

# HILARIOUS HUMaNS TEAM

```
In [4]: #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
```

```
In [5]: #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',
    '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']
```

```
In [6]: #List of Diseases is listed in list disease.

disease=['Fungal infection', 'Allergy', 'GERD', 'Chronic cholestasis',
          'Drug Reaction', 'Peptic ulcer disease', '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)', 'Heart attack', 'Varicose veins',
          'Hypothyroidism', 'Hyperthyroidism', 'Hypoglycemia',
          'Osteoarthritis', 'Arthritis',
          '(vertigo) Paroymsal  Positional Vertigo', 'Acne',
          'Urinary tract infection', 'Psoriasis', 'Impetigo']

#disease = [df['prognosis'].unique()]
#print(disease)
```

```
In [7]: l2=[]
for i in range(0,len(l1)):
    l2.append(0)
print(l2)
```

[illegible]

```

In [8]: #Reading the training .csv file
df=pd.read_csv("training.csv")
DF= pd.read_csv('training.csv', index_col='prognosis')
#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 disease':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 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':31,'Hypoglycemia':33,'Osteoarthritis':34,'Arthritis':35,'(vertigo) Paroymsal Positional Vertigo':36,'Acne':37,'Urinary tract infection':38,'Psoriasis':39,'Impetigo':40}},inplace=True)
#df.head()
DF.head()

```

Out [8]:

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on_
prognosis										
Fungal infection	1	1	1	0	0	0	0	0	0	0
Fungal infection	0	1	1	0	0	0	0	0	0	0
Fungal infection	1	0	1	0	0	0	0	0	0	0
Fungal infection	1	1	0	0	0	0	0	0	0	0
Fungal infection	1	1	1	0	0	0	0	0	0	0

5 rows × 133 columns

```

In [9]: # 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
    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 = df1.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()

```

```

In [10]: # 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 df1 if df1[col].nunique() > 1]] # keep columns where there are more than 1 unique values
    columnNames = list(df1)
    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', size=textSize)

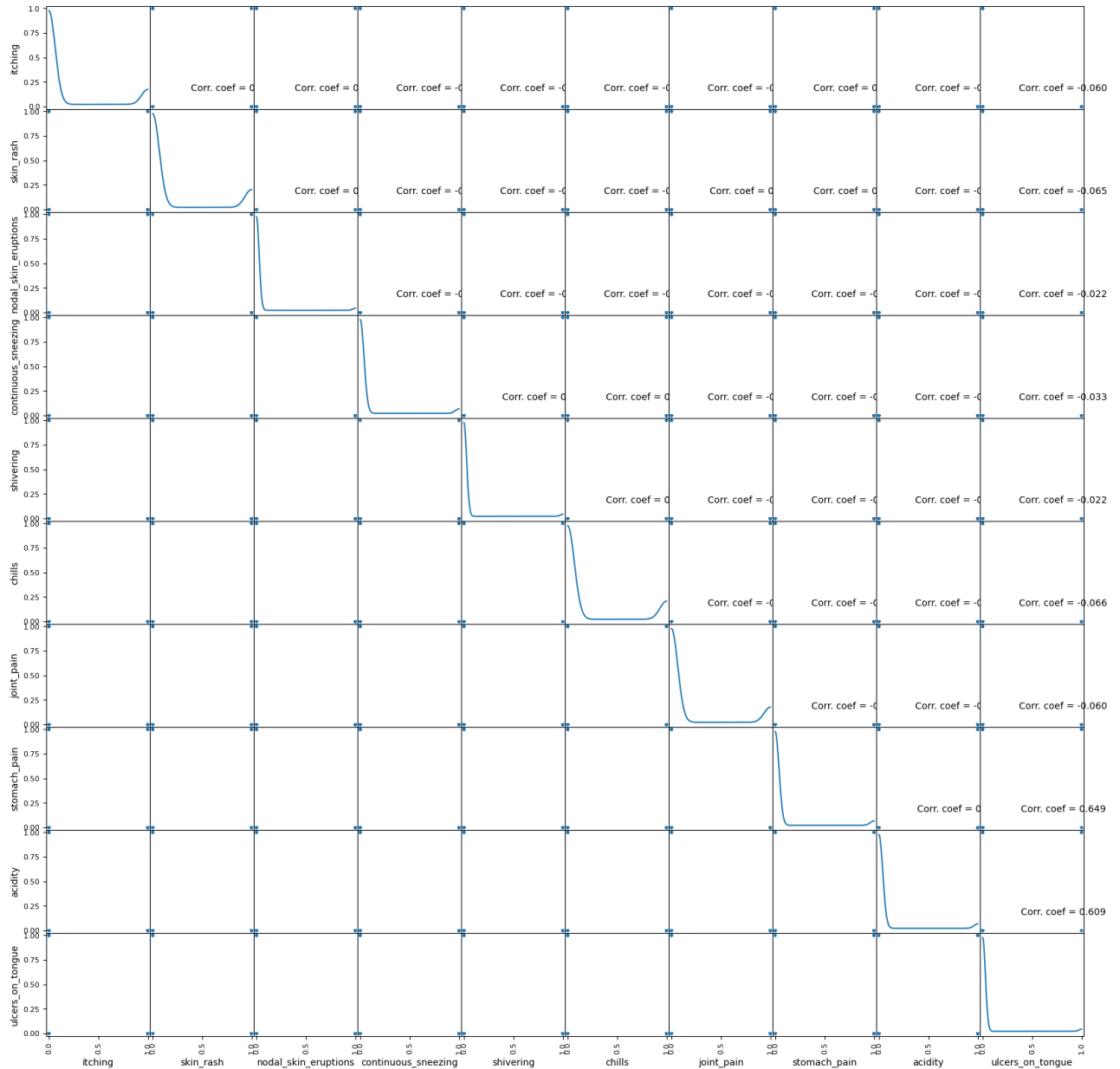
```

```
plt.suptitle('Scatter and Density Plot')
plt.show()
```

```
In [11]: plotScatterMatrix(df, 20, 10)
```

C:\Users\madhu sravanthi\AppData\Local\Temp\ipykernel\_13304\1304029198.py:5: FutureWarning: In a future version of pandas all arguments of DataFrame.dropna will be keyword-only.  
df1 = df1.dropna('columns')

Scatter and Density Plot



```
In [12]: X= df[11]
y = df[["prognosis"]]
np.ravel(y)
print(X)
```

	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	
...	...	...	...	...	...	
4915	0	0	0	0	0	
4916	0	0	0	0	0	
4917	0	0	0	0	0	
4918	0	0	0	0	0	
4919	0	0	0	0	0	

	yellow_urine	yellowing_of_eyes	acute_liver_failure	fluid_overload	\
0	0	0	0	0	
1	0	0	0	0	
2	0	0	0	0	
3	0	0	0	0	
4	0	0	0	0	
...	...	...	...	...	
4915	0	0	0	0	

```

4916      0      0      0      0      0
4917      0      0      0      0      0
4918      0      0      0      0      0
4919      0      0      0      0      0

      swelling_of_stomach  ...  pus_filled_pimples  blackheads  scurring  \
0      0      ...      0      0      0
1      0      ...      0      0      0
2      0      ...      0      0      0
3      0      ...      0      0      0
4      0      ...      0      0      0
...      ...      ...      ...      ...      ...
4915      0      ...      0      0      0
4916      0      ...      1      1      1
4917      0      ...      0      0      0
4918      0      ...      0      0      0
4919      0      ...      0      0      0

      skin_peeling  silver_like_dusting  small_dents_in_nails  \
0      0      0      0
1      0      0      0
2      0      0      0
3      0      0      0
4      0      0      0
...      ...      ...      ...
4915      0      0      0
4916      0      0      0
4917      0      0      0
4918      1      1      1
4919      0      0      0

      inflammatory_nails  blister  red_sore_around_nose  yellow_crust_ooze
0      0      0      0      0
1      0      0      0      0
2      0      0      0      0
3      0      0      0      0
4      0      0      0      0
...      ...      ...      ...      ...
4915      0      0      0      0
4916      0      0      0      0
4917      0      0      0      0
4918      1      0      0      0
4919      0      1      1      1

```

[4920 rows x 95 columns]

In [13]: `print(y)`

```

      prognosis
0      0
1      0
2      0
3      0
4      0
...      ...
4915      36
4916      37
4917      38
4918      39
4919      40

```

[4920 rows x 1 columns]

```

In [14]: #Reading the testing.csv file
tr=pd.read_csv("testing.csv")

#Using inbuilt function replace in pandas for replacing the values

tr.replace({'prognosis':{'Fungal infection':0,'Allergy':1,'GERD':2,'Chronic cholestasis':3,'Drug Reaction':4,'Peptic ulcer disease':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 B':19,'Hepatitis C':20,'Hepatitis D':21,'Hepatitis E':22,'Alcoholic hepatitis':23,'Tuberculosis':24,'Common Cold':25,'Pneumonia':26,'Dimorphic hemmorhoids(piles)':27,'Heart attack':28,'Varicose veins':29,'Hypothyroidism':30,'Hypoglycemia':31,'Osteoarthritis':32,'Arthritis':33,'(vertigo) Paroymsal Positional Vertigo':34,'Acne':35,'Urinary tract infection':36,'Psoriasis':37,'Impetigo':38}},inplace=True)

tr.head()

```

```

Out [14]:
      itching  skin_rash  nodal_skin_eruptions  continuous_sneezing  shivering  chills  joint_pain  stomach_pain  acidity  ulcers_on_tongue
0  1  1  1  0  0  0  0  0  0  0
1  0  0  0  1  1  1  0  0  0  0
2  0  0  0  0  0  0  1  1  1  1
3  1  0  0  0  0  0  0  0  0  0
4  1  1  0  0  0  0  0  1  0  0

```

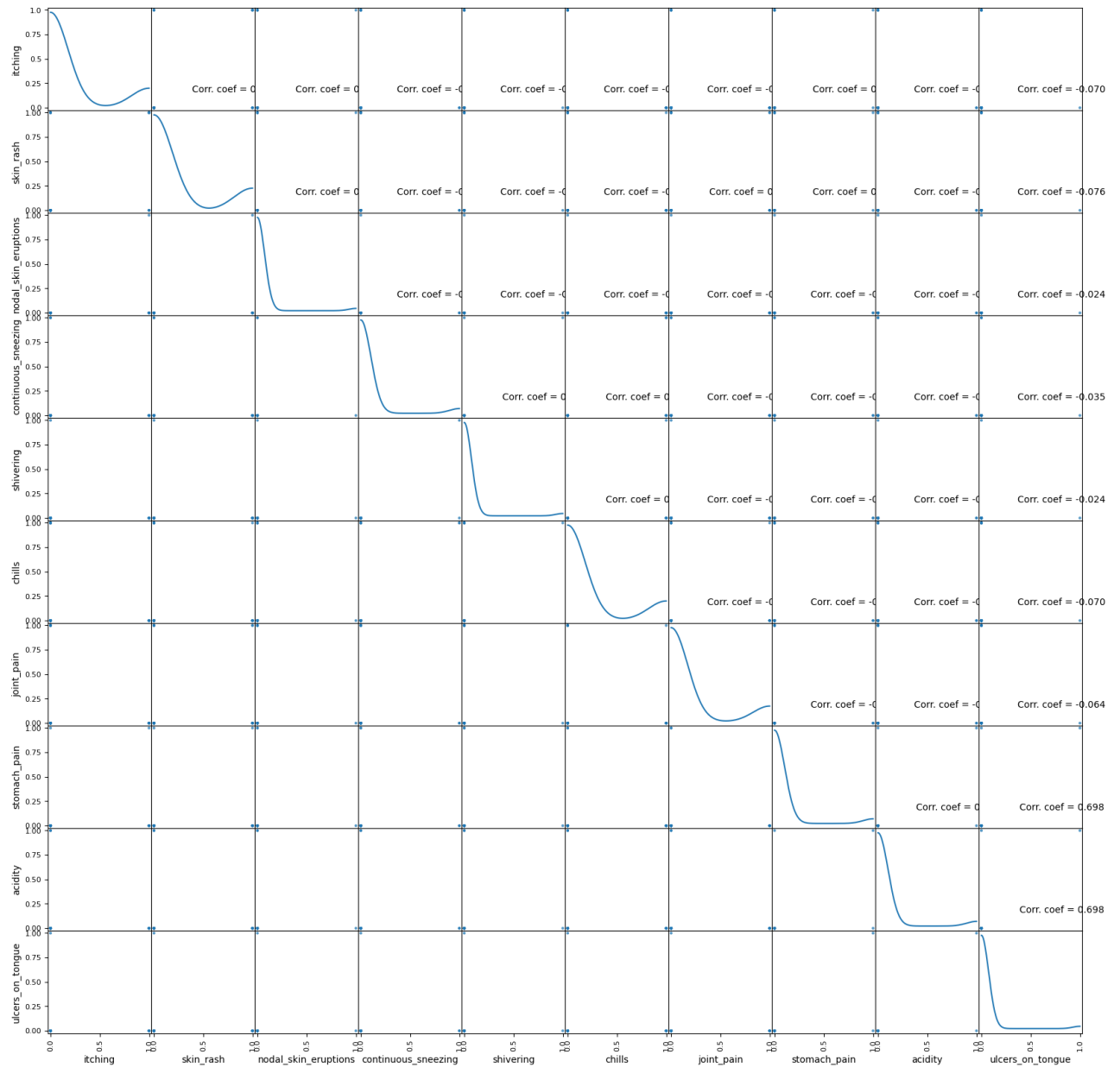
5 rows x 133 columns

In [15]: `plotScatterMatrix(tr, 20, 10)`

C:\Users\madhu sravanthi\AppData\Local\Temp\ipykernel\_13304\1304029198.py:5: FutureWarning: In a future version of pandas all arguments of DataFrame.dropna will be keyword-only.

```
df1 = df1.dropna('columns')
```

# Scatter and Density Plot



```
In [16]: X_test= tr[11]
y_test = tr[["prognosis"]]
np.ravel(y_test)
print(X_test)
```

	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	1	0	0	
4	0	0	0	0	0	
5	0	0	1	0	0	
6	0	0	0	0	0	
7	0	0	0	0	0	
8	0	0	0	1	0	
9	0	0	0	0	0	
10	0	0	0	0	0	
11	0	0	0	0	0	
12	1	0	0	0	0	
13	0	0	0	0	0	
14	0	0	1	0	0	
15	0	0	0	1	0	
16	0	0	0	0	1	
17	1	0	0	0	0	
18	0	1	1	1	0	
19	0	0	1	1	1	
20	0	0	1	0	0	
21	0	0	0	0	0	
22	0	0	1	0	0	
23	0	0	1	0	0	
24	0	0	1	0	0	
25	0	0	0	0	1	
26	0	0	0	0	0	
27	0	0	0	0	0	
28	0	1	0	0	0	
29	0	0	0	0	0	
30	0	0	0	0	0	

31	0	0	0	0	0
32	0	0	0	1	0
33	0	0	0	0	0
34	0	0	0	0	0
35	0	0	0	0	0
36	0	0	0	0	0
37	0	0	0	0	0
38	0	0	0	0	0
39	0	0	0	0	0
40	0	0	0	0	0
41	0	0	0	0	0

	yellow_urine	yellowing_of_eyes	acute_liver_failure	fluid_overload	\
0	0	0	0	0	0
1	0	0	0	0	0
2	0	0	0	0	0
3	0	1	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
19	0	1	0	0	0
20	1	1	0	0	0
21	0	1	0	0	0
22	0	1	0	0	0
23	0	1	1	0	0
24	0	0	0	0	0
25	0	1	0	0	0
26	0	0	0	0	0
27	0	0	0	0	0
28	0	0	0	0	0
29	0	0	0	0	0
30	0	0	0	0	0
31	0	0	0	0	0
32	0	0	0	0	0
33	0	0	0	0	0
34	0	0	0	0	0
35	0	0	0	0	0
36	0	0	0	0	0
37	0	0	0	0	0
38	0	0	0	0	0
39	0	0	0	0	0
40	0	0	0	0	0
41	0	0	0	0	0

	swelling_of_stomach	...	pus_filled_pimples	blackheads	scurrying	\
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
19	0	...	0	0	0	0
20	0	...	0	0	0	0
21	0	...	0	0	0	0
22	0	...	0	0	0	0
23	0	...	0	0	0	0
24	1	...	0	0	0	0
25	0	...	0	0	0	0
26	0	...	0	0	0	0
27	0	...	0	0	0	0
28	0	...	0	0	0	0
29	0	...	0	0	0	0
30	0	...	0	0	0	0
31	0	...	0	0	0	0
32	0	...	0	0	0	0
33	0	...	0	0	0	0
34	0	...	0	0	0	0
35	0	...	0	0	0	0
36	0	...	0	0	0	0
37	0	...	1	1	1	1
38	0	...	0	0	0	0
39	0	...	0	0	0	0
40	0	...	0	0	0	0
41	0	...	0	0	0	0

	skin_peeling	silver_like_dusting	small_dents_in_nails	\
0	0	0	0	0
1	0	0	0	0
2	0	0	0	0
3	0	0	0	0
4	0	0	0	0
5	0	0	0	0
6	0	0	0	0
7	0	0	0	0
8	0	0	0	0
9	0	0	0	0
10	0	0	0	0

11	0	0	0
12	0	0	0
13	0	0	0
14	0	0	0
15	0	0	0
16	0	0	0
17	0	0	0
18	0	0	0
19	0	0	0
20	0	0	0
21	0	0	0
22	0	0	0
23	0	0	0
24	0	0	0
25	0	0	0
26	0	0	0
27	0	0	0
28	0	0	0
29	0	0	0
30	0	0	0
31	0	0	0
32	0	0	0
33	0	0	0
34	0	0	0
35	0	0	0
36	0	0	0
37	0	0	0
38	0	0	0
39	1	1	1
40	0	0	0
41	1	0	0

	inflammatory_nails	blister	red_sore_around_nose	yellow_crust_ooze
0	0	0	0	0
1	0	0	0	0
2	0	0	0	0
3	0	0	0	0
4	0	0	0	0
5	0	0	0	0
6	0	0	0	0
7	0	0	0	0
8	0	0	0	0
9	0	0	0	0
10	0	0	0	0
11	0	0	0	0
12	0	0	0	0
13	0	0	0	0
14	0	0	0	0
15	0	0	0	0
16	0	0	0	0
17	0	0	0	0
18	0	0	0	0
19	0	0	0	0
20	0	0	0	0
21	0	0	0	0
22	0	0	0	0
23	0	0	0	0
24	0	0	0	0
25	0	0	0	0
26	0	0	0	0
27	0	0	0	0
28	0	0	0	0
29	0	0	0	0
30	0	0	0	0
31	0	0	0	0
32	0	0	0	0
33	0	0	0	0
34	0	0	0	0
35	0	0	0	0
36	0	0	0	0
37	0	0	0	0
38	0	0	0	0
39	1	0	0	0
40	0	1	1	1
41	0	0	1	0

[42 rows x 95 columns]

In [17]: `print(y_test)`

	prognosis
0	0
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29

```

30      30
31      31
32      32
33      33
34      34
35      35
36      36
37      37
38      38
39      39
40      40
41      0

```

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

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

```

In [18]: #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)#dropping 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()

```

## Decision Tree Algorithm

```

In [19]: root = Tk()
pred1=StringVar()
def DecisionTree():
    if len(NameEn.get()) == 0:
        pred1.set(" ")
        comp=messagebox.askokcancel("System","Kindly Fill the Name")
        if comp:
            root.mainloop()
    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()
    else:
        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")
#Creating the database if not exists named as database.db and creating table if not exists n
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS DecisionTree(Name StringVar,Symtom1 StringVar,Symtom2 :
c.execute("INSERT INTO DecisionTree(Name,Symtom1,Symtom2,Symtom3,Symtom4,Symtom5,Disease) VA
conn.commit()
c.close()
conn.close()

#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())

```

## Random Forest Algorithm

```

In [20]: pred2=StringVar()
def randomforest():
    if len(NameEn.get()) == 0:
        pred1.set(" ")
        comp=messagebox.askokcancel("System","Kindly Fill the Name")
        if comp:
            root.mainloop()
    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()
    else:
        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")
    #Creating the database if not exists named as database.db and creating table if not exists
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS RandomForest(Name StringVar,Symtom1 StringVar,Symtom2 :
c.execute("INSERT INTO RandomForest(Name,Symtom1,Symtom2,Symtom3,Symtom4,Symtom5,Disease) VA
conn.commit()
c.close()
conn.close()
#printing scatter plot of disease predicted vs its symptoms
scatterplt(pred2.get())

```

## KNearestNeighbour Algorithm

```

In [21]: pred4=StringVar()
def KNN():
    if len(NameEn.get()) == 0:
        pred1.set(" ")
        comp=messagebox.askokcancel("System","Kindly Fill the Name")
        if comp:
            root.mainloop()
    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()
    else:
        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")
    #Creating the database if not exists named as database.db and creating table if not exists
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS KNearestNeighbour(Name StringVar,Symptom1 StringVar,Symptom2 StringVar,Symptom3 StringVar,Symptom4 StringVar,Symptom5 StringVar,Disease StringVar)")
c.execute("INSERT INTO KNearestNeighbour(Name,Symptom1,Symptom2,Symptom3,Symptom4,Symptom5,Disease) VALUES ('', '', '', '', '', '', '')")
conn.commit()
c.close()
conn.close()
#printing scatter plot of disease predicted vs its symptoms

scatterplt(pred4.get())

```

## Naive Bayes Algorithm

```

In [24]: pred3=StringVar()
def NaiveBayes():
    if len(NameEn.get()) == 0:
        pred1.set(" ")
        comp=messagebox.askokcancel("System","Kindly Fill the Name")
        if comp:
            root.mainloop()
    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()
    else:
        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")
    #Creating the database if not exists named as database.db and creating table if not exists
    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 StringVar,Symtom5 StringVar,Disease StringVar)")
    c.execute("INSERT INTO NaiveBayes(Name,Symtom1,Symtom2,Symtom3,Symtom4,Symtom5,Disease) VALUES('',' ',' ',' ',' ',' ',' ')")
    conn.commit()
    c.close()
    conn.close()
    #printing scatter plot of disease predicted vs its symptoms
    scatterplt(pred3.get())

```

## Building Graphical User Interface

```

In [25]: #Tk class is used to create a root window
root.configure(background='Ivory')
root.title('Smart Disease Predictor System')
root.resizable(0,0)

```

Out [25]: ''

```

In [26]: 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()

```

```

In [27]: 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:
    pass

```

```

In [28]: from tkinter import messagebox
def Exit():
    qExit=messagebox.askyesno("System","Do you want to exit the system")

    if qExit:
        root.destroy()
        exit()

```

```

In [29]: #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: Madhu,Harsha,Nikitha,Uma shankar,sanjana", fg="Pi
w2.config(font=("Times",30,"bold italic"))
w2.grid(row=2, column=0, columnspan=2, padx=100)

```

```

In [30]: #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)

```

```

In [31]: #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)

```

```

In [32]: #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)

```

```

In [33]: #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)
```

In [34]:

```
#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)
```

In [35]:

```
#Showing the output of different algorithms
```

```
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)
```

In [ ]:

```
#calling this function because the application is ready to run
```

```
root.mainloop()
```

```
Decision Tree
```

```
Accuracy
```

```
0.9285714285714286
```

```
39
```

```
Confusion matrix
```

```
[[1 0 0 ... 0 1 0]
```

```
[0 1 0 ... 0 0 0]
```

```
[0 0 1 ... 0 0 0]
```

```
...
```

```
[0 0 0 ... 1 0 0]
```

```
[0 0 0 ... 0 1 0]
```

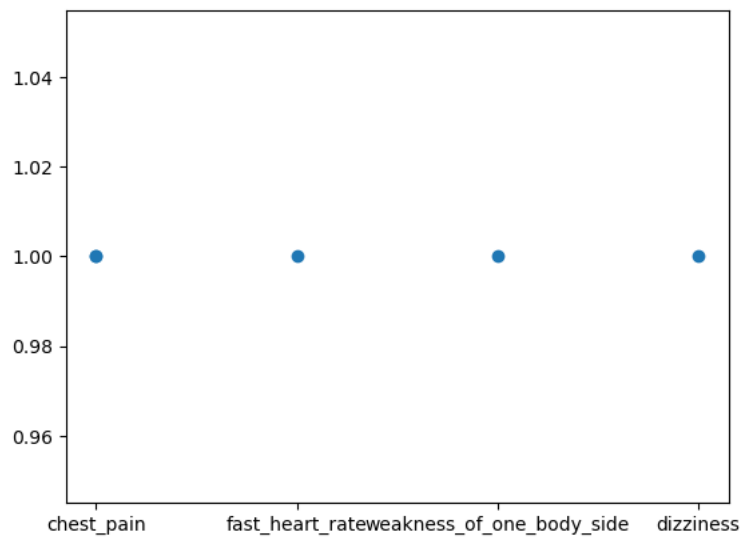
```
[0 0 0 ... 0 0 1]]
```

```
['chest_pain', 'fast_heart_rate', 'weakness_of_one_body_side', 'dizziness', 'chest_pain']
```

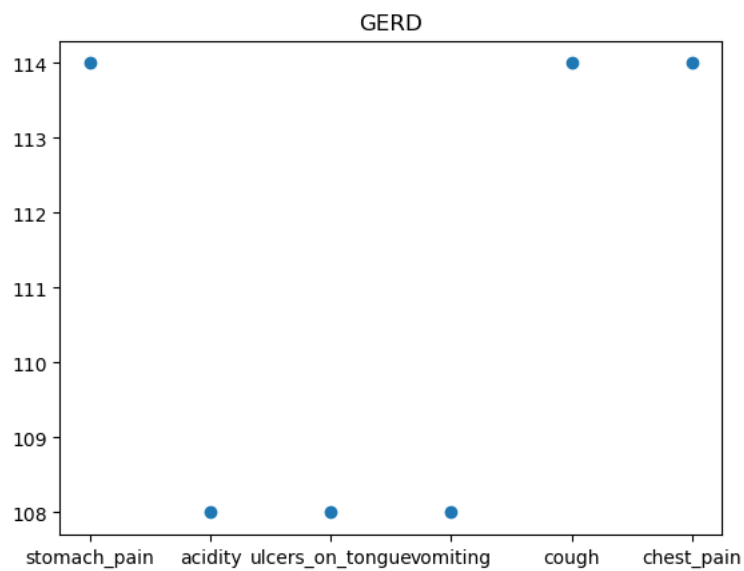
```
[1, 1, 1, 1, 1]
```

```
C:\Users\madhu sravanthi\anaconda3\lib\site-packages\sklearn\base.py:420: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
```

```
warnings.warn(
```

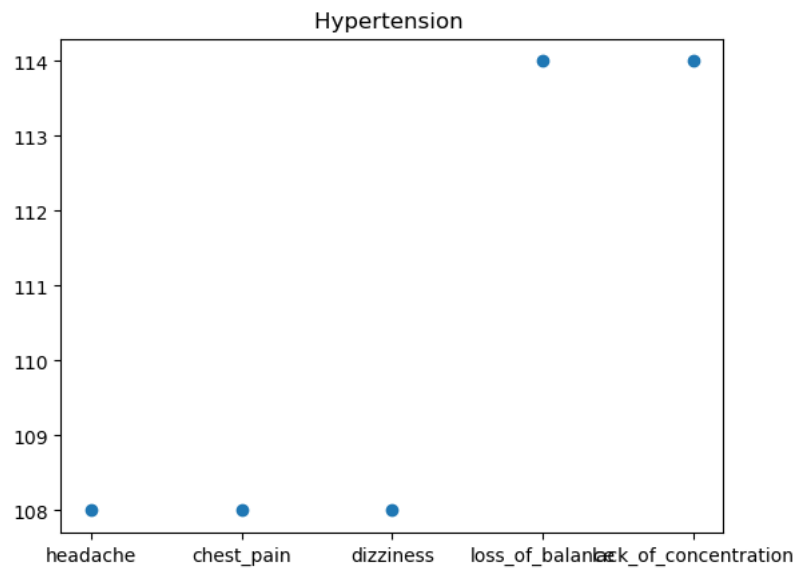


```
[114. 108. 108. 108. 114. 114.]  
6  
6
```



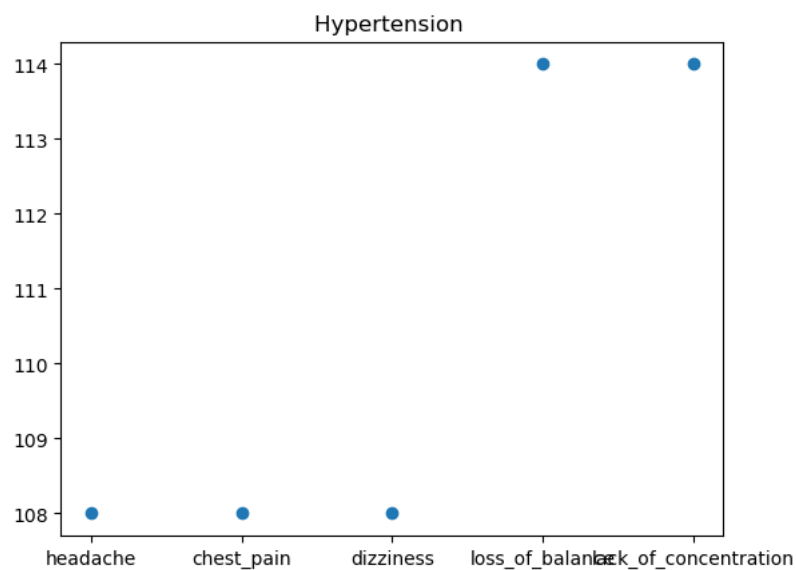
```
Random Forest  
Accuracy  
0.9285714285714286  
39  
Confusion matrix  
[[1 0 0 ... 0 0 1]  
 [0 1 0 ... 0 0 0]  
 [0 0 0 ... 0 0 0]  
 ...  
 [0 0 0 ... 1 0 0]  
 [0 0 0 ... 0 1 0]  
 [0 0 0 ... 0 0 1]]  
[108. 108. 108. 114. 114.]  
5  
5
```

```
C:\Users\madhu sravanthi\anaconda3\lib\site-packages\sklearn\base.py:420: UserWarning: X does not have valid feature  
names, but RandomForestClassifier was fitted with feature names  
warnings.warn(
```



```
Naive Bayes
Accuracy
0.9285714285714286
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[108. 108. 108. 114. 114.]
5
5
```

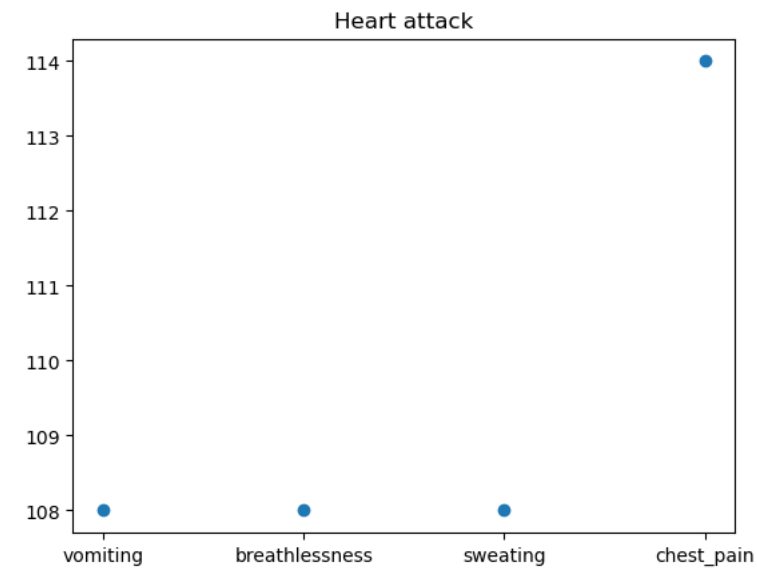
C:\Users\madhu sravanthi\anaconda3\lib\site-packages\sklearn\base.py:420: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names  
warnings.warn(



```
kNearest Neighbour
Accuracy
0.9285714285714286
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 0 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[108. 108. 108. 114.]
4
4
```

C:\Users\madhu sravanthi\anaconda3\lib\site-packages\sklearn\base.py:420: UserWarning: X does not have valid feature names, but KNeighborsClassifier was fitted with feature names  
warnings.warn(



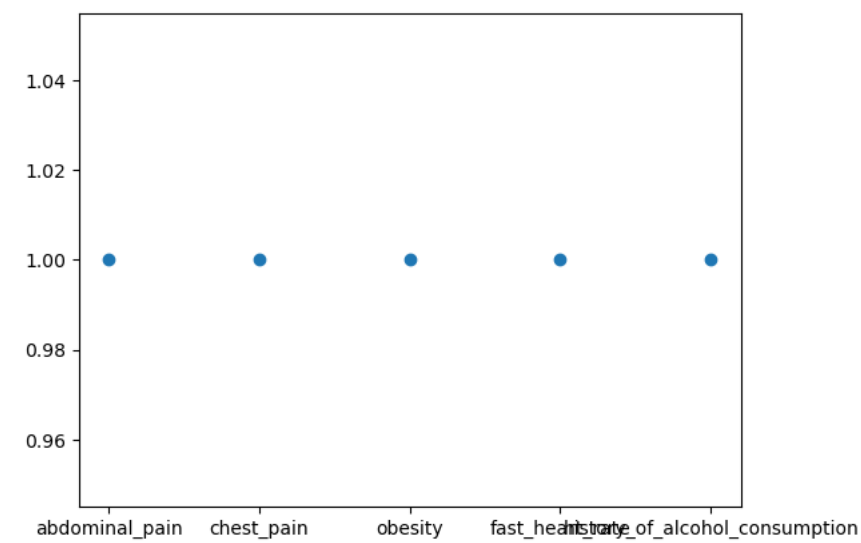


```

Decision Tree
Accuracy
0.9285714285714286
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
['abdominal_pain', 'chest_pain', 'obesity', 'fast_heart_rate', 'history_of_alcohol_consumption']
[1, 1, 1, 1, 1]

```

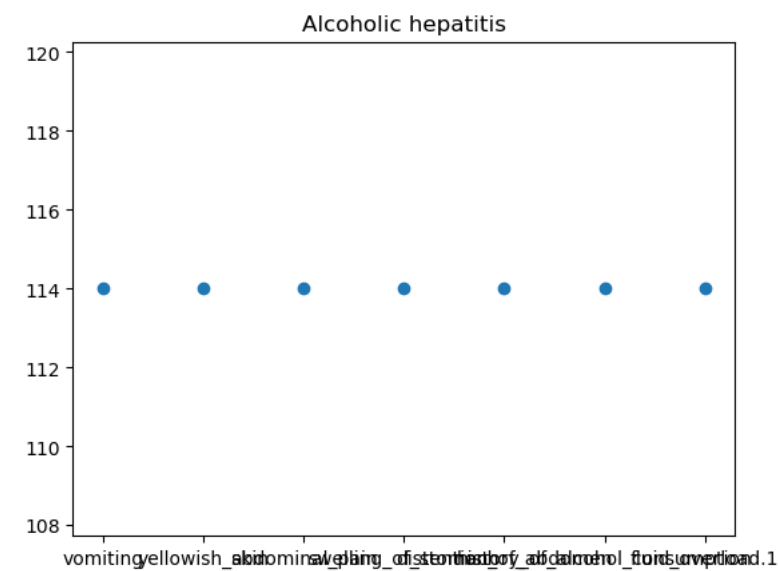
C:\Users\madhu sravanthi\anaconda3\lib\site-packages\sklearn\base.py:420: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names  
warnings.warn(



```

[114. 114. 114. 114. 114. 114.]
7
7

```

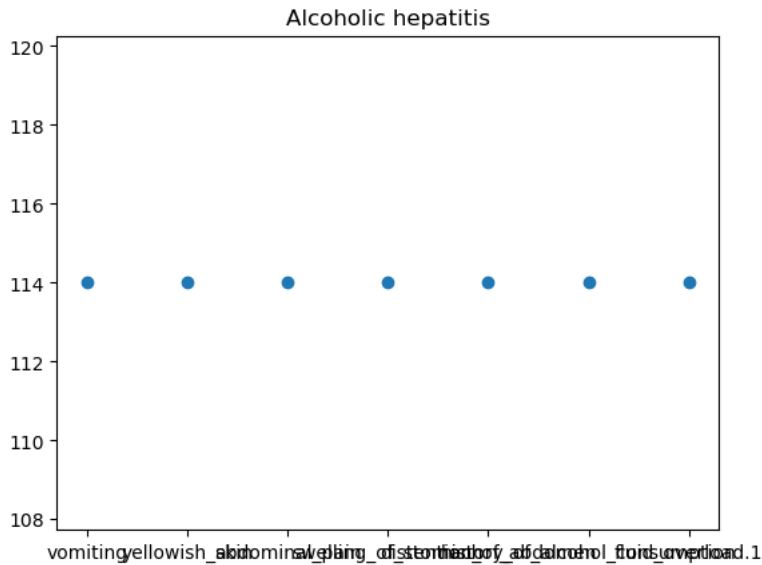


```

Random Forest
Accuracy
0.9285714285714286
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 0 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[114. 114. 114. 114. 114. 114.]
7
7

```

C:\Users\madhu sravanthi\anaconda3\lib\site-packages\sklearn\base.py:420: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names  
warnings.warn(

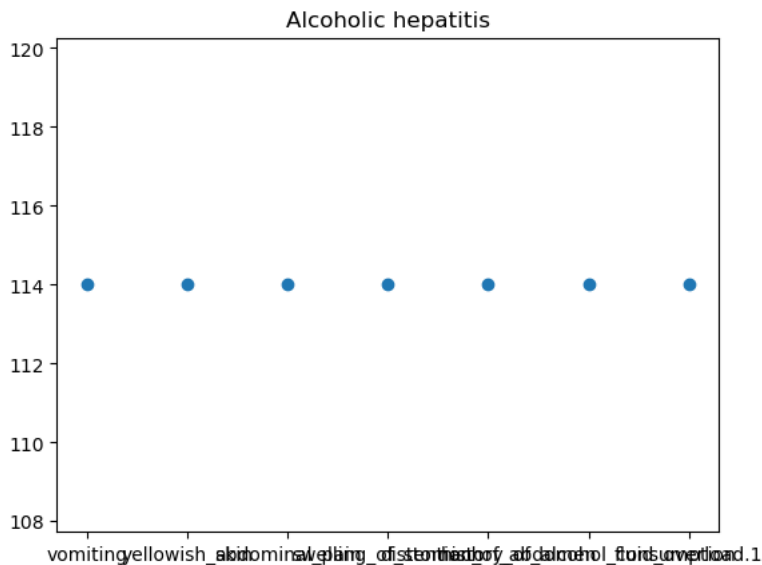


```

Naive Bayes
Accuracy
0.9285714285714286
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[114. 114. 114. 114. 114. 114.]
7
7

```

C:\Users\madhu sravanthi\anaconda3\lib\site-packages\sklearn\base.py:420: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names  
warnings.warn(



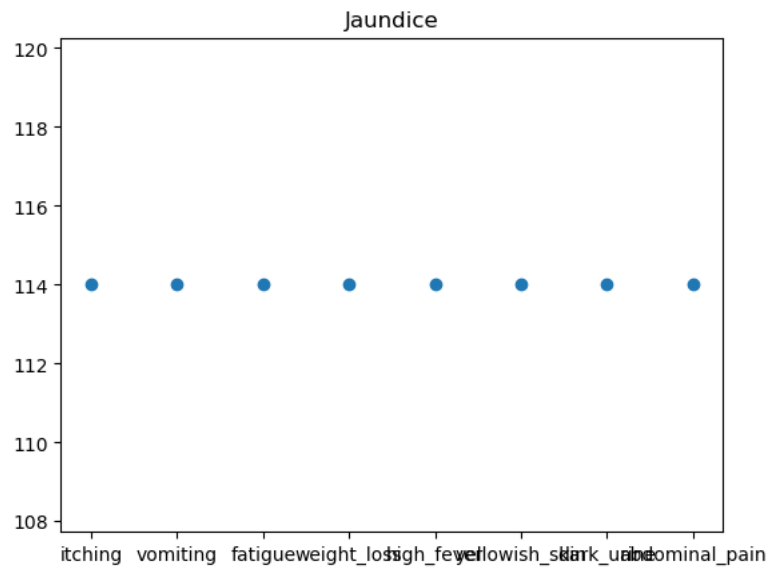
```

kNearest Neighbour
Accuracy
0.9285714285714286
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 0 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]

```

```
[0 0 0 ... 0 0 1]]
[114. 114. 114. 114. 114. 114. 114. 114.]
8
8
```

```
C:\Users\madhu sravanthi\anaconda3\lib\site-packages\sklearn\base.py:420: UserWarning: X does not have valid feature
names, but KNeighborsClassifier was fitted with feature names
warnings.warn(
```



In [ ]: