ct-bio-signal-analysis-for-smoking

January 22, 2024

1 Bio Signal Analysis for Smoking

[1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

[2]:
```
df = pd.read_csv('smoking.csv')
df = df.drop(columns=['ID','oral'])
df
```

[2]:
```
      gender  age  height(cm)  weight(kg)  waist(cm)  eyesight(left)  \
0          F   40         155          60       81.3             1.2
1          F   40         160          60       81.0             0.8
2          M   55         170          60       80.0             0.8
3          M   40         165          70       88.0             1.5
4          F   40         155          60       86.0             1.0
…        …  …          …         …        …            …
55687      F   40         170          65       75.0             0.9
55688      F   45         160          50       70.0             1.2
55689      F   55         160          50       68.5             1.0
55690      M   60         165          60       78.0             0.8
55691      M   55         160          65       85.0             0.9

       eyesight(right)  hearing(left)  hearing(right)  systolic  …    LDL  \
0                  1.0            1.0             1.0     114.0  …  126.0
1                  0.6            1.0             1.0     119.0  …  127.0
2                  0.8            1.0             1.0     138.0  …  151.0
3                  1.5            1.0             1.0     100.0  …  226.0
4                  1.0            1.0             1.0     120.0  …  107.0
…                …            …              …       …  …    …
55687              0.9            1.0             1.0     110.0  …  118.0
55688              1.2            1.0             1.0     101.0  …   79.0
55689              1.2            1.0             1.0     117.0  …   63.0
55690              1.0            1.0             1.0     133.0  …  146.0
55691              0.7            1.0             1.0     124.0  …  150.0
```

```
       hemoglobin  Urine protein  serum creatinine   AST   ALT   Gtp  \
0            12.9            1.0               0.7  18.0  19.0  27.0
1            12.7            1.0               0.6  22.0  19.0  18.0
2            15.8            1.0               1.0  21.0  16.0  22.0
3            14.7            1.0               1.0  19.0  26.0  18.0
4            12.5            1.0               0.6  16.0  14.0  22.0
…             …             …                …    …    …    …
55687        12.3            1.0               0.6  14.0   7.0  10.0
55688        14.0            1.0               0.9  20.0  12.0  14.0
55689        12.4            1.0               0.5  17.0  11.0  12.0
55690        14.4            1.0               0.7  20.0  19.0  18.0
55691        15.0            1.0               0.8  26.0  29.0  41.0

       dental caries  tartar  smoking
0                  0       Y        0
1                  0       Y        0
2                  0       N        1
3                  0       Y        0
4                  0       N        0
…                …     …       …
55687              1       Y        0
55688              0       Y        0
55689              0       N        0
55690              0       N        0
55691              0       Y        1

[55692 rows x 25 columns]
```

Exploratory Data Analysis (EDA)

[3]:
```python
df.shape
```

[3]:
```
(55692, 25)
```

[4]:
```python
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 55692 entries, 0 to 55691
Data columns (total 25 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   gender               55692 non-null  object
 1   age                  55692 non-null  int64
 2   height(cm)           55692 non-null  int64
 3   weight(kg)           55692 non-null  int64
 4   waist(cm)            55692 non-null  float64
 5   eyesight(left)       55692 non-null  float64
 6   eyesight(right)      55692 non-null  float64
```

```
 7   hearing(left)        55692 non-null  float64
 8   hearing(right)       55692 non-null  float64
 9   systolic             55692 non-null  float64
 10  relaxation           55692 non-null  float64
 11  fasting blood sugar  55692 non-null  float64
 12  Cholesterol          55692 non-null  float64
 13  triglyceride         55692 non-null  float64
 14  HDL                  55692 non-null  float64
 15  LDL                  55692 non-null  float64
 16  hemoglobin           55692 non-null  float64
 17  Urine protein        55692 non-null  float64
 18  serum creatinine     55692 non-null  float64
 19  AST                  55692 non-null  float64
 20  ALT                  55692 non-null  float64
 21  Gtp                  55692 non-null  float64
 22  dental caries        55692 non-null  int64
 23  tartar               55692 non-null  object
 24  smoking              55692 non-null  int64
dtypes: float64(18), int64(5), object(2)
memory usage: 10.6+ MB
```

[5]:
```
df.describe()
```

[5]:
```
                age    height(cm)    weight(kg)     waist(cm)  eyesight(left)  \
count  55692.000000  55692.000000  55692.000000  55692.000000    55692.000000
mean      44.182917    164.649321     65.864936     82.046418        1.012623
std       12.071418      9.194597     12.820306      9.274223        0.486873
min       20.000000    130.000000     30.000000     51.000000        0.100000
25%       40.000000    160.000000     55.000000     76.000000        0.800000
50%       40.000000    165.000000     65.000000     82.000000        1.000000
75%       55.000000    170.000000     75.000000     88.000000        1.200000
max       85.000000    190.000000    135.000000    129.000000        9.900000

       eyesight(right)  hearing(left)  hearing(right)      systolic  \
count     55692.000000   55692.000000    55692.000000  55692.000000
mean          1.007443       1.025587        1.026144    121.494218
std           0.485964       0.157902        0.159564     13.675989
min           0.100000       1.000000        1.000000     71.000000
25%           0.800000       1.000000        1.000000    112.000000
50%           1.000000       1.000000        1.000000    120.000000
75%           1.200000       1.000000        1.000000    130.000000
max           9.900000       2.000000        2.000000    240.000000

         relaxation  …           HDL           LDL    hemoglobin  \
count  55692.000000  …  55692.000000  55692.000000  55692.000000
mean      76.004830  …     57.290347    114.964501     14.622592
std        9.679278  …     14.738963     40.926476      1.564498
```

```
min       40.000000  …     4.000000     1.000000     4.900000
25%       70.000000  …    47.000000    92.000000    13.600000
50%       76.000000  …    55.000000   113.000000    14.800000
75%       82.000000  …    66.000000   136.000000    15.800000
max      146.000000  …   618.000000  1860.000000    21.100000

       Urine protein  serum creatinine           AST           ALT  \
count   55692.000000      55692.000000  55692.000000  55692.000000
mean        1.087212          0.885738     26.182935     27.036037
std         0.404882          0.221524     19.355460     30.947853
min         1.000000          0.100000      6.000000      1.000000
25%         1.000000          0.800000     19.000000     15.000000
50%         1.000000          0.900000     23.000000     21.000000
75%         1.000000          1.000000     28.000000     31.000000
max         6.000000         11.600000   1311.000000   2914.000000

                Gtp  dental caries       smoking
count  55692.000000   55692.000000  55692.000000
mean      39.952201       0.213334      0.367288
std       50.290539       0.409665      0.482070
min        1.000000       0.000000      0.000000
25%       17.000000       0.000000      0.000000
50%       25.000000       0.000000      0.000000
75%       43.000000       0.000000      1.000000
max      999.000000       1.000000      1.000000

[8 rows x 23 columns]
```

[6]:

```
df.isnull().sum()
```

[6]:

```
gender                 0
age                    0
height(cm)             0
weight(kg)             0
waist(cm)              0
eyesight(left)         0
eyesight(right)        0
hearing(left)          0
hearing(right)         0
systolic               0
relaxation             0
fasting blood sugar    0
Cholesterol            0
triglyceride           0
HDL                    0
LDL                    0
hemoglobin             0
```

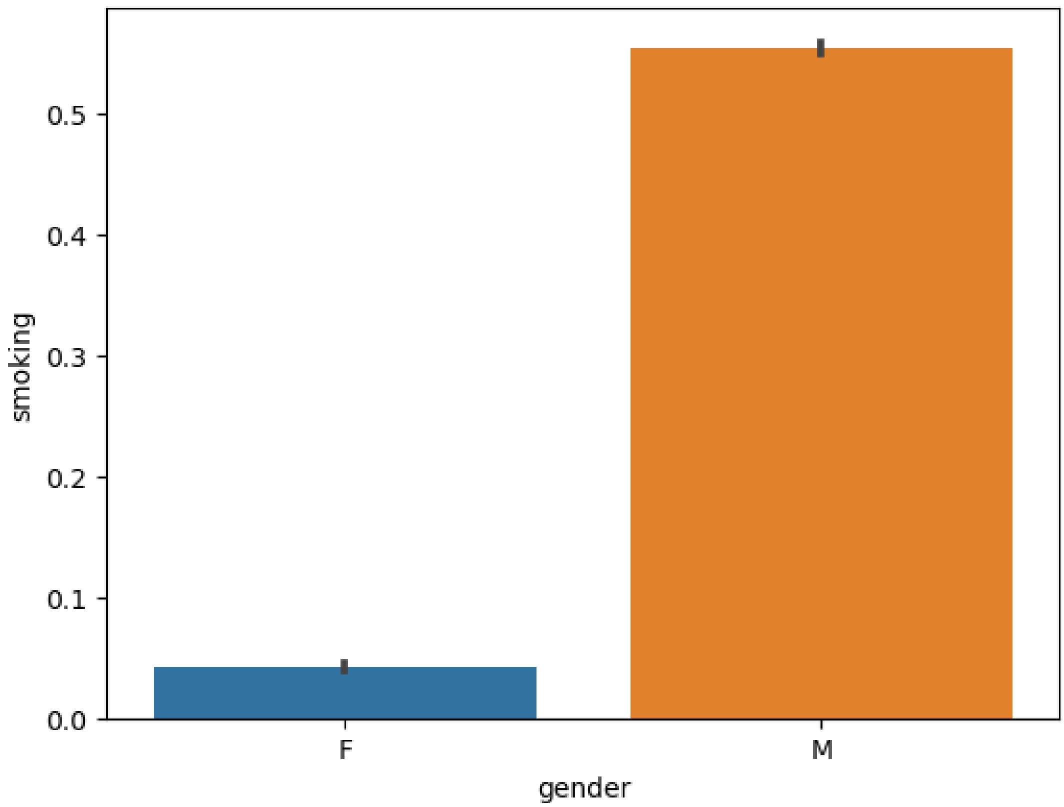
```
Urine protein         0
serum creatinine      0
AST                   0
ALT                   0
Gtp                   0
dental caries         0
tartar                0
smoking               0
dtype: int64
```

[7]:
```python
df.apply(lambda x: x.unique())
```

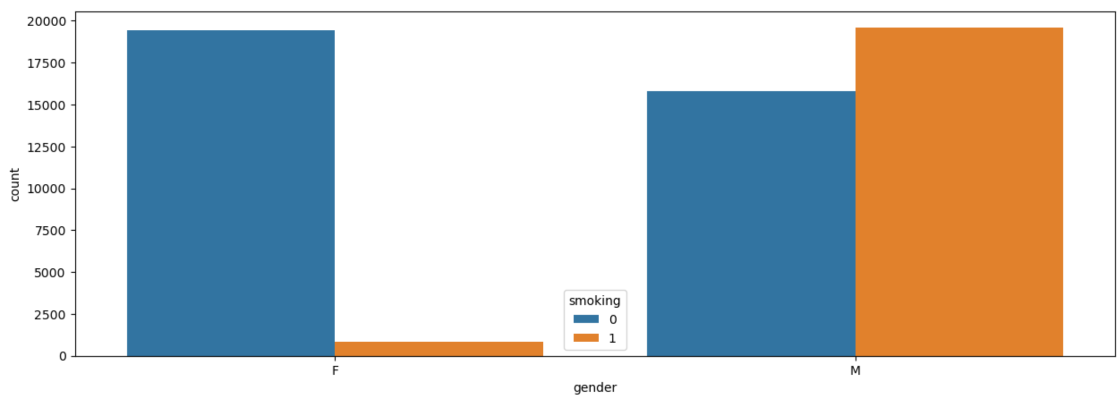
[7]:
```
gender                                                            [F, M]
age                 [40, 55, 30, 45, 50, 35, 60, 25, 65, 20, 80, 7…
height(cm)          [155, 160, 170, 165, 180, 150, 175, 140, 185, …
weight(kg)          [60, 70, 75, 90, 65, 45, 55, 50, 85, 80, 100, …
waist(cm)           [81.3, 81.0, 80.0, 88.0, 86.0, 85.0, 85.5, 96…
eyesight(left)      [1.2, 0.8, 1.5, 1.0, 0.7, 0.9, 0.3, 0.2, 0.1, …
eyesight(right)     [1.0, 0.6, 0.8, 1.5, 1.2, 0.7, 0.4, 0.9, 0.3, …
hearing(left)                                                 [1.0, 2.0]
hearing(right)                                                [1.0, 2.0]
systolic            [114.0, 119.0, 138.0, 100.0, 120.0, 128.0, 116…
relaxation          [73.0, 70.0, 86.0, 60.0, 74.0, 76.0, 82.0, 96…
fasting blood sugar [94.0, 130.0, 89.0, 96.0, 80.0, 95.0, 158.0, 8…
Cholesterol         [215.0, 192.0, 242.0, 322.0, 184.0, 217.0, 226…
triglyceride        [82.0, 115.0, 182.0, 254.0, 74.0, 199.0, 68.0,…
HDL                 [73.0, 42.0, 55.0, 45.0, 62.0, 48.0, 34.0, 43…
LDL                 [126.0, 127.0, 151.0, 226.0, 107.0, 129.0, 157…
hemoglobin          [12.9, 12.7, 15.8, 14.7, 12.5, 16.2, 17.0, 15…
Urine protein                           [1.0, 3.0, 2.0, 4.0, 5.0, 6.0]
serum creatinine    [0.7, 0.6, 1.0, 1.2, 1.3, 0.8, 1.1, 0.9, 0.5, …
AST                 [18.0, 22.0, 21.0, 19.0, 16.0, 38.0, 31.0, 26…
ALT                 [19.0, 16.0, 26.0, 14.0, 27.0, 71.0, 31.0, 24…
Gtp                 [27.0, 18.0, 22.0, 33.0, 39.0, 111.0, 14.0, 63…
dental caries                                                     [0, 1]
tartar                                                            [Y, N]
smoking                                                           [0, 1]
dtype: object
```

DATA VISUALIZATION

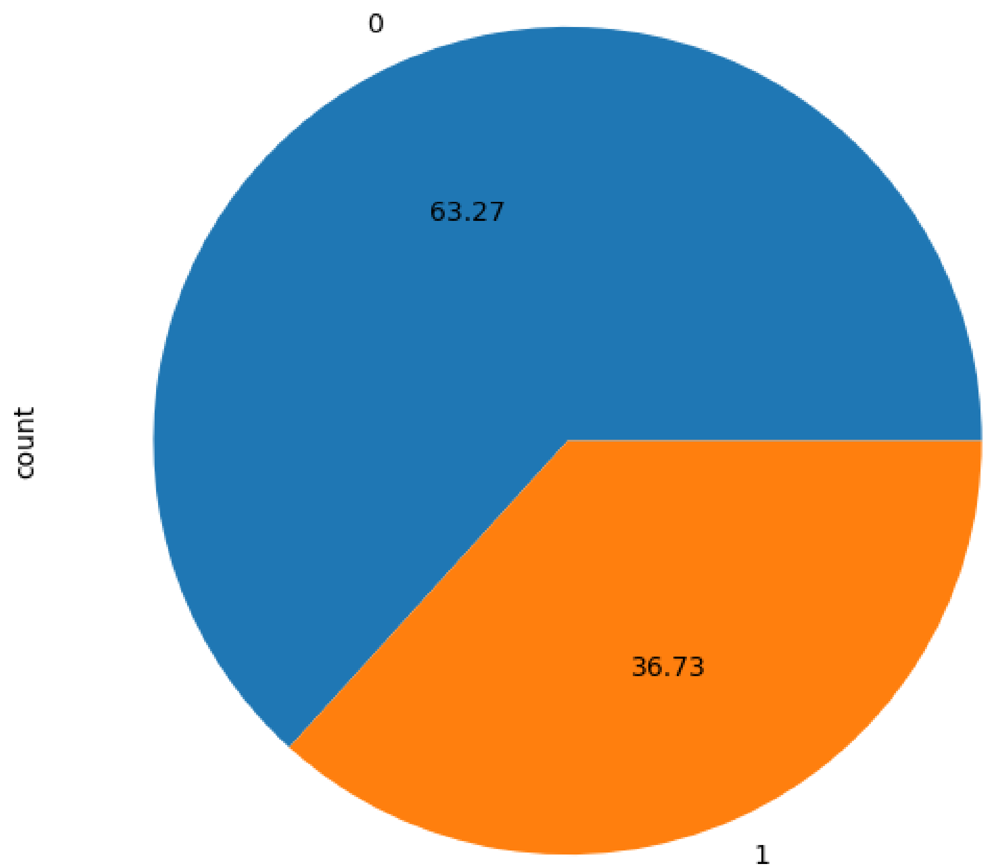
[8]:
```python
sns.barplot(x=df['gender'],y=df['smoking'])
plt.show()
```



