

In [6]:

```
#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

df.replace({'prognosis': {'Fungal infection':0,'Allergy':1,'GERD':2,'Chronic cholestasi':3,'Peptic ulcer disease':5,'AIDS':6,'Diabetes ':7,'Gastroenteritis':8,'Bronchial Asthma':9,'Migraine':11,'Cervical spondylosis':12,'Paralysis (brain hemorrhage)':13,'Jaundice':14,'Malaria':15,'Chicken pox':16,'Dengue':17,'Hepatitis B':20,'Hepatitis C':21,'Hepatitis D':22,'Hepatitis E':23,'Alcoholic hepatitis':24,'Common Cold':26,'Pneumonia':27,'Dimorphic hemmorhoids(piles)':28,'Heart attack':29,'Hyperthyroidism':32,'Hypoglycemia':33,'Osteoarthristis':34,'Arthritis':35,'(vertigo) Paroxysmal Positional Vertigo':36,'Acne':37,'Urinary tract infection':38,'Impetigo':40}},inplace=True)
#df.head()
DF.head()
```

```

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```

FileNotFoundException Traceback (most recent call last)

```

Input In [6], in <cell line: 2>()
      1 #Reading the training .csv file
----> 2 df=pd.read_csv("training.csv")
      3 DF= pd.read_csv('training.csv', index_col='prognosis')
      4 #Replace the values in the imported file by pandas by the inbuilt function re
place in pandas.

File ~\anaconda3\lib\site-packages\pandas\util\_decorators.py:311, in deprecate_nonke
yword_arguments.<locals>.decorate.<locals>.wrapper(*args, **kwargs)
 305 if len(args) > num_allow_args:
 306     warnings.warn(
 307         msg.format(arguments=arguments),
 308         FutureWarning,
 309         stacklevel=stacklevel,
 310     )
--> 311 return func(*args, **kwargs)

File ~\anaconda3\lib\site-packages\pandas\io\parsers\readers.py:680, in read_csv(file
path_or_buffer, sep, delimiter, header, names, index_col, usecols, squeeze, prefix, m
angle_dupe_cols, dtype, engine, converters, true_values, false_values, skipinitialspa
ce, skiprows, skipfooter, nrows, na_values, keep_default_na, na_filter, verbose, skip
_blank_lines, parse_dates, infer_datetime_format, keep_date_col, date_parser, dayfirs
t, cache_dates, iterator, chunksize, compression, thousands, decimal, lineterminator,
quotechar, quoting, doublequote, escapechar, comment, encoding, encoding_errors, dial
ect, error_bad_lines, warn_bad_lines, on_bad_lines, delim_whitespace, low_memory, mem
ory_map, float_precision, storage_options)
 665 kwds_defaults = _refine_defaults_read(
 666     dialect,
 667     delimiter,
 668     defaults={"delimiter": ",",
 669     })
 670 kwds.update(kwds_defaults)
--> 680 return _read(filepath_or_buffer, kwds)

File ~\anaconda3\lib\site-packages\pandas\io\parsers\readers.py:575, in _read(filepat
h_or_buffer, kwds)
 572 _validate_names(kwds.get("names", None))
 573 # Create the parser.
--> 575 parser = TextFileReader(filepath_or_buffer, **kwds)
 576 if chunksize or iterator:
 577     return parser

File ~\anaconda3\lib\site-packages\pandas\io\parsers\readers.py:933, in TextFileReade
r.__init__(self, f, engine, **kwds)
 930     self.options["has_index_names"] = kwds["has_index_names"]
 931     self.handles: IOHandles | None = None
--> 933 self._engine = self._make_engine(f, self.engine)

File ~\anaconda3\lib\site-packages\pandas\io\parsers\readers.py:1217, in TextFileRead
er._make_engine(self, f, engine)
 1213     mode = "rb"
 1214     # error: No overload variant of "get_handle" matches argument types
 1215     # "Union[str, PathLike[str], ReadCsvBuffer[bytes], ReadCsvBuffer[str]]"
 1216     # , "str", "bool", "Any", "Any", "Any", "Any", "Any"
--> 1217 self.handles = get_handle( # type: ignore[call-overload]
 1218     f,
 1219     mode,
```

```

1220     encoding=self.options.get("encoding", None),
1221     compression=self.options.get("compression", None),
1222     memory_map=self.options.get("memory_map", False),
1223     is_text=is_text,
1224     errors=self.options.get("encoding errors", "strict"),
1225     storage_options=self.options.get("storage_options", None),
1226 )
1227 assert self.handles is not None
1228 f = self.handles.handle

File ~\anaconda3\lib\site-packages\pandas\io\common.py:789, in get_handle(path_or_bu
f, mode, encoding, compression, memory_map, is_text, errors, storage_options)
    784 elif isinstance(handle, str):
    785     # Check whether the filename is to be opened in binary mode.
    786     # Binary mode does not support 'encoding' and 'newline'.
    787     if ioargs.encoding and "b" not in ioargs.mode:
    788         # Encoding
    789         handle = open(
--> 790             handle,
    791             ioargs.mode,
    792             encoding=ioargs.encoding,
    793             errors=errors,
    794             newline="",
    795         )
    796     else:
    797         # Binary mode
    798         handle = open(handle, ioargs.mode)


```

`FileNotFoundException: [Errno 2] No such file or directory: 'training.csv'`

In []:

```

In [7]: #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

df.replace({'prognosis':{'Fungal infection':0,'Allergy':1,'GERD':2,'Chronic cholestasi
'Peptic ulcer diseae':5,'AIDS':6,'Diabetes ':7,'Gastroenteritis':8,'Bronchial Asth
'Migraine':11,'Cervical spondylosis':12,
'Paralysis (brain hemorrhage)':13,'Jaundice':14,'Malaria':15,'Chicken pox':16,'Der
'Hepatitis B':20,'Hepatitis C':21,'Hepatitis D':22,'Hepatitis E':23,'Alcoholic hep
'Common Cold':26,'Pneumonia':27,'Dimorphic hemmorhoids(piles)':28,'Heart attack':2
'Hyperthyroidism':32,'Hypoglycemia':33,'Osteoarthristis':34,'Arthritis':35,
'(vertigo) Paroxysmal Positional Vertigo':36,'Acne':37,'Urinary tract infection':3
'Impetigo':40}},inplace=True)
#df.head()
DF.head()

```

```

-----
```

FileNotFoundException Traceback (most recent call last)

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Input In [7], in <cell line: 2>()
      1 #Reading the training .csv file
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 786     # Binary mode does not support 'encoding' and 'newline'.
 787     if ioargs.encoding and "b" not in ioargs.mode:
 788         # Encoding
--> 789         handle = open(
 790             handle,
 791             ioargs.mode,
 792             encoding=ioargs.encoding,
 793             errors=errors,
 794             newline="",
 795         )
 796     else:
 797         # Binary mode
 798         handle = open(handle, ioargs.mode)

FileNotFoundException: [Errno 2] No such file or directory: 'training.csv'

```

In [10]:

```

#Reading the training .csv file
df=pd.read_csv("C:/Users/Sazna/OneDrive/Desktop/training.csv")
DF= pd.read_csv( 'C:\Users\Sazna\OneDrive\Desktop\training.csv', index_col='prognosis'
#Replace the values in the imported file by pandas by the inbuilt function replace in

df.replace({'prognosis': {'Fungal infection':0,'Allergy':1,'GERD':2,'Chronic cholestasi
    'Peptic ulcer diseae':5,'AIDS':6,'Diabetes ':7,'Gastroenteritis':8,'Bronchial Asth
    'Migraine':11,'Cervical spondylosis':12,
    'Paralysis (brain hemorrhage)':13,'Jaundice':14,'Malaria':15,'Chicken pox':16,'Der
    'Hepatitis B':20,'Hepatitis C':21,'Hepatitis D':22,'Hepatitis E':23,'Alcoholic hep
    'Common Cold':26,'Pneumonia':27,'Dimorphic hemmorhoids(piles)':28,'Heart attack':2
    'Hyperthyroidism':32,'Hypoglycemia':33,'Osteoarthristis':34,'Arthritis':35,
    '(vertigo) Paroxysmal Positional Vertigo':36,'Acne':37,'Urinary tract infection':3
    'Impetigo':40}},inplace=True)
#df.head()
DF.head()

```

Input In [10]

```
DF= pd.read_csv( 'C:\Users\Sazna\OneDrive\Desktop\training.csv', index_col='progn
osis')
```

SyntaxError: (unicode error) 'unicodeescape' codec can't decode bytes in position 2-
3: truncated \UXXXXXXXXX escape

In [11]:

```

#Reading the training .csv file
df=pd.read_csv("C:/Users/Sazna/OneDrive/Desktop/training.csv")
DF= pd.read_csv( 'C:/Users/Sazna/OneDrive/Desktop/training.csv', index_col='prognosis'
#Replace the values in the imported file by pandas by the inbuilt function replace in

df.replace({'prognosis': {'Fungal infection':0,'Allergy':1,'GERD':2,'Chronic cholestasi

```

```
'Peptic ulcer diseae':5,'AIDS':6,'Diabetes ':7,'Gastroenteritis':8,'Bronchial Asth
'Migraine':11,'Cervical spondylosis':12,
'Paralysis (brain hemorrhage)':13,'Jaundice':14,'Malaria':15,'Chicken pox':16,'Der
'Hepatitis B':20,'Hepatitis C':21,'Hepatitis D':22,'Hepatitis E':23,'Alcoholic hep
'Common Cold':26,'Pneumonia':27,'Dimorphic hemmorhoids(piles)':28,'Heart attack':2
'Hyperthyroidism':32,'Hypoglycemia':33,'Osteoarthristis':34,'Arthritis':35,
'(vertigo) Paroxysmal Positional Vertigo':36,'Acne':37,'Urinary tract infection':3
'Impetigo':40}},inplace=True)
#df.head()
DF.head()
```

Input In [11]

```
DF= pd.read_csv( 'C:/Users/Sazna/OneDrive/Desktop/training.csv', index_col='progn
osis')
```

SyntaxError: (unicode error) 'unicodedeescape' codec can't decode bytes in position 2-
3: truncated \UXXXXXXXXX escape

In [12]:

```
#Reading the training .csv file
df=pd.read_csv("C:/Users/Sazna/OneDrive/Desktop/training.csv")
DF= pd.read_csv( 'C:/Users/Sazna/OneDrive/Desktop/training.csv', index_col='prognosis'
#Replace the values in the imported file by pandas by the inbuilt function replace in

df.replace({'prognosis': {'Fungal infection':0,'Allergy':1,'GERD':2,'Chronic cholestasi
'Peptic ulcer diseae':5,'AIDS':6,'Diabetes ':7,'Gastroenteritis':8,'Bronchial Asth
'Migraine':11,'Cervical spondylosis':12,
'Paralysis (brain hemorrhage)':13,'Jaundice':14,'Malaria':15,'Chicken pox':16,'Der
'Hepatitis B':20,'Hepatitis C':21,'Hepatitis D':22,'Hepatitis E':23,'Alcoholic hep
'Common Cold':26,'Pneumonia':27,'Dimorphic hemmorhoids(piles)':28,'Heart attack':2
'Hyperthyroidism':32,'Hypoglycemia':33,'Osteoarthristis':34,'Arthritis':35,
'(vertigo) Paroxysmal Positional Vertigo':36,'Acne':37,'Urinary tract infection':3
'Impetigo':40}},inplace=True)
#df.head()
DF.head()
```

Out[12]:

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain
prognosis							

Fungal infection	1	1		1	0	0	0	0
Fungal infection	0	1		1	0	0	0	0
Fungal infection	1	0		1	0	0	0	0
Fungal infection	1	1		0	0	0	0	0
Fungal infection	1	1		1	0	0	0	0

5 rows × 132 columns

```
# 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 disease prediction
nRow, nCol = df1.shape
columnNames = list(df1)
nGraphRow = (nCol + nGraphPerRow - 1) / nGraphPerRow
plt.figure(num = None, figsize = (6 * nGraphPerRow, 8 * nGraphRow), dpi = 80, facecolor = 'white')
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()

```

In [14]:

```

# 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 k by k
        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')
    plt.suptitle('Scatter and Density Plot')
    plt.show()

```

In [15]:

```
plotPerColumnDistribution(df, 10, 5)
```

```

-----
ValueError                                     Traceback (most recent call last)
Input In [15], in <cell line: 1>()
----> 1 plotPerColumnDistribution(df, 10, 5)

Input In [13], in plotPerColumnDistribution(df1, nGraphShown, nGraphPerRow)
      8 plt.figure(num = None, figsize = (6 * nGraphPerRow, 8 * nGraphRow), dpi = 80,
     facecolor = 'w', edgecolor = 'k')
      9 for i in range(min(nCol, nGraphShown)):
---> 10     plt.subplot(nGraphRow, nGraphPerRow, i + 1)
     11     columnDf = df.iloc[:, i]
     12     if (not np.issubdtype(type(columnDf.iloc[0]), np.number)):

File ~\anaconda3\lib\site-packages\matplotlib\pyplot.py:1268, in subplot(*args, **kwargs)
1265 fig = gcf()
1267 # First, search for an existing subplot with a matching spec.
-> 1268 key = SubplotSpec._from_subplot_args(fig, args)
1270 for ax in fig.axes:
1271     # if we found an axes at the position sort out if we can re-use it
1272     if hasattr(ax, 'get_subplotspec') and ax.get_subplotspec() == key:
1273         # if the user passed no kwargs, re-use

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:597, in SubplotSpec._from_subplot_args.figure, args)
593 else:
594     raise TypeError(f"subplot() takes 1 or 3 positional arguments but "
595                     f"{len(args)} were given")
--> 597 gs = GridSpec._check_gridspec_exists.figure, rows, cols)
598 if gs is None:
599     gs = GridSpec(rows, cols, figure=figure)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:225, in GridSpecBase._check_gridspec_exists.figure, nrows, ncols)
223         return gs
224 # else gridspec not found:
--> 225 return GridSpec(nrows, ncols, figure=figure)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:385, in GridSpec.__init__(self, nrows, ncols, figure, left, bottom, right, top, wspace, hspace, width_ratios, height_ratios)
382 self.hspace = hspace
383 self.figure = figure
--> 385 super().__init__(nrows, ncols,
386                      width_ratios=width_ratios,
387                      height_ratios=height_ratios)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:49, in GridSpecBase.__init__(self, nrows, ncols, height_ratios, width_ratios)
34 """
35 Parameters
36 -----
37 (...)
38     If not given, all rows will have the same height.
39 """
40 if not isinstance(nrows, Integral) or nrows <= 0:
--> 41     raise ValueError(
42         f"Number of rows must be a positive integer, not {nrows!r}")
43 if not isinstance(ncols, Integral) or ncols <= 0:
44     raise ValueError(

```

```
53     f"Number of columns must be a positive integer, not {ncols!r}")
```

```
ValueError: Number of rows must be a positive integer, not 27.2
<Figure size 2400x17408 with 0 Axes>
```

```
In [16]: plotPerColumnDistribution(df, 10, 5)
```

```

-----
ValueError                                     Traceback (most recent call last)
Input In [16], in <cell line: 1>()
----> 1 plotPerColumnDistribution(df, 10, 5)

Input In [13], in plotPerColumnDistribution(df1, nGraphShown, nGraphPerRow)
      8 plt.figure(num = None, figsize = (6 * nGraphPerRow, 8 * nGraphRow), dpi = 80,
     facecolor = 'w', edgecolor = 'k')
      9 for i in range(min(nCol, nGraphShown)):
---> 10     plt.subplot(nGraphRow, nGraphPerRow, i + 1)
     11     columnDf = df.iloc[:, i]
     12     if (not np.issubdtype(type(columnDf.iloc[0]), np.number)):

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```

```
53     f"Number of columns must be a positive integer, not {ncols!r}")
```

```
ValueError: Number of rows must be a positive integer, not 27.2
<Figure size 2400x17408 with 0 Axes>
```

```
In [17]: # 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
    columnNames = list(df)
    if len(columnNames) > 10: # reduce the number of columns for matrix inversion of k
        columnNames = columnNames[:10]
    df1 = df1[columnNames]
    ax = pd.plotting.scatter_matrix(df1, alpha=0.75, figsize=[plotSize, plotSize], dia
    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='ax
    plt.suptitle('Scatter and Density Plot')
    plt.show()
```

```
In [18]: plotPerColumnDistribution(df, 10, 5)
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File ~\anaconda3\lib\site-packages\matplotlib\pyplot.py:1268, in subplot(*args, **kwargs)
1265 fig = gcf()
1266 # First, search for an existing subplot with a matching spec.
-> 1268 key = SubplotSpec._from_subplot_args(fig, args)
1270 for ax in fig.axes:
1271     # if we found an axes at the position sort out if we can re-use it
1272     if hasattr(ax, 'get_subplotspec') and ax.get_subplotspec() == key:
1273         # if the user passed no kwargs, re-use

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:597, in SubplotSpec._from_subplot_args.figure, args)
593 else:
594     raise TypeError(f"subplot() takes 1 or 3 positional arguments but "
595                     f"{len(args)} were given")
--> 597 gs = GridSpec._check_gridspec_exists.figure, rows, cols)
598 if gs is None:
599     gs = GridSpec(rows, cols, figure=figure)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:225, in GridSpecBase._check_gridspec_exists.figure, nrows, ncols)
223         return gs
224 # else gridspec not found:
--> 225 return GridSpec(nrows, ncols, figure=figure)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:385, in GridSpec.__init__(self, nrows, ncols, figure, left, bottom, right, top, wspace, hspace, width_ratios, height_ratios)
382 self.hspace = hspace
383 self.figure = figure
--> 385 super().__init__(nrows, ncols,
386                      width_ratios=width_ratios,
387                      height_ratios=height_ratios)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:49, in GridSpecBase.__init__(self, nrows, ncols, height_ratios, width_ratios)
34 """
35 Parameters
36 -----
37 (...)
38     If not given, all rows will have the same height.
39 """
40 if not isinstance(nrows, Integral) or nrows <= 0:
--> 41     raise ValueError(
42         f"Number of rows must be a positive integer, not {nrows!r}")
43 if not isinstance(ncols, Integral) or ncols <= 0:
44     raise ValueError(

```

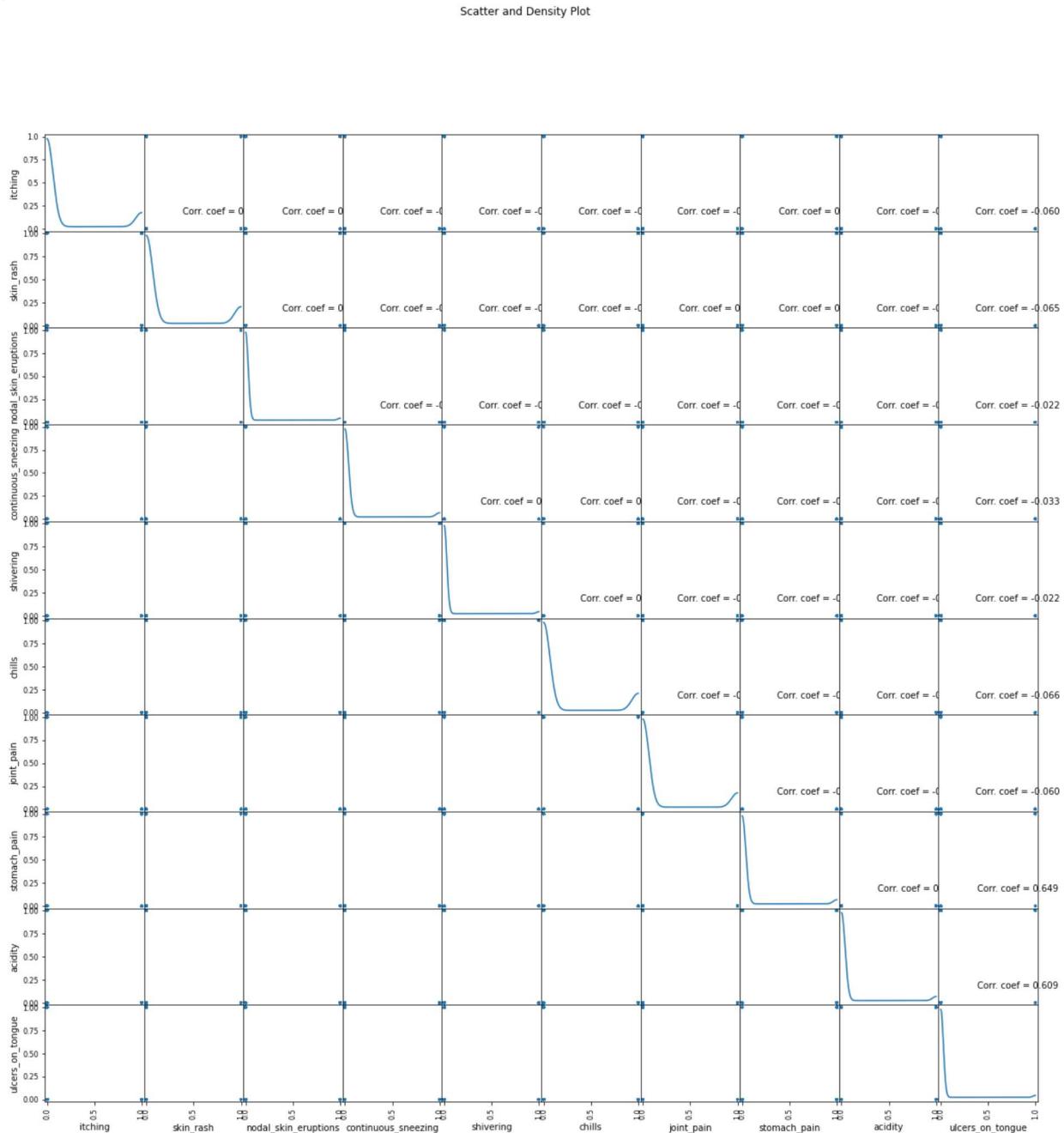
53

f"Number of columns must be a positive integer, not {ncols!r}")

ValueError: Number of rows must be a positive integer, not 27.2
<Figure size 2400x17408 with 0 Axes>

In [19]: plotScatterMatrix(df, 20, 10)

C:\Users\Sazna\AppData\Local\Temp\ipykernel_8196\1304029198.py:5: FutureWarning: In a future version of pandas all arguments of DataFrame.dropna will be keyword-only.
df1 = df1.dropna('columns')



In [20]:
X = df[11]
y = df[["prognosis"]]
np.ravel(y)
print(X)

symptom based disease prediction

	back_pain	constipation	abdominal_pain	diarrhoea	mild_fever	\
0	0	0	0	0	0	0
1	0	0	0	0	0	0
2	0	0	0	0	0	0
3	0	0	0	0	0	0
4	0	0	0	0	0	0
...
4915	0	0	0	0	0	0
4916	0	0	0	0	0	0
4917	0	0	0	0	0	0
4918	0	0	0	0	0	0
4919	0	0	0	0	0	0
	yellow_urine	yellowing_of_eyes	acute_liver_failure	fluid_overload		\
0	0	0	0	0	0	0
1	0	0	0	0	0	0
2	0	0	0	0	0	0
3	0	0	0	0	0	0
4	0	0	0	0	0	0
...
4915	0	0	0	0	0	0
4916	0	0	0	0	0	0
4917	0	0	0	0	0	0
4918	0	0	0	0	0	0
4919	0	0	0	0	0	0
	swelling_of_stomach	...	pus_filled_pimples	blackheads	scurring	\
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	...	1	1	1	1
4917	0	...	0	0	0	0
4918	0	...	0	0	0	0
4919	0	...	0	0	0	0
	skin_peeling	silver_like_dusting	small_dents_in_nails		\	
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	1	1	1	1	1	
4919	0	0	0	0	0	
	inflammatory_nails	blister	red_sore_around_nose	yellow_crust_ooze		
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
4917	0	0	0	0
4918	1	0	0	0
4919	0	1	1	1

[4920 rows x 95 columns]

In [21]: `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 [22]: `#Reading the testing.csv file
tr=pd.read_csv("C:/Users/Sazna/OneDrive/Desktop/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, 'Peptic ulcer disease': 4, 'AIDS': 5, 'Diabetes ': 6, 'Gastroenteritis': 7, 'Bronchial Asthma': 8, 'Migraine': 9, 'Cervical spondylosis': 10, 'Paralysis (brain hemorrhage)': 11, 'Jaundice': 12, 'Malaria': 13, 'Chicken pox': 14, 'Dengue': 15, 'Hepatitis B': 16, 'Hepatitis C': 17, 'Hepatitis D': 18, 'Hepatitis E': 19, 'Alcoholic hepatitis': 20, 'Common Cold': 21, 'Pneumonia': 22, 'Dimorphic hemmorhoids(piles)': 23, 'Heart attack': 24, 'Hyperthyroidism': 25, 'Hypoglycemia': 26, 'Osteoarthristis': 27, 'Arthritis': 28, '(vertigo) Paroxysmal Positional Vertigo': 29, 'Acne': 30, 'Urinary tract infection': 31, 'Impetigo': 32}, inplace=True)
tr.head()`

```

-----
```

FileNotFoundException Traceback (most recent call last)

```

Input In [22], in <cell line: 2>()
    1 #Reading the testing.csv file
----> 2 tr=pd.read_csv("testing.csv")
    3 #Using inbuilt function replace in pandas for replacing the values
    4 tr.replace({'prognosis': {'Fungal infection': 0, 'Allergy': 1, 'GERD': 2, 'Chronic c
holestasis': 3, 'Drug Reaction': 4,
    5     'Peptic ulcer diseae': 5, 'AIDS': 6, 'Diabetes ': 7, 'Gastroenteritis': 8, 'Bronc
hial Asthma': 9, 'Hypertension ': 10,
    6     'Migraine': 11, 'Cervical spondylosis': 12,
    7     (...),
    8     '(vertigo) Paroxysmal Positional Vertigo': 13, 'Acne': 14, 'Urinary tract inf
ection': 15, 'Psoriasis': 16,
    9     'Impetigo': 17}}, inplace=True)

File ~\anaconda3\lib\site-packages\pandas\util\_decorators.py:311, in deprecate_nonke
yword_arguments.<locals>.decorate.<locals>.wrapper(*args, **kwargs)
    305 if len(args) > num_allow_args:
    306     warnings.warn(
    307         msg.format(arguments=arguments),
    308         FutureWarning,
    309         stacklevel=stacklevel,
    310     )
--> 311 return func(*args, **kwargs)

File ~\anaconda3\lib\site-packages\pandas\io\parsers\readers.py:680, in read_csv(file
path_or_buffer, sep, delimiter, header, names, index_col, usecols, squeeze, prefix, m
angle_dupe_cols, dtype, engine, converters, true_values, false_values, skipinitialspa
ce, skiprows, skipfooter, nrows, na_values, keep_default_na, na_filter, verbose, skip
_blank_lines, parse_dates, infer_datetime_format, keep_date_col, date_parser, dayfirs
t, cache_dates, iterator, chunksize, compression, thousands, decimal, lineterminator,
quotechar, quoting, doublequote, escapechar, comment, encoding, encoding_errors, dial
ect, error_bad_lines, warn_bad_lines, on_bad_lines, delim_whitespace, low_memory, mem
ory_map, float_precision, storage_options)
    665 kwds_defaults = _refine_defaults_read(
    666     dialect,
    667     delimiter,
    668     defaults={"delimiter": ",",
    669     }
    670 kwds.update(kwds_defaults)
--> 680 return _read(filepath_or_buffer, kwds)

File ~\anaconda3\lib\site-packages\pandas\io\parsers\readers.py:575, in _read(filepat
h_or_buffer, kwds)
    572 _validate_names(kwds.get("names", None))
    573 # Create the parser.
--> 575 parser = TextFileReader(filepath_or_buffer, **kwds)
    576 if chunksize or iterator:
    577     return parser

File ~\anaconda3\lib\site-packages\pandas\io\parsers\readers.py:933, in TextFileReade
r.__init__(self, f, engine, **kwds)
    930     self.options["has_index_names"] = kwds["has_index_names"]
    931 self.handles: IOHandles | None = None
--> 933 self._engine = self._make_engine(f, self.engine)

File ~\anaconda3\lib\site-packages\pandas\io\parsers\readers.py:1217, in TextFileRead
er._make_engine(self, f, engine)

```

```

1213     mode = "rb"
1214 # error: No overload variant of "get_handle" matches argument types
1215 # "Union[str, PathLike[str], ReadCsvBuffer[bytes], ReadCsvBuffer[str]]"
1216 # , "str", "bool", "Any", "Any", "Any", "Any", "Any"
-> 1217 self.handles = get_handle( # type: ignore[call-overload]
1218     f,
1219     mode,
1220     encoding=self.options.get("encoding", None),
1221     compression=self.options.get("compression", None),
1222     memory_map=self.options.get("memory_map", False),
1223     is_text=is_text,
1224     errors=self.options.get("encoding_errors", "strict"),
1225     storage_options=self.options.get("storage_options", None),
1226 )
1227 assert self.handles is not None
1228 f = self.handles.handle

File ~\anaconda3\lib\site-packages\pandas\io\common.py:789, in get_handle(path_or_bu
f, mode, encoding, compression, memory_map, is_text, errors, storage_options)
784 elif isinstance(handle, str):
785     # Check whether the filename is to be opened in binary mode.
786     # Binary mode does not support 'encoding' and 'newline'.
787     if ioargs.encoding and "b" not in ioargs.mode:
788         # Encoding
-> 789         handle = open(
790             handle,
791             ioargs.mode,
792             encoding=ioargs.encoding,
793             errors=errors,
794             newline="",
795         )
796     else:
797         # Binary mode
798         handle = open(handle, ioargs.mode)

```

`FileNotFoundException: [Errno 2] No such file or directory: 'testing.csv'`

```

In [23]: #Reading the testing.csv file
tr=pd.read_csv("C:/Users/Sazna/OneDrive/Desktop/testing.csv")

#Using inbuilt function replace in pandas for replacing the values

tr.replace({'prognosis':{'Fungal infection':0,'Allergy':1,'GERD':2,'Chronic cholestasi
    'Peptic ulcer diseae':5,'AIDS':6,'Diabetes ':7,'Gastroenteritis':8,'Bronchial Asth
    'Migraine':11,'Cervical spondylosis':12,
    'Paralysis (brain hemorrhage)':13,'Jaundice':14,'Malaria':15,'Chicken pox':16,'Der
    'Hepatitis B':20,'Hepatitis C':21,'Hepatitis D':22,'Hepatitis E':23,'Alcoholic hep
    'Common Cold':26,'Pneumonia':27,'Dimorphic hemmorhoids(piles)':28,'Heart attack':2
    'Hyperthyroidism':32,'Hypoglycemia':33,'Osteoarthristis':34,'Arthritis':35,
    '(vertigo) Paroxysmal Positional Vertigo':36,'Acne':37,'Urinary tract infection':3
    'Impetigo':40}},inplace=True)
tr.head()

```

Out[23]:

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach
0	1	1		1	0	0	0	0
1	0	0		0	1	1	1	0
2	0	0		0	0	0	0	0
3	1	0		0	0	0	0	0
4	1	1		0	0	0	0	0

5 rows × 133 columns

In [25]: `plotPerColumnDistribution(tr, 10, 6)`

```

-----
ValueError                                     Traceback (most recent call last)
Input In [25], in <cell line: 1>()
----> 1 plotPerColumnDistribution(tr, 10, 6)

Input In [13], in plotPerColumnDistribution(df1, nGraphShown, nGraphPerRow)
     8 plt.figure(num = None, figsize = (6 * nGraphPerRow, 8 * nGraphRow), dpi = 80,
  facecolor = 'w', edgecolor = 'k')
     9 for i in range(min(nCol, nGraphShown)):
--> 10     plt.subplot(nGraphRow, nGraphPerRow, i + 1)
    11     columnDf = df.iloc[:, i]
    12     if (not np.issubdtype(type(columnDf.iloc[0]), np.number)):

File ~\anaconda3\lib\site-packages\matplotlib\pyplot.py:1268, in subplot(*args, **kwargs)
1265 fig = gcf()
1267 # First, search for an existing subplot with a matching spec.
-> 1268 key = SubplotSpec._from_subplot_args(fig, args)
1270 for ax in fig.axes:
1271     # if we found an axes at the position sort out if we can re-use it
1272     if hasattr(ax, 'get_subplotspec') and ax.get_subplotspec() == key:
1273         # if the user passed no kwargs, re-use

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:597, in SubplotSpec._from_subplot_args.figure, args)
593 else:
594     raise TypeError(f"subplot() takes 1 or 3 positional arguments but "
595                     f"{len(args)} were given")
--> 597 gs = GridSpec._check_gridspec_exists.figure, rows, cols)
598 if gs is None:
599     gs = GridSpec(rows, cols, figure=figure)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:225, in GridSpecBase._check_gridspec_exists.figure, nrows, ncols)
223         return gs
224 # else gridspec not found:
--> 225 return GridSpec(nrows, ncols, figure=figure)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:385, in GridSpec.__init__(self, nrows, ncols, figure, left, bottom, right, top, wspace, hspace, width_ratios, height_ratios)
382 self.hspace = hspace
383 self.figure = figure
--> 385 super().__init__(nrows, ncols,
386                      width_ratios=width_ratios,
387                      height_ratios=height_ratios)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:49, in GridSpecBase.__init__(self, nrows, ncols, height_ratios, width_ratios)
34 """
35 Parameters
36 -----
(...):
46     If not given, all rows will have the same height.
47 """
48 if not isinstance(nrows, Integral) or nrows <= 0:
--> 49     raise ValueError(
50             f"Number of rows must be a positive integer, not {nrows!r}")
51 if not isinstance(ncols, Integral) or ncols <= 0:
52     raise ValueError(

```

```
53     f"Number of columns must be a positive integer, not {ncols!r}")
```

```
ValueError: Number of rows must be a positive integer, not 22.833333333333332
<Figure size 2880x14613.3 with 0 Axes>
```

```
In [26]: plotPerColumnDistribution(tr, 10, 6)
```

```

-----
ValueError                                     Traceback (most recent call last)
Input In [26], in <cell line: 1>()
----> 1 plotPerColumnDistribution(tr, 10, 6)

Input In [13], in plotPerColumnDistribution(df1, nGraphShown, nGraphPerRow)
     8 plt.figure(num = None, figsize = (6 * nGraphPerRow, 8 * nGraphRow), dpi = 80,
  facecolor = 'w', edgecolor = 'k')
     9 for i in range(min(nCol, nGraphShown)):
--> 10     plt.subplot(nGraphRow, nGraphPerRow, i + 1)
    11     columnDf = df.iloc[:, i]
    12     if (not np.issubdtype(type(columnDf.iloc[0]), np.number)):

File ~\anaconda3\lib\site-packages\matplotlib\pyplot.py:1268, in subplot(*args, **kwargs)
1265 fig = gcf()
1266 # First, search for an existing subplot with a matching spec.
-> 1268 key = SubplotSpec._from_subplot_args(fig, args)
1270 for ax in fig.axes:
1271     # if we found an axes at the position sort out if we can re-use it
1272     if hasattr(ax, 'get_subplotspec') and ax.get_subplotspec() == key:
1273         # if the user passed no kwargs, re-use

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:597, in SubplotSpec._from_subplot_args.figure, args)
593 else:
594     raise TypeError(f"subplot() takes 1 or 3 positional arguments but "
595                     f"{len(args)} were given")
--> 597 gs = GridSpec._check_gridspec_exists.figure, rows, cols)
598 if gs is None:
599     gs = GridSpec(rows, cols, figure=figure)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:225, in GridSpecBase._check_gridspec_exists.figure, nrows, ncols)
223         return gs
224 # else gridspec not found:
--> 225 return GridSpec(nrows, ncols, figure=figure)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:385, in GridSpec.__init__(self, nrows, ncols, figure, left, bottom, right, top, wspace, hspace, width_ratios, height_ratios)
382 self.hspace = hspace
383 self.figure = figure
--> 385 super().__init__(nrows, ncols,
386                      width_ratios=width_ratios,
387                      height_ratios=height_ratios)

File ~\anaconda3\lib\site-packages\matplotlib\gridspec.py:49, in GridSpecBase.__init__(self, nrows, ncols, height_ratios, width_ratios)
34 """
35 Parameters
36 -----
37 (...)
38     If not given, all rows will have the same height.
39 """
40 if not isinstance(nrows, Integral) or nrows <= 0:
--> 41     raise ValueError(
42         f"Number of rows must be a positive integer, not {nrows!r}")
43 if not isinstance(ncols, Integral) or ncols <= 0:
44     raise ValueError(

```

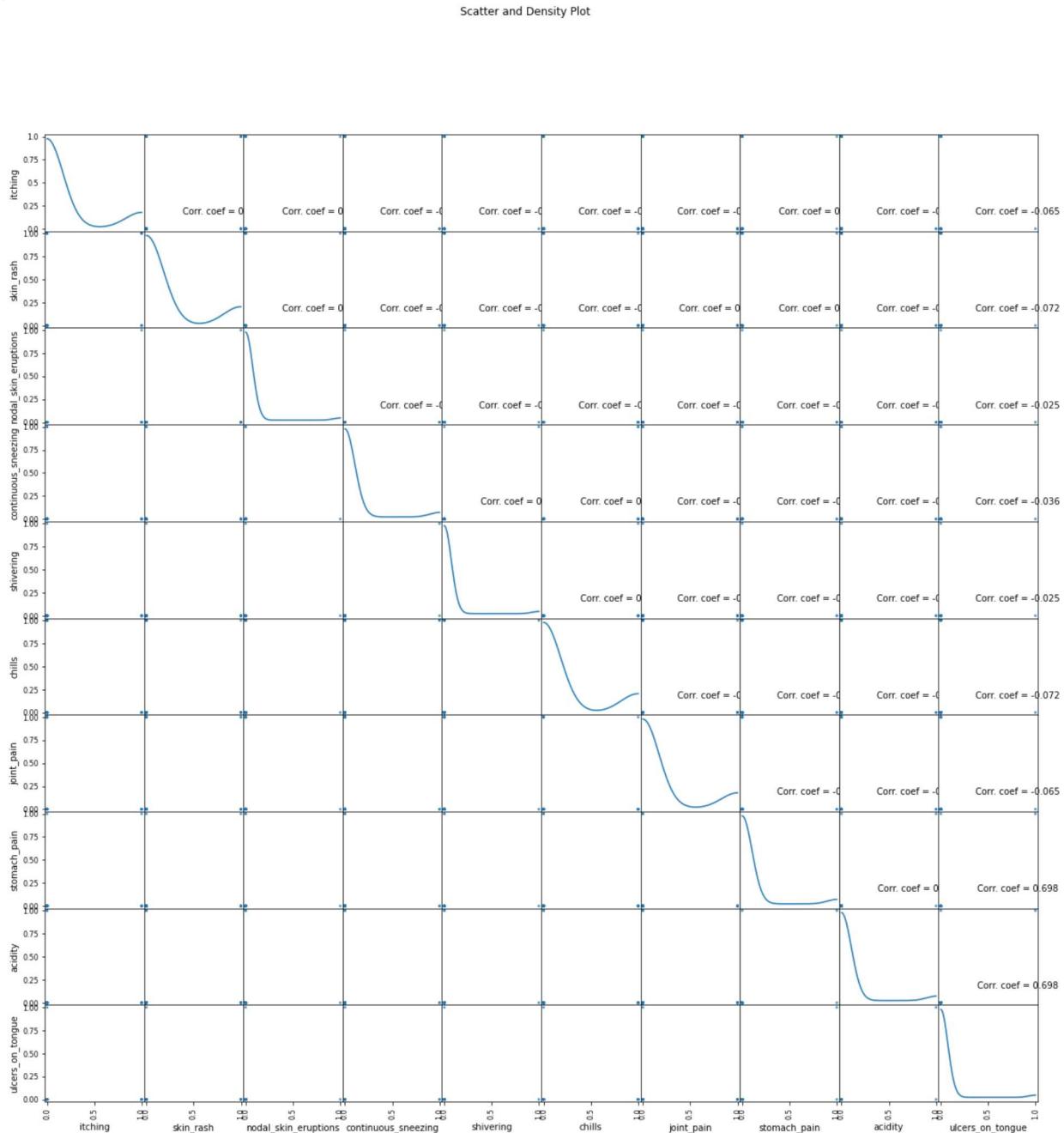
53

f"Number of columns must be a positive integer, not {ncols!r}")

ValueError: Number of rows must be a positive integer, not 22.833333333333332
<Figure size 2880x14613.3 with 0 Axes>

In [27]: plotScatterMatrix(tr, 20, 10)

C:\Users\Sazna\AppData\Local\Temp\ipykernel_8196\1304029198.py:5: FutureWarning: In a future version of pandas all arguments of DataFrame.dropna will be keyword-only.
df1 = df1.dropna('columns')



In [28]:
X_test= tr[11]
y_test = tr[["prognosis"]]
np.ravel(y_test)
print(X_test)

symptom based disease prediction

	back_pain	constipation	abdominal_pain	diarrhoea	mild_fever	\
0	0	0	0	0	0	0
1	0	0	0	0	0	0
2	0	0	0	0	0	0
3	0	0	1	0	0	0
4	0	0	0	0	0	0
5	0	0	1	0	0	0
6	0	0	0	0	0	0
7	0	0	0	0	0	0
8	0	0	0	1	0	0
9	0	0	0	0	0	0
10	0	0	0	0	0	0
11	0	0	0	0	0	0
12	1	0	0	0	0	0
13	0	0	0	0	0	0
14	0	0	1	0	0	0
15	0	0	0	1	0	0
16	0	0	0	0	0	1
17	1	0	0	0	0	0
18	0	1	1	1	0	0
19	0	0	1	1	1	1
20	0	0	1	0	0	0
21	0	0	0	0	0	0
22	0	0	1	0	0	0
23	0	0	1	0	0	0
24	0	0	1	0	0	0
25	0	0	0	0	0	1
26	0	0	0	0	0	0
27	0	0	0	0	0	0
28	0	1	0	0	0	0
29	0	0	0	0	0	0
30	0	0	0	0	0	0
31	0	0	0	0	0	0
32	0	0	0	0	1	0
33	0	0	0	0	0	0
34	0	0	0	0	0	0
35	0	0	0	0	0	0
36	0	0	0	0	0	0
37	0	0	0	0	0	0
38	0	0	0	0	0	0
39	0	0	0	0	0	0
40	0	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

	swelling_of_stomach	...	pus_filled_pimples	blackheads	scurrинг	\
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	1	...	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	...	1	1	1
38	0	...	0	0	0
39	0	...	0	0	0
40	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	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	1	1	1
40	0	0	0	0

	inflammatory_nails	blister	red_sore_around_nose	yellow_crust_ooze	
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
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 rows x 95 columns]

In [29]: `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

```

```

In [30]: #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()

```

```

In [33]: 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 in it
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,Symtom4 StringVar,Prediction StringVar)")
c.execute("INSERT INTO DecisionTree(Name,Symtom1,Symtom2,Symtom3,Symtom4,Prediction) VALUES ('John','Cough','Headache','Fever','Runny Nose','Yes')")
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())

```

In [34]:

```

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
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS RandomForest(Name StringVar,Syntom1 StringVar,Syntom2 StringVar,Syntom3 StringVar,Syntom4 StringVar,Syntom5 StringVar,Syntom6 StringVar,Syntom7 StringVar,Syntom8 StringVar,Syntom9 StringVar,Syntom10 StringVar,Syntom11 StringVar,Syntom12 StringVar,Disease StringVar)")
c.execute("INSERT INTO RandomForest(Name,Syntom1,Syntom2,Syntom3,Syntom4,Syntom5,Syntom6,Syntom7,Syntom8,Syntom9,Syntom10,Syntom11,Syntom12,Disease) VALUES ('{}','{}','{}','{}','{}','{}','{}','{}','{}','{}','{}','{}','{}','{}')".format(NameEn.get(),Symptom1.get(),Symptom2.get(),Symptom3.get(),Symptom4.get(),Symptom5.get(),Symptom6.get(),Symptom7.get(),Symptom8.get(),Symptom9.get(),Symptom10.get(),Symptom11.get(),Symptom12.get(),DiseaseEn.get()))
conn.commit()
c.close()
conn.close()
#printing scatter plot of disease predicted vs its symptoms
scatterplt(pred2.get())

```

```

In [35]: 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
import sqlite3
conn = sqlite3.connect('database.db')
c = conn.cursor()
c.execute("CREATE TABLE IF NOT EXISTS NaiveBayes(Name StringVar,Symtom1 String")
c.execute("INSERT INTO NaiveBayes(Name,Symtom1,Symtom2,Symtom3,Symtom4,Symtom5
conn.commit()
c.close()
conn.close()
#printing scatter plot of disease predicted vs its symptoms
scatterplt(pred3.get())

```

In [36]: #Tk class is used to create a root window
root.configure(background='Ivory')
root.title('Smart Disease Predictor System')
root.resizable(0,0)

Out[36]: ''

In [37]: 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 [38]: 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 [39]: 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 [40]: from tkinter import messagebox
def Exit():
    qExit=messagebox.askyesno("System","Do you want to exit the system")

    if qExit:
        root.destroy()
        exit()

```

```

In [41]: #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)

```

```

In [42]: #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 [43]: #Creating Labels for the symptoms
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 [44]:

```
#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 [45]:

```
#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 [47]:

```
#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)

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 [48]: #Showing the output of different algorithms

```
t1=Label(root,font=("Times",15,"bold italic"),text="Decision Tree",height=1,bg="Light Blue",width=40,fg="red",textvariable=pred1,relief="sunken").grid(row=15, column=1,sticky=W)

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,sticky=W)

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,sticky=W)
```

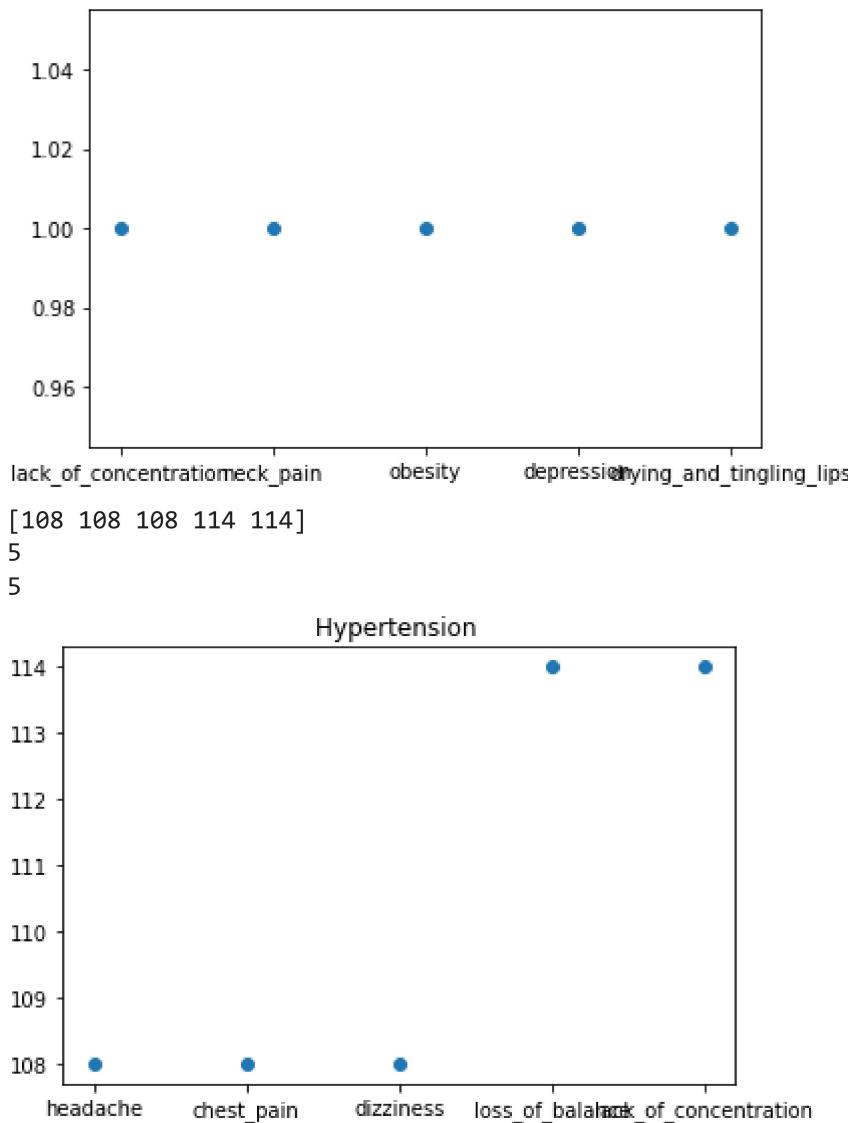
In [49]: #calling this function because the application is ready to run

```
root.mainloop()
```

```
Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'neck_pain', 'obesity', 'depression', 'drying_and_tingling_lips']
[1, 1, 1, 1, 1]
```

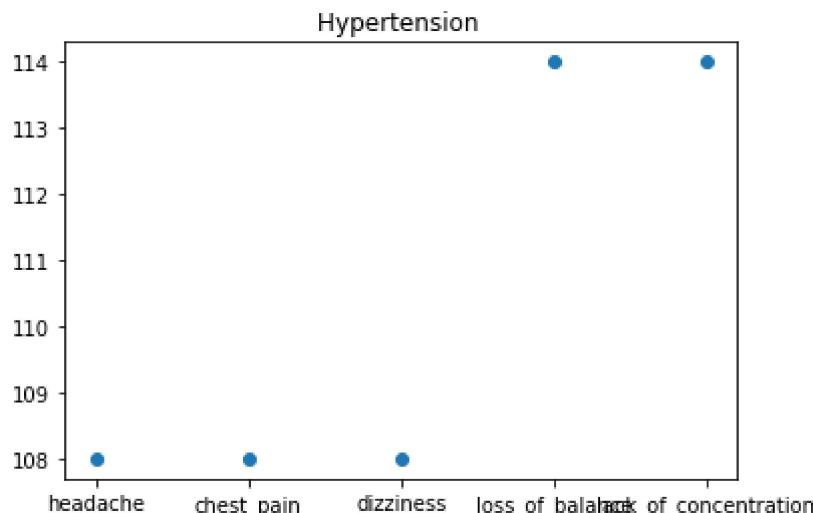
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names

```
warnings.warn(
```



```
Random Forest
Accuracy
0.9512195121951219
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]]
[108 108 108 114 114]
5
5
```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(
```



Naive Bayes

Accuracy

0.9512195121951219

39

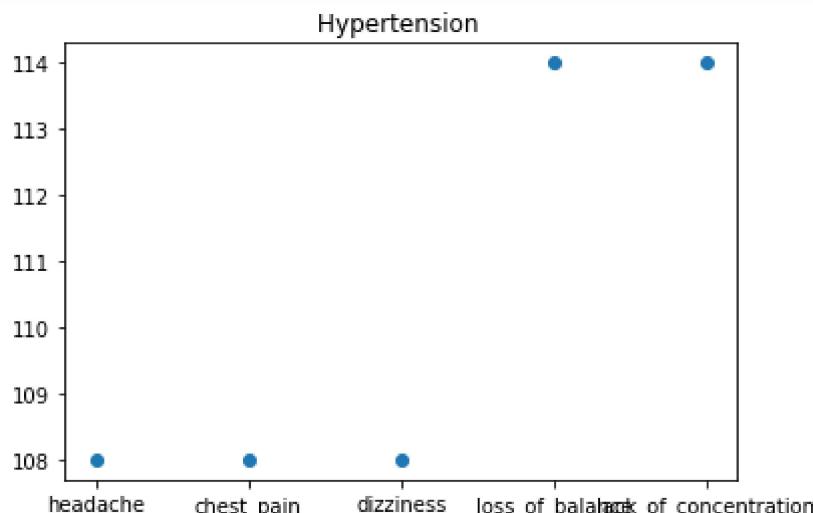
Confusion matrix

```
[[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\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
  warnings.warn(
```

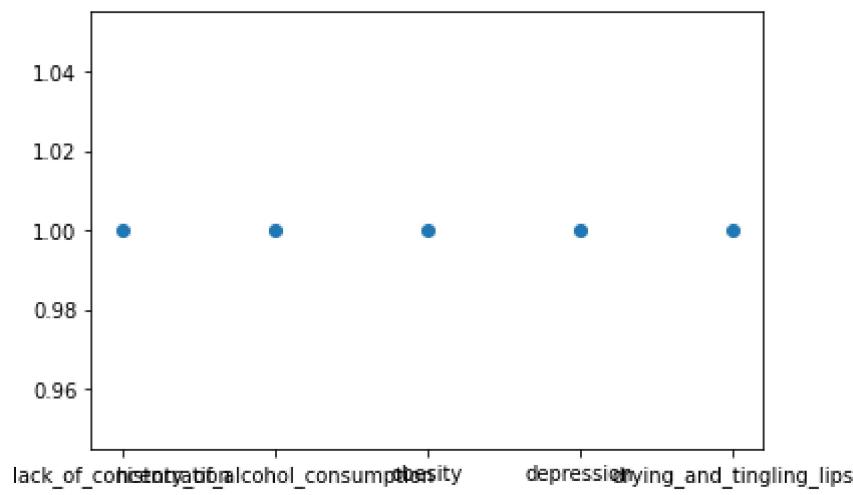


```

Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
'drying_and_tingling_lips']
[1, 1, 1, 1, 1]

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(

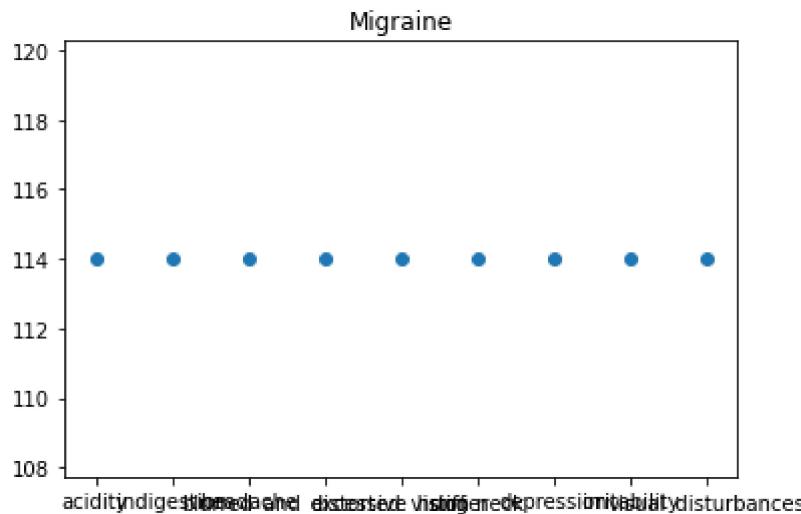
```



[114 114 114 114 114 114 114 114]

9

9

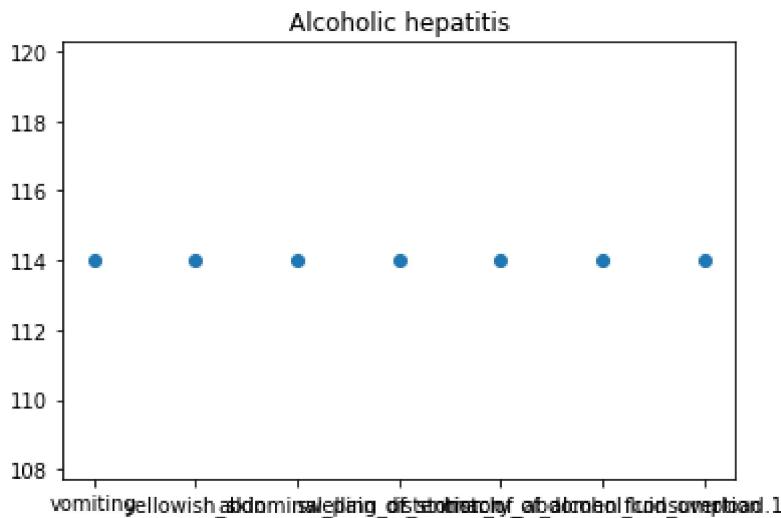


```

Random Forest
Accuracy
0.9512195121951219
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]]
[114 114 114 114 114 114 114]
7
7

```

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(

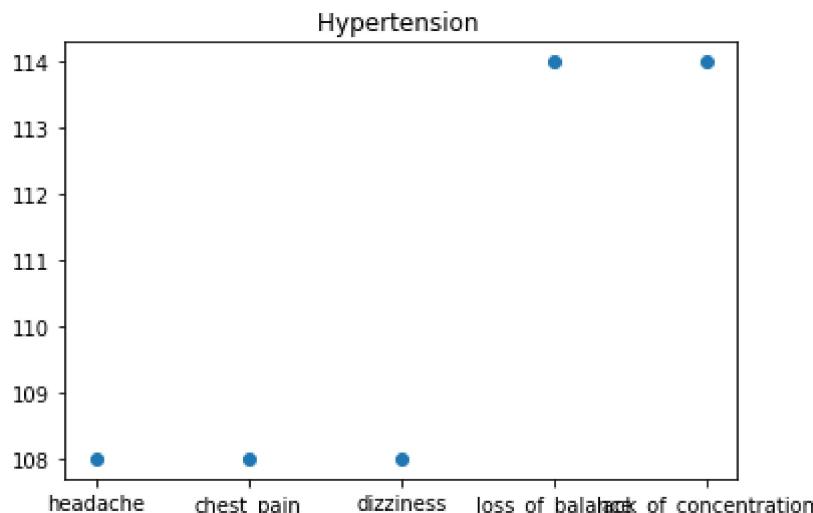


```

Naive Bayes
Accuracy
0.9512195121951219
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\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(



Naive Bayes

Accuracy

0.9512195121951219

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]`

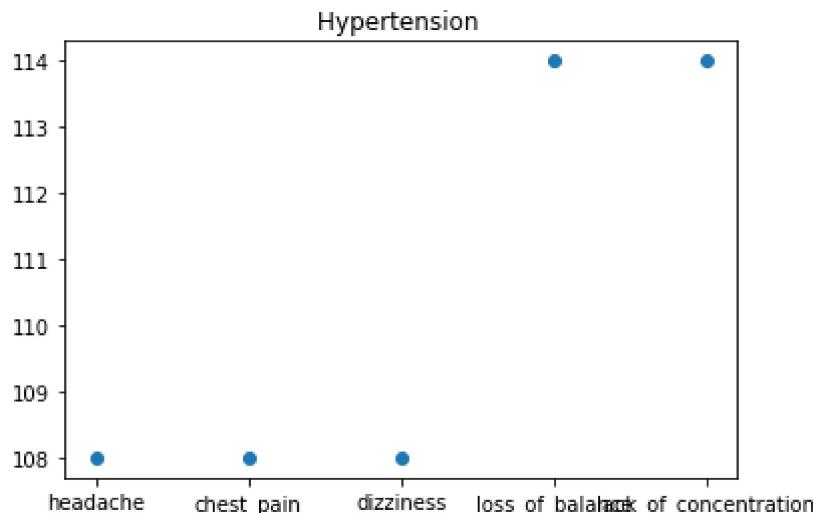
`[0 0 0 ... 0 0 1]]`

`[108 108 108 114 114]`

5

5

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(

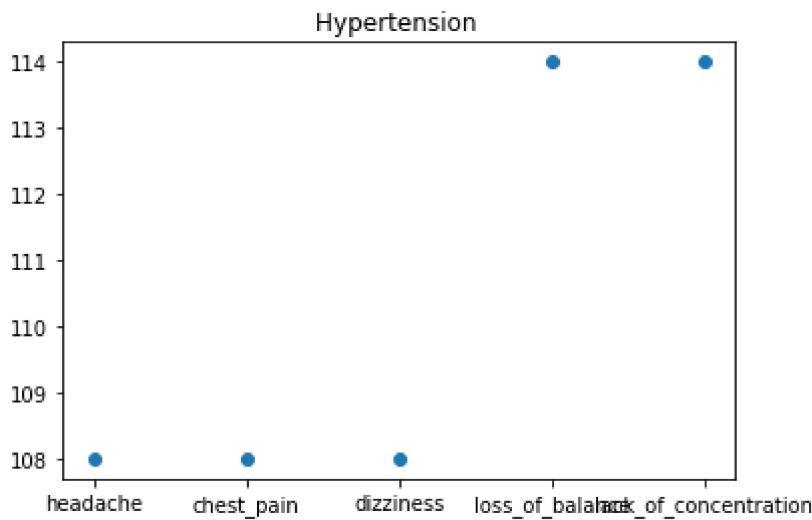


```

Naive Bayes
Accuracy
0.9512195121951219
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\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(

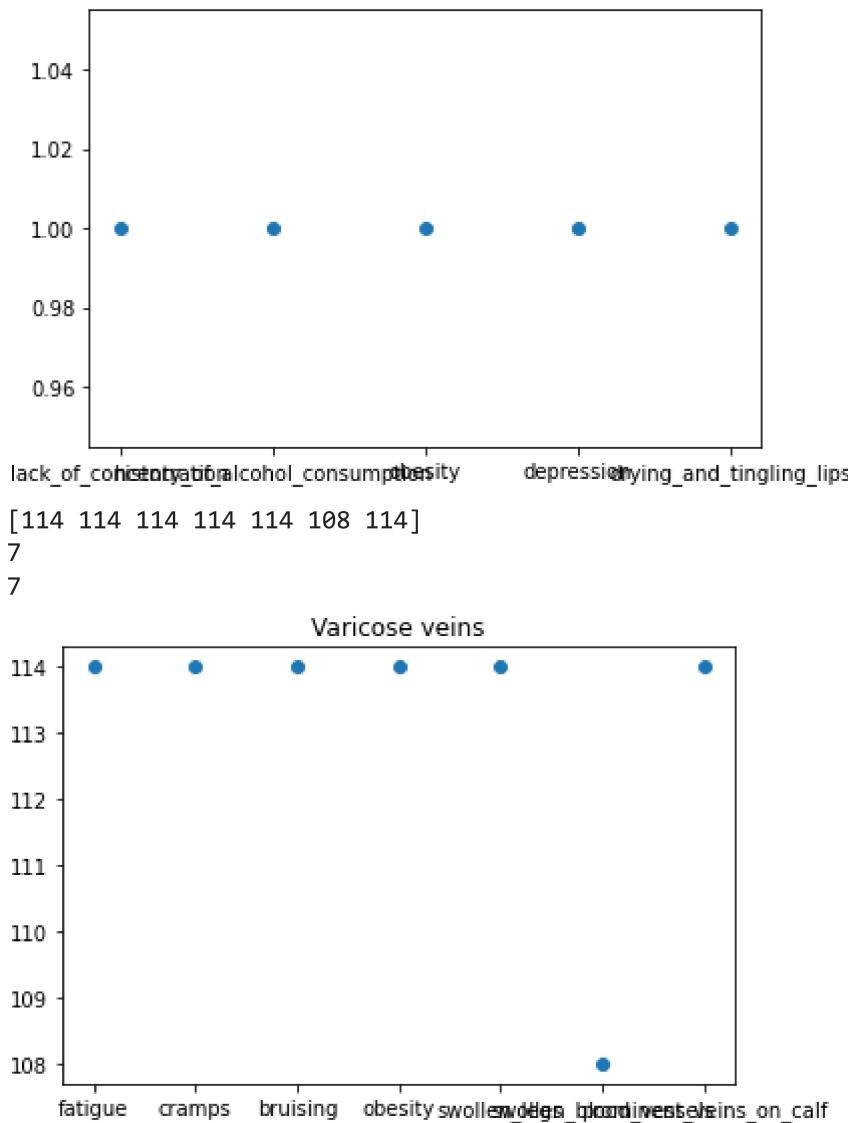


```

Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
'drying_and_tingling_lips']
[1, 1, 1, 1, 1]

```

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(



Decision Tree

Accuracy

0.9512195121951219

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]

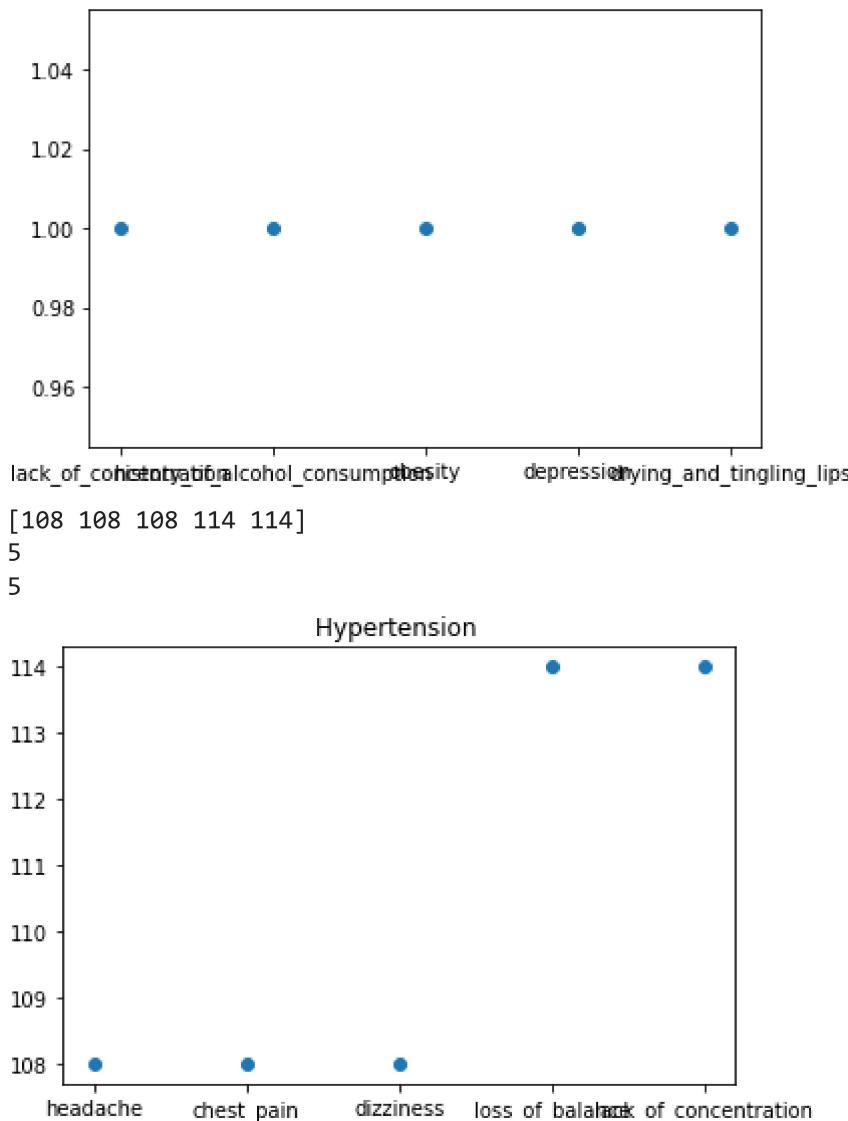
[0 0 0 ... 0 0 1]]

['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression', 'drying_and_tingling_lips']

[1, 1, 1, 1, 1]

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names

warnings.warn(

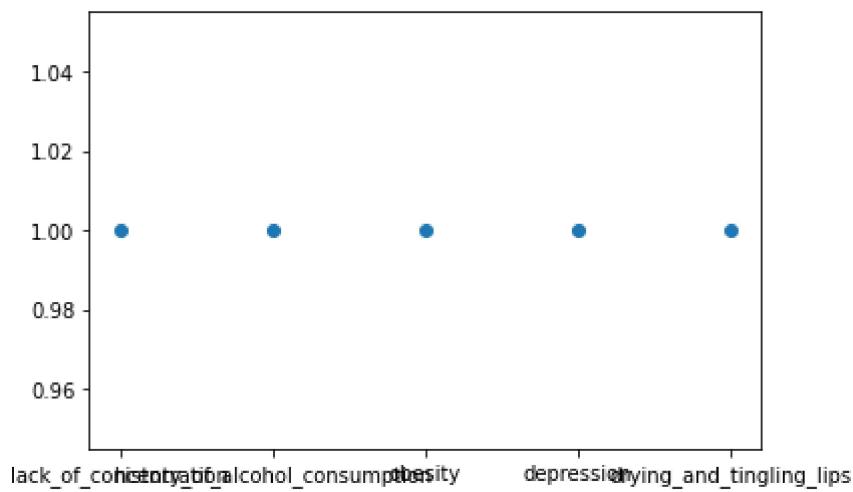


```

Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
'drying_and_tingling_lips']
[1, 1, 1, 1, 1]

```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```

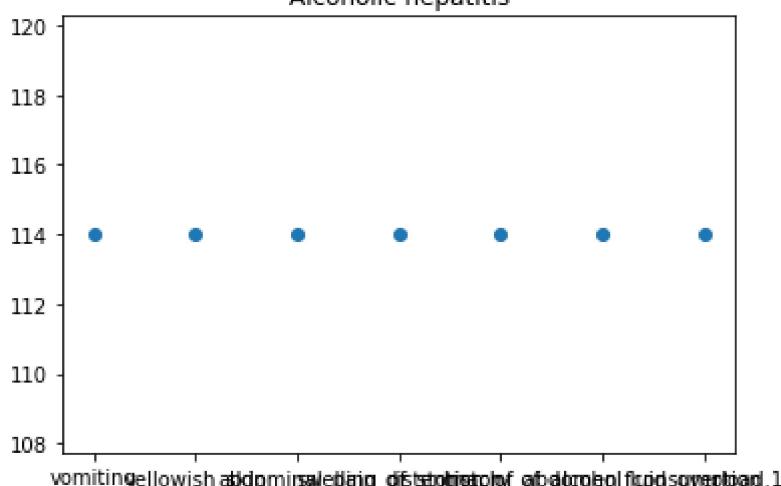


[114 114 114 114 114 114]

7

7

Alcoholic hepatitis



vomiting

yellowish_abdomen

salting_diet

history_of_alcohol_consumption

alcohol_intoxication

[114 114 114 114 114 114]

1

Random Forest

Accuracy

0.9512195121951219

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]

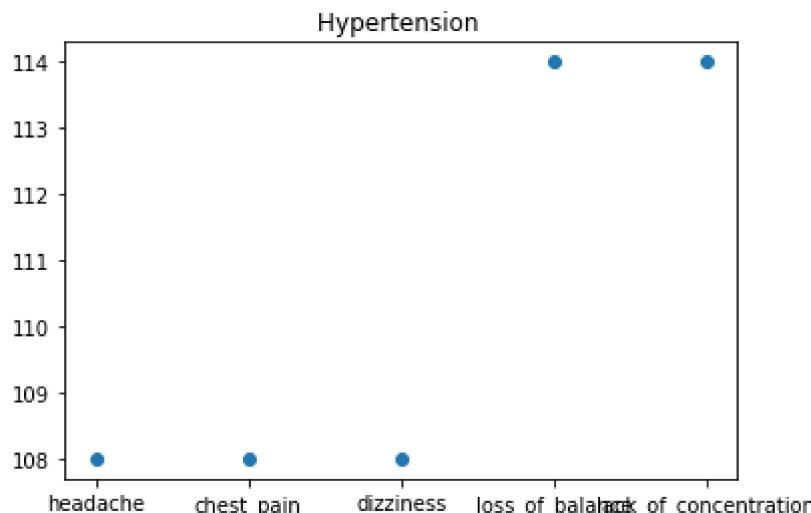
[0 0 0 ... 0 0 1]]

[108 108 108 114 114]

5

5

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(



Random Forest

Accuracy

0.9512195121951219

39

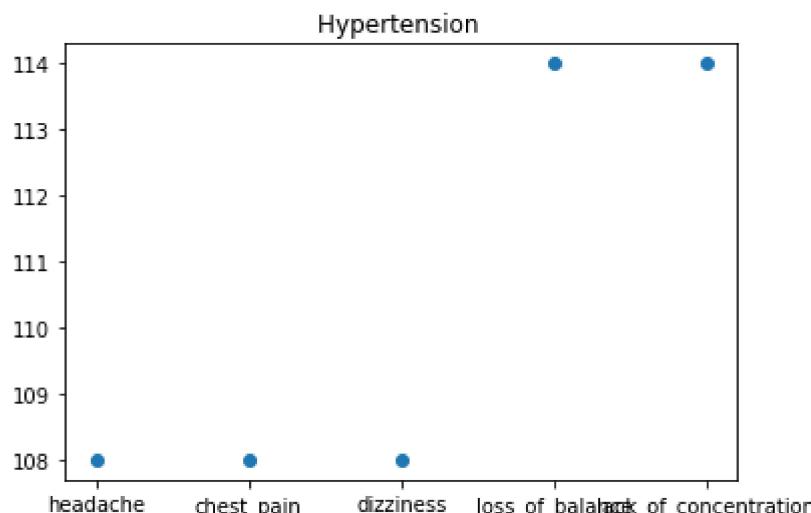
Confusion matrix

```
[[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\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(
```

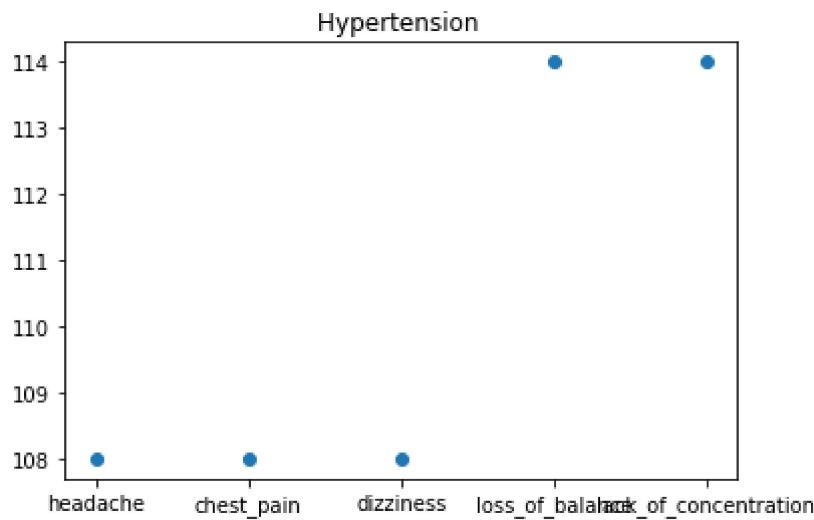


```
Random Forest
Accuracy
0.9512195121951219
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[108 108 108 114 114]
```

5

5

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(

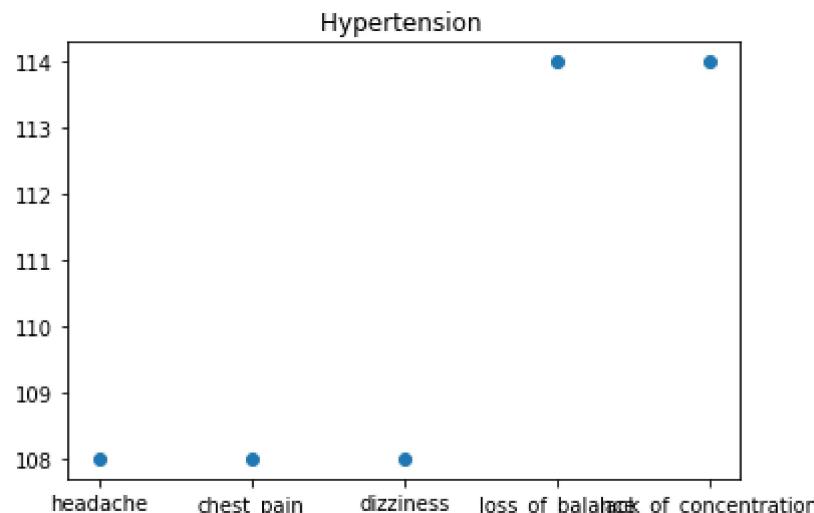


```
Naive Bayes
Accuracy
0.9512195121951219
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[108 108 108 114 114]
```

5

5

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(



Naive Bayes

Accuracy

0.9512195121951219

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]`

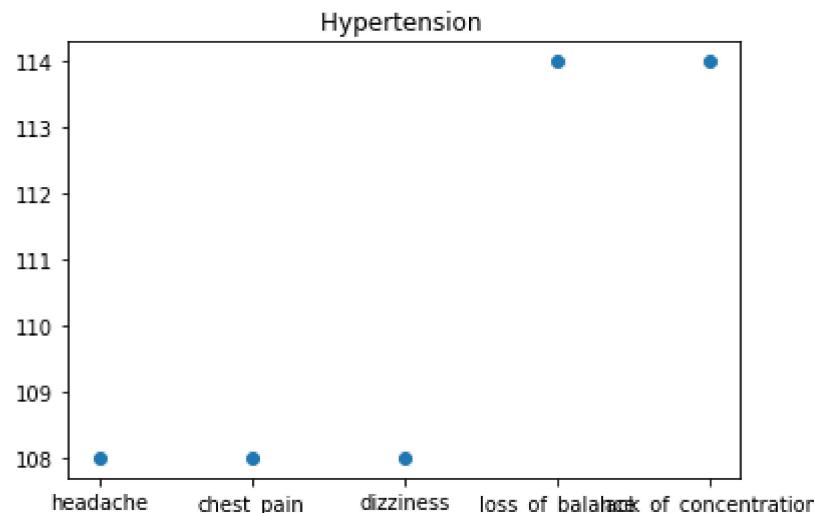
`[0 0 0 ... 0 0 1]]`

`[108 108 108 114 114]`

5

5

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(

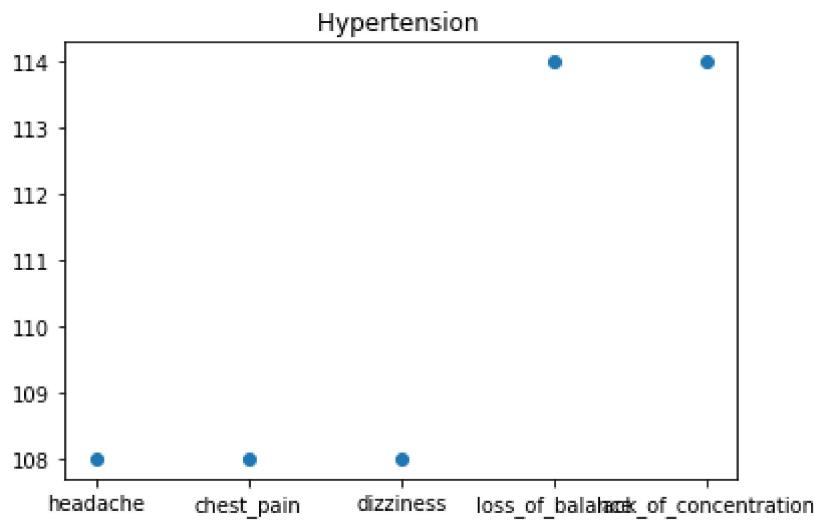


```

Naive Bayes
Accuracy
0.9512195121951219
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\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(
```

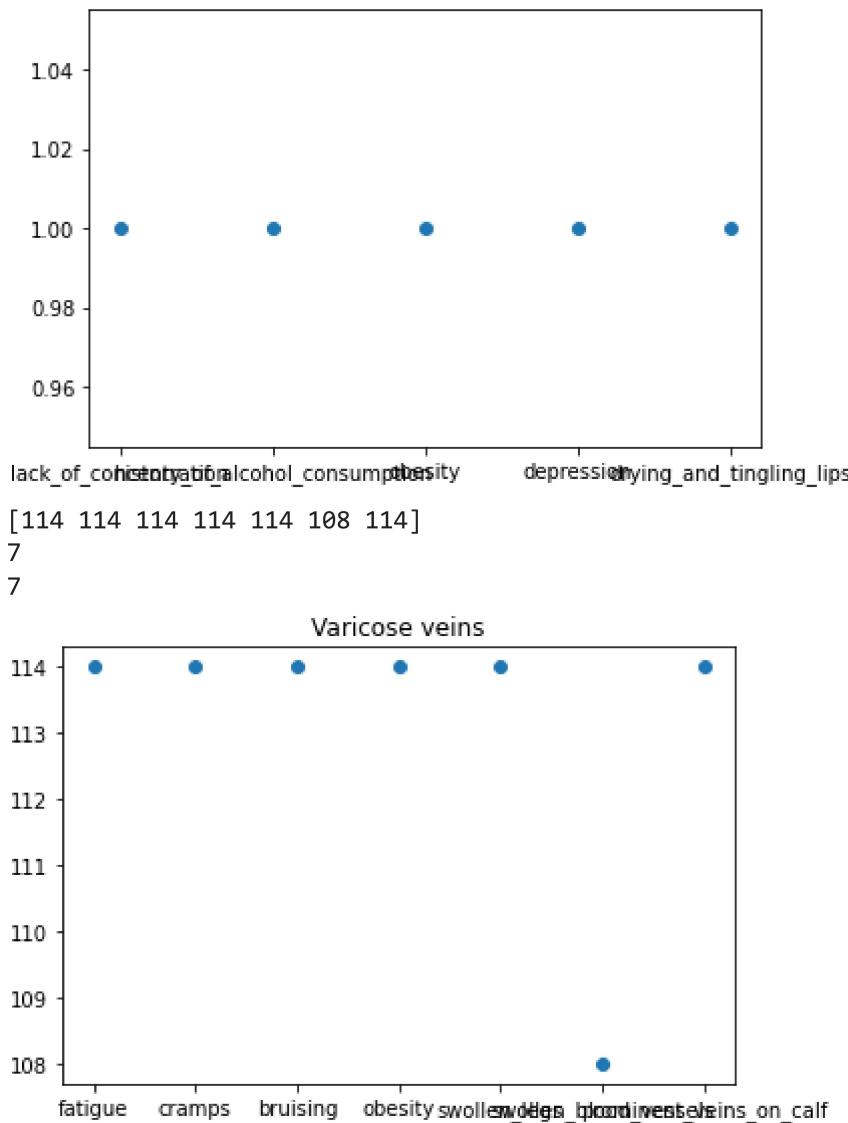


```

Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
 'dryness_and_tingling_lips']
[1, 1, 1, 1, 1]

```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```



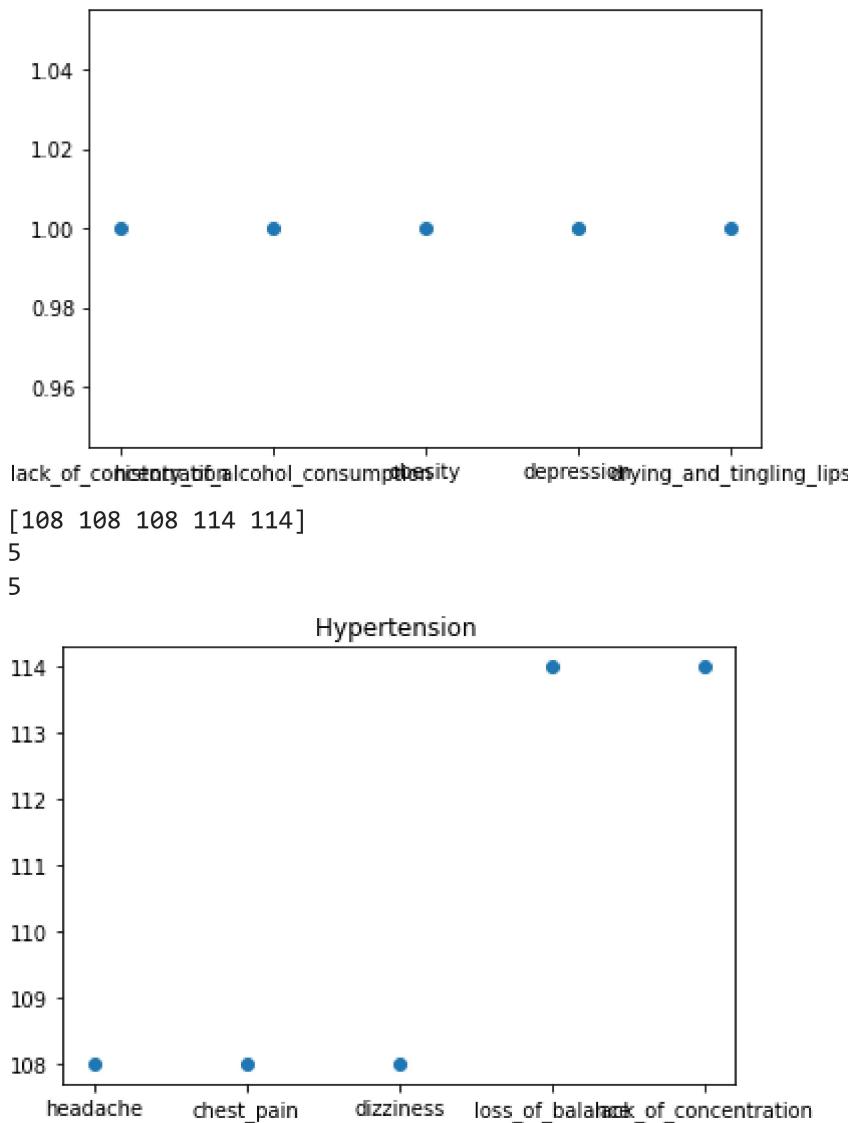
```

Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
'drying_and_tingling_lips']
[1, 1, 1, 1, 1]

```

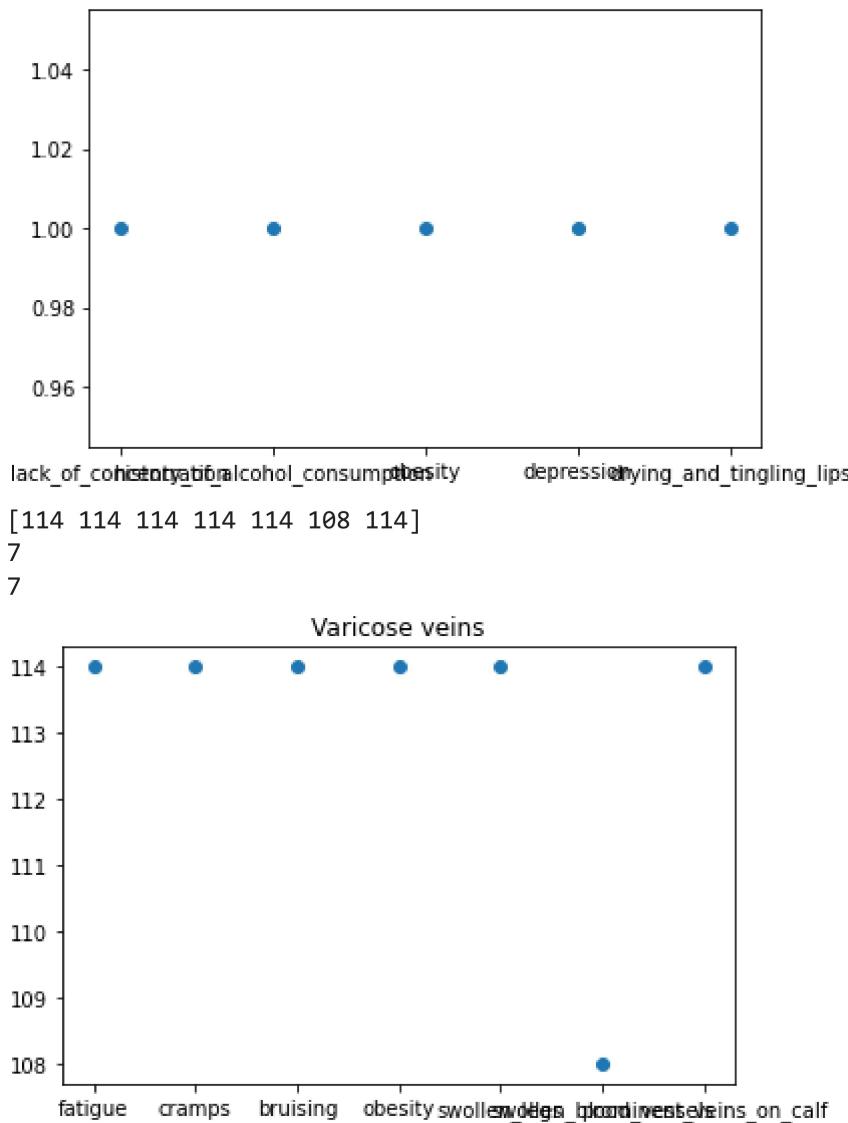
```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(

```



```
Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
'drying_and_tingling_lips']
[1, 1, 1, 1, 1]
```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```



Decision Tree

Accuracy

0.9512195121951219

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]`

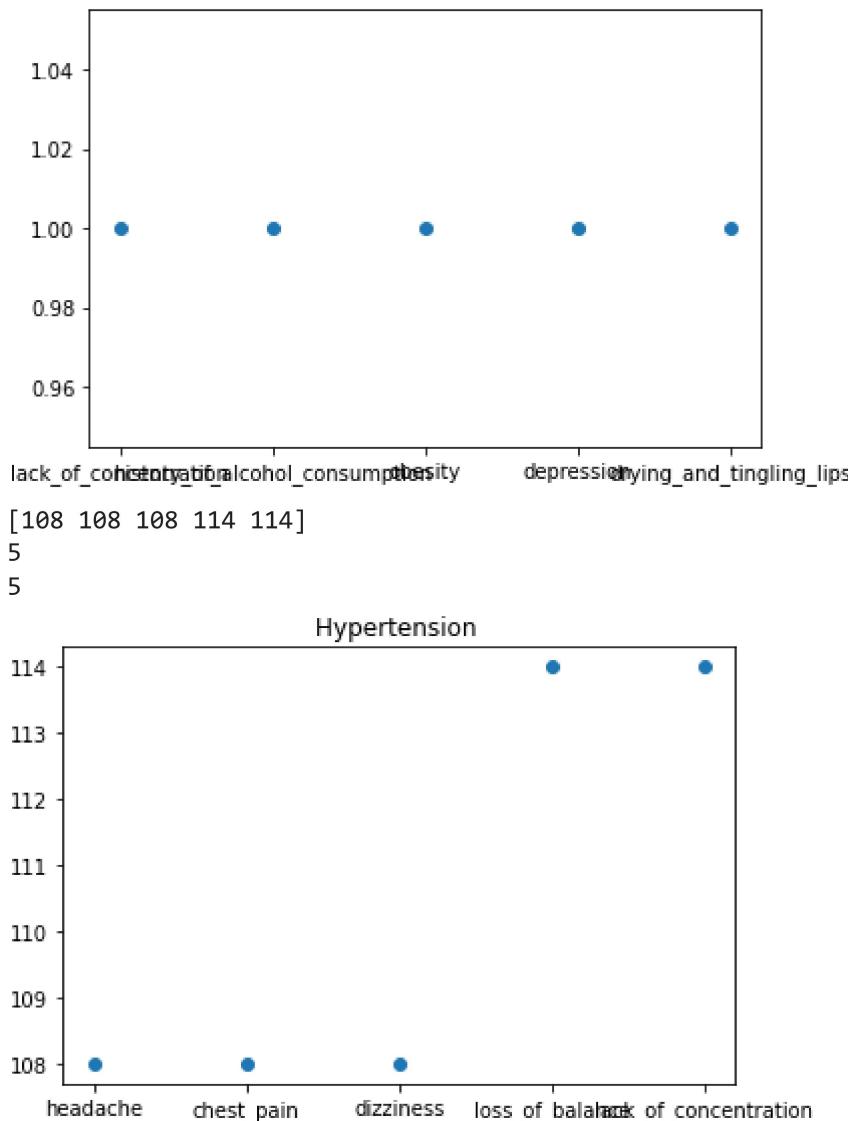
`[0 0 0 ... 0 1 0]`

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

`['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression', 'drying_and_tingling_lips']`

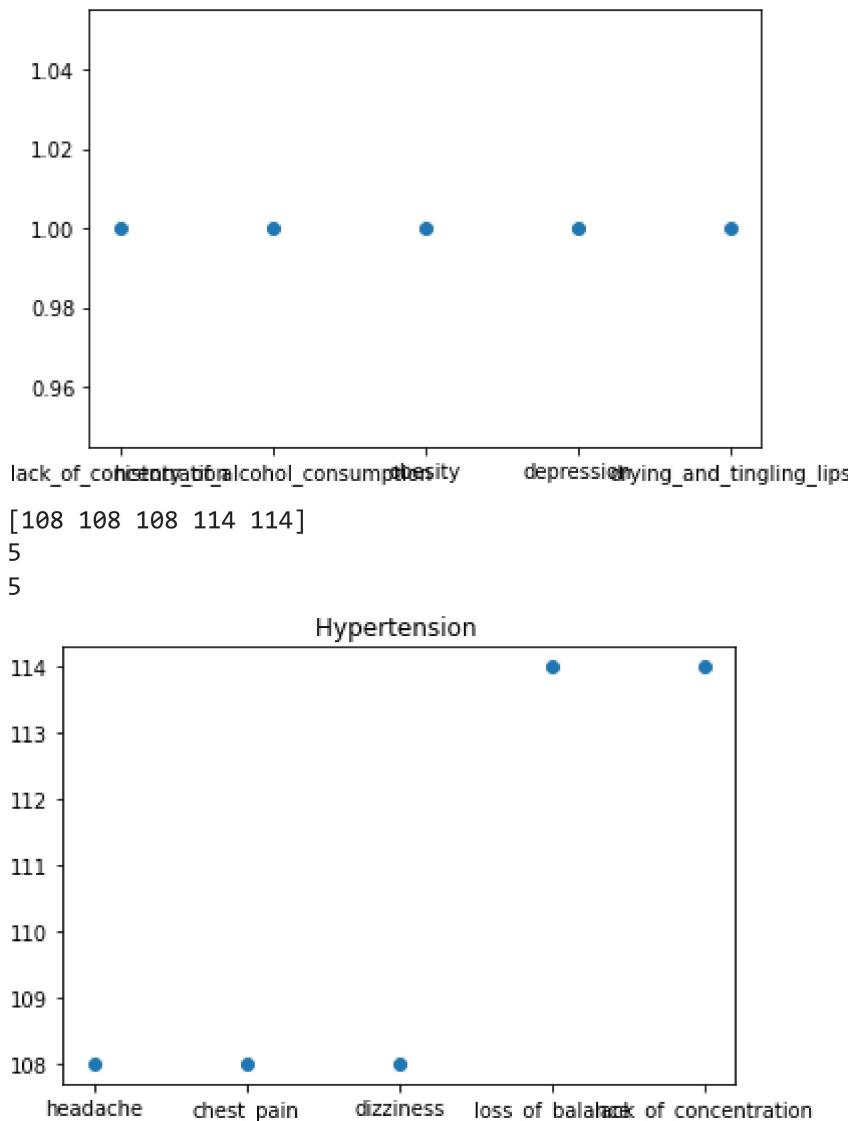
`[1, 1, 1, 1, 1]`

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(



```
Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
'drying_and_tingling_lips']
[1, 1, 1, 1, 1]
```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```



Decision Tree

Accuracy

0.9512195121951219

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]`

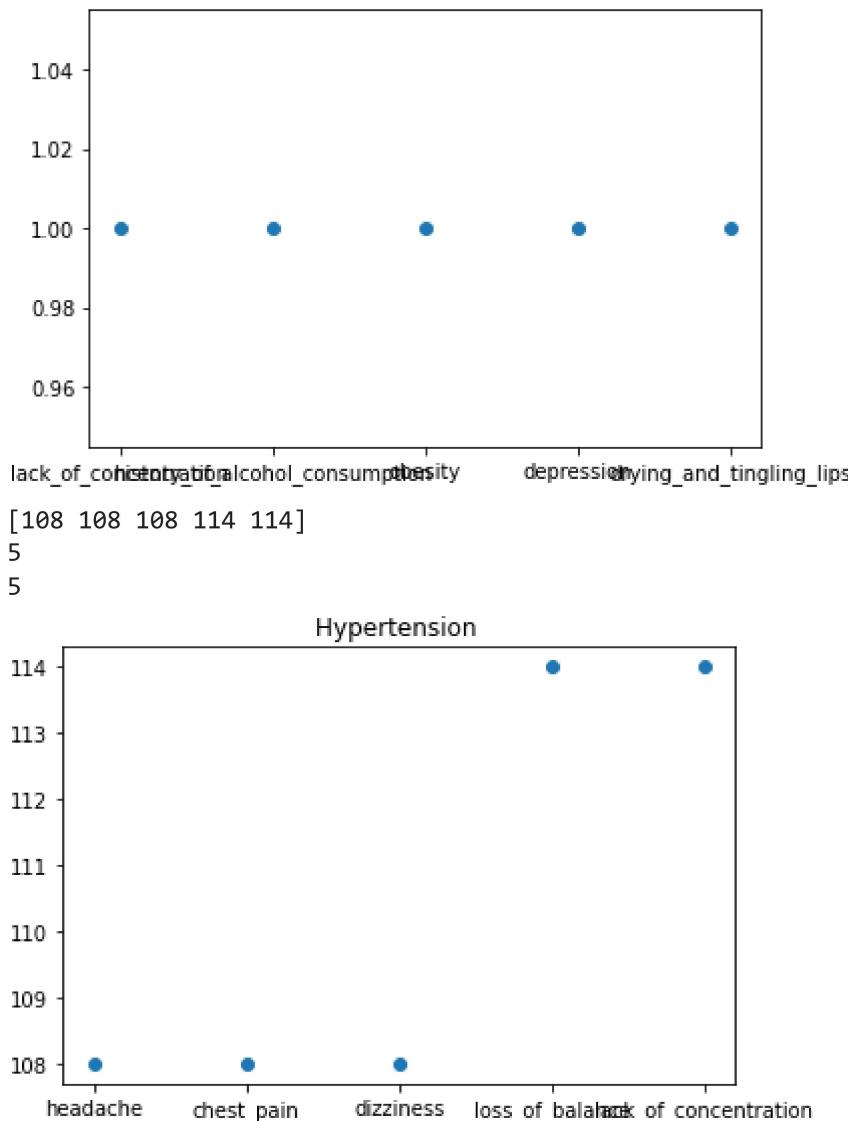
`[0 0 0 ... 0 0 1]]`

`['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',`

`'drying_and_tingling_lips']`

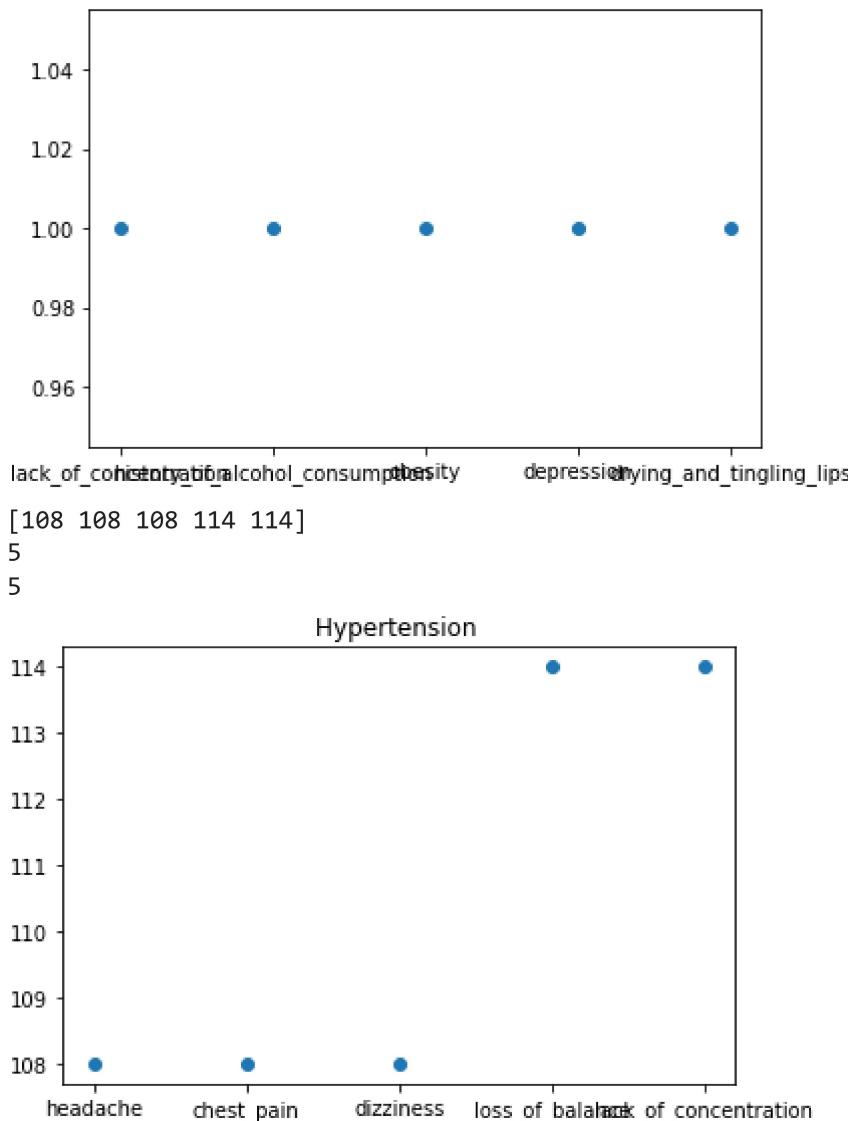
`[1, 1, 1, 1, 1]`

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(



```
Decision Tree
Accuracy
0.9512195121951219
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]]
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
'drying_and_tingling_lips']
[1, 1, 1, 1, 1]
```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```



Decision Tree

Accuracy

0.9512195121951219

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]`

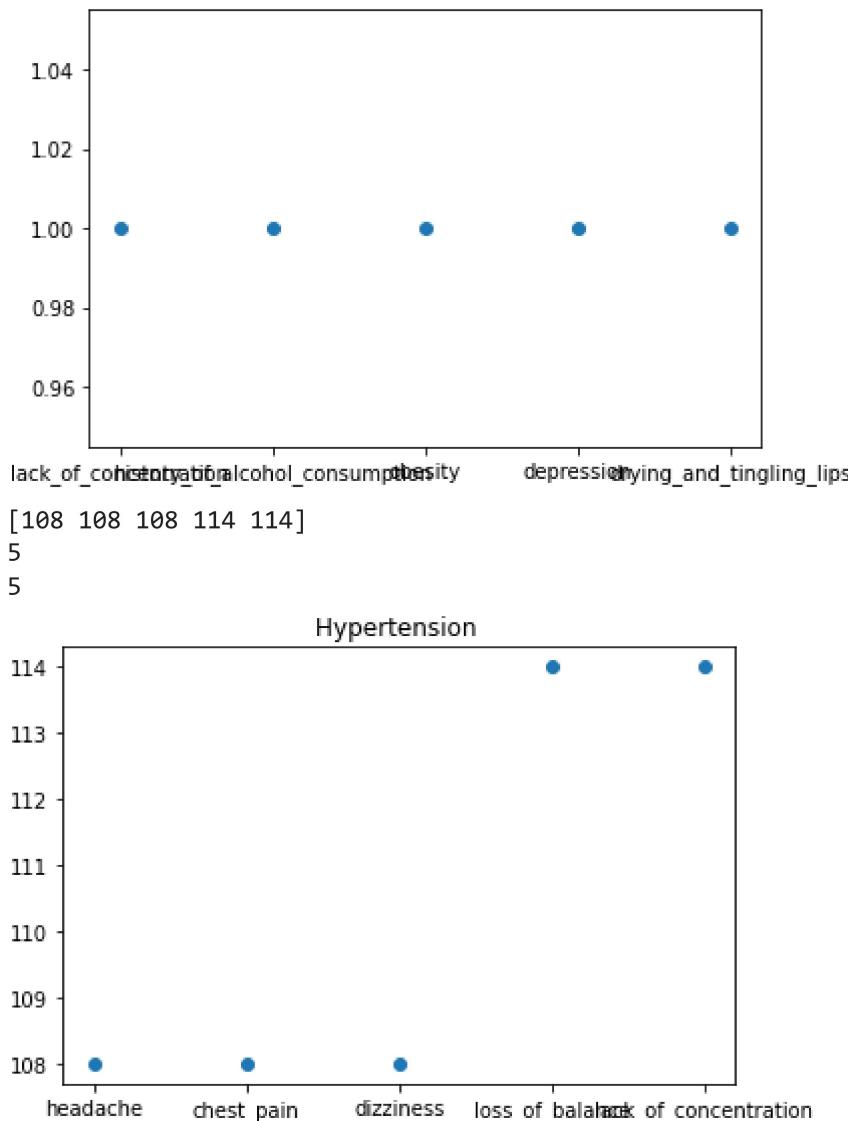
`[0 0 0 ... 0 0 1]]`

`['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',`

`'drying_and_tingling_lips']`

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

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(



Decision Tree
Accuracy
0.9512195121951219

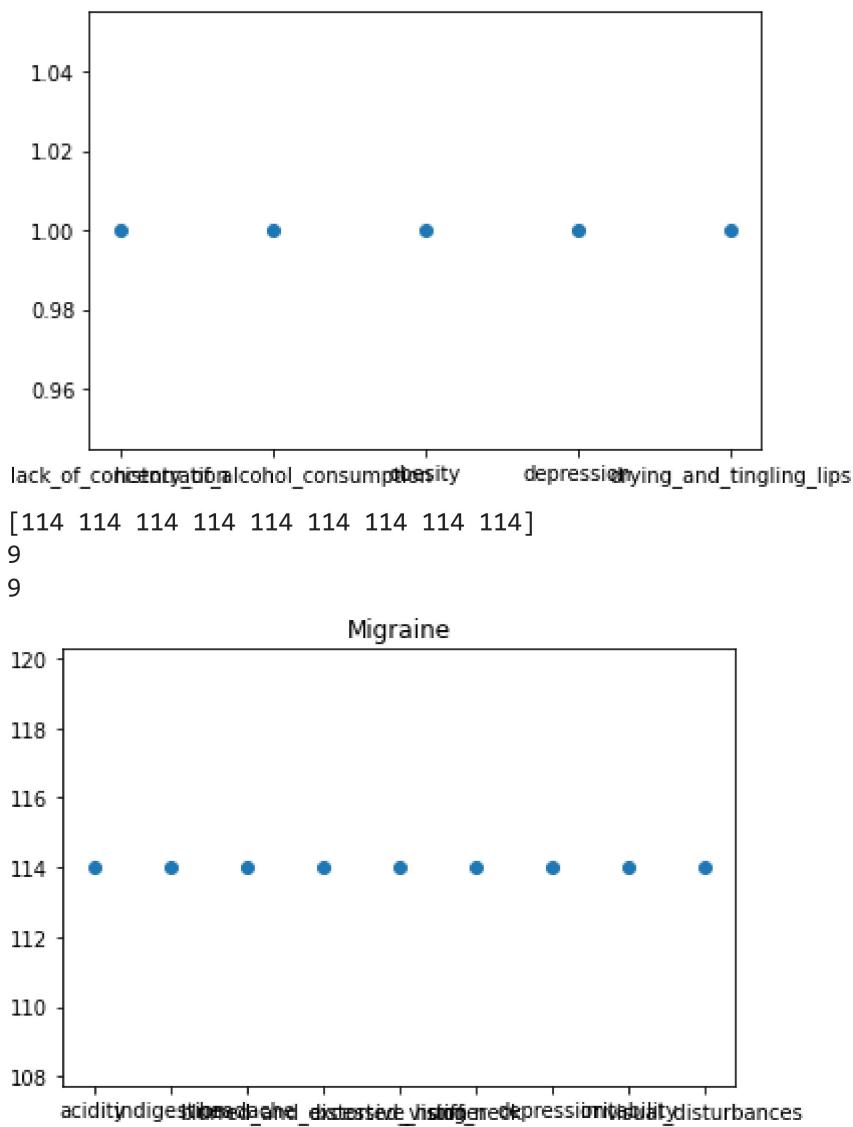
39

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]]
```

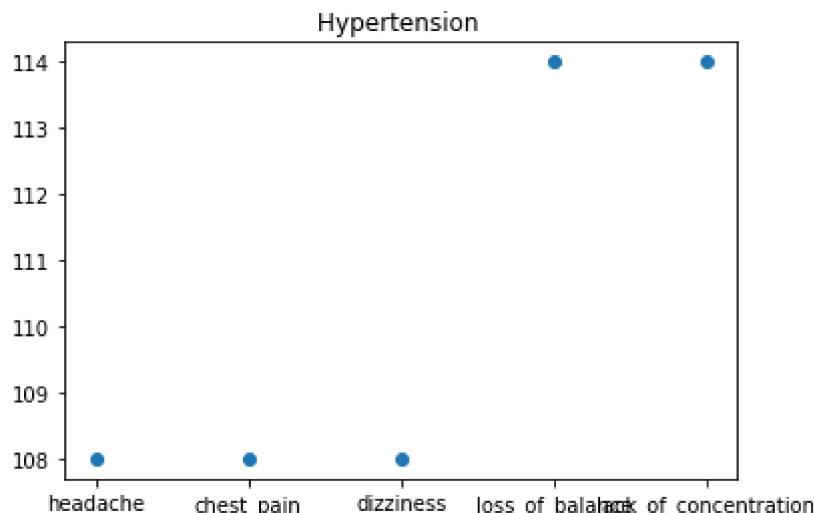
```
['lack_of_concentration', 'history_of_alcohol_consumption', 'obesity', 'depression',
'drying_and_tingling_lips']  
[1, 1, 1, 1, 1]
```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```



```
Random Forest
Accuracy
0.9512195121951219
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]
```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does n
ot have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(
```



Random Forest

Accuracy

0.9512195121951219

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]`

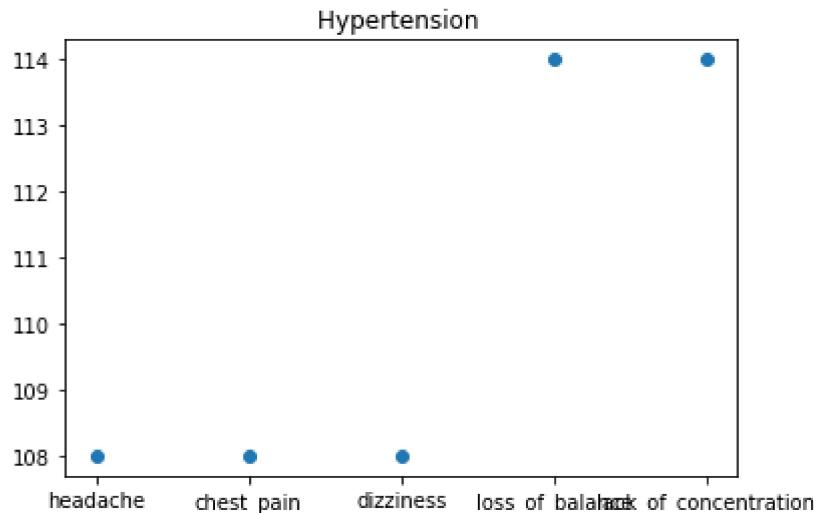
`[0 0 0 ... 0 0 1]]`

`[108 108 108 114 114]`

5

5

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(

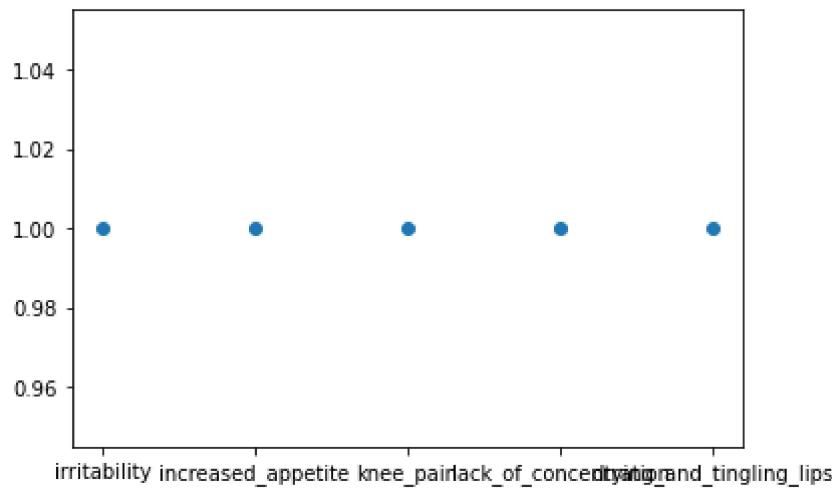


```

Decision Tree
Accuracy
0.9512195121951219
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]]
['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'drying_and_tingling_lips']
[1, 1, 1, 1, 1]

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(

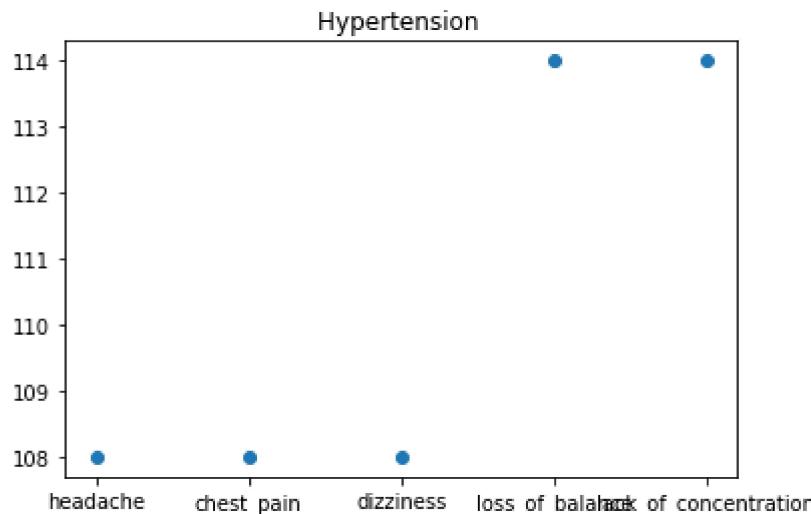
```



[108 108 108 114 114]

5

5

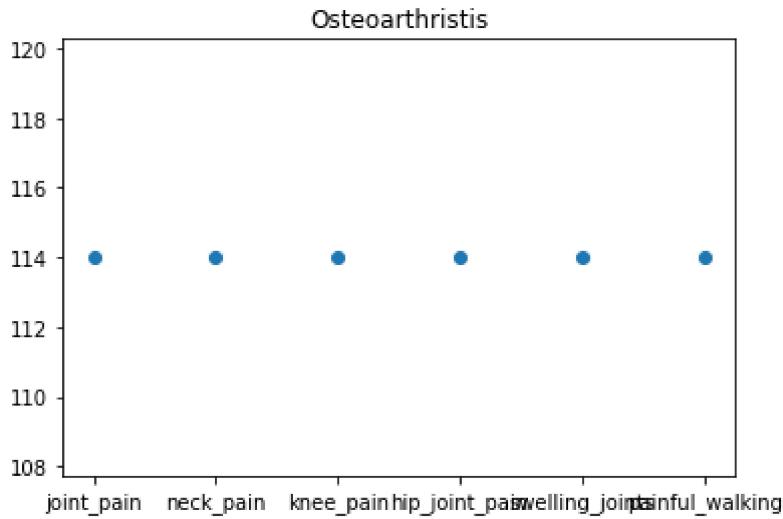


```
Random Forest
Accuracy
0.9512195121951219
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[114 114 114 114 114 114]
```

6

6

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(



Naive Bayes

Accuracy

0.9512195121951219

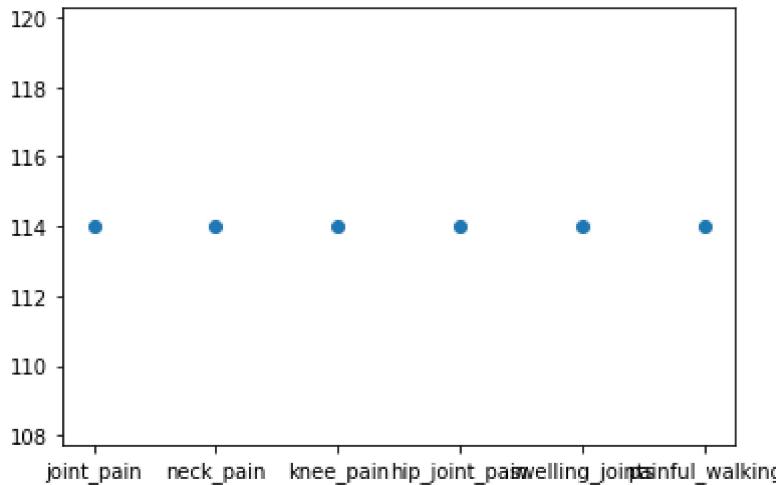
39

```
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]
```

6

6

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(

Osteoarthritis

Decision Tree

Accuracy

0.9512195121951219

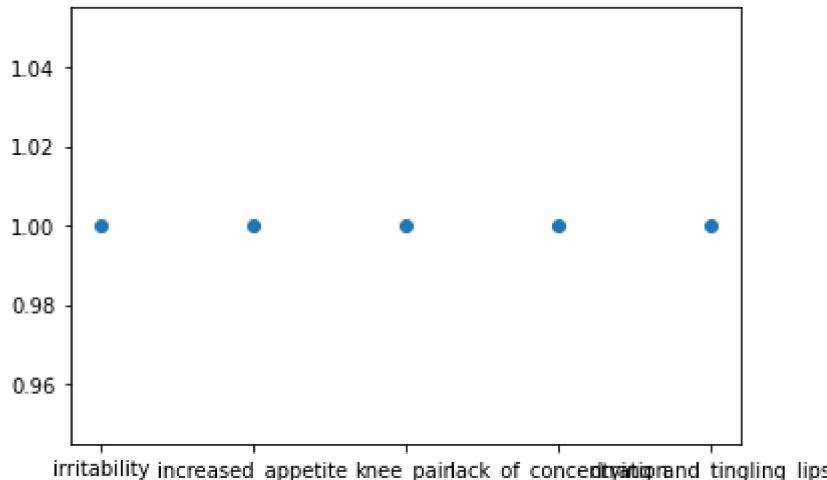
39

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]]
```

```
['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'drying_and_tingling_lips']
[1, 1, 1, 1, 1]
```

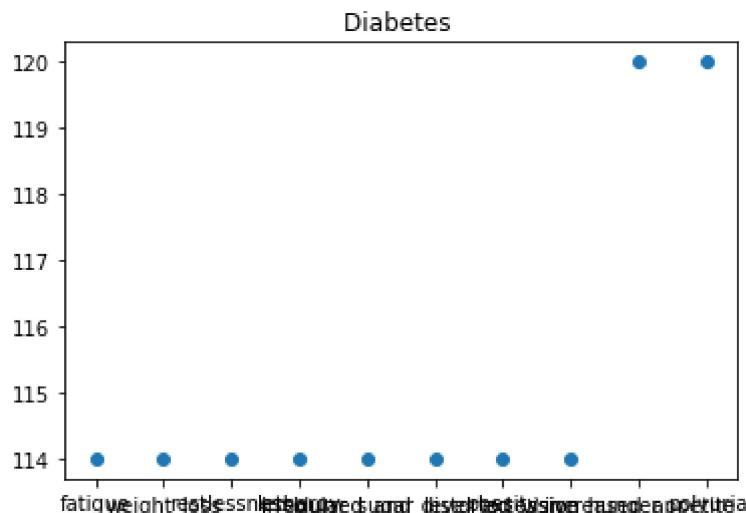
```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```



```
[114 114 114 114 114 114 114 114 114 120 120]
```

10

10



Decision Tree

Accuracy

0.9512195121951219

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]`

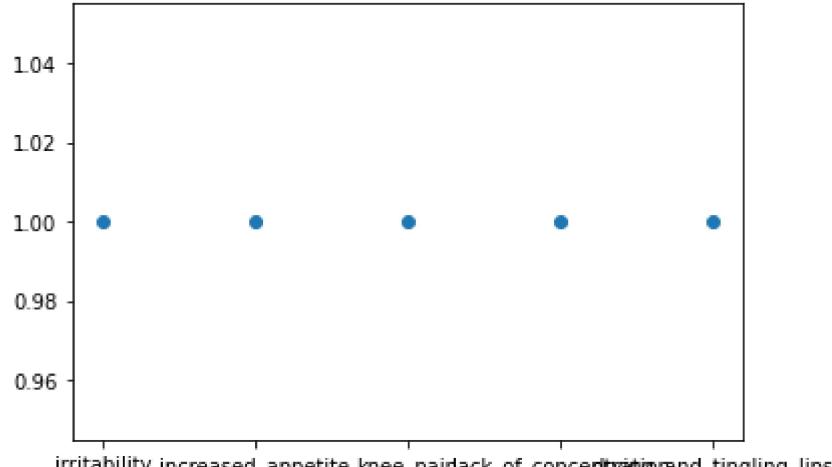
`[0 0 0 ... 0 1 0]`

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

`['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'dryng_and_tingling_lips']`

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

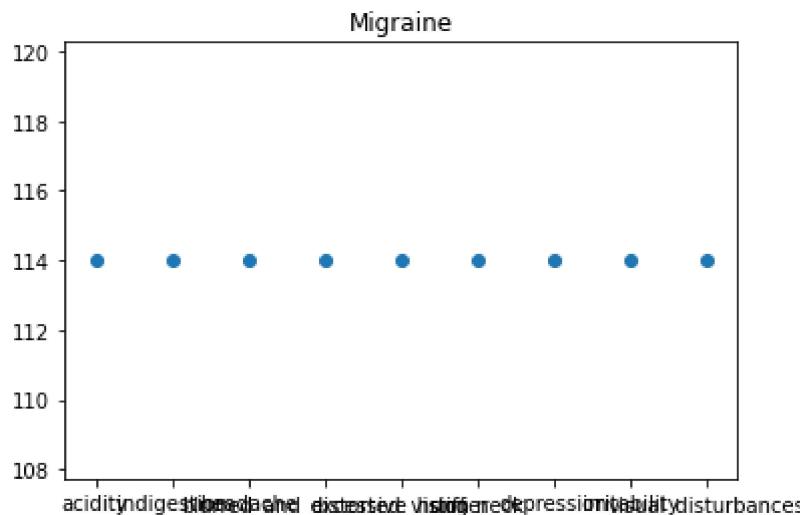
```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```



`[114 114 114 114 114 114]`

9

9



```
Decision Tree
```

```
Accuracy
```

```
0.9512195121951219
```

```
39
```

```
Confusion matrix
```

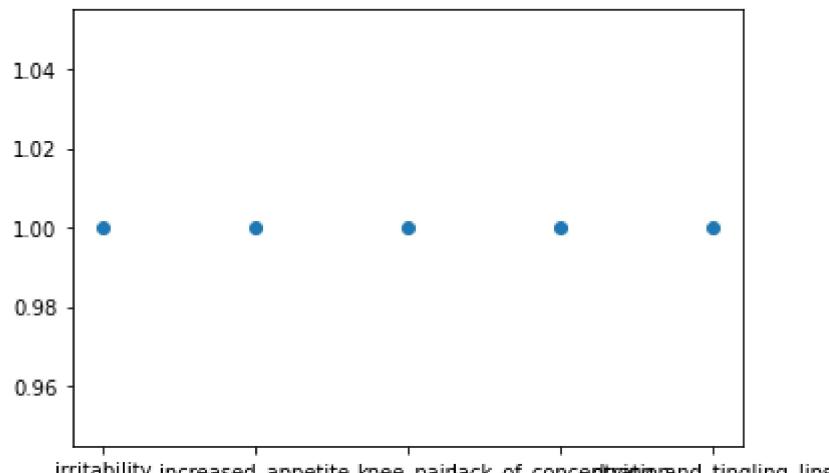
```
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
```

```
...
```

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

```
['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'drying_and_tingling_lips']
 [1, 1, 1, 1, 1]
```

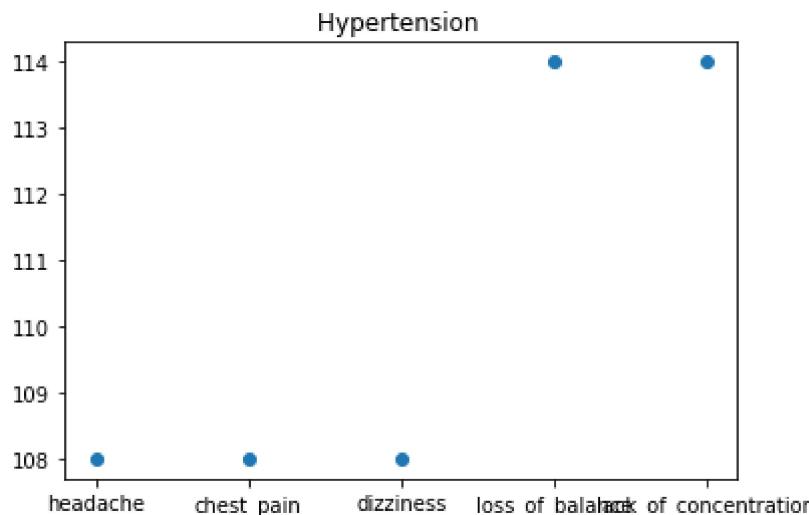
```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
 warnings.warn(
```



```
[108 108 108 114 114]
```

```
5
```

```
5
```



Decision Tree

Accuracy

0.9512195121951219

39

Confusion matrix

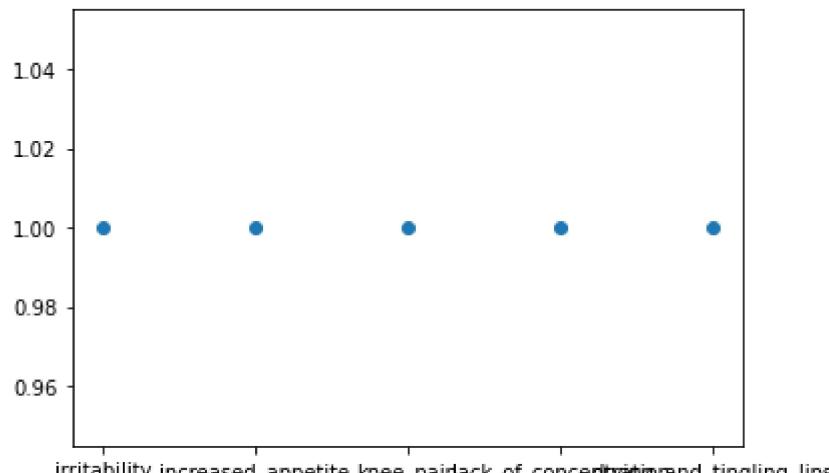
```
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
```

...

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

```
['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'drying_and_tingling_lips']
 [1, 1, 1, 1, 1]
```

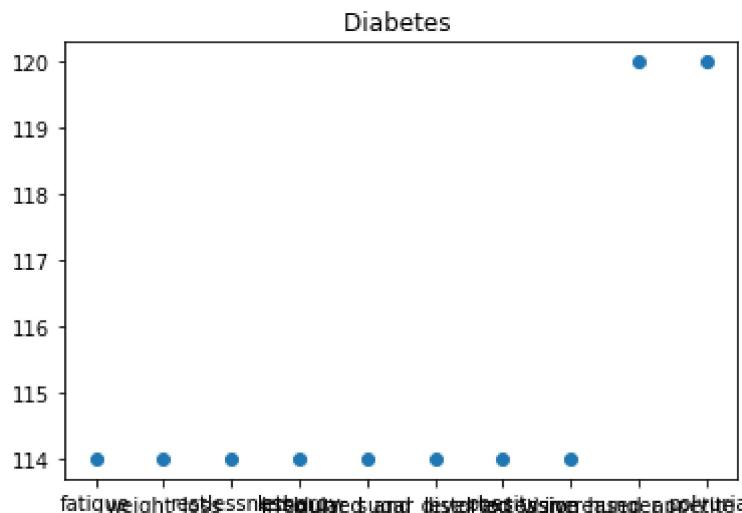
```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
 warnings.warn(
```



```
[114 114 114 114 114 114 114 114 114 120 120]
```

10

10



Decision Tree

Accuracy

0.9512195121951219

39

Confusion matrix

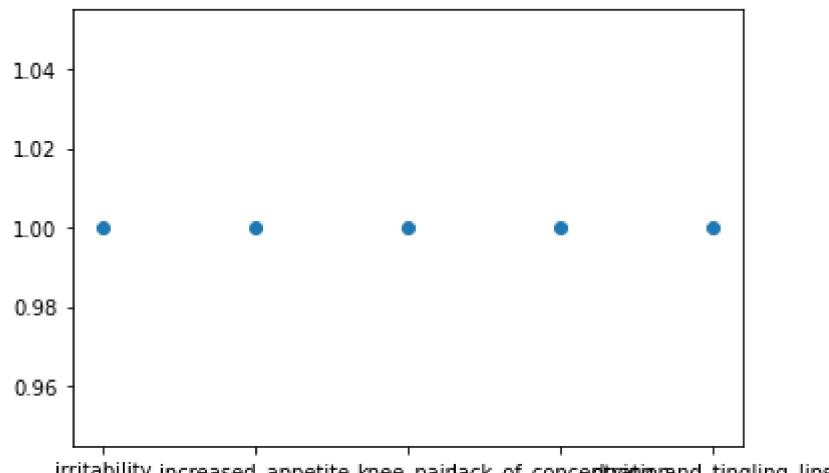
```
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
```

...

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

['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'dryng_and_tingling_lips']
[1, 1, 1, 1, 1]

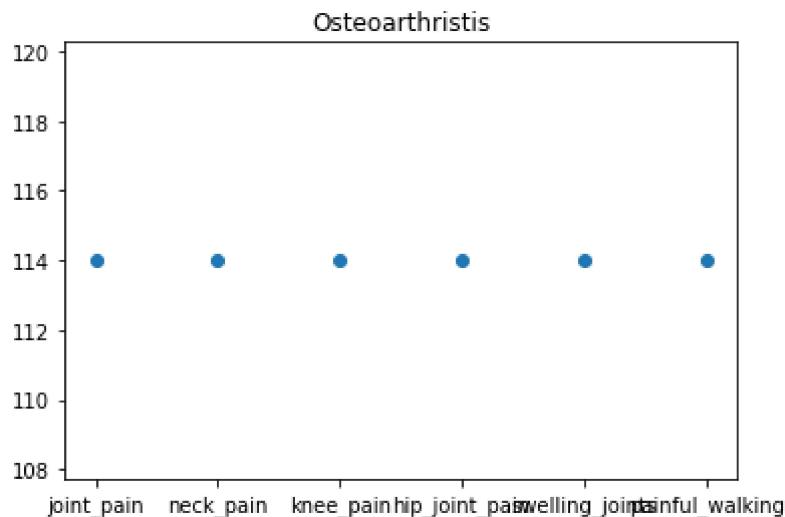
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(



[114 114 114 114 114]

6

6

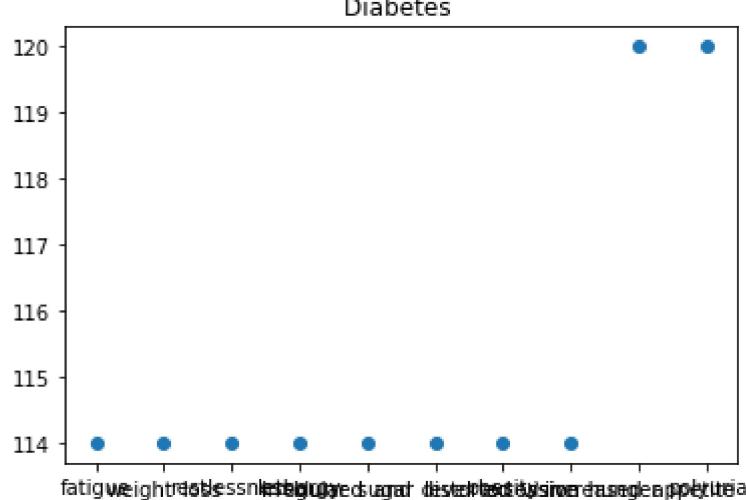


```
Random Forest
Accuracy
0.9512195121951219
39
Confusion matrix
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[114 114 114 114 114 114 114 114 120 120]
```

10

10

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(
```

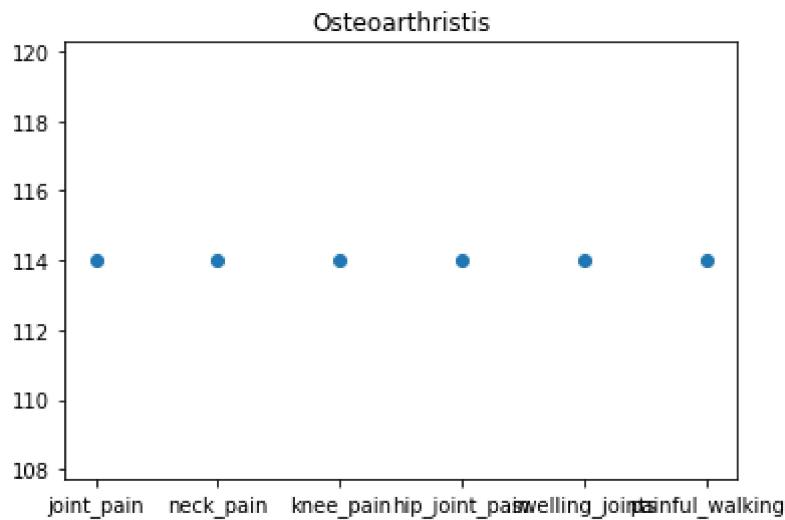


```

Naive Bayes
Accuracy
0.9512195121951219
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]
6
6

```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(
```

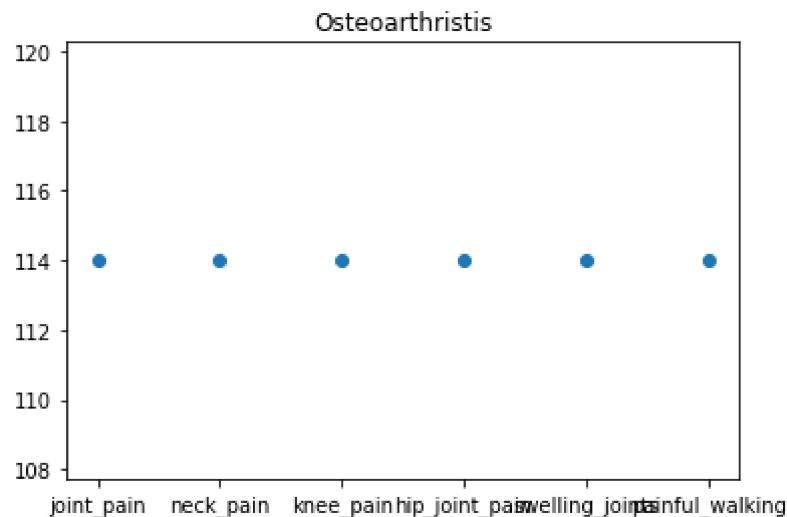


```

Naive Bayes
Accuracy
0.9512195121951219
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]
6
6

```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(
```



Naive Bayes

Accuracy

0.9512195121951219

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]`

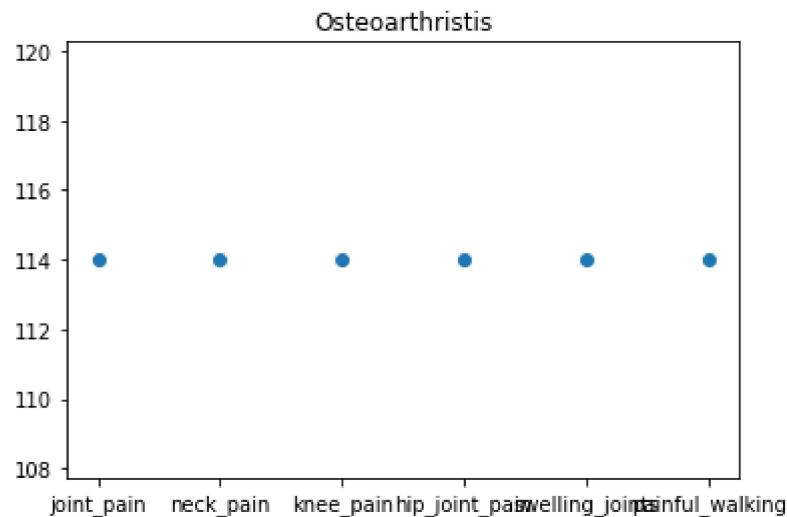
`[0 0 0 ... 0 0 1]]`

`[114 114 114 114 114 114]`

6

6

C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(

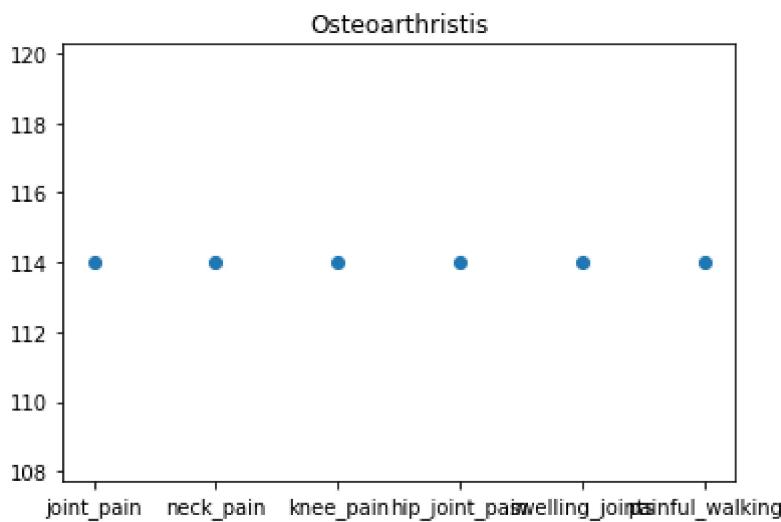


```

Naive Bayes
Accuracy
0.9512195121951219
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]
6
6

```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
warnings.warn(
```

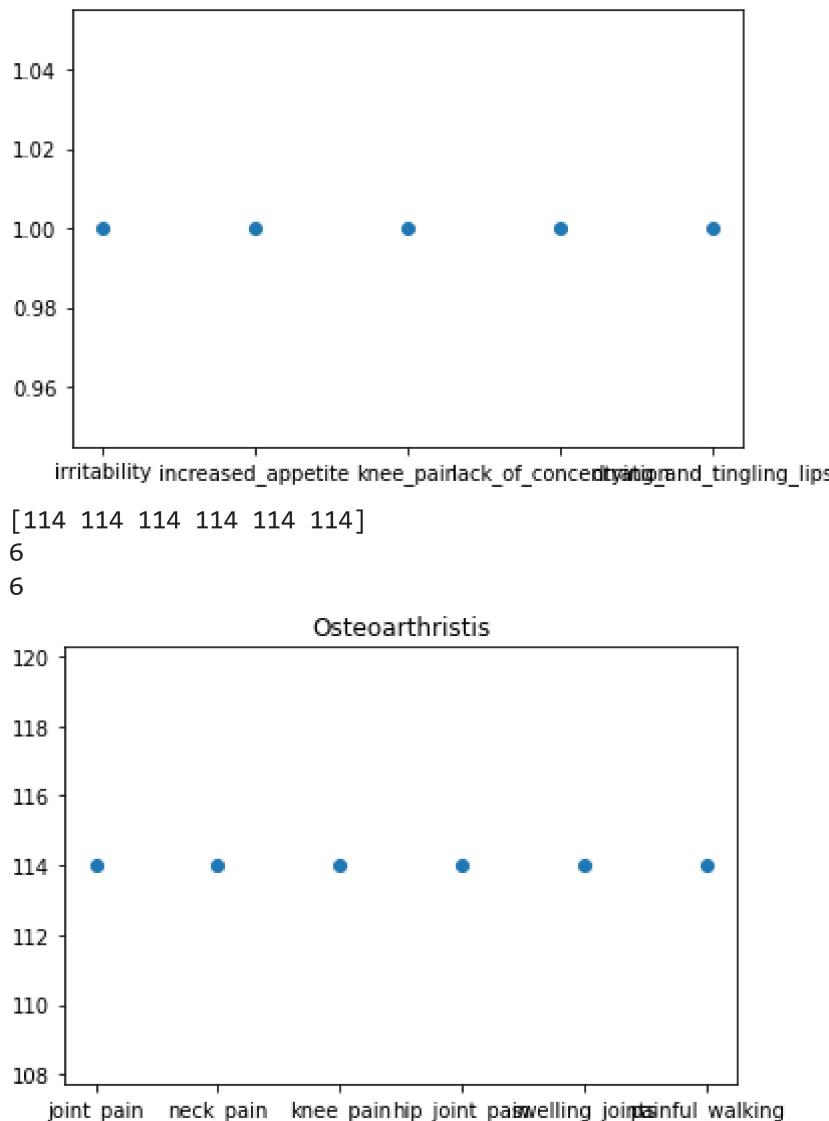


```

Decision Tree
Accuracy
0.9512195121951219
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]]
['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'drying_and_tingling_lips']
[1, 1, 1, 1, 1]

```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```



Decision Tree

Accuracy

0.9512195121951219

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]`

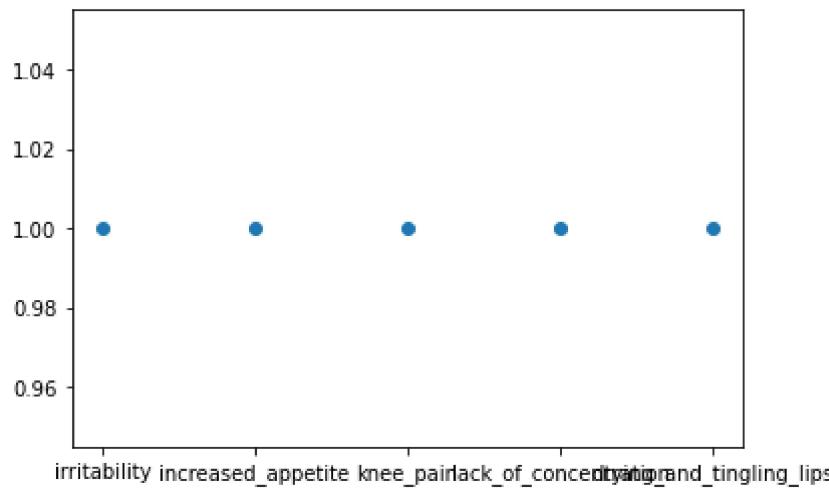
`[0 0 0 ... 0 1 0]`

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

`['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'drying_and_tingling_lips']`

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

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
  warnings.warn(
```

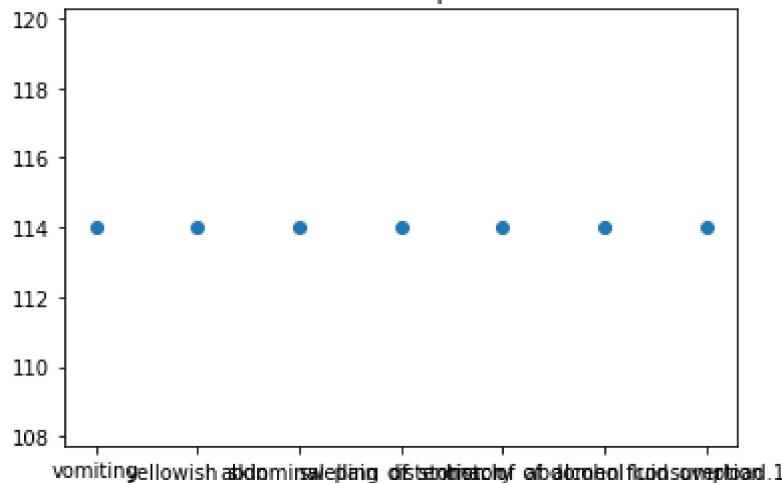


```
[114 114 114 114 114 114]
```

```
7
```

```
7
```

Alcoholic hepatitis



```
Decision Tree
```

```
Accuracy
```

```
0.9512195121951219
```

```
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]
```

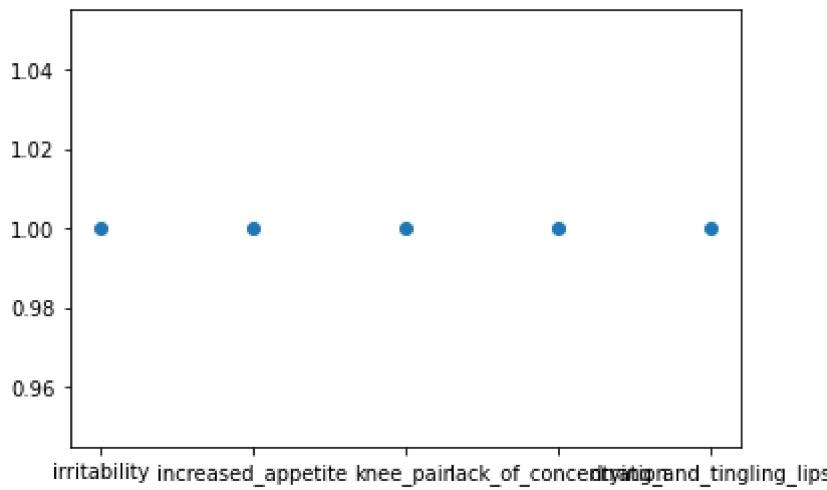
```
[0 0 0 ... 0 0 1]]
```

```
['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'drying_and_tingling_lips']
```

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

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
```

```
warnings.warn(
```

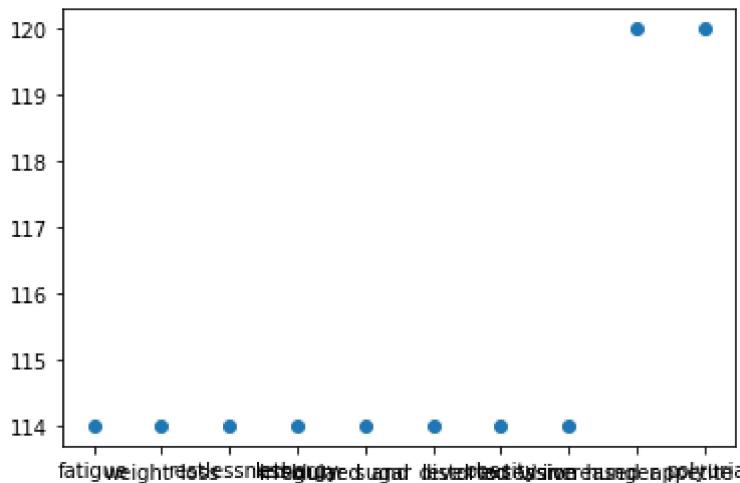


```
[114 114 114 114 114 114 114 114 114 120 120]
```

```
10
```

```
10
```

Diabetes



Decision Tree

Accuracy

```
0.9512195121951219
```

```
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]
```

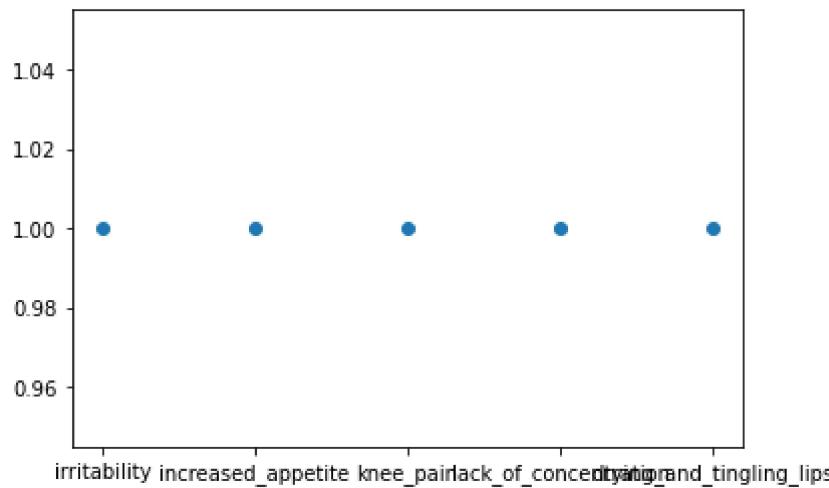
```
[0 0 0 ... 0 1 0]
```

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

`['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'dryng_and_tingling_lips']`

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

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
warnings.warn(
```

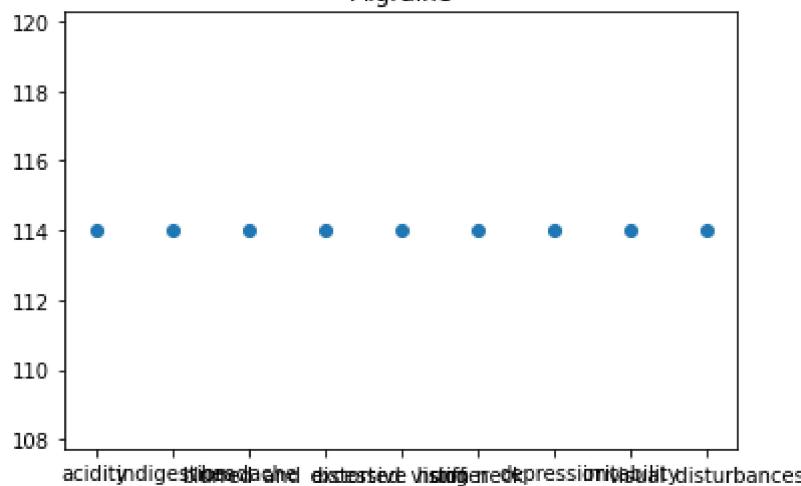


```
[114 114 114 114 114 114 114 114 114]
```

```
9
```

```
9
```

Migraine



```
Decision Tree
```

```
Accuracy
```

```
0.9512195121951219
```

```
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]
```

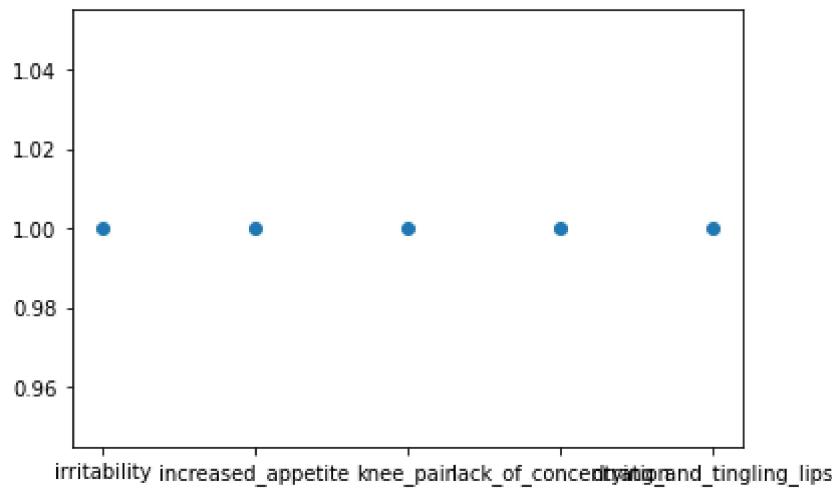
```
[0 0 0 ... 0 0 1]]
```

```
['irritability', 'increased_appetite', 'knee_pain', 'lack_of_concentration', 'drying_and_tingling_lips']
```

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

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names
```

```
warnings.warn(
```

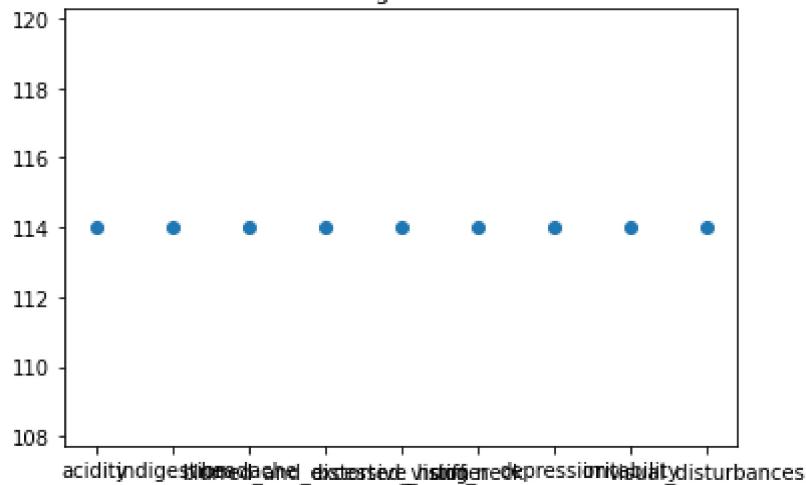


```
[114 114 114 114 114 114]
```

```
9
```

```
9
```

Migraine



```
Random Forest
```

```
Accuracy
```

```
0.9512195121951219
```

```
39
```

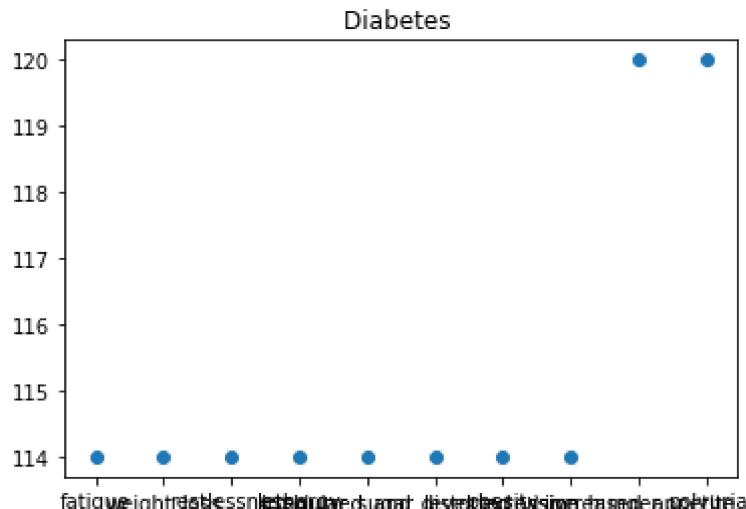
```
Confusion matrix
```

```
[[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]]
[114 114 114 114 114 114 114 114 120 120]
```

```
10
```

```
10
```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(
```



Naive Bayes

Accuracy

0.9512195121951219

39

Confusion matrix

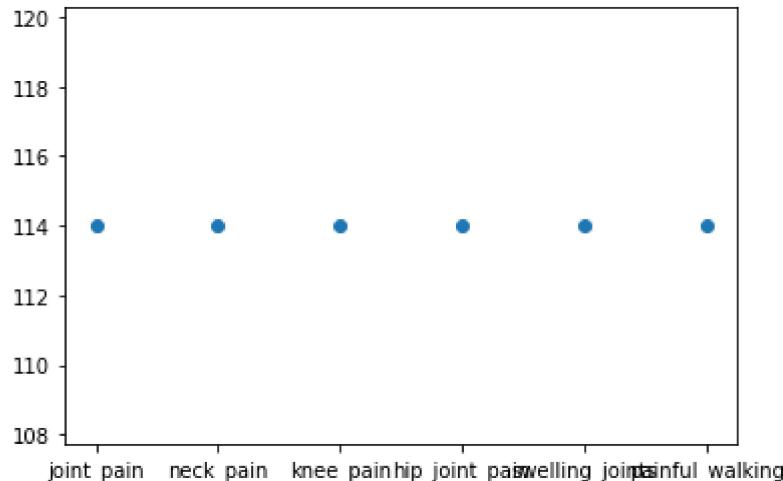
```
[[1 0 0 ... 0 0 0]
 [0 1 0 ... 0 0 0]
 [0 0 1 ... 0 0 0]
 ...
 [0 0 0 ... 1 0 0]
 [0 0 0 ... 0 1 0]
 [0 0 0 ... 0 0 1]]
[114 114 114 114 114 114]
```

6

6

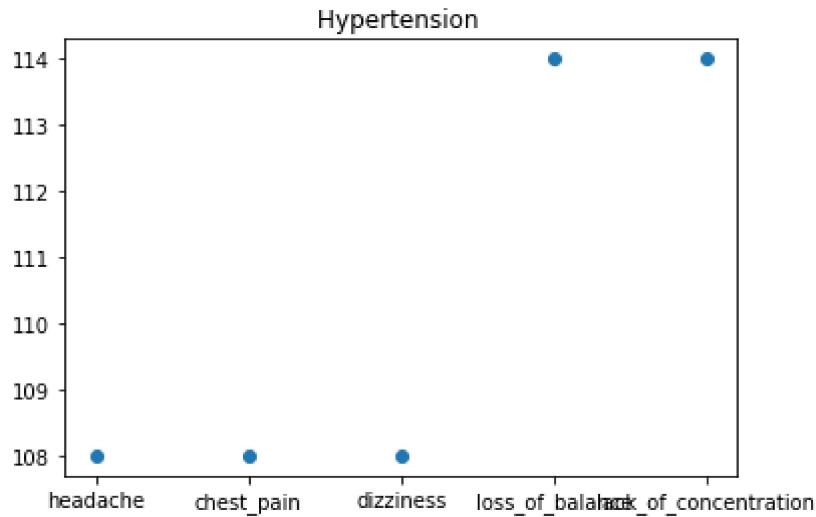
```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but GaussianNB was fitted with feature names
  warnings.warn(
```

Osteoarthritis



```
Random Forest
Accuracy
0.9512195121951219
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]]
[108 108 108 114 114]
5
5
```

```
C:\Users\Sazna\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature names
warnings.warn(
```



In []: