urine',
    'continuous_feel_of_urine','passage_of_gases','internal_itching','toxic_look_(typhos)',
    'depression','irritability','muscle_pain','altered_sensorium','red_spots_over_body','belly_pain',
    'abnormal_menstruation','dischromic _patches','watering_from_eyes','increased_appetite','polyuria',
    'family_history','mucoid_sputum','rusty_sputum','lack_of_concentration','visual_disturbances',
    'receiving_blood_transfusion','receiving_unsterile_injections','coma','stomach_bleeding','distention_of_abdomen',
    'history_of_alcohol_consumption','fluid_overload','blood_in_sputum','prominent_veins_on_calf',
    'palpitations','painful_walking','pus_filled_pimples','blackheads','scurring','skin_peeling',
    'silver_like_dusting','small_dents_in_nails','inflammatory_nails','blister','red_sore_around_nose',
    'yellow_crust_ooze']
```

L1 is the list made for various Symptoms which are generally showed up in people for various Diseases.

```
#List of Diseases is listed in list disease.

disease=['Fungal infection','Allergy','GERD','Chronic cholestasis','Drug Reaction',
    'Peptic ulcer diseae','AIDS','Diabetes','Gastroenteritis','Bronchial Asthma','Hypertension',
    ' Migraine','Cervical spondylosis',
    'Paralysis (brain hemorrhage)','Jaundice','Malaria','Chicken pox','Dengue','Typhoid','hepatitis A',
    'Hepatitis B','Hepatitis C','Hepatitis D','Hepatitis E','Alcoholic hepatitis','Tuberculosis',
    'Common Cold','Pneumonia','Dimorphic hemmorhoids(piles)',
    'Heartattack','Varicoseveins','Hypothyroidism','Hyperthyroidism','Hypoglycemia','Osteoarthristis',
    'Arthritis','(vertigo) Paroymsal  Positional Vertigo','Acne','Urinary tract infection','Psoriasis',
    'Impetigo']
```

Disease is the list made for different Diseases which are for the most part appeared in different individuals.

```
l2=[]
for i in range(0,len(l1)):
    l2.append(0)
print(l2)
```

First L2 is the vacant list made. At that point, equivalent to a number of diseases in list L1, L2 is appended in a number of zeroes.

```
#Reading the training .csv file
df=pd.read_csv("training.csv")
#Replace the values in the imported file by pandas by the inbuilt function replace in pandas.
df.replace({'prognosis':{'Fungal infection':0,'Allergy':1,'GERD':2,'Chronic cholestasis':3,'Drug Reaction':4,
    'Peptic ulcer diseae':5,'AIDS':6,'Diabetes ':7,'Gastroenteritis':8,'Bronchial Asthma':9,'Hypertension ':10,
    'Migraine':11,'Cervical spondylosis':12,
    'Paralysis (brain hemorrhage)':13,'Jaundice':14,'Malaria':15,'Chicken pox':16,'Dengue':17,'Typhoid':18,'hepatitis A':19,
    'Hepatitis B':20,'Hepatitis C':21,'Hepatitis D':22,'Hepatitis E':23,'Alcoholic hepatitis':24,'Tuberculosis':25,
    'Common Cold':26,'Pneumonia':27,'Dimorphic hemmorhoids(piles)':28,'Heart attack':29,'Varicose veins':30,'Hypothyroidism':
    'Hyperthyroidism':32,'Hypoglycemia':33,'Osteoarthristis':34,'Arthritis':35,
    '(vertigo) Paroymsal  Positional Vertigo':36,'Acne':37,'Urinary tract infection':38,'Psoriasis':39,
    'Impetigo':40}},inplace=True)
df.head()
```

There is a CSV document containing diseases and symptoms, named training.csv, which is utilized to prepare the model. Read_csv() function is utilized to store the information in the dataframe, named df. Utilizing replace() function, prognosis column that are the different diseases, it is replaced by the numbers from 0 to n-1, where n is the number of different diseases present in .csv record. Head() function is utilized to print the initial five rows of the preparation dataframe.

Out[179]:

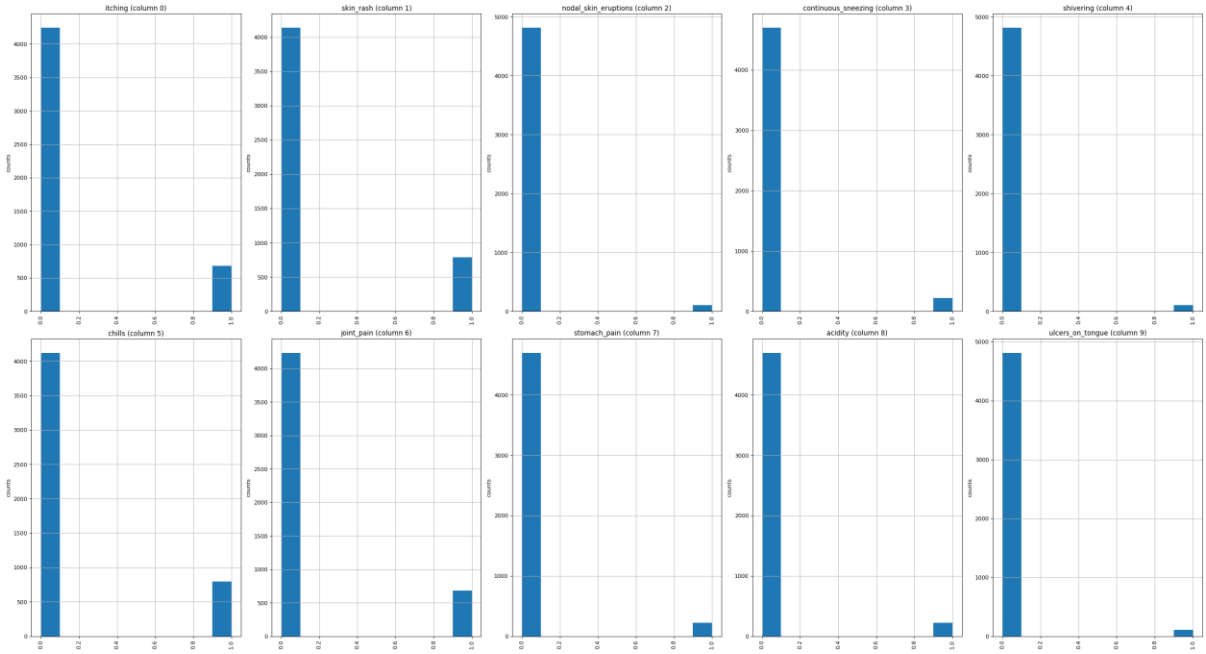
	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on_tongue	...	blackheads	scurri
0	1	1	1	0	0	0	0	0	0	0	...	0	
1	0	1	1	0	0	0	0	0	0	0	...	0	
2	1	0	1	0	0	0	0	0	0	0	...	0	
3	1	1	0	0	0	0	0	0	0	0	...	0	
4	1	1	1	0	0	0	0	0	0	0	...	0	

5 rows × 133 columns

This is the output produced which contains the initial five rows of the dataframe df.

```
# Distribution graphs (histogram/bar graph) of column data
def plotPerColumnDistribution(df1, nGraphShown, nGraphPerRow):
    nunique = df1.nunique()
    df1 = df1[[col for col in df if nunique[col] > 1 and nunique[col] < 50]] # For displaying purposes, pick columns that have b
    nRow, nCol = df1.shape
    columnNames = list(df1)
    nGraphRow = (nCol + nGraphPerRow - 1) / nGraphPerRow
    plt.figure(num = None, figsize = (6 * nGraphPerRow, 8 * nGraphRow), dpi = 80, facecolor = 'w', edgecolor = 'k')
    for i in range(min(nCol, nGraphShown)):
        plt.subplot(nGraphRow, nGraphPerRow, i + 1)
        columnDf = df.iloc[:, i]
        if (not np.issubdtype(type(columnDf.iloc[0]), np.number)):
            valueCounts = columnDf.value_counts()
            valueCounts.plot.bar()
        else:
            columnDf.hist()
        plt.ylabel('counts')
        plt.xticks(rotation = 90)
        plt.title(f'{columnNames[i]} (column {i})')
    plt.tight_layout(pad = 1.0, w_pad = 1.0, h_pad = 1.0)
    plt.show()
plotPerColumnDistribution(df, 10, 5)
```

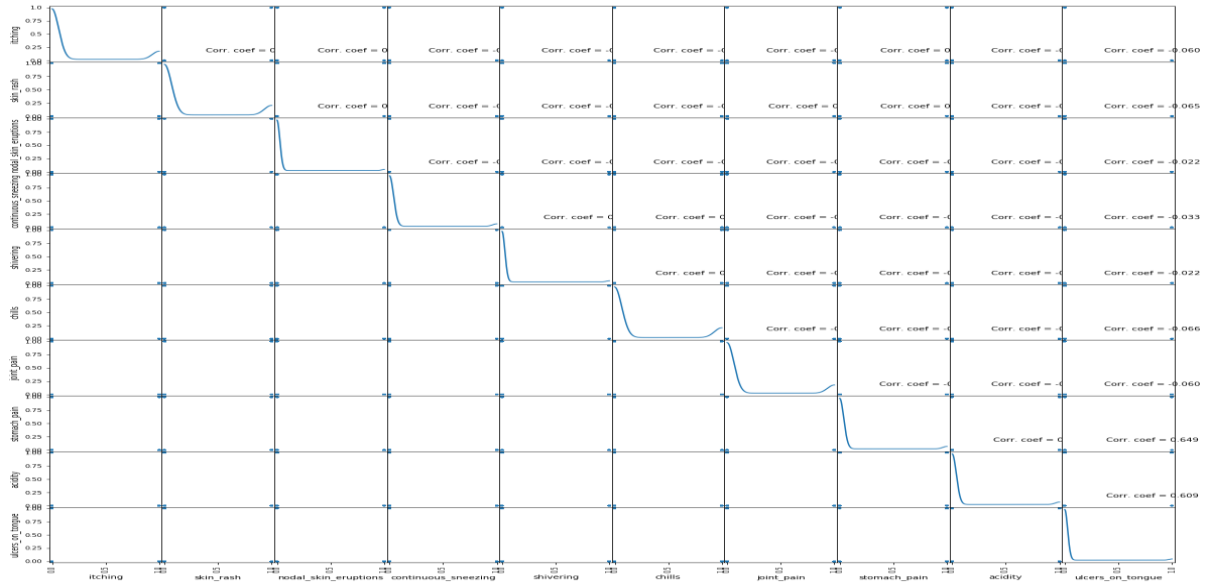
This is the code for the distribution graph of the columns of training.csv file.



Output for the distribution graph of the columns of training.csv file.

```
# Scatter and density plots
def plotScatterMatrix(df1, plotSize, textSize):
    df1 = df1.select_dtypes(include =[np.number]) # keep only numerical columns
    # Remove rows and columns that would lead to df being singular
    df1 = df1.dropna('columns')
    df1 = df1[[col for col in df if df[col].nunique() > 1]] # keep columns where there are more than 1 unique values
    columnNames = list(df)
    if len(columnNames) > 10: # reduce the number of columns for matrix inversion of kernel density plots
        columnNames = columnNames[:10]
    df1 = df1[columnNames]
    ax = pd.plotting.scatter_matrix(df1, alpha=0.75, figsize=[plotSize, plotSize], diagonal='kde')
    corrs = df1.corr().values
    for i, j in zip(*plt.np.triu_indices_from(ax, k = 1)):
        ax[i, j].annotate('Corr. coef = %.3f' % corrs[i, j], (0.8, 0.2), xycoords='axes fraction', ha='center', va='center', siz
    plt.suptitle('Scatter and Density Plot')
    plt.show()
plotScatterMatrix(df, 20, 10)
```

This is the code for the scatter and density plots of the columns of training.csv file.



Output for the distribution graph of the columns of training.csv file.

```
X= df[l1]
y = df[["prognosis"]]
np.ravel(y)
print(X)
```

Putting the Symptoms in X and prognosis/diseases in y for training the model.

```
    back_pain  constipation  abdominal_pain  diarrhoea  mild_fever  \
0           0             0               0          0           0
1           0             0               0          0           0
2           0             0               0          0           0
3           0             0               0          0           0
4           0             0               0          0           0
5           0             0               0          0           0
6           0             0               0          0           0
7           0             0               0          0           0
8           0             0               0          0           0
9           0             0               0          0           0
10          0             0               0          0           0
11          0             0               0          0           0
12          0             0               0          0           0
13          0             0               0          0           0
14          0             0               0          0           0
15          0             0               0          0           0
16          0             0               0          0           0
17          0             0               0          0           0
18          0             0               0          0           0
```

Output for the print(X) in which different symtoms has the values ‘0’ or ‘1’ according to their presence in the particular diseases

```
: print(y)
```

	prognosis
0	0
1	0
2	0
3	0
4	0
5	0
6	0
7	0
8	0
9	0
10	1
11	1
12	1
13	1
14	1
15	1
16	1
17	1
18	1
19	1
20	2
21	2

Output for the print(y) in whci different disease has values according to their symptoms.

To build the precision of the model, we utilized four distinctive algorithms which are as per the following

- Decision Tree algorithm
- Random Forest algorithm
- KNearestNeighbour algorithm
- Naive Bayes algorithm

```
#list1 = DF['prognosis'].unique()
def scatterplt(disea):
    x = ((DF.loc[disea]).sum())#total sum of symptom reported for given disease
    x.drop(x[x==0].index,inplace=True)#droping symptoms with values 0
    print(x.values)
    y = x.keys()#storing nameof symptoms in y
    print(len(x))
    print(len(y))
    plt.title(disea)
    plt.scatter(y,x.values)
    plt.show()

def scatterinp(sym1,sym2,sym3,sym4,sym5):
    x = [sym1,sym2,sym3,sym4,sym5]#storing input symptoms in y
    y = [0,0,0,0,0]#creating and giving values to the input symptoms
    if(sym1!='Select Here'):
        y[0]=1
    if(sym2!='Select Here'):
        y[1]=1
    if(sym3!='Select Here'):
        y[2]=1
    if(sym4!='Select Here'):
        y[3]=1
    if(sym5!='Select Here'):
        y[4]=1
    print(x)
    print(y)
    plt.scatter(x,y)
    plt.show()
```

These are the function to plot the scatterplot of the predictions of the diseases and the symptoms entered by the user.

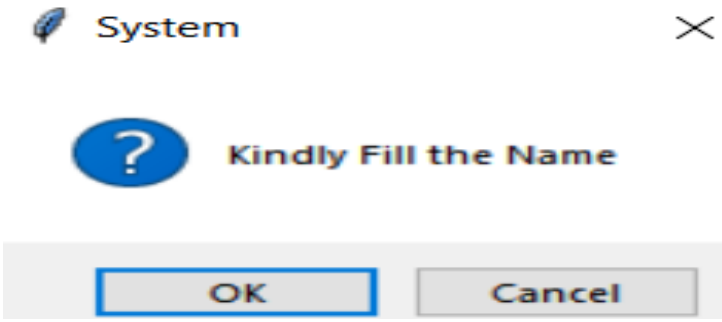
Decision Tree Function:

```
root = Tk()
pred1=StringVar()
def DecisionTree():
```

Root=Tk() is used to for start working with the tkinter to build the gui. Definition of DecisionTree() function. “pred1” is used to store the predicted disease using decision tree algorithm.

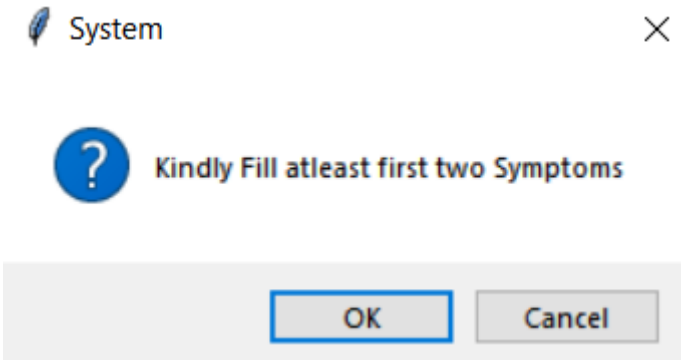
```
if len(NameEn.get()) == 0:
    pred1.set(" ")
    comp=messagebox.askokcancel("System","Kindly Fill the Name")
    if comp:
        root.mainloop()
```

If user tries to run the gui without entering the name, then System will prompt the following message.




```
elif((Symptom1.get()=="Select Here") or (Symptom2.get()=="Select Here")):
    pred1.set(" ")
    sym=messagebox.askokcancel("System","Kindly Fill atleast first two Symptoms")
    if sym:
        root.mainloop()
```

After filling the name, user have to fill five symptoms and out of which first two are compulsory. If user will not select atleast two symptoms, then following message will be prompt from the system



```
    from sklearn import tree
    clf3 = tree.DecisionTreeClassifier()
    clf3 = clf3.fit(X,y)
    from sklearn.metrics import classification_report,confusion_matrix,accuracy_score
    y_pred=clf3.predict(X_test)
    print("Decision Tree")
    print("Accuracy")
    print(accuracy_score(y_test, y_pred))
    print(accuracy_score(y_test, y_pred,normalize=False))
    print("Confusion matrix")
    conf_matrix=confusion_matrix(y_test,y_pred)
    print(conf_matrix)
    psymptoms = [Symptom1.get(),Symptom2.get(),Symptom3.get(),Symptom4.get(),Symptom5.get()]
    for k in range(0,len(l1)):
        for z in psymptoms:
            if(z==l1[k]):
                l2[k]=1
    inputtest = [l2]
    predict = clf3.predict(inputtest)
    predicted=predict[0]

    h='no'
    for a in range(0,len(disease)):
        if(predicted == a):
            h='yes'
            break
    if (h=='yes'):
        pred1.set(" ")
        pred1.set(disease[a])
    else:
        pred1.set(" ")
        pred1.set("Not Found")
```

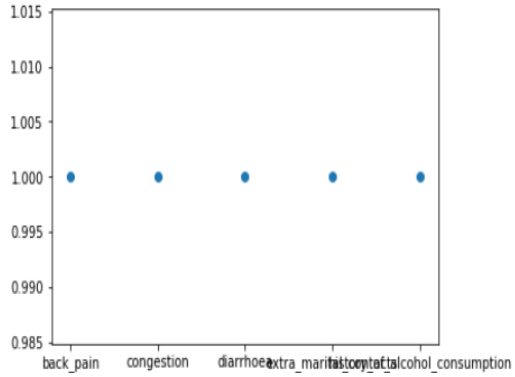
DecisionTreeClassifier() is used to train the model and predict the disease on testing dataset according to symptoms entered by the user. Final disease for decision tree is stored in a variable named “pred1”. Accuracy of predicting the disease is printed using accuracy_score and confusion matrix is created using confusion_matrix which are imported from sklearn.metrices.

```
#Creating the database if not exists named as database.db and creating table if not exists named as DecisionTree using sqlite3
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS DecisionTree(Name StringVar,Symtom1 StringVar,Symtom2 StringVar,Symtom3 StringVar,Symtom
c.execute("INSERT INTO DecisionTree(Name,Symtom1,Symtom2,Symtom3,Symtom4,Symtom5,Disease) VALUES(?,?,?,?,?,?,?)",(NameEn.get()
conn.commit()
c.close()
conn.close()
```

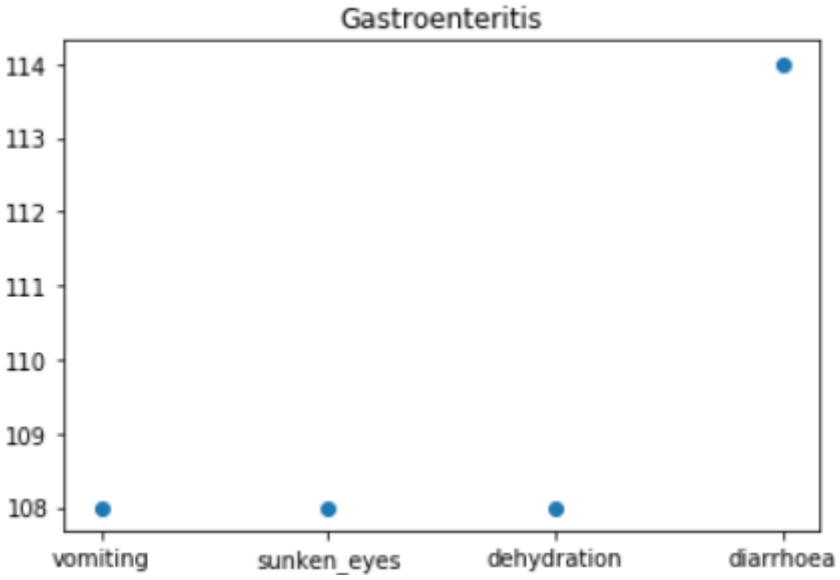
Creating a database named “database.db”, if not exists, using “sqlite3” database. For storing data for decision tree algorithm "DecisionTree" table is created, if not exists, in database.db using “CREATE” function in sqlite. Values are inserted in DecisionTree table using “INSERT” function in sqlite.

```
#printing scatter plot of input symptoms
#printing scatter plot of disease predicted vs its symptoms
scatterinp(Symptom1.get(),Symptom2.get(),Symptom3.get(),Symptom4.get(),Symptom5.get())
scatterplt(pred1.get())
```

```
['back_pain', 'congestion', 'diarrhoea', 'extra_marital_contacts', 'history_of_alcohol_consumption']
[1, 1, 1, 1, 1]
```



The scatterplot for the symtoms which are given by the user as input



The scatter plot for the disease on the basis of symptoms which given by the user as input

Random Forest function:

```
pred2=StringVar()
def randomforest():
```

Definition of randomforest() function. “pred2” is used to store the predicted disease using random forest algorithm.

```
from sklearn.ensemble import RandomForestClassifier
clf4 = RandomForestClassifier(n_estimators=100)
clf4 = clf4.fit(X,np.ravel(y))
# calculating accuracy
from sklearn.metrics import classification_report,confusion_matrix,accuracy_score
y_pred=clf4.predict(X_test)
print("Random Forest")
print("Accuracy")
print(accuracy_score(y_test, y_pred))
print(accuracy_score(y_test, y_pred,normalize=False))
print("Confusion matrix")
conf_matrix=confusion_matrix(y_test,y_pred)
print(conf_matrix)
psymptoms = [Symptom1.get(),Symptom2.get(),Symptom3.get(),Symptom4.get(),Symptom5.get()]
for k in range(0,len(l1)):
    for z in psymptoms:
        if(z==l1[k]):
            l2[k]=1
inputtest = [l2]
predict = clf4.predict(inputtest)
predicted=predict[0]
h='no'
for a in range(0,len(disease)):
    if(predicted == a):
        h='yes'
        break
if (h=='yes'):
    pred2.set(" ")
    pred2.set(disease[a])
else:
    pred2.set(" ")
    pred2.set("Not Found")
```

RandomForestClassifier() is used to train the model and predict the disease on testing dataset according to symptoms entered by the user. Final disease for random forest is stored in a variable named “pred2”. Accuracy of predicting the disease is calculated using accuracy_score and confusion matrix is created using confusion_matrix which are imported from sklearn.metrices.

```
#Creating the database if not exists named as database.db and creating table if not exists named as RandomForest using sqlite3
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS RandomForest(Name StringVar,Symtom1 StringVar,Symtom2 StringVar,Symtom3 StringVar,Symtom4
c.execute("INSERT INTO RandomForest(Name,Symtom1,Symtom2,Symtom3,Symtom4,Symtom5,Disease) VALUES(?,?,?,?,?,?,?)",(NameEn.get(),
conn.commit()
c.close()
conn.close()
```

Same databse is used i.e.,databse.db that is used in decision tree algorithm with different table for random forest algorithm which is name as “RandomForest”.

kNearest Neighbour function:

```
pred4=StringVar()
def KNN():
    if len(NameEn.get()) == 0:
```

Definition of KNN() function. “pred4” is used to store the predicted disease using kNearestNeighbour algorithm.

```
from sklearn.neighbors import KNeighborsClassifier
knn=KNeighborsClassifier(n_neighbors=5,metric='minkowski',p=2)
knn=knn.fit(X,np.ravel(y))
from sklearn.metrics import classification_report,confusion_matrix,accuracy_score
y_pred=knn.predict(X_test)
print("kNearest Neighbour")
print("Accuracy")
print(accuracy_score(y_test, y_pred))
print(accuracy_score(y_test, y_pred,normalize=False))
print("Confusion matrix")
conf_matrix=confusion_matrix(y_test,y_pred)
print(conf_matrix)
psymptoms = [Symptom1.get(),Symptom2.get(),Symptom3.get(),Symptom4.get(),Symptom5.get()]
for k in range(0,len(l1)):
    for z in psymptoms:
        if(z==l1[k]):
            l2[k]=1
inputtest = [l2]
predict = knn.predict(inputtest)
predicted=predict[0]
h='no'
for a in range(0,len(disease)):
    if(predicted == a):
        h='yes'
        break
if (h=='yes'):
    pred4.set(" ")
    pred4.set(disease[a])
else:
    pred4.set(" ")
    pred4.set("Not Found")
```

KNeighboursClassifier() is used to train the model and predict the disease on testing dataset according to symptoms entered by the user. Final disease for kNearestNeighbour is stored in a variable named “pred4”. Accuracy of predicting the disease is calculated using accuracy_score and confusion matrix is created using confusion_matrix which are imported from sklearn.metrices.

```
#Creating the database if not exists named as database.db and creating table if not exists named as KNearestNeighbour using sql
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS KNearestNeighbour(Name StringVar,Symtom1 StringVar,Symtom2 StringVar,Symtom3 StringVar,Sym
c.execute("INSERT INTO KNearestNeighbour(Name,Symtom1,Symtom2,Symtom3,Symtom4,Symtom5,Disease) VALUES(?,?,?,?,?,?,?)",(NameEn.ge
conn.commit()
c.close()
conn.close()
```

Same databse is used i.e.,databse.db that is used in all previous algorithms with different table for kNearest Neighbour algorithm which is name as “KNearestNeighbour”.

Naïve Bayes function:

```
pred3=StringVar()
def NaiveBayes():
```

Definition of NaiveBayes() function. “pred3” is used to store the predicted disease using Naïve Bayes algorithm.

```
from sklearn.naive_bayes import GaussianNB
gnb = GaussianNB()
gnb=gnb.fit(X,np.ravel(y))
from sklearn.metrics import classification_report,confusion_matrix,accuracy_score
y_pred=gnb.predict(X_test)
print("Naive Bayes")
print("Accuracy")
print(accuracy_score(y_test, y_pred))
print(accuracy_score(y_test, y_pred,normalize=False))
print("Confusion matrix")
conf_matrix=confusion_matrix(y_test,y_pred)
print(conf_matrix)
psymptoms = [Symptom1.get(),Symptom2.get(),Symptom3.get(),Symptom4.get(),Symptom5.get()]
for k in range(0,len(l1)):
    for z in psymptoms:
        if(z==l1[k]):
            l2[k]=1
inputtest = [l2]
predict = gnb.predict(inputtest)
predicted=predict[0]
h='no'
for a in range(0,len(disease)):
    if(predicted == a):
        h='yes'
        break
if (h=='yes'):
    pred3.set(" ")
    pred3.set(disease[a])
else:
    pred3.set(" ")
    pred3.set("Not Found")
```

GaussianNB() is used to train the model and predict the disease on testing dataset according to symptoms entered by the user. Final disease for Naïve Bayes is stored in a variable named “pred3”. Accuracy of predicting the disease is calculated using accuracy_score and confusion matrix is created using confusion_matrix which are imported from sklearn.metrices.

```
#Creating the database if not exists named as database.db and creating table if not exists named as NaiveBayes using sqlite3
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS NaiveBayes(Name StringVar,Symtom1 StringVar,Symtom2 StringVar,Symtom3 StringVar,Symtom4 TE
c.execute("INSERT INTO NaiveBayes(Name,Symtom1,Symtom2,Symtom3,Symtom4,Symtom5,Disease) VALUES(?,?,?,?,?,?,?)",(NameEn.get(),Sym
conn.commit()
c.close()
conn.close()
```

Same databse is used i.e.,databse.db that is used in all previous algorithms with different table for Naïve Bayes algorithm which is name as “NaiveBayes”.

Building the Graphical User Interface:

```
#Tk class is used to create a root window
root.configure(background='Ivory')
root.title('Smart Disease Predictor System')
root.resizable(0,0)
```

Graphical User Interface is build using tkinter library in Python. Root is used to start the GUI. It is configured with the background that is set to “Ivory”. GUI titlt is given as “Smart Disease Predictor System” using title() function in tkinter library. Resizable function is used to fix the size GUI.

```
Symptom1 = StringVar()
Symptom1.set("Select Here")

Symptom2 = StringVar()
Symptom2.set("Select Here")

Symptom3 = StringVar()
Symptom3.set("Select Here")

Symptom4 = StringVar()
Symptom4.set("Select Here")

Symptom5 = StringVar()
Symptom5.set("Select Here")
Name = StringVar()
```

Here, variables are defined like Name, Symptom1, Symptom2, etc and they initialised to “Select Here” using set() function in tkinter library.

This is how the above variables are looking like in GUI.

```
prev_win=None
def Reset():
    global prev_win

    Symptom1.set("Select Here")
    Symptom2.set("Select Here")
    Symptom3.set("Select Here")
    Symptom4.set("Select Here")
    Symptom5.set("Select Here")
    NameEn.delete(first=0,last=100)
    pred1.set(" ")
    pred2.set(" ")
    pred3.set(" ")
    pred4.set(" ")
    try:
        prev_win.destroy()
        prev_win=None
    except AttributeError:
```

It is the definition of the function “Reset()” which is used to reset the GUI inputs which are given by the user. It is called when user click on the button “Reset Inputs” from the GUI.

“Reset Inputs” button in GUI

```
from tkinter import messagebox
def Exit():
    qExit=messagebox.askyesno("System","Do you want to exit the system")

    if qExit:
        root.destroy()
        exit()
```

It is the definition of the function “Exit()” which is used to come out from the GUI. It is called when user click on the button “Exit System” from the GUI.

“Exit System” button in GUI

```
#Headings for the GUI written at the top of GUI
w2 = Label(root, justify=LEFT, text="Disease Predictor using Machine Learning", fg="Red", bg="Ivory")
w2.config(font=("Times",30,"bold italic"))
w2.grid(row=1, column=0, columnspan=2, padx=100)
w2 = Label(root, justify=LEFT, text="Contributors: Sudhanshu,Rohan,Aditya", fg="Pink", bg="Ivory")
w2.config(font=("Times",30,"bold italic"))
w2.grid(row=2, column=0, columnspan=2, padx=100)
```

“W2” is the label created for showing the headings in the GUI using label() function from tkinter library. Two text are written under label w2 in row1 and row2 with font features as “Times”,”30”,”bold italic”.

This is how w2 label is available in the GUI

```
#Label for the name
NameLb = Label(root, text="Name of the Patient *", fg="Red", bg="Ivory")
NameLb.config(font=("Times",15,"bold italic"))
NameLb.grid(row=6, column=0, pady=15, sticky=W)
```

“NameLb” is the label created for showing the “Name of the Patient *” using label() function in tkinter library. It is configured using config() function and the grid of the label is set using grid() function.

NameLb label in GUI. ‘ * ’ shows that it is compulsory for the user to give his/her name.

```
#Creating Labels for the symtoms
S1Lb = Label(root, text="Symptom 1 *", fg="Black", bg="Ivory")
S1Lb.config(font=("Times",15,"bold italic"))
S1Lb.grid(row=7, column=0, pady=10, sticky=W)

S2Lb = Label(root, text="Symptom 2 *", fg="Black", bg="Ivory")
S2Lb.config(font=("Times",15,"bold italic"))
S2Lb.grid(row=8, column=0, pady=10, sticky=W)

S3Lb = Label(root, text="Symptom 3", fg="Black",bg="Ivory")
S3Lb.config(font=("Times",15,"bold italic"))
S3Lb.grid(row=9, column=0, pady=10, sticky=W)

S4Lb = Label(root, text="Symptom 4", fg="Black", bg="Ivory")
S4Lb.config(font=("Times",15,"bold italic"))
S4Lb.grid(row=10, column=0, pady=10, sticky=W)

S5Lb = Label(root, text="Symptom 5", fg="Black", bg="Ivory")
S5Lb.config(font=("Times",15,"bold italic"))
S5Lb.grid(row=11, column=0, pady=10, sticky=W)
```

These are the labels for showing the Symptoms of the disease. It is created using label() function from tkinter library. Its features are configured using config() function and their grid is set by using grid() function from tkinter library.

```
#Taking name as input from user
NameEn = Entry(root, textvariable=Name)
NameEn.grid(row=6, column=1)

#Taking Symptoms as input from the dropdown from the user
S1 = OptionMenu(root, Symptom1,*OPTIONS)
S1.grid(row=7, column=1)

S2 = OptionMenu(root, Symptom2,*OPTIONS)
S2.grid(row=8, column=1)

S3 = OptionMenu(root, Symptom3,*OPTIONS)
S3.grid(row=9, column=1)

S4 = OptionMenu(root, Symptom4,*OPTIONS)
S4.grid(row=10, column=1)

S5 = OptionMenu(root, Symptom5,*OPTIONS)
S5.grid(row=11, column=1)
```

NameEn is the entry box created for getting the name of the patient using Entry() function in tknirter library. S1, S2, S3, S4, S5 are the option menu used to get symtoms from the user which is created using Optionmenu in tkinter library. *OPTIONS is the list of unique symtoms.

List of symptoms available for user

```
#Labels for the different algorithms
lrLb = Label(root, text="DecisionTree", fg="white", bg="red", width = 20)
lrLb.config(font=("Times",15,"bold italic"))
lrLb.grid(row=15, column=0, pady=10,sticky=W)

destreeLb = Label(root, text="RandomForest", fg="Red", bg="Orange", width = 20)
destreeLb.config(font=("Times",15,"bold italic"))
destreeLb.grid(row=17, column=0, pady=10, sticky=W)

ranfLb = Label(root, text="NaiveBayes", fg="White", bg="green", width = 20)
ranfLb.config(font=("Times",15,"bold italic"))
ranfLb.grid(row=19, column=0, pady=10, sticky=W)

knnLb = Label(root, text="kNearestNeighbour", fg="Red", bg="Sky Blue", width = 20)
knnLb.config(font=("Times",15,"bold italic"))
knnLb.grid(row=21, column=0, pady=10, sticky=W)
OPTIONS = sorted(l1)
```

These are the labels created for showing the texts of different algorithms

```
#Buttons for predicting the disease using different algorithms
dst = Button(root, text="Prediction 1", command=DecisionTree,bg="Red",fg="yellow")
dst.config(font=("Times",15,"bold italic"))
dst.grid(row=6, column=3,padx=10)

rnf = Button(root, text="Prediction 2", command=randomforest,bg="Light green",fg="red")
rnf.config(font=("Times",15,"bold italic"))
rnf.grid(row=7, column=3,padx=10)

lr = Button(root, text="Prediction 3", command=NaiveBayes,bg="Blue",fg="white")
lr.config(font=("Times",15,"bold italic"))
lr.grid(row=8, column=3,padx=10)

kn = Button(root, text="Prediction 4", command=KNN,bg="sky blue",fg="red")
kn.config(font=("Times",15,"bold italic"))
kn.grid(row=9, column=3,padx=10)

rs = Button(root,text="Reset Inputs", command=Reset,bg="yellow",fg="purple",width=15)
rs.config(font=("Times",15,"bold italic"))
rs.grid(row=10,column=3,padx=10)

ex = Button(root,text="Exit System", command=Exit,bg="yellow",fg="purple",width=15)
ex.config(font=("Times",15,"bold italic"))
ex.grid(row=11,column=3,padx=10)
```

Buttons created for predicting the disease using different algorithms.

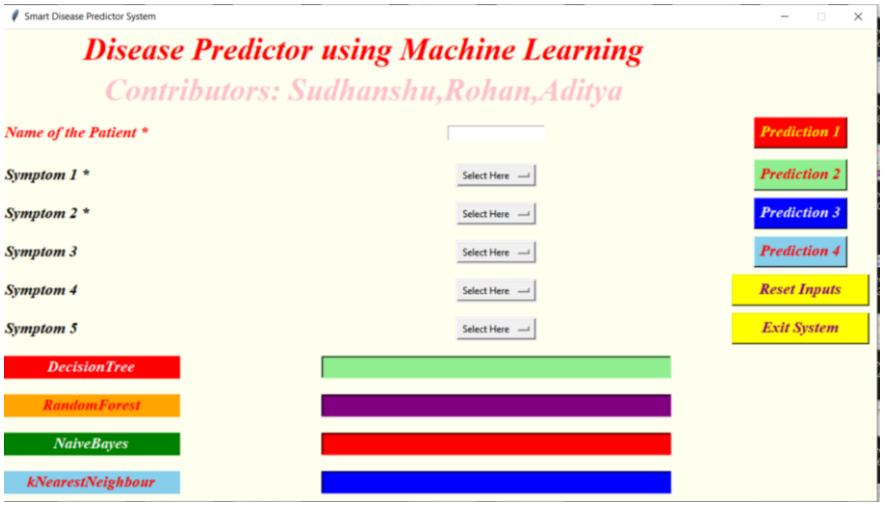
- Press Prediction 1 for Decision tree algorithm
- Press Prediction 2 for Random forest algorithm
- Press Prediction 3 for Naive bayes algorithm
- Press Prediction 4 for K-Nearest neighbour
- Press Reset Inputs for resetting the inputs
- Press Exit System for Exiting from the System


```
#Showing the output of different aldorithms
t1=Label(root,font=("Times",15,"bold italic"),text="Decision Tree",height=1,bg="Light green"
         ,width=40,fg="red",textvariable=pred1,relief="sunken").grid(row=15, column=1, padx=10)

t2=Label(root,font=("Times",15,"bold italic"),text="Random Forest",height=1,bg="Purple"
         ,width=40,fg="white",textvariable=pred2,relief="sunken").grid(row=17, column=1, padx=10)

t3=Label(root,font=("Times",15,"bold italic"),text="Naive Bayes",height=1,bg="red"
         ,width=40,fg="orange",textvariable=pred3,relief="sunken").grid(row=19, column=1, padx=10)

t4=Label(root,font=("Times",15,"bold italic"),text="kNearest Neighbour",height=1,bg="Blue"
         ,width=40,fg="yellow",textvariable=pred4,relief="sunken").grid(row=21, column=1, padx=10)
```

These are label created for showing the predicted disease using different algorithm.


```
#calling this function because the application is ready to run
root.mainloop()
```

This is the calling of the GUI.



The Final GUI presented to the user.