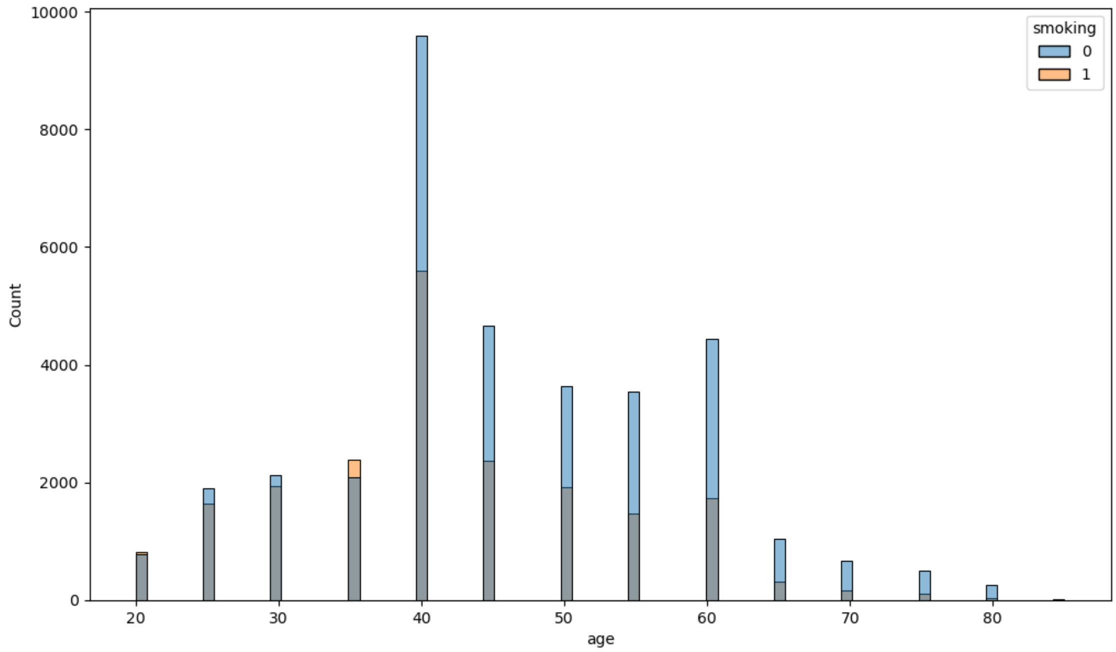
[9]:
```
plt.figure(figsize=(15, 5))
sns.countplot(x=df['gender'], hue=df['smoking'])
plt.show()
```



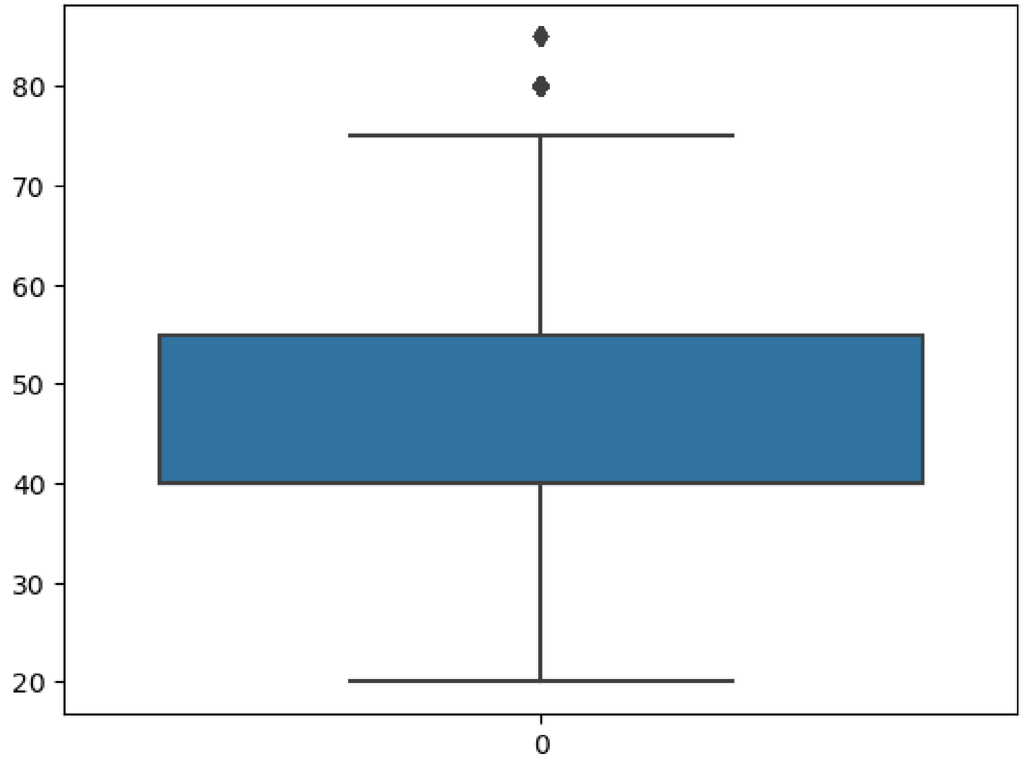
[10]:
```
plt.figure(figsize=(10,7))
df['smoking'].value_counts().plot.pie(autopct='%0.2f')
plt.show()
```

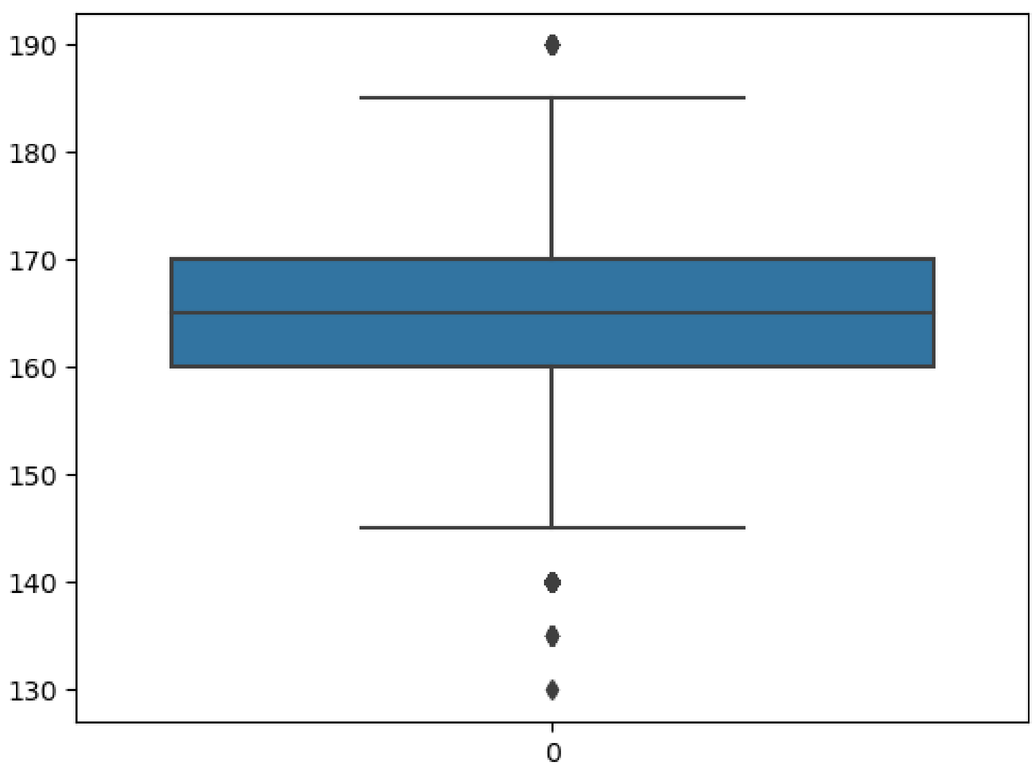


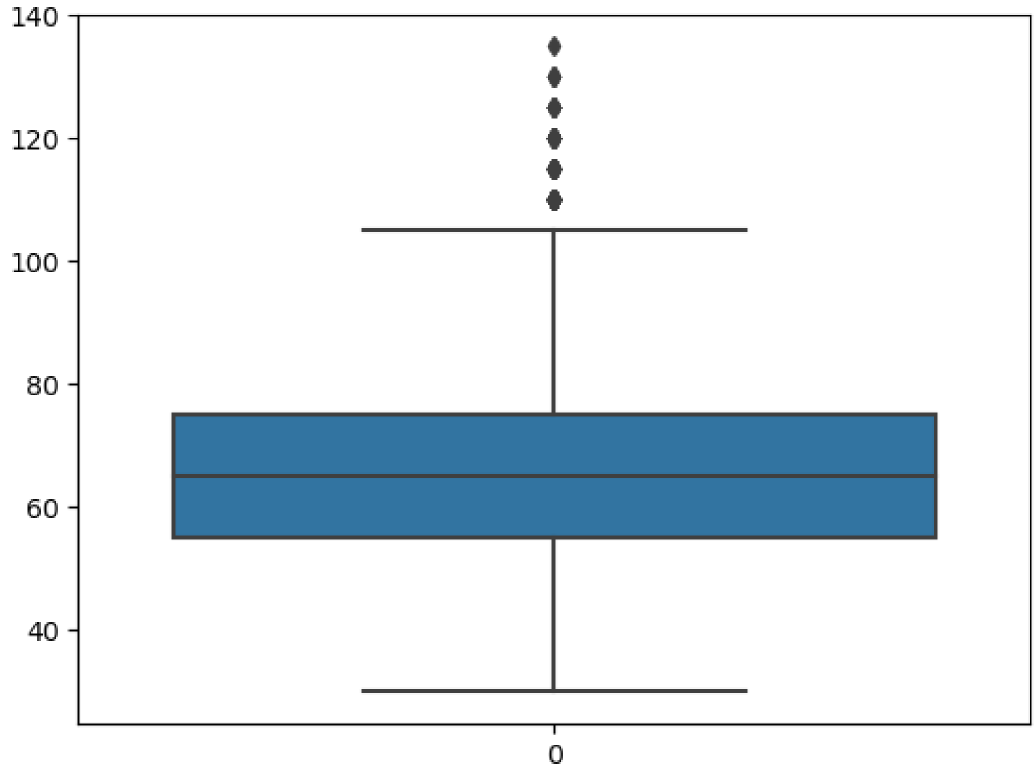
[11]:
```
# Suppress FutureWarning related to use_inf_as_na
import warnings
warnings.simplefilter(action='ignore', category=FutureWarning)

plt.figure(figsize=(12,7))
sns.histplot(x=df['age'],hue=df['smoking'])
plt.show()
```



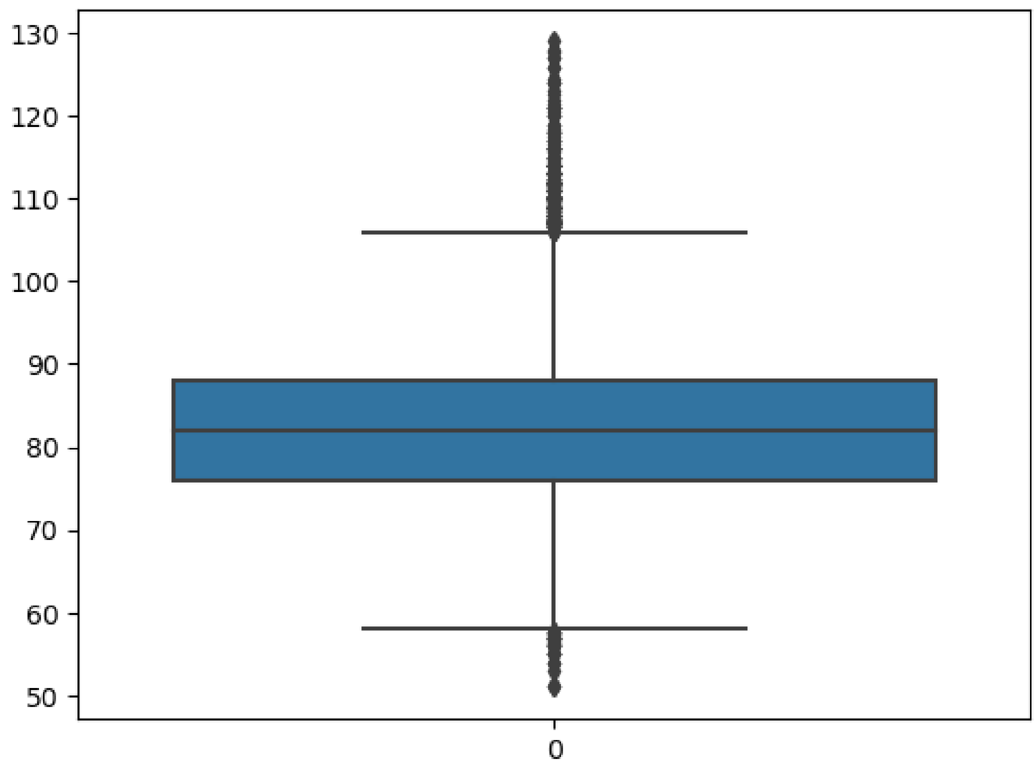
[12]:
```
for i in df.columns:
    if(df[i].dtypes=='int64' or df[i].dtypes=='float64'):
        sns.boxplot(df[i])
        plt.show()
```

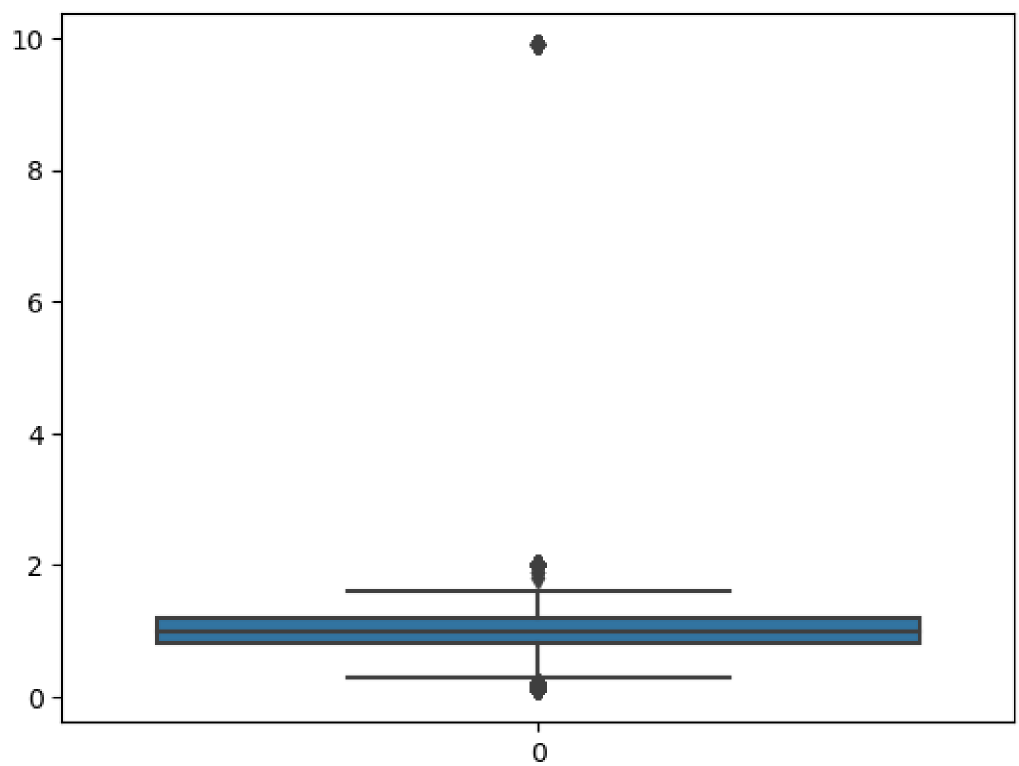

80
70
60
50
40
30
20
0

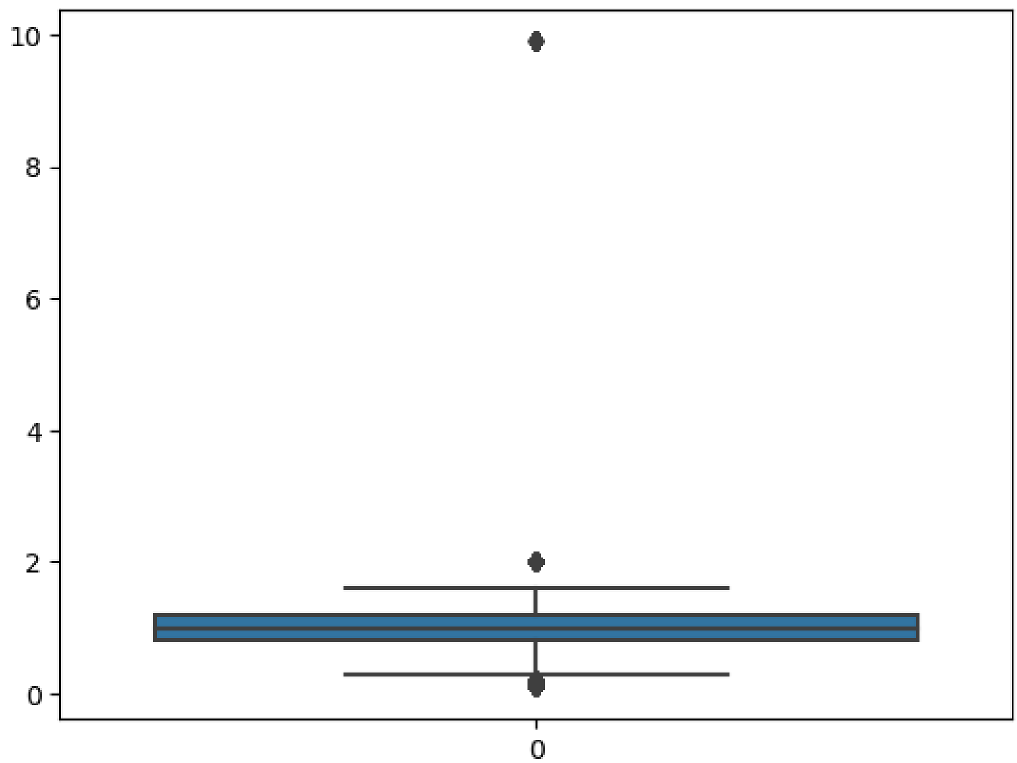

190
180
170
160
150
140
130
0

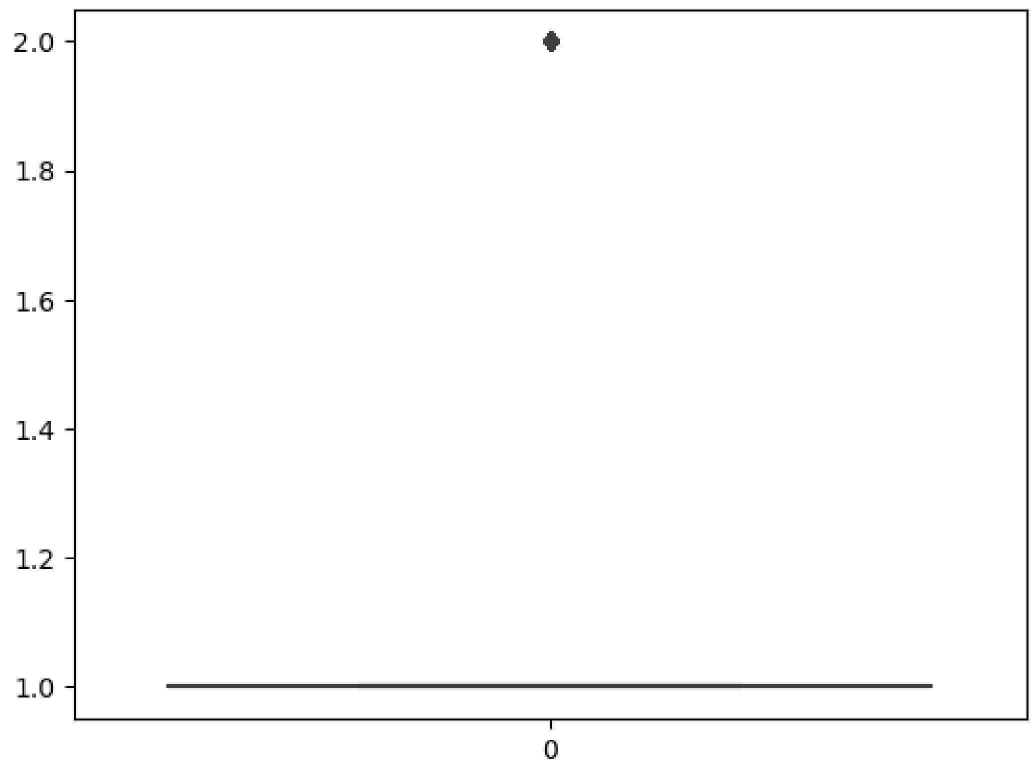


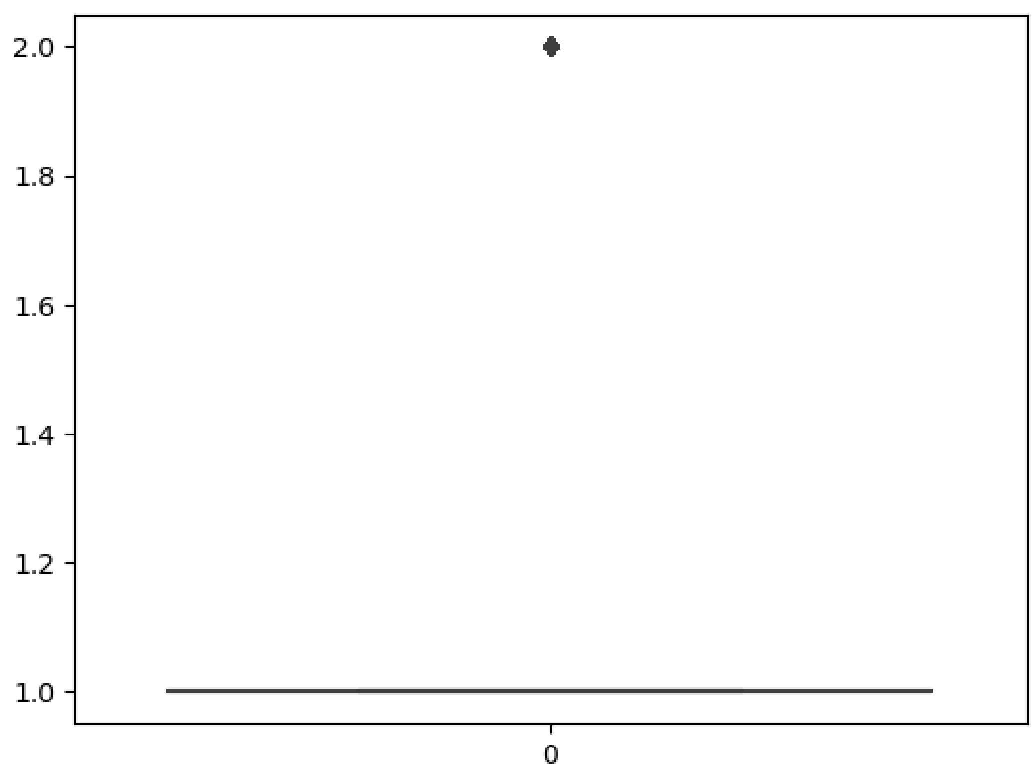
140
120
100
80
60
40
0

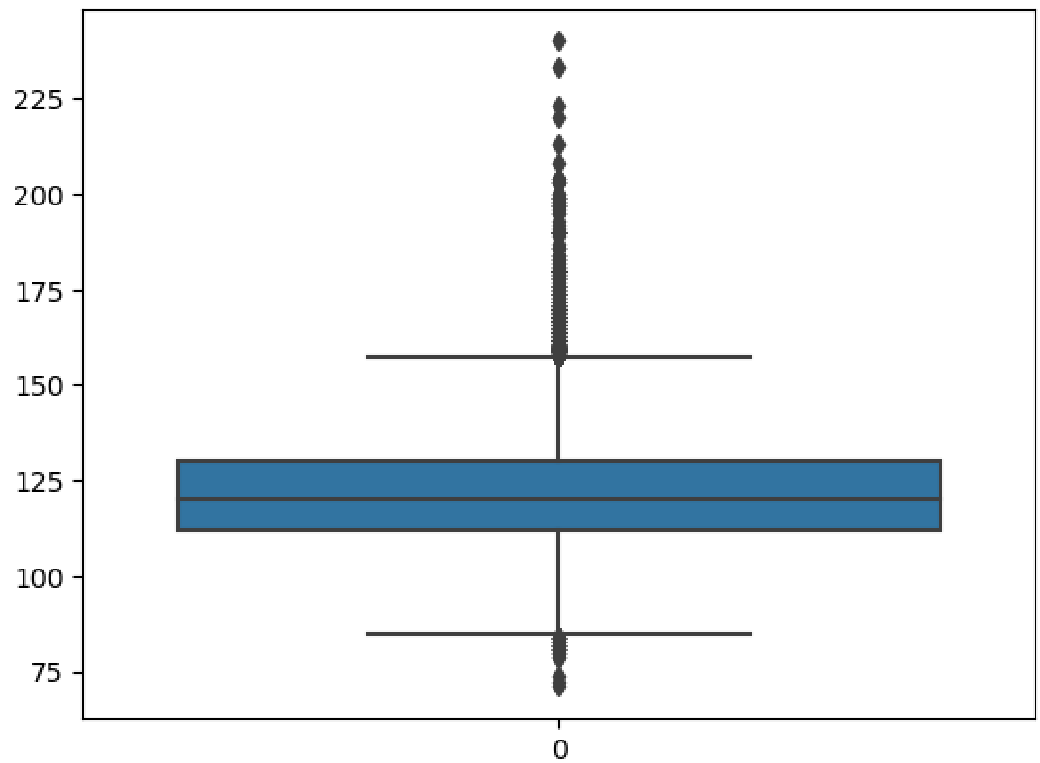

130
120
110
100
90
80
70
60
50
0

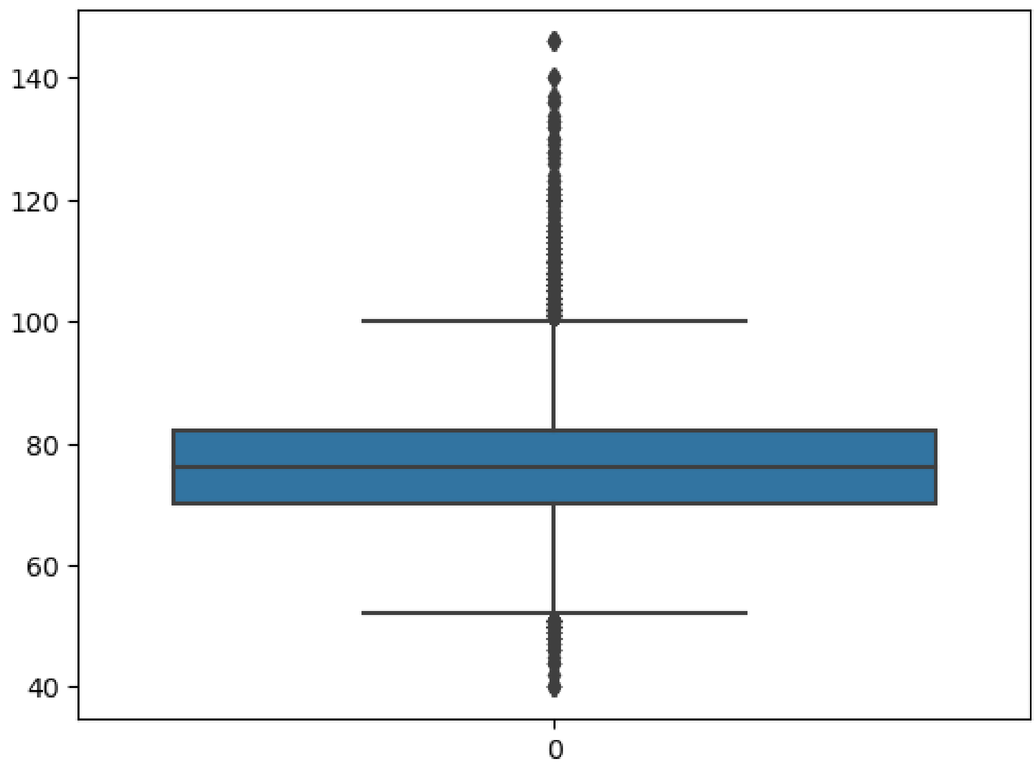

10
8
6
4
2
0
0

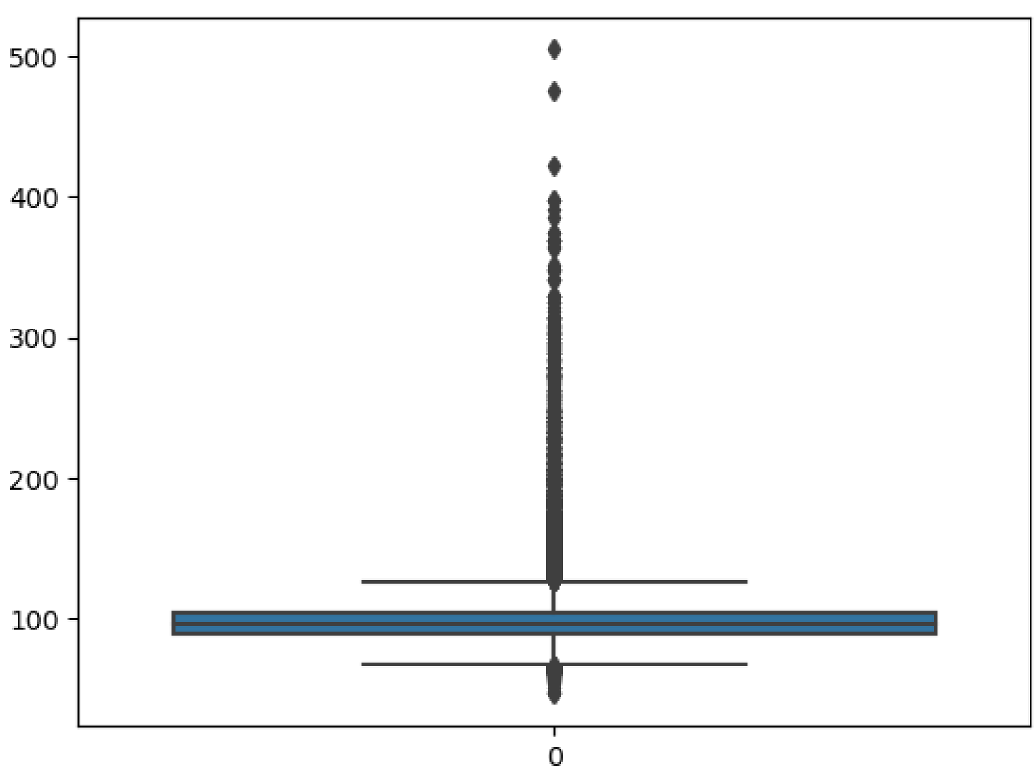

10
8
6
4
2
0
0

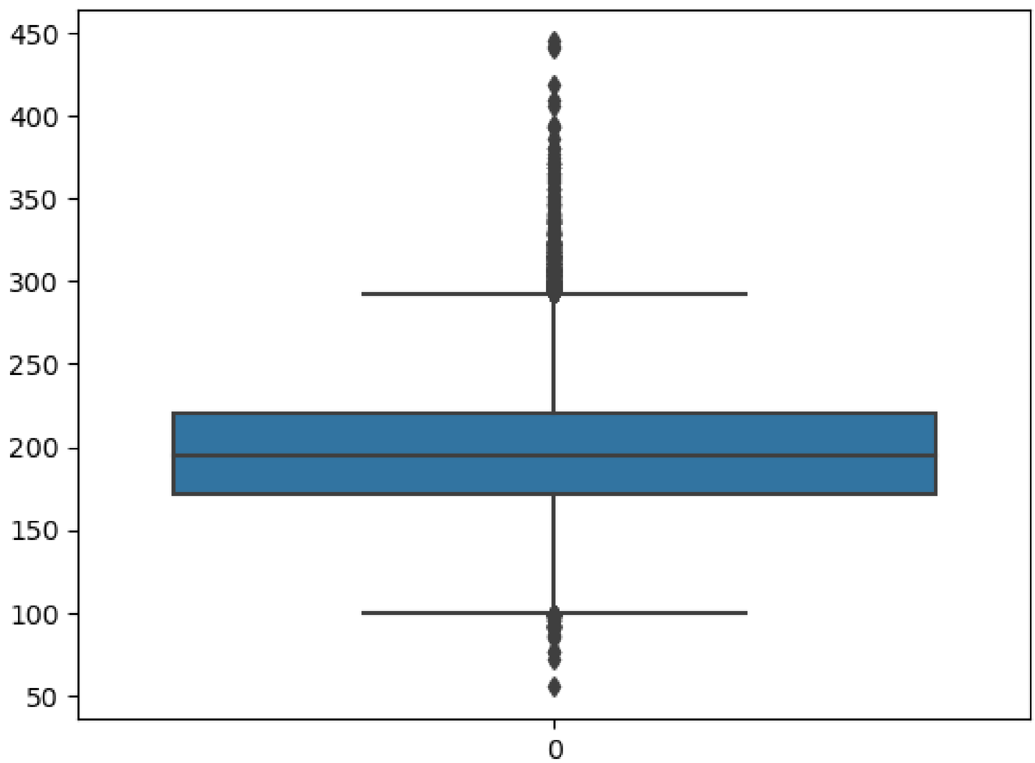

2.0
1.8
1.6
1.4
1.2
1.0
0

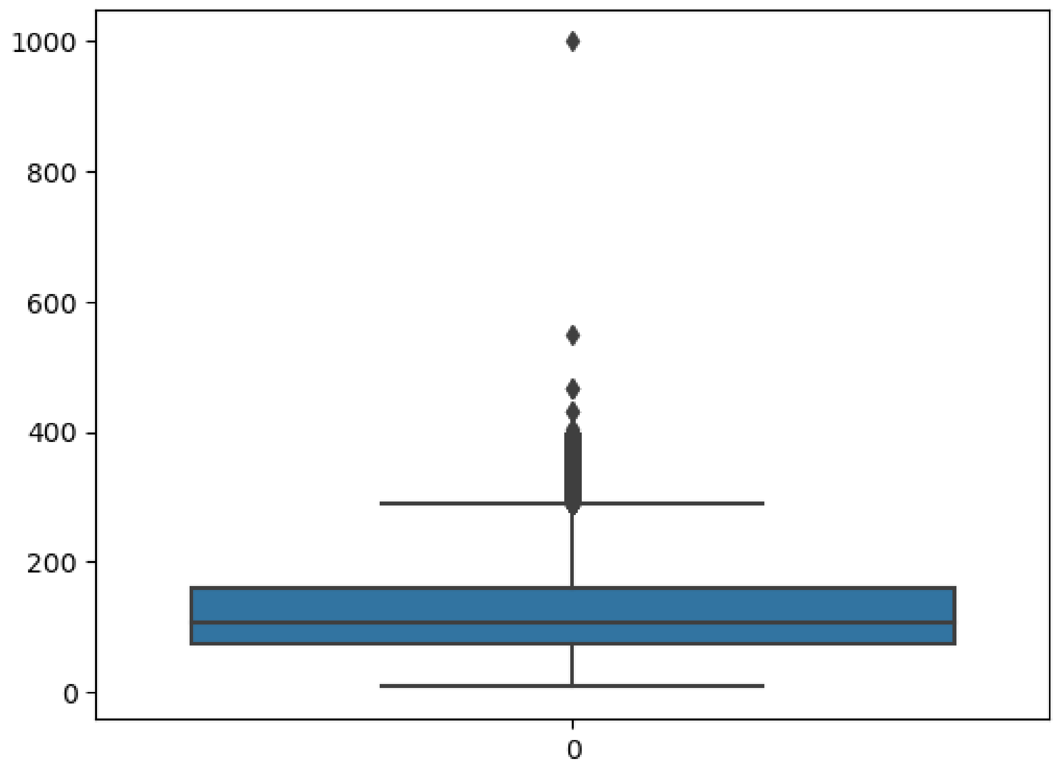

2.0
1.8
1.6
1.4
1.2
1.0
0

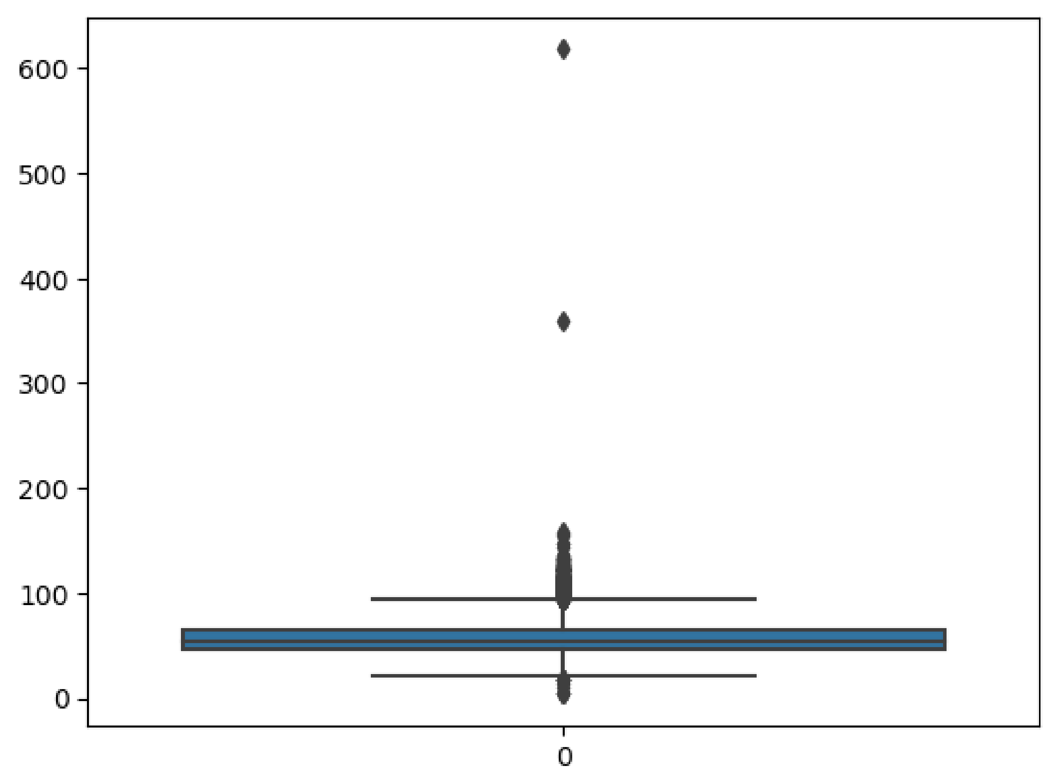

225
200
175
150
125
100
75
0

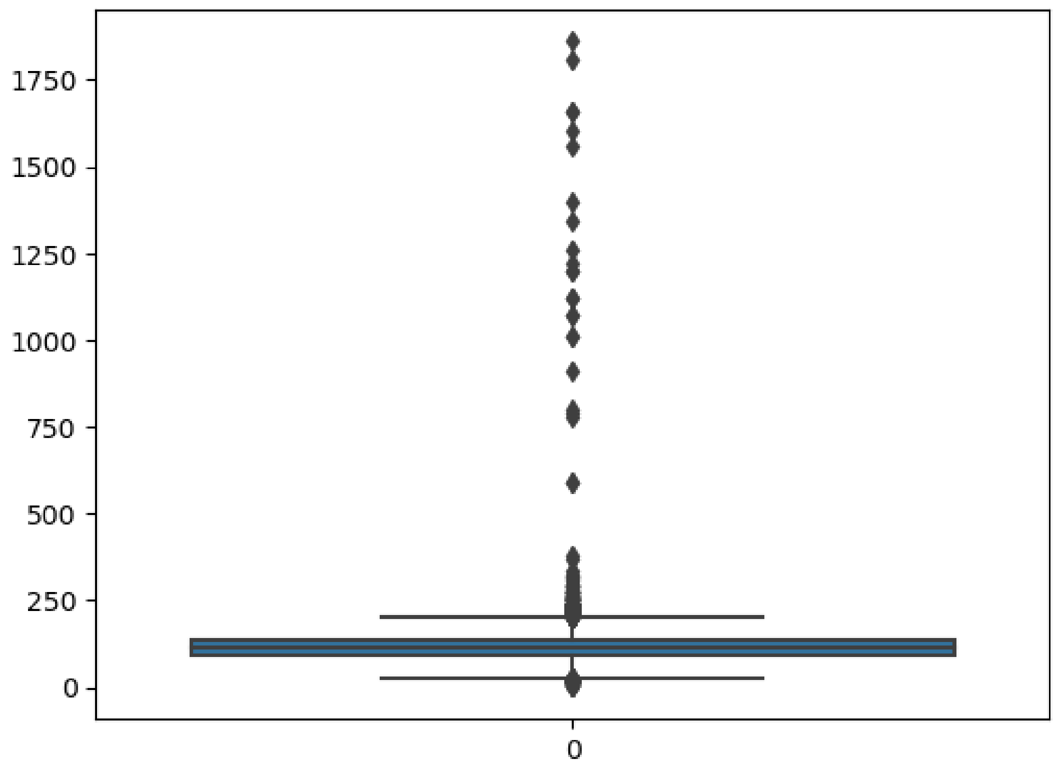

140
120
100
80
60
40
0

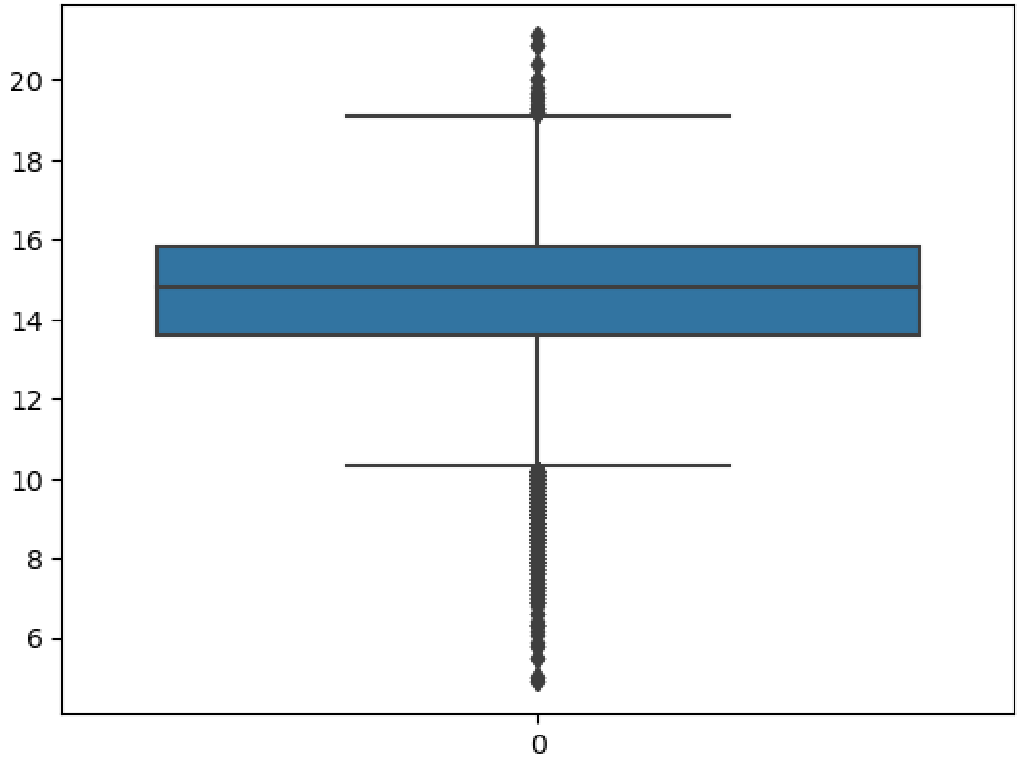

500
400
300
200
100
0

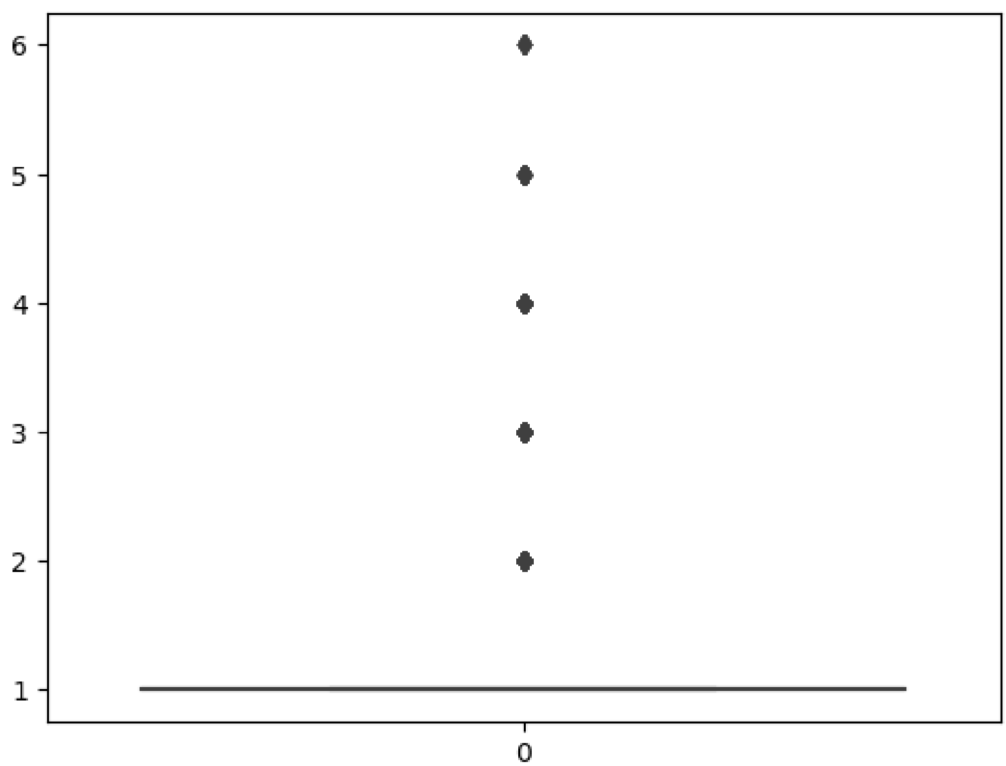

450
400
350
300
250
200
150
100
50
0

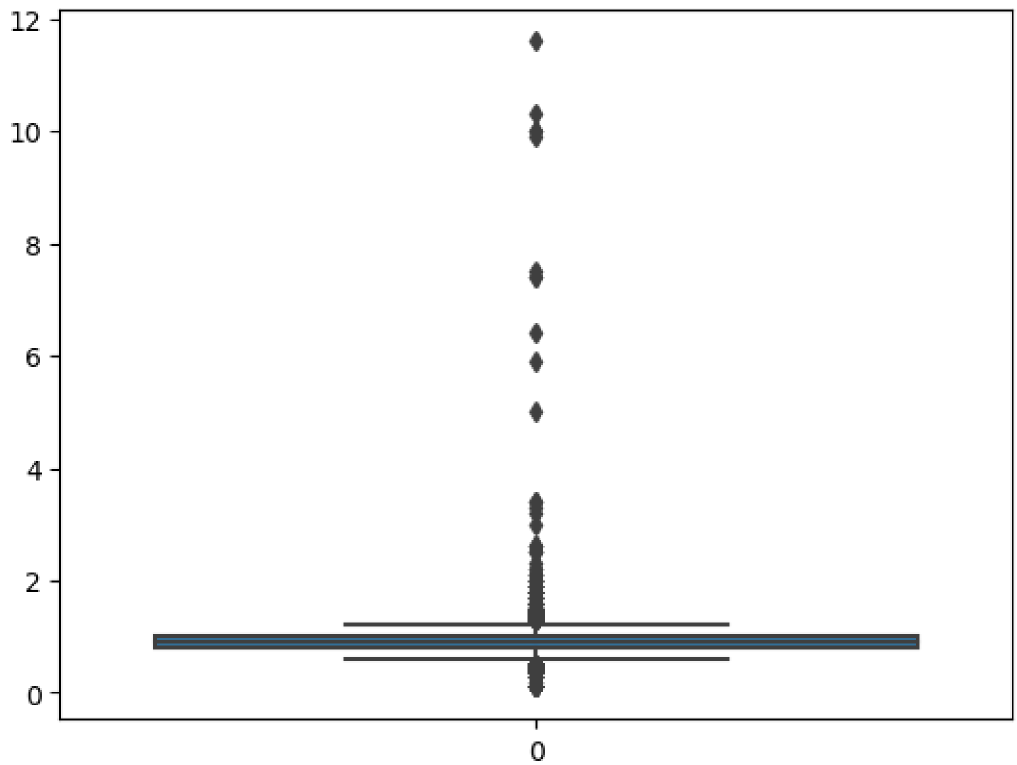

1000
800
600
400
200
0
0

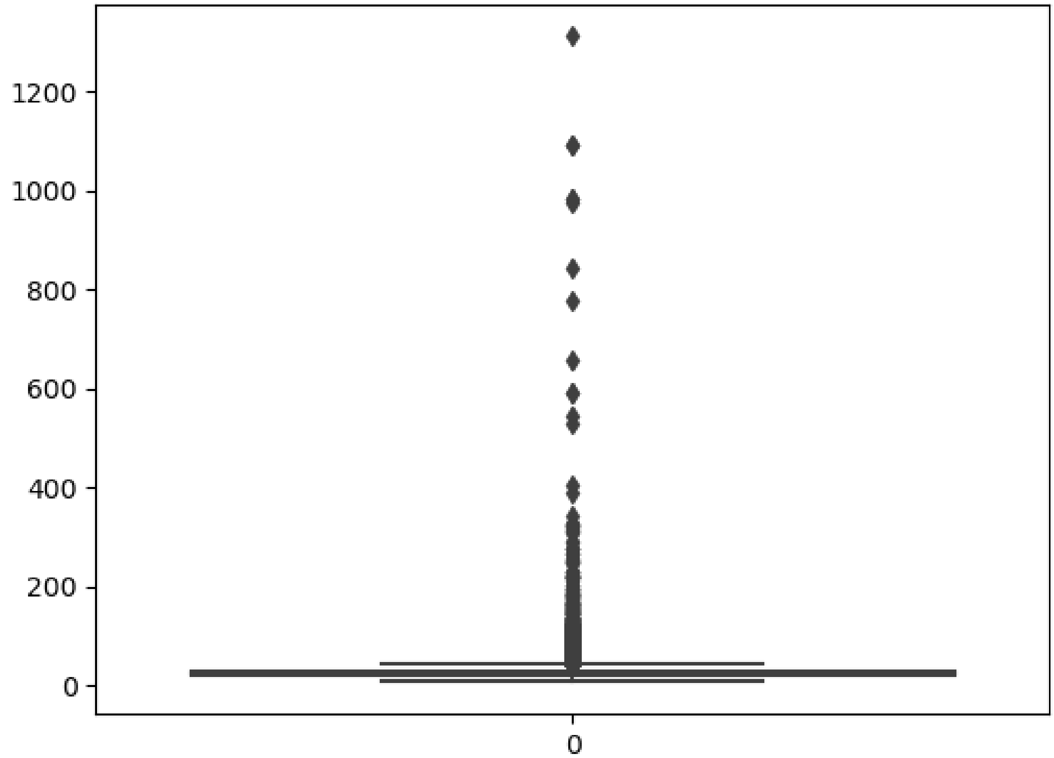

600
500
400
300
200
100
0
0


1750
1500
1250
1000
750
500
250
0
0

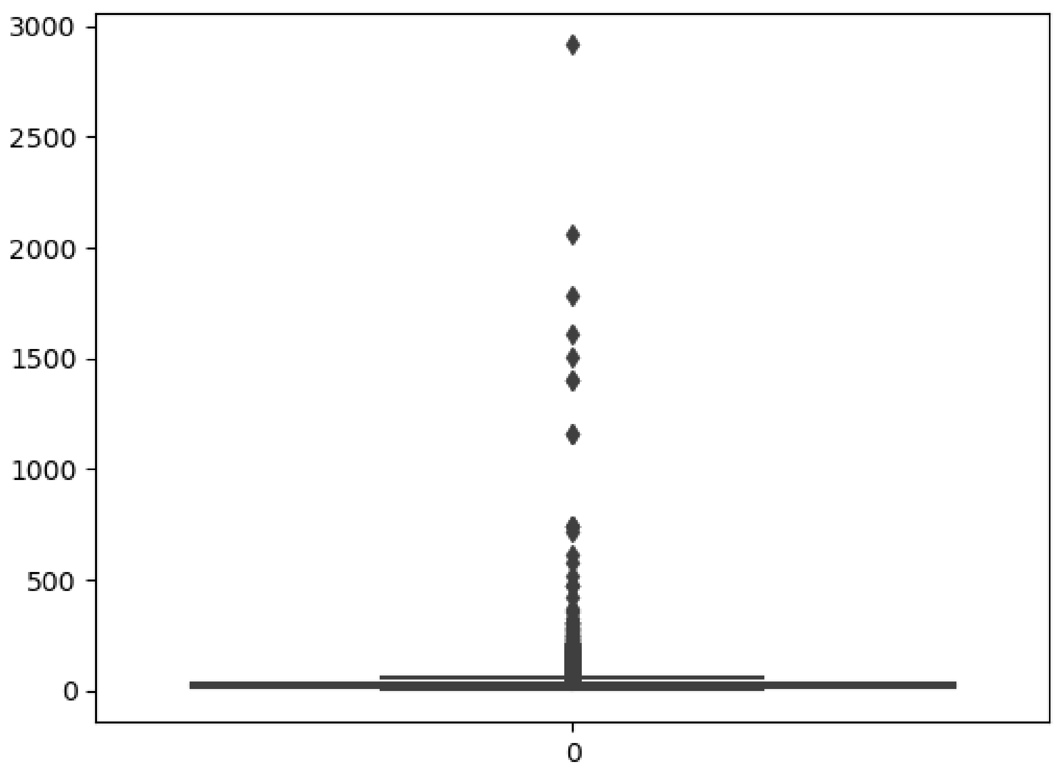

20
18
16
14
12
10
8
6
0


6
5
4
3
2
1
0

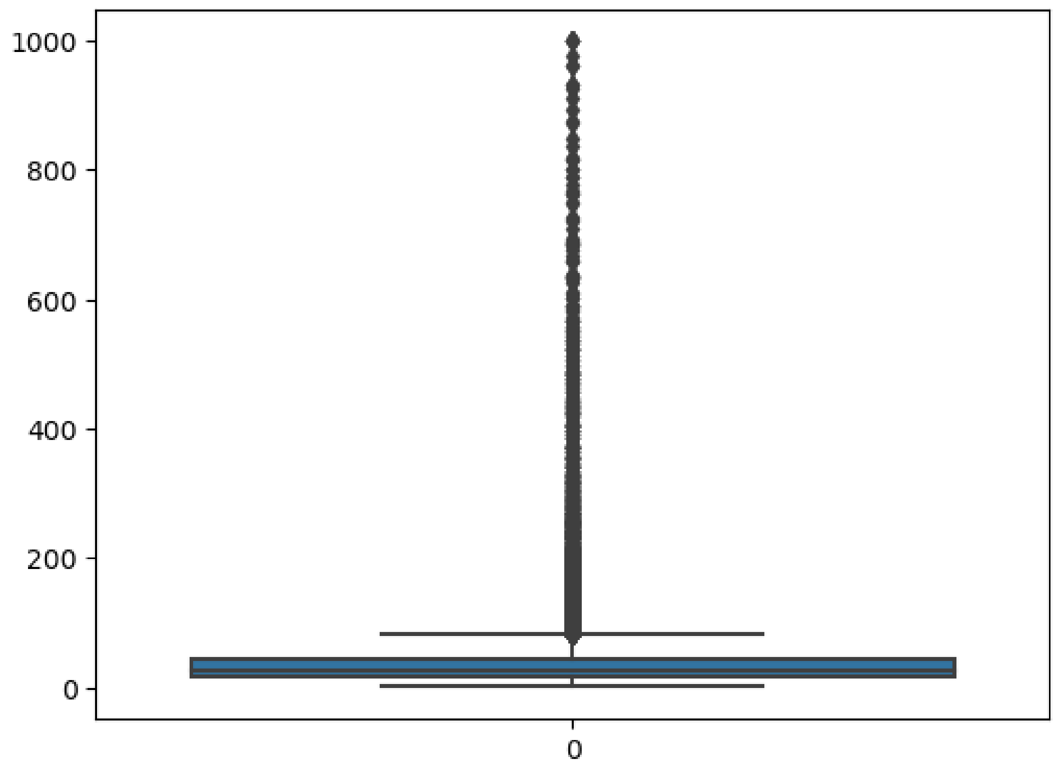

12
10
8
6
4
2
0
0

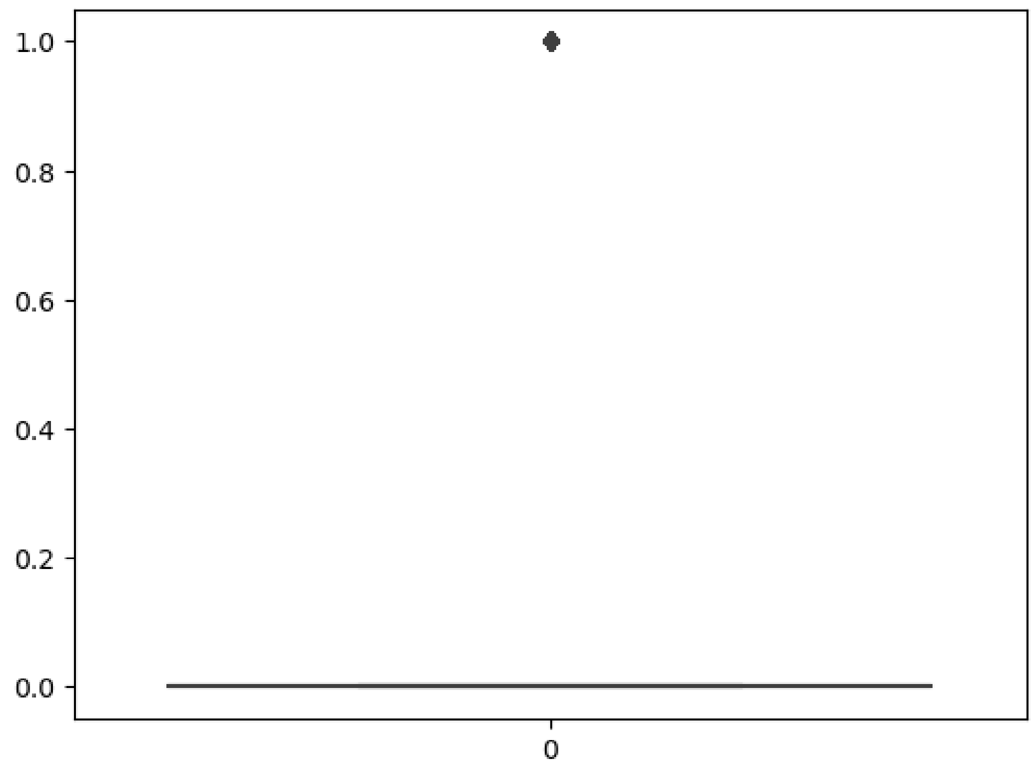


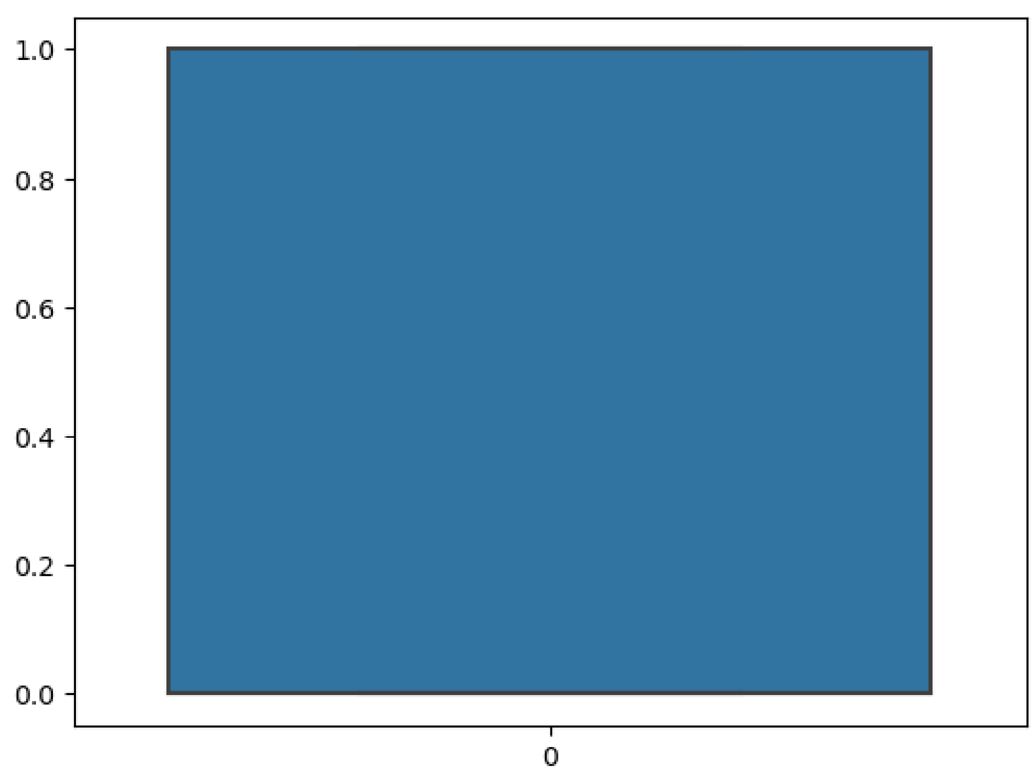
1200
1000
800
600
400
200
0
0



3000
2500
2000
1500
1000
500
0
0


1000
800
600
400
200
0
0


1.0
0.8
0.6
0.4
0.2
0.0
0


1.0
0.8
0.6
0.4
0.2
0.0
0

DATA PREPROCESSING

[13]:
```python
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

# Apply label encoding to each categorical column and convert to int64
c_cols = ['gender' , 'tartar', 'dental caries' ]
df[c_cols] = df[c_cols].apply(lambda col: le.fit_transform(col).astype('int64'))

df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 55692 entries, 0 to 55691
Data columns (total 25 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   gender               55692 non-null  int64
 1   age                  55692 non-null  int64
 2   height(cm)           55692 non-null  int64
 3   weight(kg)           55692 non-null  int64
 4   waist(cm)            55692 non-null  float64
 5   eyesight(left)       55692 non-null  float64
 6   eyesight(right)      55692 non-null  float64
 7   hearing(left)        55692 non-null  float64
 8   hearing(right)       55692 non-null  float64
 9   systolic             55692 non-null  float64
 10  relaxation           55692 non-null  float64
 11  fasting blood sugar  55692 non-null  float64
 12  Cholesterol          55692 non-null  float64
 13  triglyceride         55692 non-null  float64
 14  HDL                  55692 non-null  float64
 15  LDL                  55692 non-null  float64
 16  hemoglobin           55692 non-null  float64
 17  Urine protein        55692 non-null  float64
 18  serum creatinine     55692 non-null  float64
 19  AST                  55692 non-null  float64
 20  ALT                  55692 non-null  float64
 21  Gtp                  55692 non-null  float64
 22  dental caries        55692 non-null  int64
 23  tartar               55692 non-null  int64
 24  smoking              55692 non-null  int64
dtypes: float64(18), int64(7)
memory usage: 10.6 MB
```

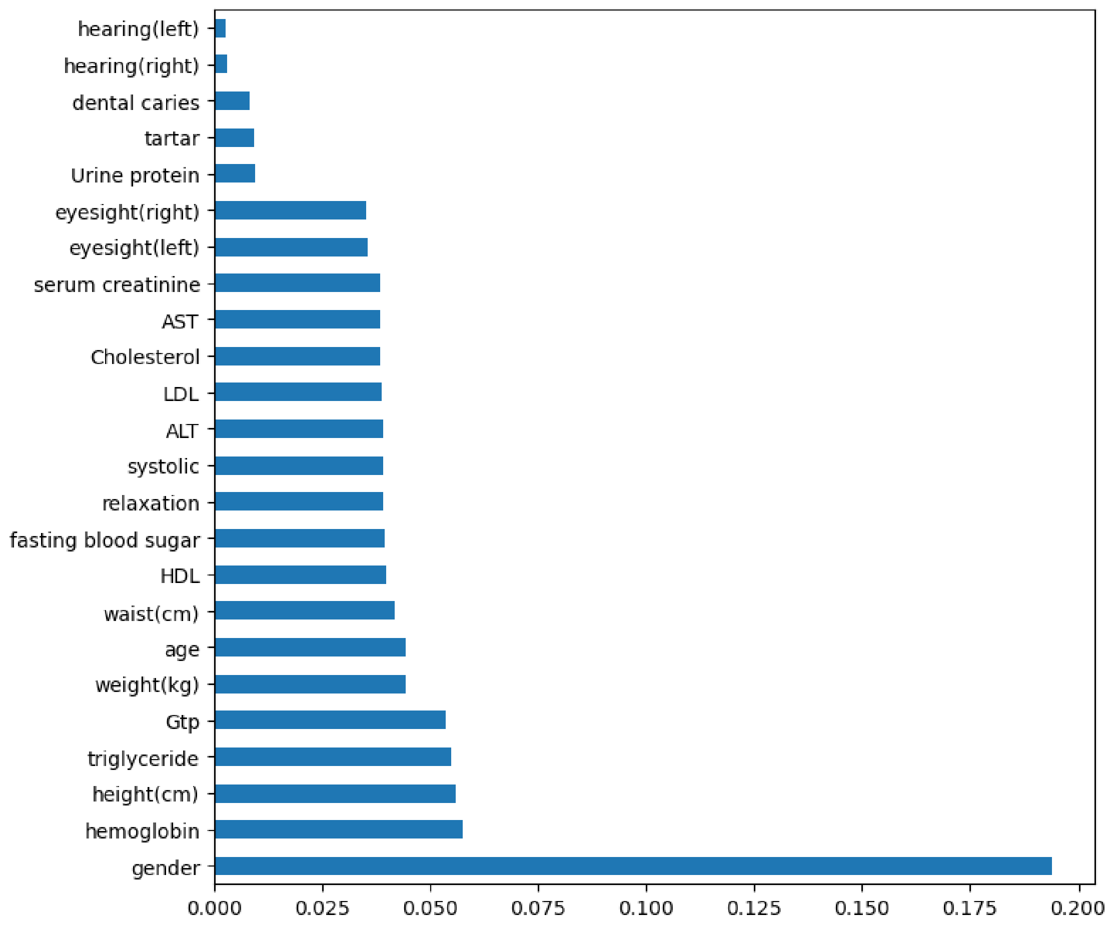
2 FEATURE SELECTION USING FEATURE IMPORTANCE

[14]:
```
X = df.iloc[:,:-1]
y = df.iloc[:, -1]
```

[15]:
```
from sklearn.ensemble import ExtraTreesClassifier
model = ExtraTreesClassifier()
model.fit(X,y)
```

[15]:
```
ExtraTreesClassifier()
```

[16]:
```
df1= pd.Series(model.feature_importances_,index=X.columns)
plt.figure(figsize=(8,8))
df1.nlargest(24).plot(kind='barh')
plt.show()
```



[17]:
```
X = df[['gender','triglyceride','height(cm)','hemoglobin','Gtp','weight(kg)',
```

```
        'waist(cm)','age','HDL','fasting blood␣
↪sugar','LDL','relaxation','ALT','systolic','Cholesterol']]
y = df.iloc[:, -1]
```

Logistic Regression

[18]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)

from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)

from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
lr.fit(X_train, y_train)

y_pred = lr.predict(X_test)

pd.DataFrame({"actaul_value":y_test,"predicted_value":y_pred})
```

[18]:

	actaul_value	predicted_value
33967	0	0
21956	1	0
15458	0	1
36215	0	1
8886	0	1
…	…	…
17853	0	0
31224	1	0
24589	0	0
43475	0	0
33600	1	1

[11139 rows x 2 columns]

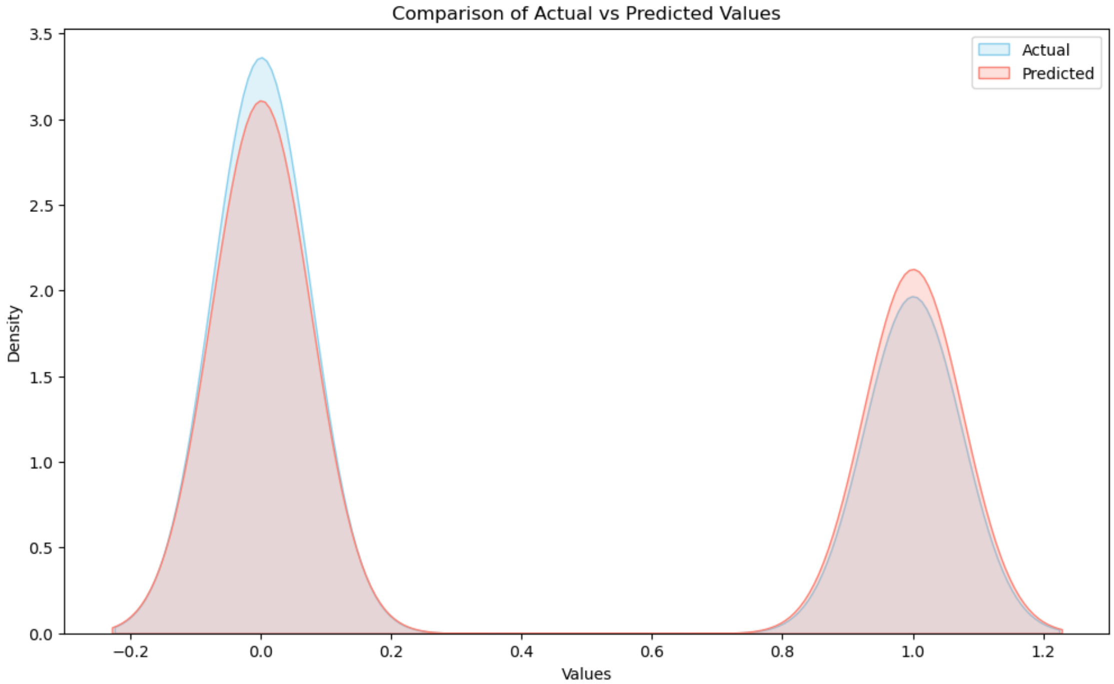
[19]:
```
from sklearn.metrics import accuracy_score, classification_report,␣
↪confusion_matrix
# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")

print("\nClassification Report:")
print(classification_report(y_test, y_pred))
```

```
print("\nConfusion Matrix:")
print(confusion_matrix(y_test, y_pred))
```

```
Accuracy: 0.73

Classification Report:
              precision    recall  f1-score   support

           0       0.80      0.76      0.78      7027
           1       0.62      0.69      0.65      4112

    accuracy                           0.73     11139
   macro avg       0.71      0.72      0.72     11139
weighted avg       0.74      0.73      0.73     11139


Confusion Matrix:
[[5321 1706]
 [1295 2817]]
```

[20]:

```
# Create a figure and axis
plt.figure(figsize=(12, 7))

# Plot the kernel density estimate for actual and predicted values
sns.kdeplot(y_test, label='Actual', fill=True, color='skyblue')
sns.kdeplot(y_pred, label='Predicted', fill=True, color='salmon')
plt.xlabel('Values')
plt.ylabel('Density')
plt.title('Comparison of Actual vs Predicted Values')
plt.legend()
plt.show()
```



Decision Tree Classifier

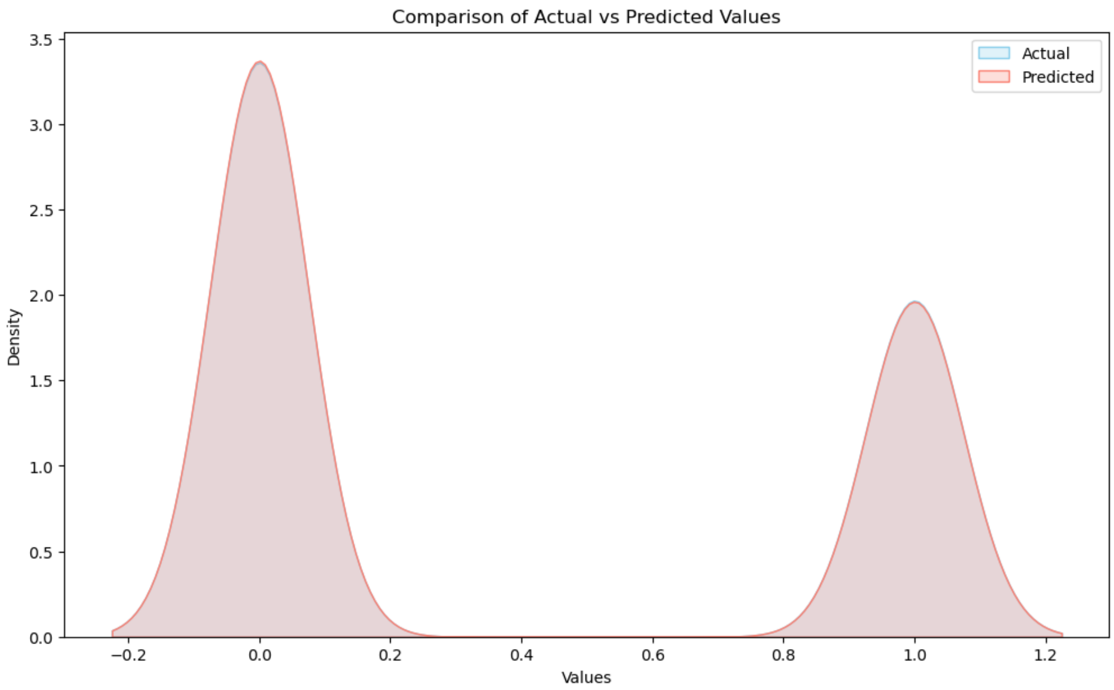
[21]:
```
from sklearn.tree import DecisionTreeClassifier
dt = DecisionTreeClassifier()
dt.fit(X_train, y_train)

y_pred = dt.predict(X_test)
```

[22]:
```
# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")

print("\nClassification Report:")
print(classification_report(y_test, y_pred))

print("\nConfusion Matrix:")
print(confusion_matrix(y_test, y_pred))
```

```
Accuracy: 0.79

Classification Report:
              precision    recall  f1-score   support

           0       0.83      0.83      0.83      7027
           1       0.72      0.71      0.71      4112
```

```
    accuracy                           0.79     11139
   macro avg       0.77      0.77      0.77     11139
weighted avg       0.79      0.79      0.79     11139


Confusion Matrix:
[[5865 1162]
 [1178 2934]]
```

[23]:
```
# Create a figure and axis
plt.figure(figsize=(12, 7))

# Plot the kernel density estimate for actual and predicted values
sns.kdeplot(y_test, label='Actual', fill=True, color='skyblue')
sns.kdeplot(y_pred, label='Predicted', fill=True, color='salmon')
plt.xlabel('Values')
plt.ylabel('Density')
plt.title('Comparison of Actual vs Predicted Values')
plt.legend()
plt.show()
```



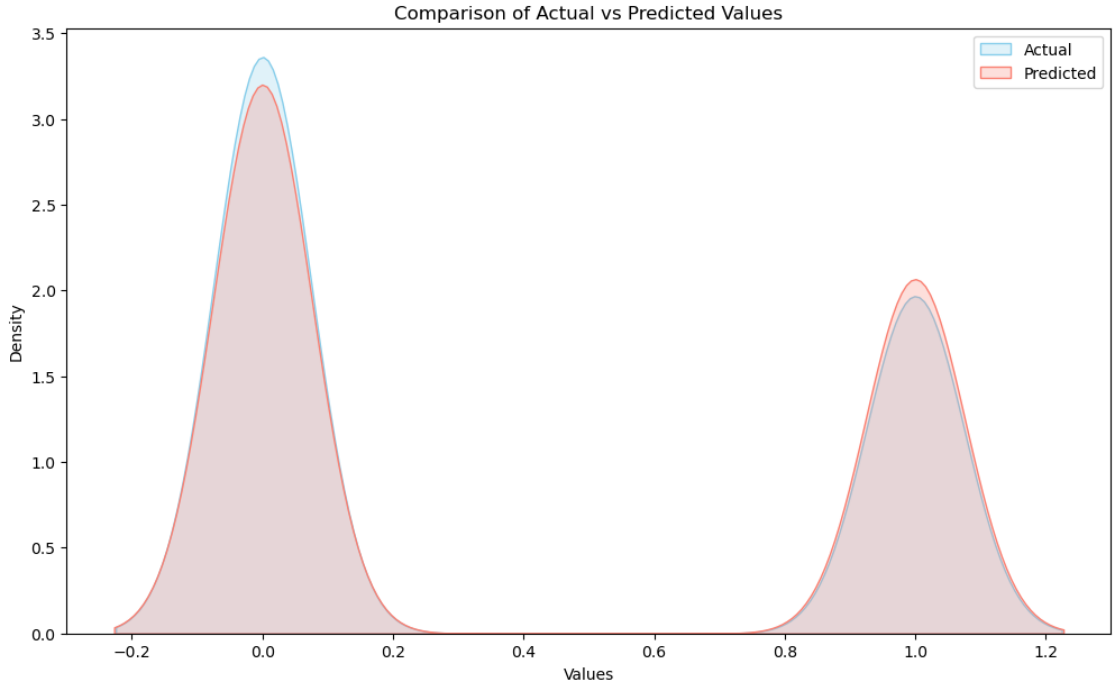
Ensemble Learning with Bagging Classifier

[24]:
```
from sklearn.ensemble import BaggingClassifier
bagg = BaggingClassifier(base_estimator =␣
 ↪DecisionTreeClassifier(),n_estimators=1000)
bagg.fit(X_train, y_train).score(X_test,y_test)

y_pred = bagg.predict(X_test)
```

[25]:
```
# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")

print("\nClassification Report:")
print(classification_report(y_test, y_pred))

print("\nConfusion Matrix:")
print(confusion_matrix(y_test, y_pred))
```

```
Accuracy: 0.83

Classification Report:
              precision    recall  f1-score   support

           0       0.88      0.84      0.86      7027
           1       0.75      0.80      0.77      4112

    accuracy                           0.83     11139
   macro avg       0.81      0.82      0.82     11139
weighted avg       0.83      0.83      0.83     11139


Confusion Matrix:
[[5927 1100]
 [ 842 3270]]
```

[26]:
```
# Create a figure and axis
plt.figure(figsize=(12, 7))

# Plot the kernel density estimate for actual and predicted values
sns.kdeplot(y_test, label='Actual', fill=True, color='skyblue')
sns.kdeplot(y_pred, label='Predicted', fill=True, color='salmon')
plt.xlabel('Values')
plt.ylabel('Density')
plt.title('Comparison of Actual vs Predicted Values')
plt.legend()
plt.show()
```



Ensemble Learning with Extra Trees Classifier

[27]:
```
from sklearn.ensemble import ExtraTreesClassifier
et = ExtraTreesClassifier(n_estimators=1000,random_state=42)
et.fit(X_train,y_train)

y_pred = et.predict(X_test)
```

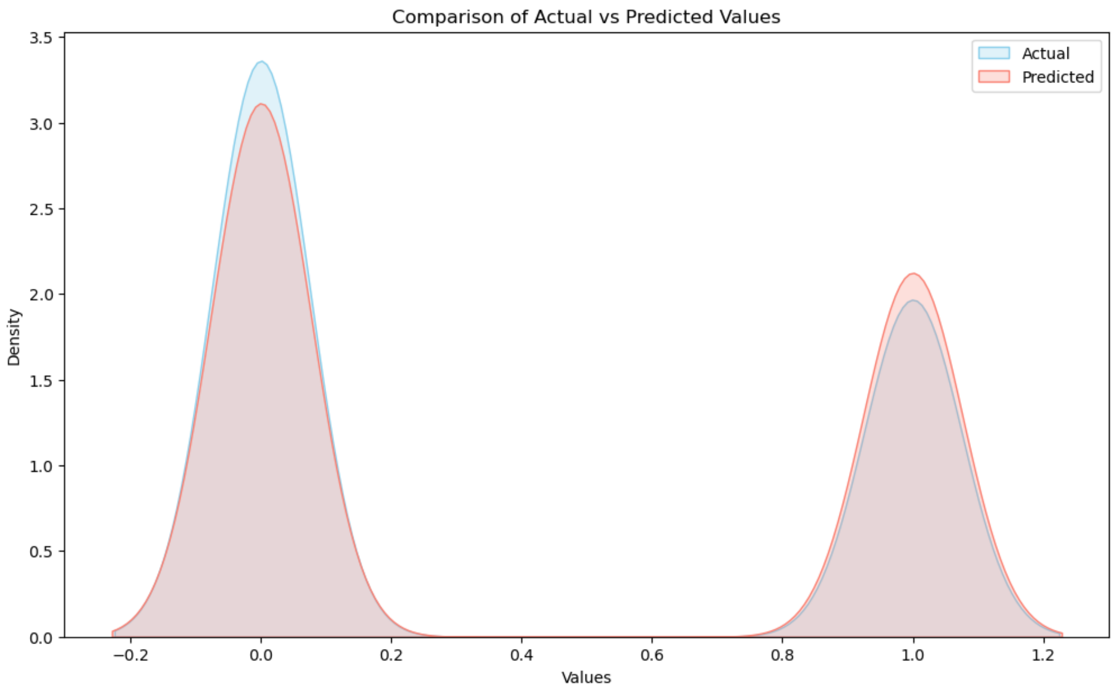
[28]:
```
# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")

print("\nClassification Report:")
print(classification_report(y_test, y_pred))

print("\nConfusion Matrix:")
print(confusion_matrix(y_test, y_pred))
```

```
Accuracy: 0.83

Classification Report:
              precision    recall  f1-score   support

           0       0.88      0.83      0.86      7027
           1       0.74      0.81      0.78      4112
```

```
    accuracy                           0.83     11139
   macro avg       0.81      0.82      0.82     11139
weighted avg       0.83      0.83      0.83     11139


Confusion Matrix:
[[5860 1167]
 [ 762 3350]]
```

[29]:

```
# Create a figure and axis
plt.figure(figsize=(12, 7))

# Plot the kernel density estimate for actual and predicted values
sns.kdeplot(y_test, label='Actual', fill=True, color='skyblue')
sns.kdeplot(y_pred, label='Predicted', fill=True, color='salmon')
plt.xlabel('Values')
plt.ylabel('Density')
plt.title('Comparison of Actual vs Predicted Values')
plt.legend()
plt.show()
```



Random Forest Classifier

[30]:

```python
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier(n_estimators=1000)
rfc.fit(X_train, y_train)

y_pred = rfc.predict(X_test)
```

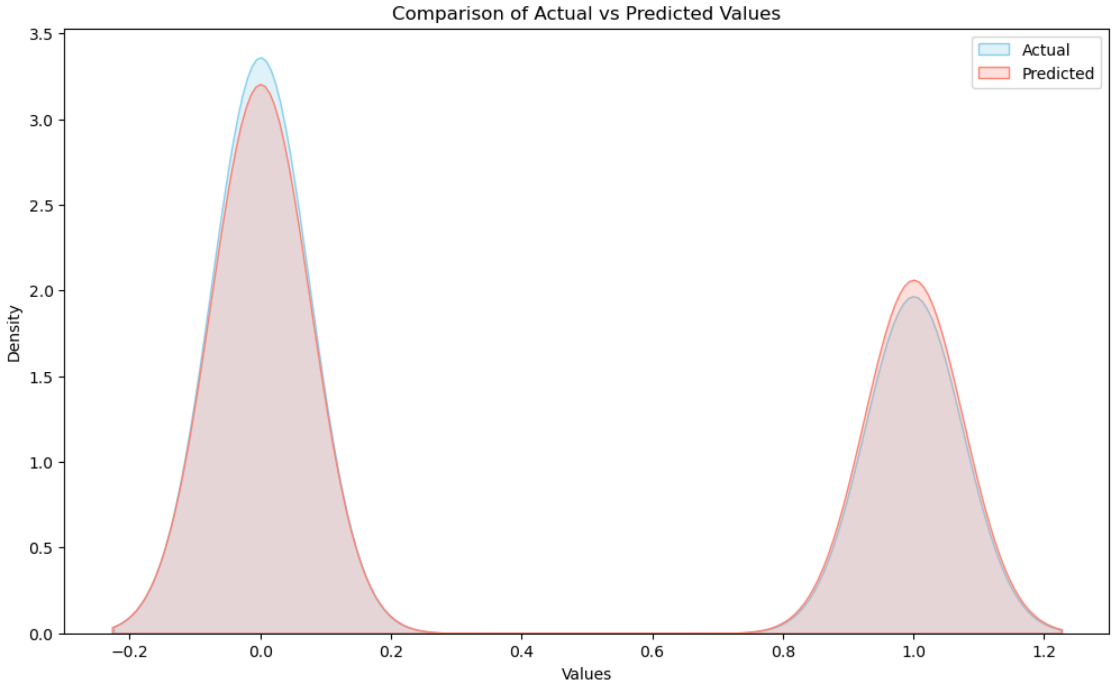
[31]:

```python
# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")

print("\nClassification Report:")
print(classification_report(y_test, y_pred))

print("\nConfusion Matrix:")
print(confusion_matrix(y_test, y_pred))
```

```
Accuracy: 0.83

Classification Report:
              precision    recall  f1-score   support

           0       0.88      0.85      0.86      7027
           1       0.75      0.80      0.77      4112

    accuracy                           0.83     11139
   macro avg       0.81      0.82      0.82     11139
weighted avg       0.83      0.83      0.83     11139


Confusion Matrix:
[[5940 1087]
 [ 837 3275]]
```

[32]:

```python
# Create a figure and axis
plt.figure(figsize=(12, 7))

# Plot the kernel density estimate for actual and predicted values
sns.kdeplot(y_test, label='Actual', fill=True, color='skyblue')
sns.kdeplot(y_pred, label='Predicted', fill=True, color='salmon')
plt.xlabel('Values')
plt.ylabel('Density')
plt.title('Comparison of Actual vs Predicted Values')
plt.legend()
plt.show()
```



SELECTING THE BEST MODEL

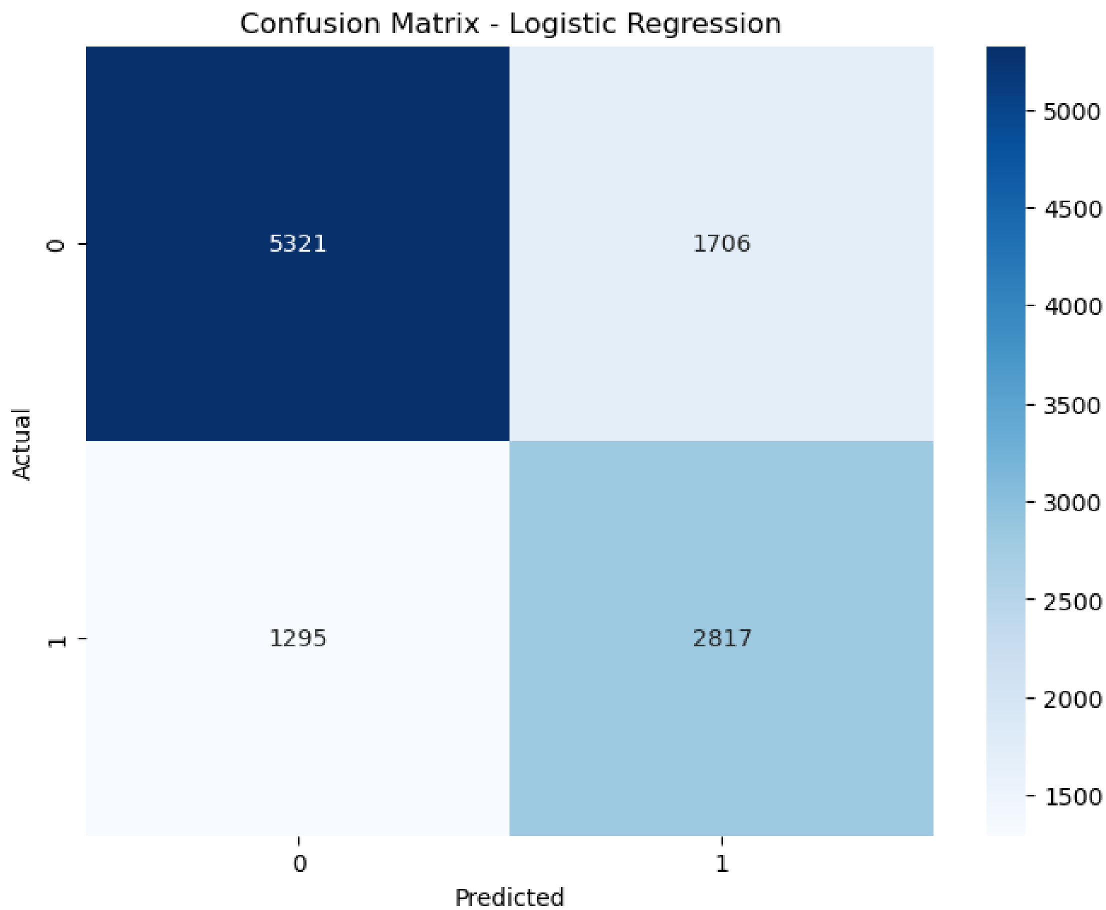
[35]:
```
from sklearn.metrics import recall_score, precision_score, f1_score

# List of classifiers
classifiers = [lr, dt, bagg, et, rfc]  # Assuming these are the names of your␣
↪classifiers
classifier_names = ['Logistic Regression', 'Decision Tree', 'Bagging␣
↪Classifier', 'Extra Trees Classifier', 'Random Forest']

# Initialize lists to store metrics
models = []
confusion_matrices = []
classification_reports = []
accuracies = []
recalls = []
precisions = []
f1_scores = []

# Loop through each classifier
for clf, clf_name in zip(classifiers, classifier_names):
    # Get predictions
    y_pred = clf.predict(X_test)

    # Store metrics in lists
```

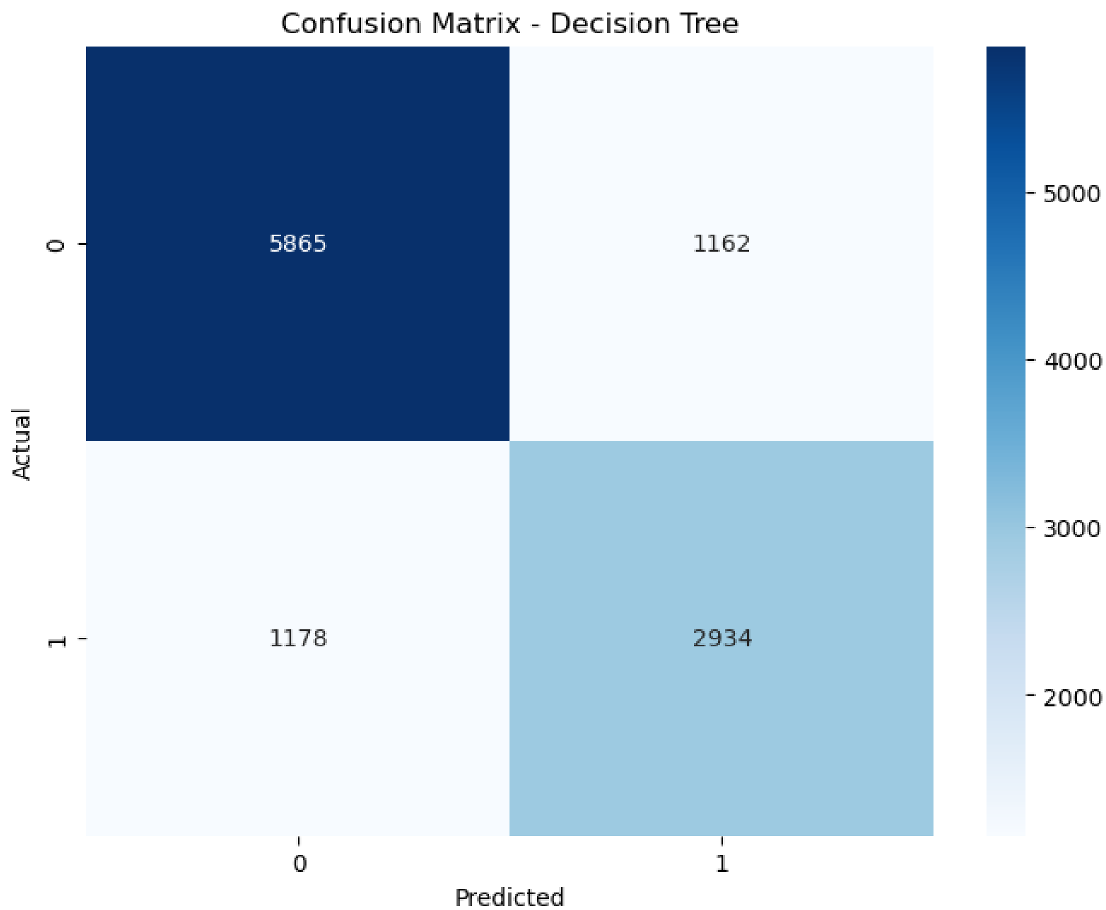
```
    models.append(clf_name)
    confusion_matrices.append(confusion_matrix(y_test, y_pred))
    classification_reports.append(classification_report(y_test, y_pred))
    accuracies.append(accuracy_score(y_test, y_pred))
    recalls.append(recall_score(y_test, y_pred, average='weighted'))
    precisions.append(precision_score(y_test, y_pred, average='weighted'))
    f1_scores.append(f1_score(y_test, y_pred, average='weighted'))

# Create a DataFrame with metrics
metrics_df = pd.DataFrame({
    'Model': models,
    'Accuracy': accuracies,
    'Recall': recalls,
    'Precision': precisions,
    'F1 Score': f1_scores
})

# Display the metrics table
print("Metrics for Each Model:")
print(metrics_df)
```

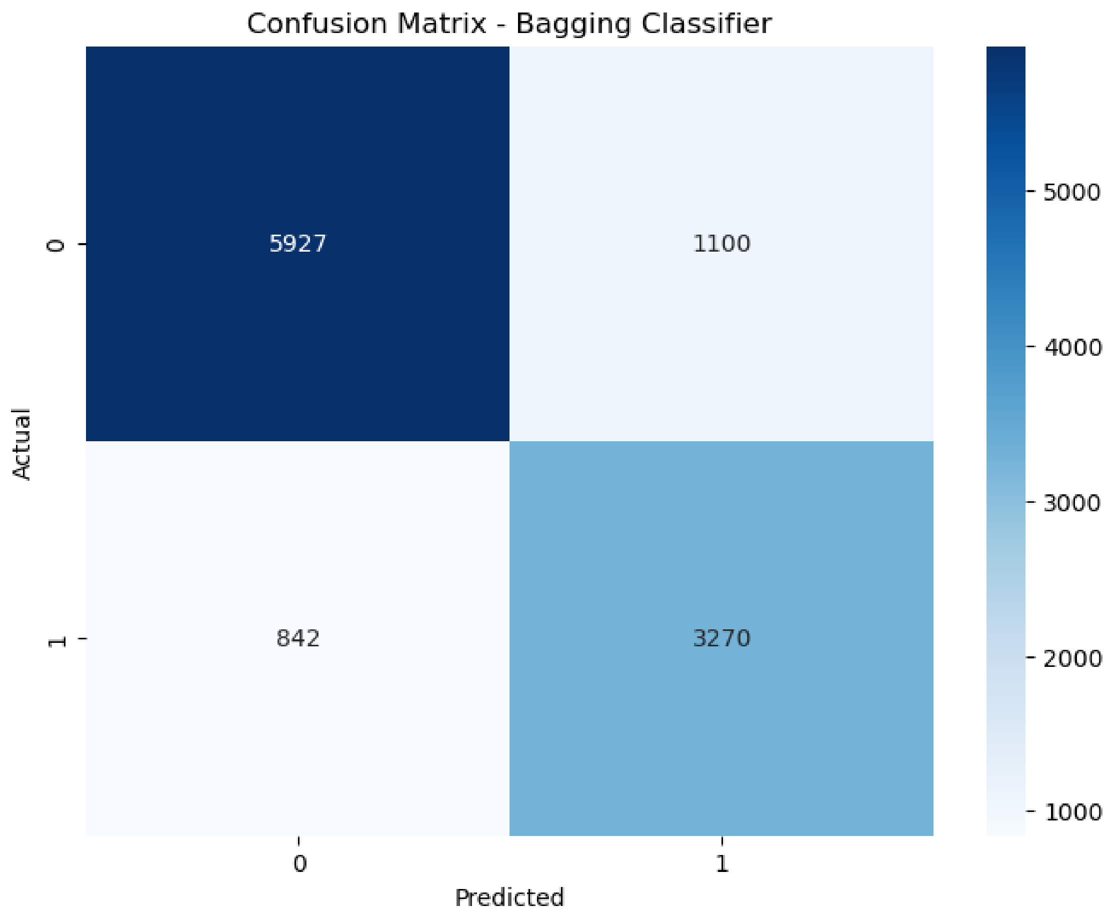
```
Metrics for Each Model:
                   Model  Accuracy    Recall  Precision  F1 Score
0    Logistic Regression  0.730586  0.730586   0.737281  0.732940
1          Decision Tree  0.789927  0.789927   0.789760  0.789842
2      Bagging Classifier  0.825658  0.825658   0.828607  0.826679
3  Extra Trees Classifier  0.826825  0.826825   0.832034  0.828319
4          Random Forest  0.827274  0.827274   0.830095  0.828257
```

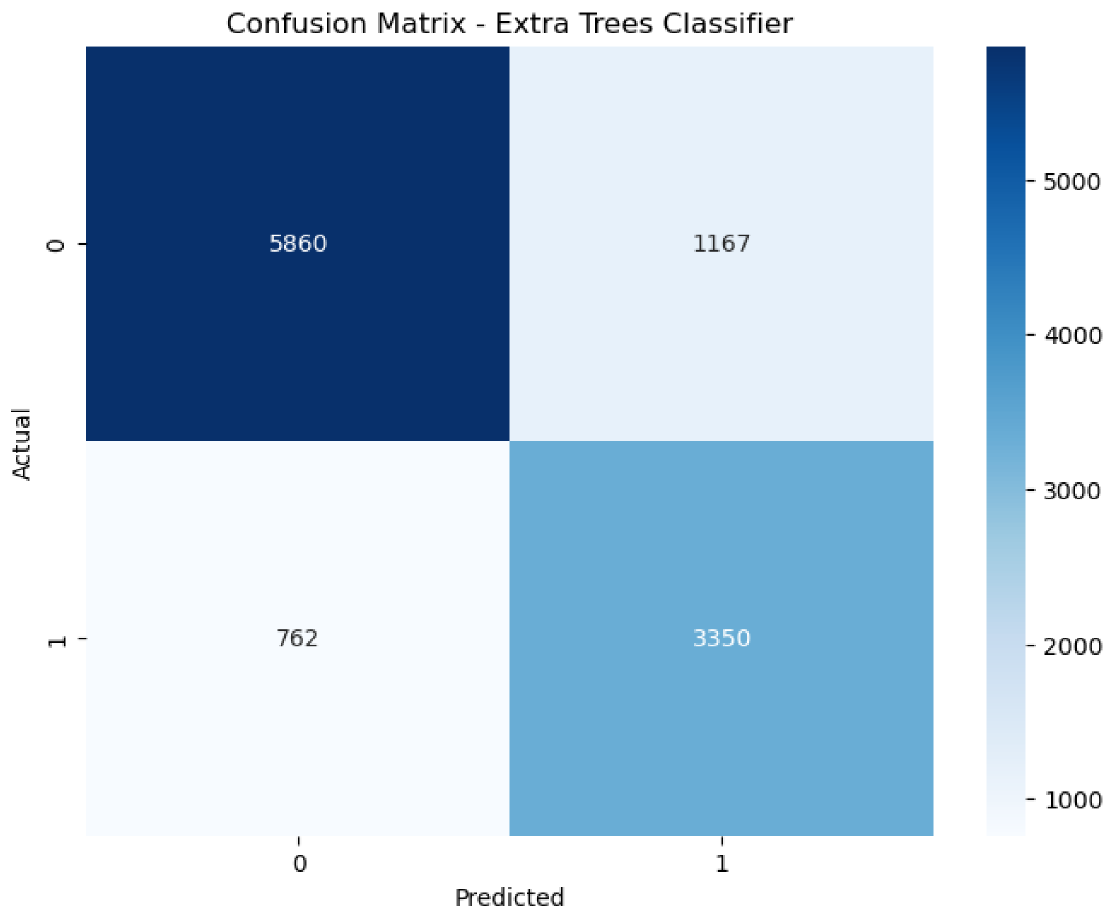
[36]:

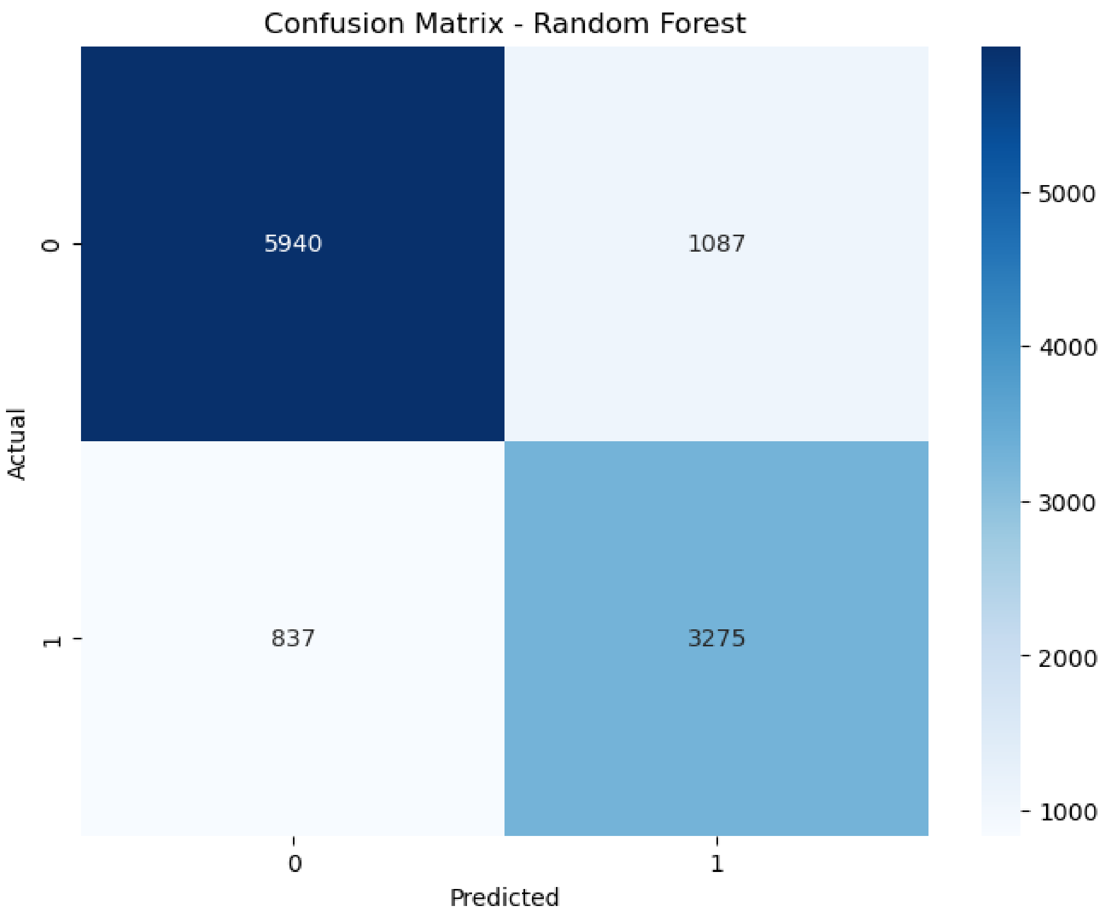
```
# Visualize confusion matrices using heatmaps
for clf, clf_name, confusion_matrix in zip(classifiers, classifier_names,␣
 ↪confusion_matrices):
    plt.figure(figsize=(8, 6))
    sns.heatmap(confusion_matrix, annot=True, cmap='Blues', fmt='g')
    plt.title(f'Confusion Matrix - {clf_name}')
    plt.xlabel('Predicted')
    plt.ylabel('Actual')
    plt.show()
```


Confusion Matrix - Logistic Regression
5321
1706
1295
2817
Actual
Predicted
0
1
0
1
5000
4500
4000
3500
3000
2500
2000
1500


Confusion Matrix - Decision Tree
5865
1162
1178
2934
Actual
Predicted
0
1
0
1
5000
4000
3000
2000


Confusion Matrix - Bagging Classifier
5927
1100
842
3270
Actual
Predicted
0
1
0
1
5000
4000
3000
2000
1000


Confusion Matrix - Extra Trees Classifier
5860
1167
762
3350
Actual
Predicted
0
1
0
1
5000
4000
3000
2000
1000



[37]:
```
# Select the best model based on highest accuracy
best_model_index = accuracies.index(max(accuracies))
best_model_name = models[best_model_index]
print(f"\nThe best model is {best_model_name} with an accuracy of␣
 ↪{accuracies[best_model_index]:.2f}")
```

```
The best model is Random Forest with an accuracy of 0.83
```

[ ]:
```
```