```
import numpy as np
import pandas as pd
import matplotlib as plt
import seaborn as sns
import datetime as dt
import sklearn
```

```
retail_dt=pd.read_csv("heart_v2.csv")
```

```
retail_dt.head()
```

```
   age  sex   BP  cholestrol  heart disease
0   70    1  130         322              1
1   67    0  115         564              0
2   57    1  124         261              1
3   64    1  128         263              0
4   74    0  120         269              0
```

```
retail_dt.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 270 entries, 0 to 269
Data columns (total 5 columns):
 #   Column         Non-Null Count  Dtype
---  ------         --------------  -----
 0   age            270 non-null    int64
 1   sex            270 non-null    int64
 2   BP             270 non-null    int64
 3   cholestrol     270 non-null    int64
 4   heart disease  270 non-null    int64
dtypes: int64(5)
memory usage: 10.7 KB
```

```
retail_dt.isnull().sum()
```

```
age              0
sex              0
BP               0
cholestrol       0
heart disease    0
dtype: int64
```

```
retail_dt.isnull().sum().sum()
```

```
0
```

```
retail_dt['heart disease'].value_counts()
```

```
0    150
1    120
Name: heart disease, dtype: int64
```

```
retail_dt=retail_dt.dropna()
retail_dt.shape
```

```
(270, 5)
```

```
retail_dt.head()
```

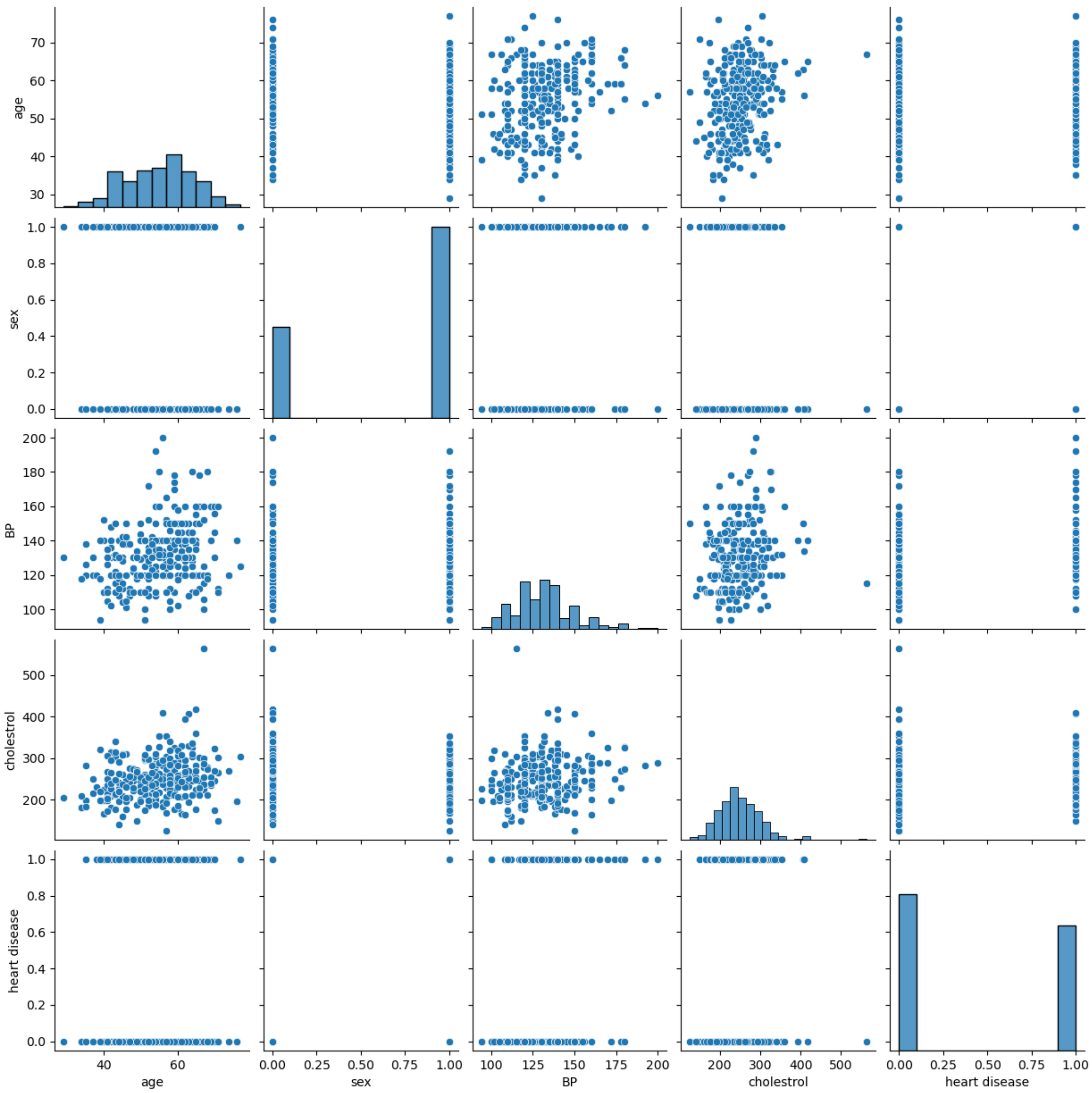
```
   age  sex   BP  cholestrol  heart disease
0   70    1  130         322              1
1   67    0  115         564              0
2   57    1  124         261              1
3   64    1  128         263              0
4   74    0  120         269              0
```

```
retail_dt.columns
```

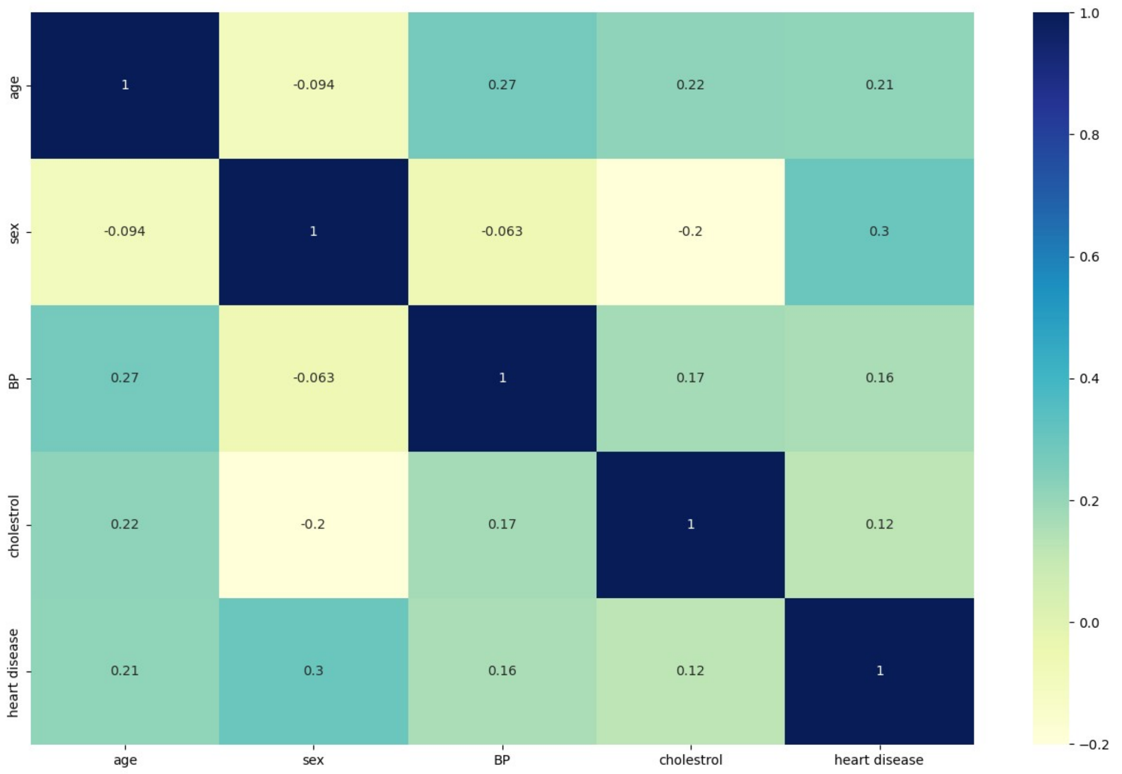
```
Index(['age', 'sex', 'BP', 'cholestrol', 'heart disease'],
dtype='object')
```

```
import matplotlib.pyplot as plt
```

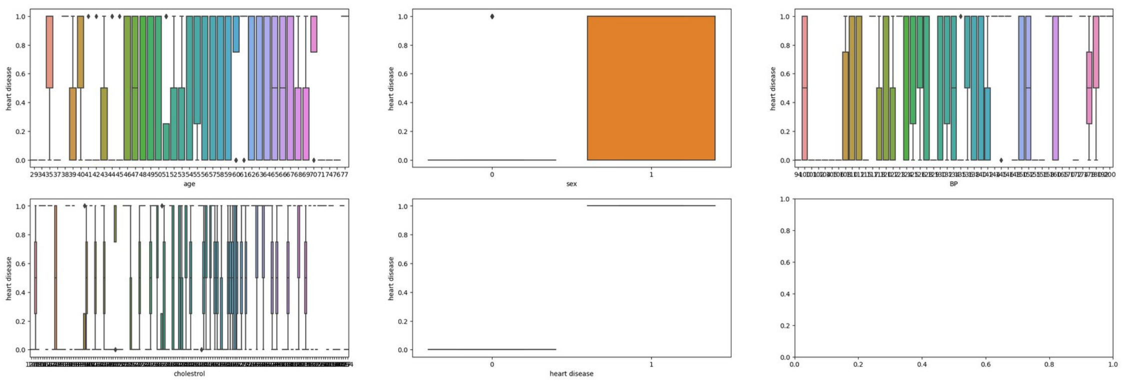
```
###visualisation
sns.pairplot(retail_dt, vars=['age', 'sex', 'BP', 'cholestrol', 'heart
disease'])
plt.show()
```



```
plt.figure(figsize = (16, 10))
sns.heatmap(retail_dt.corr(), annot = True, cmap="YlGnBu")
plt.show()
```



```
#Visualising categorical Variables to understand data better
plt.figure(figsize=(30, 15))
plt.subplot(3,3,1)
sns.boxplot(x = 'age', y = 'heart disease', data = retail_dt)
plt.subplot(3,3,2)
sns.boxplot(x = 'sex', y = 'heart disease', data =retail_dt)
plt.subplot(3,3,3)
sns.boxplot(x = 'BP', y = 'heart disease', data =retail_dt)
plt.subplot(3,3,4)
sns.boxplot(x = 'cholestrol', y = 'heart disease', data =retail_dt)
plt.subplot(3,3,5)
sns.boxplot(x = 'heart disease', y = 'heart disease', data =
retail_dt)
plt.subplot(3,3,6)
plt.show()
```



```python
import plotly.express as px
fig = px.box(retail_dt["age"], title="plotly")
fig.show()
```

```
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```
retail_dt['sex'].value_counts()
```

```
1    183
0     87
Name: sex, dtype: int64
```

```
import plotly.express as px
fig = px.box(retail_dt["sex"], title="plotly")
fig.show()
```

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fig.show()
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fig = px.box(retail_dt["cholestrol"], title="plotly")
fig.show()
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fig.show()
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lor":"white","showbackground":true,"ticks":"","zerolinecolor":"white"}
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lor":"white","showbackground":true,"ticks":"","zerolinecolor":"white"}
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lor":"white","showbackground":true,"ticks":"","zerolinecolor":"white"}
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6","caxis":
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{"standoff":15},"zerolinecolor":"white","zerolinewidth":2},"yaxis":
{"automargin":true,"gridcolor":"white","linecolor":"white","ticks":"",
"title":
{"standoff":15},"zerolinecolor":"white","zerolinewidth":2}}},"title":
```
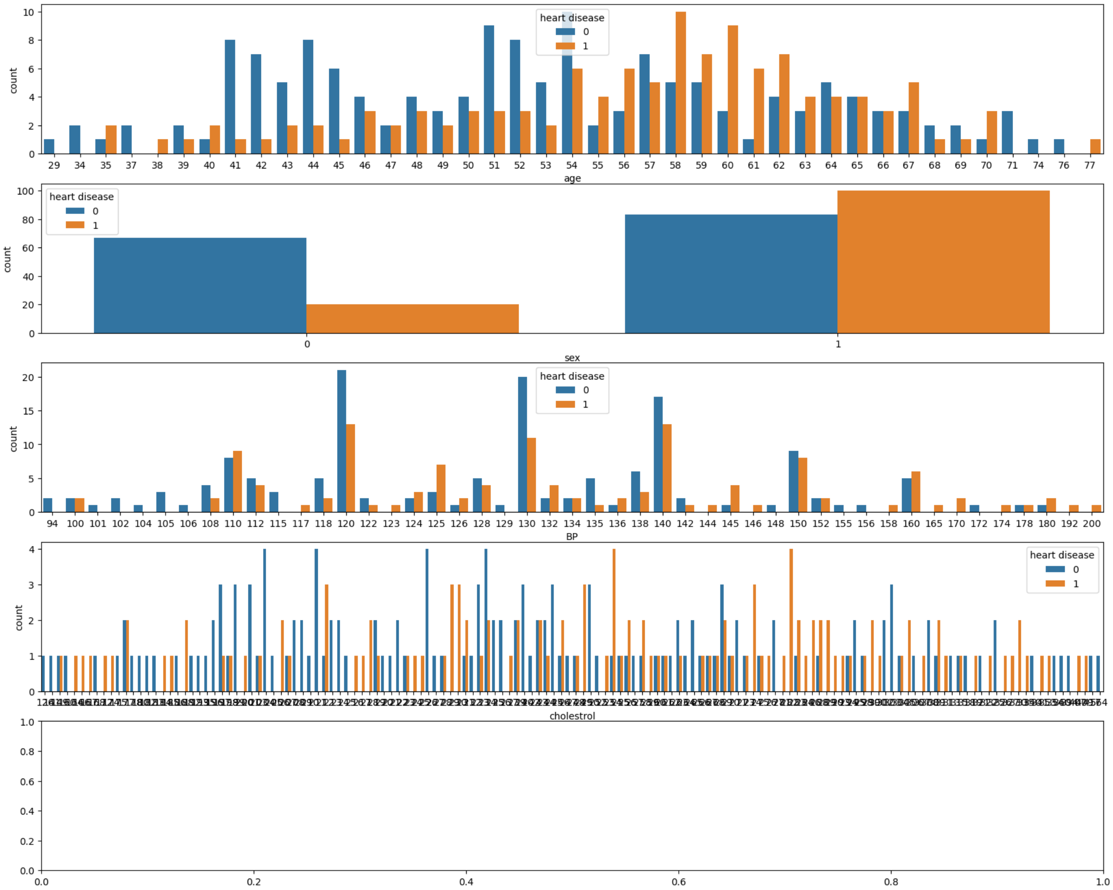

{"text":"plotly"},"xaxis":{"anchor":"y","domain":[0,1],"title":
{"text":"variable"}},"yaxis":{"anchor":"x","domain":[0,1],"title":
{"text":"value"}}}}

```
retail_dt.columns
```

```
Index(['age', 'sex', 'BP', 'cholestrol', 'heart disease'],
dtype='object')
```

```
plt.figure(figsize=(20, 30))
plt.subplot(9,1,1)
sns.countplot(x = 'age', hue = 'heart disease', data = retail_dt)
plt.subplot(9,1,2)
sns.countplot(x = 'sex', hue = 'heart disease', data = retail_dt)
plt.subplot(9,1,3)
sns.countplot(x = 'BP', hue = 'heart disease', data = retail_dt)
plt.subplot(9,1,4)
sns.countplot(x = 'cholestrol', hue = 'heart disease', data =
retail_dt)
plt.subplot(9,1,5)
plt.show()
```



```
###Scaling
```

```
# Putting feature variable to X
X = retail_dt.drop('heart disease',axis=1)

# Putting response variable to y
y = retail_dt['heart disease']
```

```
from sklearn.model_selection import train_test_split
```

```
X_train,x_test,y_train,y_test=train_test_split(X,y,train_size=0.7,rand
om_state=42)
X_train.shape,y_train.shape
```

```
((189, 4), (189,))
```

```
X_train.head()
```

```
     age  sex   BP  cholestrol
84    57    1  110         201
251   44    1  130         219
92    54    1  124         266
201   58    1  125         300
126   62    1  120         267
```

```
X_train.shape
```

```
(189, 4)
```

```
from sklearn.preprocessing import StandardScaler
```

```
scaler = StandardScaler()
```

```
X_train[['age', 'sex', 'BP', 'cholestrol']] =
scaler.fit_transform(X_train[['age', 'sex', 'BP', 'cholestrol']])
X_train.head()
```

```
          age       sex        BP  cholestrol
84   0.246885  0.665393 -1.218091   -0.964008
251 -1.180400  0.665393 -0.101064   -0.620599
92  -0.082489  0.665393 -0.436172    0.276080
201  0.356676  0.665393 -0.380321    0.924741
126  0.795841  0.665393 -0.659578    0.295158
```

```
age=(sum(retail_dt['age'])/len(retail_dt['age'].index))*100
age
```

```
5443.333333333333
```

```
plt.figure(figsize=(20,10))
sns.heatmap(retail_dt.corr(),annot=True)
plt.show
```

```
<function matplotlib.pyplot.show(close=None, block=None)>
```

```
#X_test=x_test.drop(['age', 'sex', 'BP', 'cholestrol'], 1)
#X_train = X_train.drop(['age', 'sex', 'BP', 'cholestrol'], 1)



##Logistic regression
```

```
import statsmodels.api as sm
```

```
logm1 = sm.GLM(y_train,(sm.add_constant(X_train)),
family=sm.families.Binomial())
logm1.fit().summary()
```

```
<class 'statsmodels.iolib.summary.Summary'>
"""
                 Generalized Linear Model Regression Results                  
                                                                      
======================================================================
========
Dep. Variable:          heart disease   No. Observations:             
189
Model:                            GLM   Df Residuals:                 
184
Model Family:                Binomial   Df Model:                     
4
Link Function:                  Logit   Scale:                        
1.0000
Method:                          IRLS   Log-Likelihood:               
-112.87
Date:                Tue, 14 Mar 2023   Deviance:                     
225.75
Time:                        11:51:28   Pearson chi2:                 
184.
No. Iterations:                     4   Pseudo R-squ. (CS):           
0.1707
Covariance Type:            nonrobust                                 
                                                                      
======================================================================
========
                 coef    std err          z      P>|z|      [0.025    
0.975]
----------------------------------------------------------------------
--------
const         -0.1950      0.162     -1.203      0.229      -0.513    
0.123
```

```
age              0.5421      0.181      3.000      0.003       0.188
0.896
sex              0.8073      0.187      4.327      0.000       0.442
1.173
BP               0.3449      0.168      2.058      0.040       0.016
0.673
cholestrol       0.1490      0.168      0.886      0.375      -0.180
0.478
======================================================================
========
"""
```

```
from sklearn.linear_model import LogisticRegression
logreg=LogisticRegression()
```

```
from sklearn.feature_selection import RFE
rfe = RFE(logreg, n_features_to_select=1)
rfe=rfe.fit(X_train, y_train)
```

```
rfe.support_
```

```
array([False,  True, False, False])
```

```
list(zip(X_train.columns, rfe.support_, rfe.ranking_))
```

```
[('age', False, 2),
 ('sex', True, 1),
 ('BP', False, 3),
 ('cholestrol', False, 4)]
```

```
col = X_train.columns[rfe.support_]
```

```
X_train_sm = sm.add_constant(X_train[col])
logm2 = sm.GLM(y_train,X_train_sm, family = sm.families.Binomial())
res = logm2.fit()
res.summary()
```

```
<class 'statsmodels.iolib.summary.Summary'>
"""
                 Generalized Linear Model Regression Results

======================================================================
========
Dep. Variable:          heart disease   No. Observations:
189
Model:                            GLM   Df Residuals:
187
Model Family:                Binomial   Df Model:
1
Link Function:                  Logit   Scale:
1.0000
Method:                          IRLS   Log-Likelihood:
```

```
-123.09
Date:                    Tue, 14 Mar 2023   Deviance:
246.19
Time:                            11:51:33   Pearson chi2:
189.
No. Iterations:                         4   Pseudo R-squ. (CS):
0.07593
Covariance Type:                nonrobust

======================================================================
========
                 coef    std err          z      P>|z|      [0.025
0.975]
----------------------------------------------------------------------
--------
const         -0.1638      0.153     -1.072      0.284      -0.463
0.136
sex            0.5918      0.160      3.691      0.000       0.278
0.906
======================================================================
========
"""
```

```
y_train_pred = res.predict(X_train_sm)
y_train_pred[:10]
```

```
84     0.557252
251    0.557252
92     0.557252
201    0.557252
126    0.557252
124    0.557252
78     0.258621
181    0.258621
111    0.557252
229    0.557252
dtype: float64
```

```
y_train_pred = y_train_pred.values.reshape(-1)
y_train_pred[:10]
```

```
array([0.55725191, 0.55725191, 0.55725191, 0.55725191, 0.55725191,
       0.55725191, 0.25862069, 0.25862069, 0.55725191, 0.55725191])
```

```
y_train_pred_final = pd.DataFrame({'age':y_train.values,
'age_prob':y_train_pred})
y_train_pred_final['BP'] = y_train.index
y_train_pred_final.head()
```

```
   age  age_prob   BP
0    0  0.557252   84
```

```
1    0  0.557252  251
2    1  0.557252   92
3    1  0.557252  201
4    1  0.557252  126
```

```
y_train_pred_final['predicted'] =
y_train_pred_final.age_prob.map(lambda x: 1 if x > 0.5 else 0)

# Let's see the head
y_train_pred_final.head()
```

```
   age  age_prob   BP  predicted
0    0  0.557252   84          1
1    0  0.557252  251          1
2    1  0.557252   92          1
3    1  0.557252  201          1
4    1  0.557252  126          1
```

```
%matplotlib inline
```

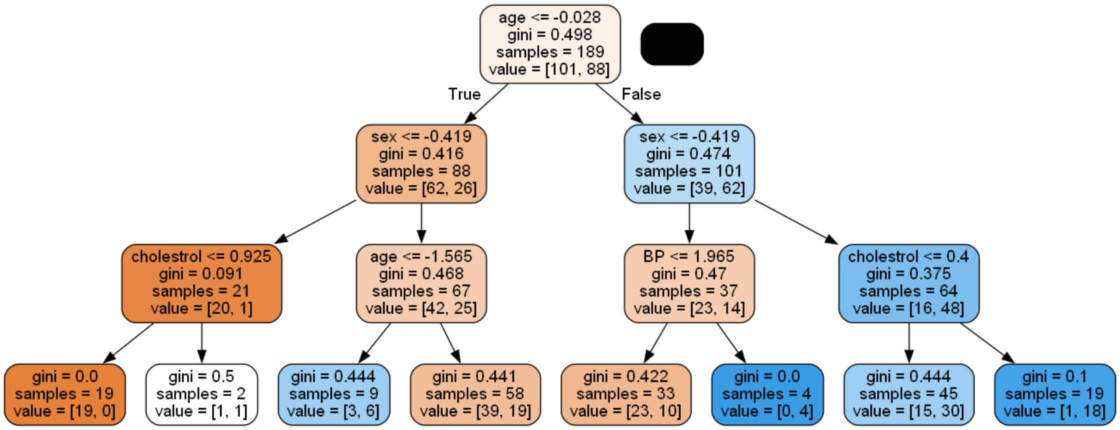
```
#Decision tree
from sklearn.tree import DecisionTreeClassifier
retail_dt = DecisionTreeClassifier(max_depth=3)
retail_dt.fit(X_train, y_train)
```

```
DecisionTreeClassifier(max_depth=3)
```

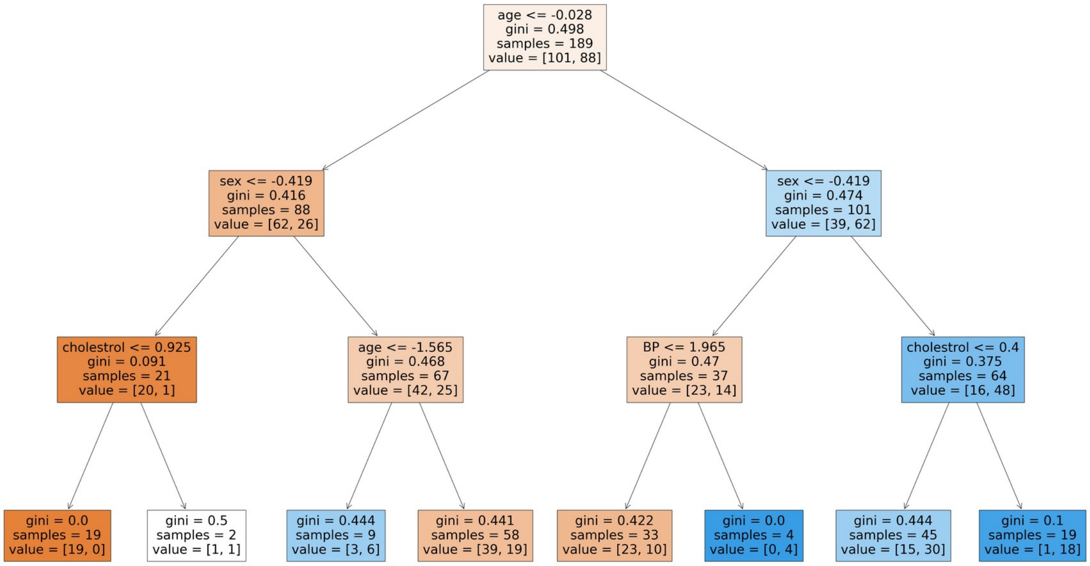
```
retail_dt = DecisionTreeClassifier(max_depth=3)
retail_dt.fit(X_train, y_train)
```

```
DecisionTreeClassifier(max_depth=3)
```

```
##Decision TREE
from IPython.display import Image
from six import StringIO
from sklearn.tree import export_graphviz
import pydotplus, graphviz

from sklearn.tree import plot_tree

dot_data = StringIO()

export_graphviz(retail_dt, out_file=dot_data, filled=True,
rounded=True,
                feature_names=X.columns, )

graph = pydotplus.graph_from_dot_data(dot_data.getvalue())
Image(graph.create_png())
#Image(graph.create_png(),width=800,height=900)
#graph.write_pdf("dt_heartdisease.pdf")
```



```
plt.figure(figsize=(50,30))
plot_tree(retail_dt, feature_names =X.columns,filled=True);
```



```
y_train_pred=retail_dt.predict(X_train)
y_test_pred=retail_dt.predict(X_train)

##Confusion matrix

from sklearn.metrics import confusion_matrix, accuracy_score

print(accuracy_score(y_train, y_train_pred))
confusion_matrix(y_train, y_train_pred)
```

```
0.7407407407407407
```

```
array([[82, 19],
       [30, 58]], dtype=int64)
```

```
print("Test Performance")
print(accuracy_score(y_test, y_test_pred))
confusion_matrix(y_test, y_test_pred)
```

```
Test Performance

---------------------------------------------------------------------------
ValueError                                Traceback (most recent call last)
~\AppData\Local\Temp\ipykernel_7504\359019888.py in <module>
      1 print("Test Performance")
----> 2 print(accuracy_score(y_test, y_test_pred))
      3 confusion_matrix(y_test, y_test_pred)

~\anaconda3\lib\site-packages\sklearn\metrics\_classification.py in accuracy_score(y_true, y_pred, normalize, sample_weight)
    209 
    210     # Compute accuracy for each possible representation
--> 211     y_type, y_true, y_pred = _check_targets(y_true, y_pred)
    212     check_consistent_length(y_true, y_pred, sample_weight)
    213     if y_type.startswith("multilabel"):

~\anaconda3\lib\site-packages\sklearn\metrics\_classification.py in _check_targets(y_true, y_pred)
     82     y_pred : array or indicator matrix
     83     """
---> 84     check_consistent_length(y_true, y_pred)
     85     type_true = type_of_target(y_true)
     86     type_pred = type_of_target(y_pred)

~\anaconda3\lib\site-packages\sklearn\utils\validation.py in check_consistent_length(*arrays)
    330     uniques = np.unique(lengths)
    331     if len(uniques) > 1:
--> 332         raise ValueError(
    333             "Found input variables with inconsistent numbers of samples: %r"
    334             % [int(l) for l in lengths]

ValueError: Found input variables with inconsistent numbers of samples: [81, 189]
```

```
from sklearn.ensemble import RandomForestClassifier
```

```
##Random forest
?RandomForestClassifier
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.3, random_state=42)
```

```
rf = RandomForestClassifier(max_depth=5, min_samples_leaf=3,
min_samples_split=5,n_jobs=-1, random_state=42)
```

```
rf.fit(X_train, y_train)
```

```
RandomForestClassifier(max_depth=5, min_samples_leaf=3,
min_samples_split=5,
                       n_jobs=-1, random_state=42)
```

```
rf.base_estimator_
```

```
DecisionTreeClassifier()
```

```
rf.n_features_
```

```
C:\Users\Shree\anaconda3\lib\site-packages\sklearn\utils\
deprecation.py:103: FutureWarning:

Attribute `n_features_` was deprecated in version 1.0 and will be
removed in 1.2. Use `n_features_in_` instead.


4
```

```
rf.feature_names_in_
```

```
array(['age', 'sex', 'BP', 'cholestrol'], dtype=object)
```

```
rf.n_outputs_
```

```
1
```

```
sample_tree = rf.estimators_[20]
```

```
classifier_rf = RandomForestClassifier(random_state=42, n_jobs=-1)
```

```
# Create the parameter grid based on the results of random search
params = {
    'max_depth': [1, 2, 5, 10, 20],
    'min_samples_leaf': [5, 10, 20, 50, 100],
    'max_features': [2,3,4],
    'n_estimators': [10, 30, 50, 100, 200]
}
```

```
classifier_rf = RandomForestClassifier(random_state=42, n_jobs=-1,
max_depth=5, n_estimators=100, oob_score=True)
```

```
rf.fit(X_train, y_train)
```

```
RandomForestClassifier(max_depth=5, min_samples_leaf=3,
min_samples_split=5,
                       n_jobs=-1, random_state=42)
```

```
y_pred = rf.predict(X_test)
```

```
accuracy = rf.score(X_test, y_test)
print('Accuracy: {:.2f}%'.format(accuracy*100))
```

```
Accuracy: 67.90%
```

```
##Kmean clusters

from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score
from scipy.cluster.hierarchy import linkage
from scipy.cluster.hierarchy import dendrogram
from scipy.cluster.hierarchy import cut_tree
```

```
retail_dt=pd.read_csv("heart_v2.csv")
```

```
retail_dt.head()
```

```
   age  sex   BP  cholestrol  heart disease
0   70    1  130         322              1
1   67    0  115         564              0
2   57    1  124         261              1
3   64    1  128         263              0
4   74    0  120         269              0
```

```
##missing values
round(100*(retail_dt.isnull().sum())/len(retail_dt),2)
```

```
age              0.0
sex              0.0
BP               0.0
cholestrol       0.0
heart disease    0.0
dtype: float64
```

```
retail_dt=retail_dt.dropna()
retail_dt.shape
```

```
(270, 5)
```

```
retail_dt.head()
```

```
   age  sex   BP  cholestrol  heart disease
0   70    1  130         322              1
1   67    0  115         564              0
```

```
2   57    1  124         261              1
3   64    1  128         263              0
4   74    0  120         269              0
```

```
retail_dt['new']=retail_dt['heart disease']*retail_dt['cholestrol']
retail_dt.head()
```

```
   age  sex   BP  cholestrol  heart disease  new
0   70    1  130         322              1  322
1   67    0  115         564              0    0
2   57    1  124         261              1  261
3   64    1  128         263              0    0
4   74    0  120         269              0    0
```

```
group_dt=retail_dt.groupby('age')['new'].sum()
group_dt=group_dt.reset_index()
group_dt.head()
```

```
   age  new
0   29    0
1   34    0
2   35  480
3   37    0
4   38  231
```

```
##frequency
frequency=retail_dt.groupby('age')['BP'].count()
frequency=frequency.reset_index()
frequency.columns=['age','frequency']
frequency.head()
```

```
   age  frequency
0   29          1
1   34          2
2   35          3
3   37          2
4   38          1
```

```
group_dt=pd.merge(group_dt,frequency, on='age',how='inner')
group_dt.head()
```

```
   age  new  frequency
0   29    0          1
1   34    0          2
2   35  480          3
3   37    0          2
4   38  231          1
```

```
retail_dt.head()
```

```
   age  sex   BP  cholestrol  heart disease  new
0   70    1  130         322              1  322
```

```
1   67    0  115         564              0    0
2   57    1  124         261              1  261
3   64    1  128         263              0    0
4   74    0  120         269              0    0
```

```
#retail_dt['diff']=group_dt

#last_patient=retail_dt.groupby('age')['diff'].min()
#last_patient=last_patient.reset_index()
#last_patient.head()

group_dt.head()
```

```
   age  new  frequency
0   29    0          1
1   34    0          2
2   35  480          3
3   37    0          2
4   38  231          1
```

```
from sklearn import preprocessing


rfm_dt=group_dt[['age','new','frequency']]
scaler=StandardScaler()

rfm_dt_scaled=scaler.fit_transform(rfm_dt)
rfm_dt_scaled.shape
```

```
(41, 3)
```

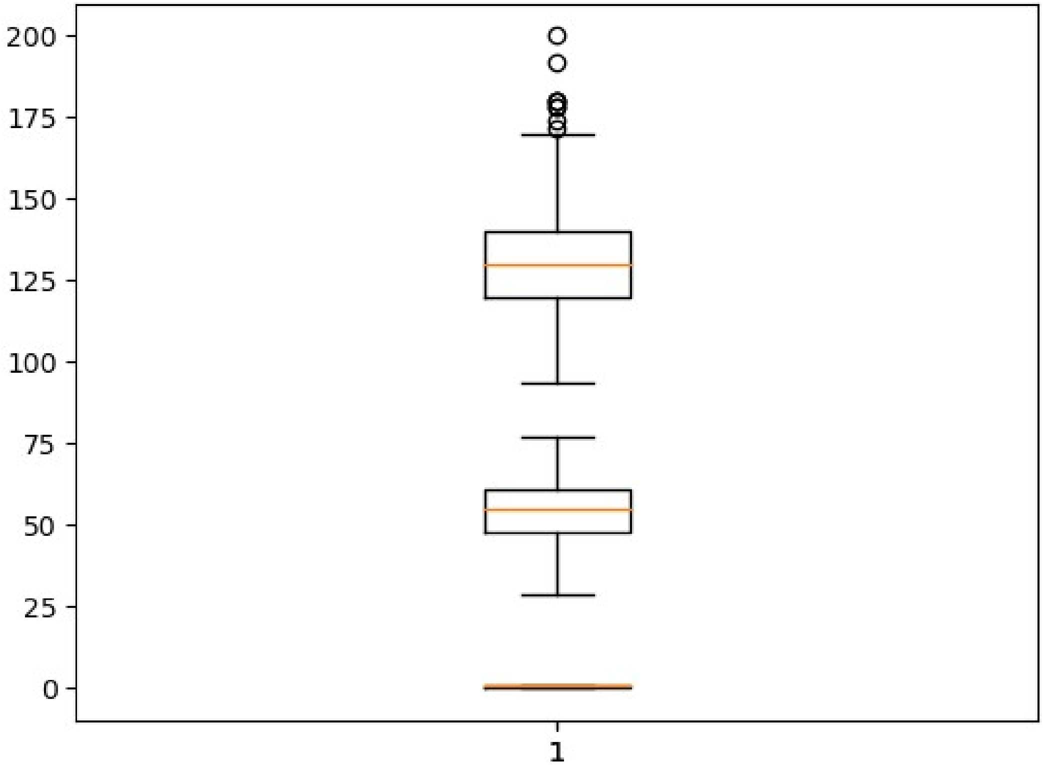
```
rfm_dt_scaled=pd.DataFrame(rfm_dt_scaled)
rfm_dt_scaled.columns=['age','new','frequency']
rfm_dt_scaled.head()
```

```
        age       new  frequency
0 -2.007801 -1.170748  -1.409344
1 -1.606632 -1.170748  -1.157016
2 -1.526398 -0.422102  -0.904688
3 -1.365931 -1.170748  -1.157016
4 -1.285697 -0.810462  -1.409344
```

```
last_patient=retail_dt.groupby('heart disease').min()
last_patient=last_patient.reset_index()
last_patient.head()
```

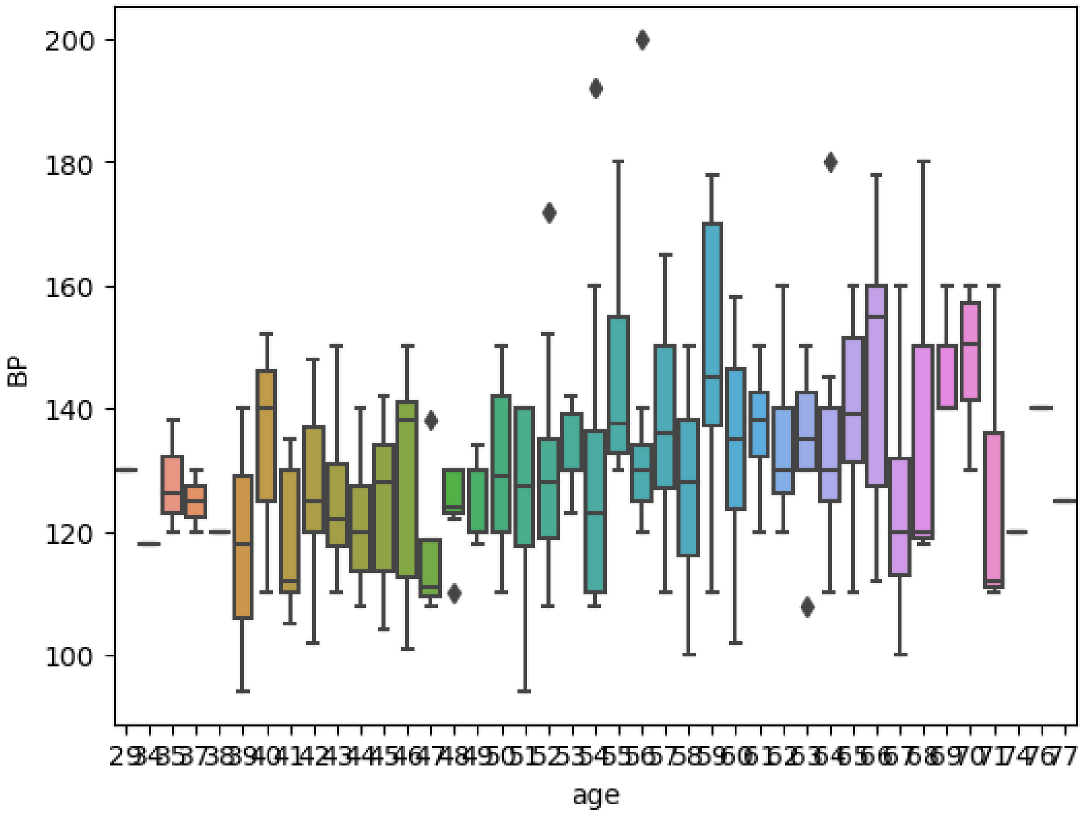
```
   heart disease  age  sex   BP  cholestrol  new
0              0   29    0   94         126    0
1              1   35    0  100         149  149
```

```
import matplotlib.pyplot as plt
plt.boxplot(retail_dt['age'])
plt.boxplot(retail_dt['sex'])
plt.boxplot(retail_dt['BP'])
plt.show()
```



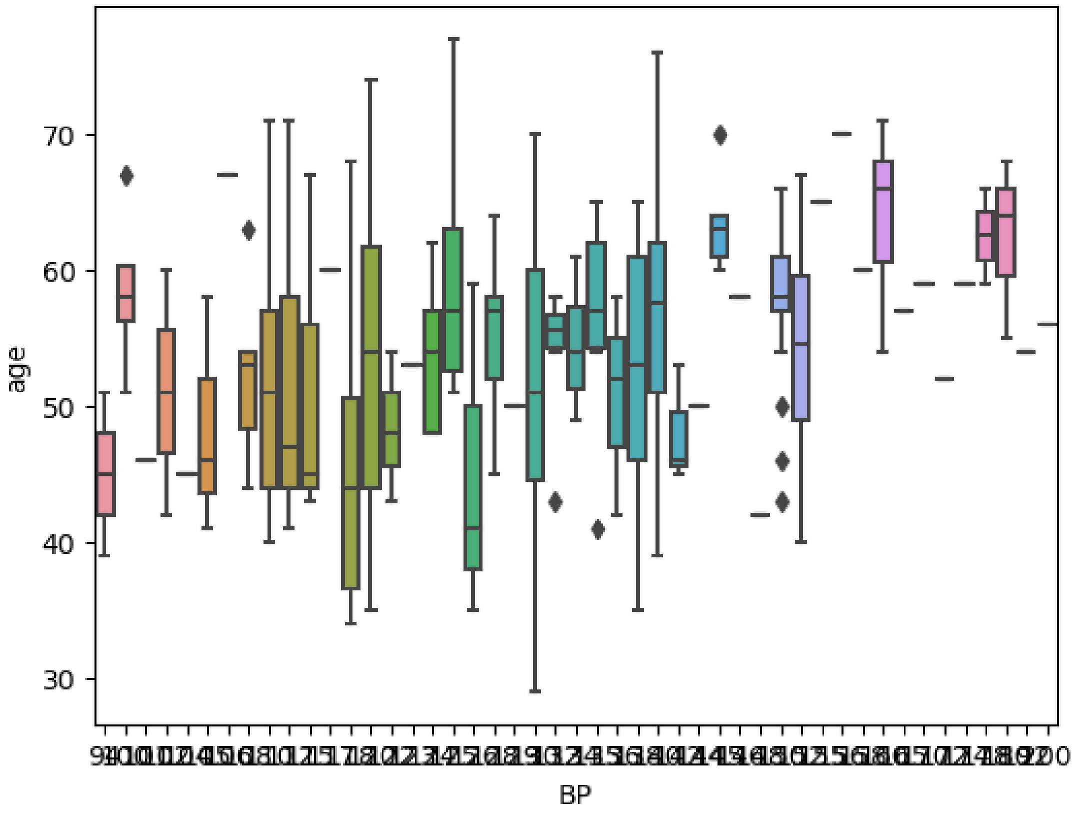
```
sns.boxplot(x='age', y='BP',data=retail_dt)
```

```
<AxesSubplot:xlabel='age', ylabel='BP'>
```



```
sns.boxplot(x='BP', y='age',data=retail_dt)
```

```
<AxesSubplot:xlabel='BP', ylabel='age'>
```



```
####Hopkins

from sklearn.neighbors import NearestNeighbors
from random import sample
from numpy.random import uniform
from math import isnan
import numpy as np

def hopkins(X):
    d = X.shape[1]
    n = len(X)
    m = int(0.1 * n)
    nbrs = NearestNeighbors(n_neighbors=1).fit(X)

    rand_X = sample(range(0, n, 1), m)
    ujd = []
    wjd = []
    for j in range(0, m):
        u_dist,_ss =
nbrs.kneighbors(uniform(np.amin(X,axis=0),np.amax(X,axis=0),d).reshape
(1, -1), 2, return_distance=True)
        ujd.append(u_dist[0][1])
        w_dist,_ = nbrs.kneighbors(X.iloc[rand_X[j]].values.reshape(1,
-1), 2, return_distance=True)
        wjd.append(w_dist[0][1])

    H = sum(ujd) / (sum(ujd) + sum(wjd))
    if isnan(H):
        print(ujd, wjd)
        H = 0

    return H
```

```
rfm_dt_scaled=pd.DataFrame(rfm_dt_scaled)
rfm_dt_scaled.columns=['age','new','frequency']
```

```
retail_dt_scaled=pd.DataFrame(retail_dt_scaled)
retail_dt_scaled.columns=['age','BP','sex','cholesrole','new','frequency'] retail_dt.head()
```

```
hopkins(rfm_dt_scaled)
```

```
C:\Users\Shree\anaconda3\lib\site-packages\sklearn\base.py:450:
UserWarning:

X does not have valid feature names, but NearestNeighbors was fitted
with feature names

C:\Users\Shree\anaconda3\lib\site-packages\sklearn\base.py:450:
UserWarning:

X does not have valid feature names, but NearestNeighbors was fitted
with feature names

C:\Users\Shree\anaconda3\lib\site-packages\sklearn\base.py:450:
UserWarning:

X does not have valid feature names, but NearestNeighbors was fitted
with feature names

C:\Users\Shree\anaconda3\lib\site-packages\sklearn\base.py:450:
UserWarning:

X does not have valid feature names, but NearestNeighbors was fitted
with feature names

C:\Users\Shree\anaconda3\lib\site-packages\sklearn\base.py:450:
UserWarning:

X does not have valid feature names, but NearestNeighbors was fitted
with feature names

C:\Users\Shree\anaconda3\lib\site-packages\sklearn\base.py:450:
UserWarning:
```

```
X does not have valid feature names, but NearestNeighbors was fitted
with feature names

C:\Users\Shree\anaconda3\lib\site-packages\sklearn\base.py:450:
UserWarning:

X does not have valid feature names, but NearestNeighbors was fitted
with feature names

C:\Users\Shree\anaconda3\lib\site-packages\sklearn\base.py:450:
UserWarning:

X does not have valid feature names, but NearestNeighbors was fitted
with feature names


0.756703202266792
```

```
##kmeans  orbitory

kmeans=KMeans(n_clusters=4,max_iter=50)
kmeans.fit(rfm_dt_scaled)

kmeans.labels_

#finding cluster
#elow curve
ssd=[]
range_n_clusters=[2,3,4,5,6,7,8]
for num_clusters in range_n_clusters:
    kmeans=KMeans(n_clusters=num_clusters,max_iter=50)
    kmeans.fit(rfm_dt_scaled)
    ssd.append(kmeans.inertia_)
    plt.plot(ssd)

##sa
range_n_clusters = [2, 3, 4, 5, 6]
for n_clusters in range_n_clusters:
    # Initialize the KMeans clustering algorithm with n_clusters
    kmeans= KMeans(n_clusters=n_clusters, random_state=10)
    kmeans.fit_predict(X)
    cluster_labels=kmeans.labels_

    # Calculate the average silhouette score for the current number of
clusters
    silhouette_avg = silhouette_score(X, cluster_labels)
    print("for n_clusters={0},the silhouette score
is{1}".format(num_clusters))
```

```
kmeans=KMeans(n_clusters=3,max_iter=50)
kmeans.fit(rfm_dt_scaled)
```

```
KMeans(max_iter=50, n_clusters=3)
```

```
kmeans.labels_
```

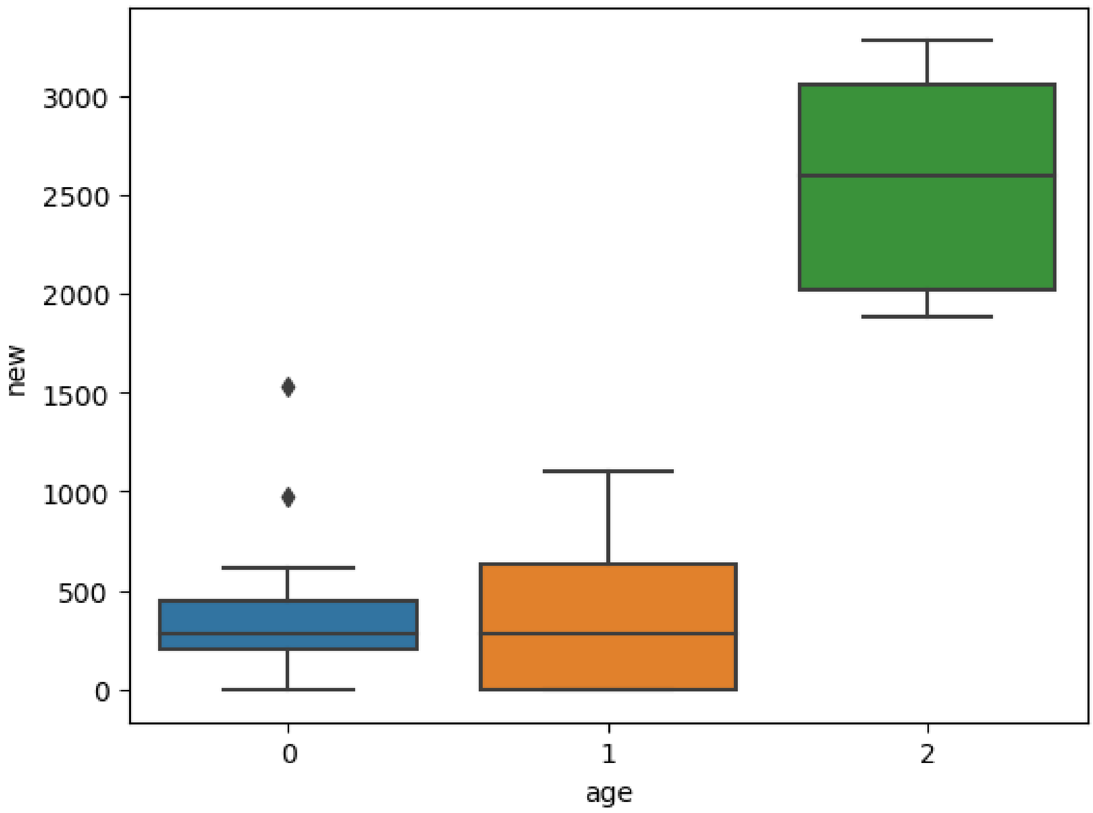
```
array([1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 2, 1, 1, 1, 2, 1, 1, 1,
2,
       1, 1, 1, 1, 1, 2, 0, 0, 0, 0, 0, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0])
```

```
group_dt['age']=kmeans.labels_
group_dt.head()
```

```
    BP  new  age
0   94    0    1
1  100  533    1
2  101    0    1
3  102    0    1
4  104    0    1
```

```
sns.boxplot(x='age',y='new',data=group_dt)
```

```
<AxesSubplot:xlabel='age', ylabel='new'>
```



```
###Hierarchical clustering
```

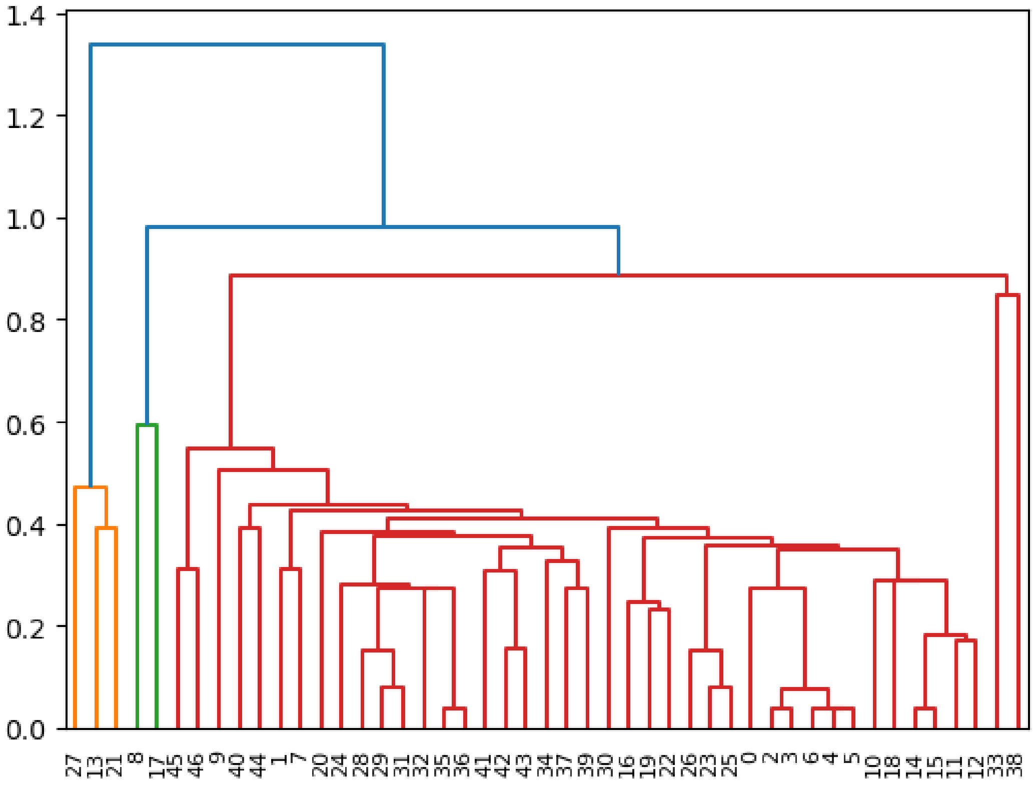
```
rfm_dt_scaled.head()
```

```
          0         1
0 -0.788227 -1.659050
1 -0.146627 -1.425474
2 -0.788227 -1.386545
3 -0.788227 -1.347615
4 -0.788227 -1.269757
```

```
group_dt.head()
```

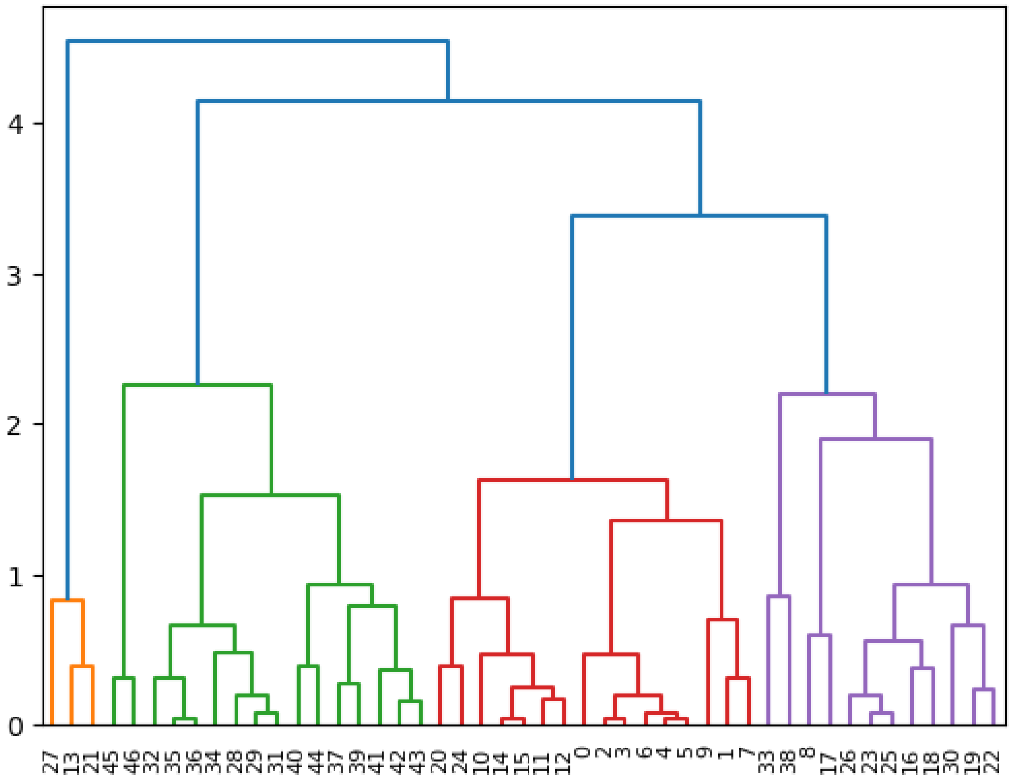
```
    BP  new  age
0   94    0    1
1  100  533    1
2  101    0    1
3  102    0    1
4  104    0    1
```

```
#single linkage
mergings=linkage(rfm_dt_scaled,method='single',metric='euclidean')
dendrogram(mergings)
plt.show()
```



```
##complete linkage
mergings=linkage(rfm_dt_scaled,method='complete',metric='euclidean')
```

```
dendrogram(mergings)
plt.show()
```



```
cluster_labels=cut_tree(mergings,n_clusters=3).reshape(-1,)
cluster_labels
```

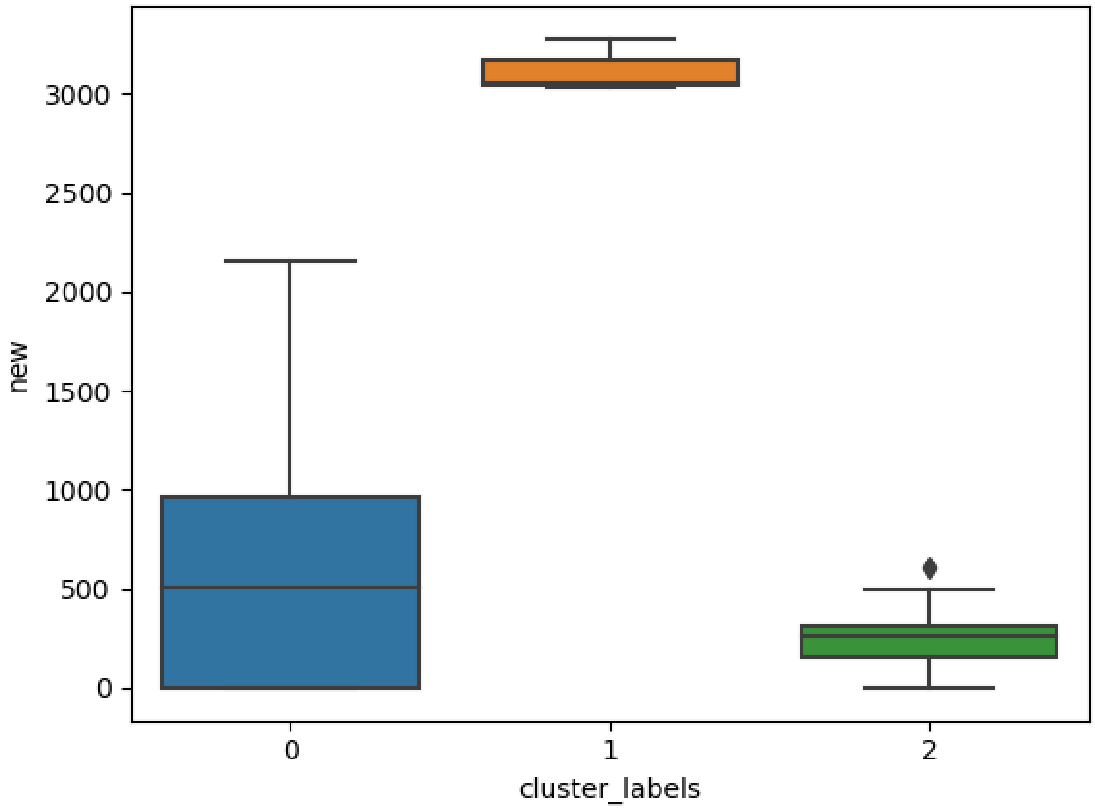
```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0,
1,
       0, 0, 0, 0, 0, 1, 2, 2, 0, 2, 2, 0, 2, 2, 2, 2, 0, 2, 2, 2, 2,
2,
       2, 2, 2])
```

```
group_dt['cluster_labels']=cluster_labels
group_dt.head()
```

```
    BP  new  age  cluster_labels
0   94    0    1               0
1  100  533    1               0
2  101    0    1               0
3  102    0    1               0
4  104    0    1               0
```

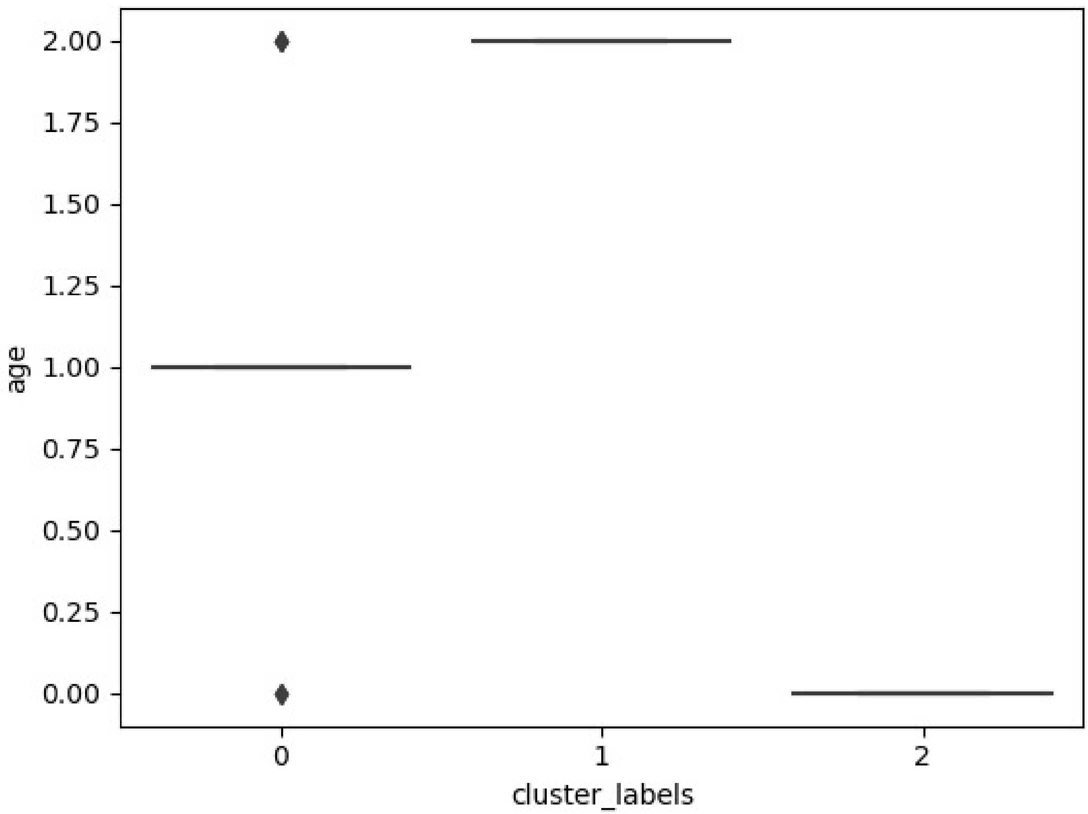
```
sns.boxplot(x='cluster_labels',y='new',data=group_dt)
```

```
<AxesSubplot:xlabel='cluster_labels', ylabel='new'>
```



```
sns.boxplot(x='cluster_labels',y='age',data=group_dt)
```

```
<AxesSubplot:xlabel='cluster_labels', ylabel='age'>
```



2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
age
0
1
2
cluster_labels