```
# Topic: Implement KNN in Water Quality Dataset
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# Date: 16th May 2024
# Submission : 17th May 2024
```

Dataset Description :

- Rows: 7,999
- Columns: 21
- Features: Chemical concentrations: Includes various chemicals like aluminium, ammonia, arsenic, barium, cadmium, chloramine, chromium, copper, flouride, lead, nitrates, nitrites, mercury, perchlorate, radium, selenium, silver, and uranium. Biological parameters: bacteria and viruses, indicating the presence of biological contaminants. Safety Indicator: is_safe (1 for safe, 0 for not safe), indicating whether the water quality is considered safe for consumption based on the measured parameters.

References :

- https://www.kaggle.com/code/sabrinajeannin/wine-pca-hierarchical-clustering
- https://www.kaggle.com/code/elisthefox/ultimate-guide-to-k-nearest-neighbors-k-nn#4.-Results-of-K-NN-implementation-after-preparation-of-data

Tools and Libraries :

- Pandas: For data manipulation and analysis.
- Matplotlib: For creating visualizations such as plots.
- Seaborn: For enhancing the visual aesthetics of plots.
- Scikit-learn: For building and evaluating machine learning models.

Sections:

- Importing Libraries
- Loading and Viewing the Dataset
- EDA
- Visualization
- Model Building
- Model Improvement
- Hyperparameter Tuning

Importing Libraries

```
# Importing required libraries
import pandas as pd
import numpy as np
from matplotlib import pyplot as plt
import seaborn as sns
```

```
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix
from sklearn.metrics import classification_report
from sklearn.model_selection import GridSearchCV
```

Loading and Viewing the dataset

```
# Loading dataset
df = pd.read_csv("waterQuality1.csv")

# Print first 5 rows of the dataframe
df.head()
```

```
   aluminium  ammonia  arsenic  barium  cadmium  chloramine  chromium 
copper  \
0       1.65     9.08     0.04    2.85    0.007        0.35      0.83 
0.17
1       2.32    21.16     0.01    3.31    0.002        5.28      0.68 
0.66
2       1.01    14.02     0.04    0.58    0.008        4.24      0.53 
0.02
3       1.36    11.33     0.04    2.96    0.001        7.23      0.03 
1.66
4       0.92    24.33     0.03    0.20    0.006        2.67      0.69 
0.57

   flouride  bacteria  ...   lead  nitrates  nitrites  mercury 
perchlorate  \
0      0.05      0.20  ...  0.054     16.08      1.13    0.007 
37.75
1      0.90      0.65  ...  0.100      2.01      1.93    0.003 
32.26
2      0.99      0.05  ...  0.078     14.16      1.11    0.006 
50.28
3      1.08      0.71  ...  0.016      1.41      1.29    0.004 
9.12
4      0.61      0.13  ...  0.117      6.74      1.11    0.003 
16.90

   radium  selenium  silver  uranium  is_safe
0    6.78      0.08    0.34     0.02        1
1    3.21      0.08    0.27     0.05        1
2    7.07      0.07    0.44     0.01        0
3    1.72      0.02    0.45     0.05        1
4    2.41      0.02    0.06     0.02        1

[5 rows x 21 columns]
```

```python
# Print last 5 rows of the dataframe
df.tail()
```

```
      aluminium  ammonia  arsenic  barium  cadmium  chloramine  
chromium  \
7991       0.05     7.78     0.00    1.95     0.04        0.10   
0.03   
7992       0.05    24.22     0.02    0.59     0.01        0.45   
0.02   
7993       0.09     6.85     0.00    0.61     0.03        0.05   
0.05   
7994       0.01    10.00     0.01    2.00     0.00        2.00   
0.00   
7995       0.04     6.85     0.01    0.70     0.03        0.05   
0.01   

      copper  flouride  bacteria  ...   lead  nitrates  nitrites  
mercury  \
7991    0.03      1.37       0.0  ...  0.197     14.29       1.0   
0.005   
7992    0.02      1.48       0.0  ...  0.031     10.27       1.0   
0.001   
7993    0.02      0.91       0.0  ...  0.182     15.92       1.0   
0.000   
7994    0.09      0.00       0.0  ...  0.000      0.00       0.0   
0.000   
7995    0.03      1.00       0.0  ...  0.182     15.92       1.0   
0.000   

      perchlorate  radium  selenium  silver  uranium  is_safe  
7991         3.57    2.13      0.09    0.06     0.03        1  
7992         1.48    1.11      0.09    0.10     0.08        1  
7993         1.35    4.84      0.00    0.04     0.05        1  
7994         0.00    0.00      0.00    0.00     0.00        1  
7995         1.35    4.84      0.00    0.04     0.05        1  

[5 rows x 21 columns]
```

```python
# Getting the shape of the dataframe
df.shape
```

```
(7996, 21)
```

EDA

```python
# Columns of the dataframe
df.columns
```

```
Index(['aluminium', 'ammonia', 'arsenic', 'barium', 'cadmium', 
'chloramine',
       'chromium', 'copper', 'flouride', 'bacteria', 'viruses',
```

```
'lead',
       'nitrates', 'nitrites', 'mercury', 'perchlorate', 'radium',
'selenium',
       'silver', 'uranium', 'is_safe'],
      dtype='object')

# Getting column information of the dataframe
df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 7996 entries, 0 to 7995
Data columns (total 21 columns):
 #   Column       Non-Null Count  Dtype  
---  ------       --------------  -----  
 0   aluminium    7996 non-null   float64
 1   ammonia      7996 non-null   float64
 2   arsenic      7996 non-null   float64
 3   barium       7996 non-null   float64
 4   cadmium      7996 non-null   float64
 5   chloramine   7996 non-null   float64
 6   chromium     7996 non-null   float64
 7   copper       7996 non-null   float64
 8   flouride     7996 non-null   float64
 9   bacteria     7996 non-null   float64
 10  viruses      7996 non-null   float64
 11  lead         7996 non-null   float64
 12  nitrates     7996 non-null   float64
 13  nitrites     7996 non-null   float64
 14  mercury      7996 non-null   float64
 15  perchlorate  7996 non-null   float64
 16  radium       7996 non-null   float64
 17  selenium     7996 non-null   float64
 18  silver       7996 non-null   float64
 19  uranium      7996 non-null   float64
 20  is_safe      7996 non-null   int64  
dtypes: float64(20), int64(1)
memory usage: 1.3 MB

# Unique values of each columns
df.nunique()

aluminium       495
ammonia        2563
arsenic         107
barium          480
cadmium          23
chloramine      812
chromium         91
copper          201
flouride        151
```

```
bacteria         101
viruses           61
lead             200
nitrates        1803
nitrites         280
mercury           11
perchlorate     2999
radium           735
selenium          11
silver            51
uranium           10
is_safe            2
dtype: int64
```

```
# Checking for null values
df.isnull().sum()
```

```
aluminium      0
ammonia        0
arsenic        0
barium         0
cadmium        0
chloramine     0
chromium       0
copper         0
flouride       0
bacteria       0
viruses        0
lead           0
nitrates       0
nitrites       0
mercury        0
perchlorate    0
radium         0
selenium       0
silver         0
uranium        0
is_safe        0
dtype: int64
```

```
# Statistical summary of the dataframe
df.describe(include='all')
```

```
         aluminium      ammonia      arsenic       barium      cadmium
\
count  7996.000000  7996.000000  7996.000000  7996.000000  7996.000000

mean      0.666396    14.278212     0.161477     1.567928     0.042803

std       1.265323     8.878930     0.252632     1.216227     0.036049
```

```
min       0.000000    -0.080000     0.000000     0.000000     0.000000
25%       0.040000     6.577500     0.030000     0.560000     0.008000
50%       0.070000    14.130000     0.050000     1.190000     0.040000
75%       0.280000    22.132500     0.100000     2.482500     0.070000
max       5.050000    29.840000     1.050000     4.940000     0.130000

        chloramine     chromium       copper     flouride     bacteria
...  \
count  7996.000000  7996.000000  7996.000000  7996.000000  7996.000000
...
mean      2.177589     0.247300     0.805940     0.771646     0.319714
...
std       2.567210     0.270663     0.653595     0.435423     0.329497
...
min       0.000000     0.000000     0.000000     0.000000     0.000000
...
25%       0.100000     0.050000     0.090000     0.407500     0.000000
...
50%       0.530000     0.090000     0.750000     0.770000     0.220000
...
75%       4.240000     0.440000     1.390000     1.160000     0.610000
...
max       8.680000     0.900000     2.000000     1.500000     1.000000
...

              lead     nitrates     nitrites      mercury  perchlorate
\
count  7996.000000  7996.000000  7996.000000  7996.000000  7996.000000
mean      0.099431     9.819250     1.329846     0.005193    16.465266
std       0.058169     5.541977     0.573271     0.002967    17.688827
min       0.000000     0.000000     0.000000     0.000000     0.000000
25%       0.048000     5.000000     1.000000     0.003000     2.170000
50%       0.102000     9.930000     1.420000     0.005000     7.745000
75%       0.151000    14.610000     1.760000     0.008000    29.487500
max       0.200000    19.830000     2.930000     0.010000    60.010000

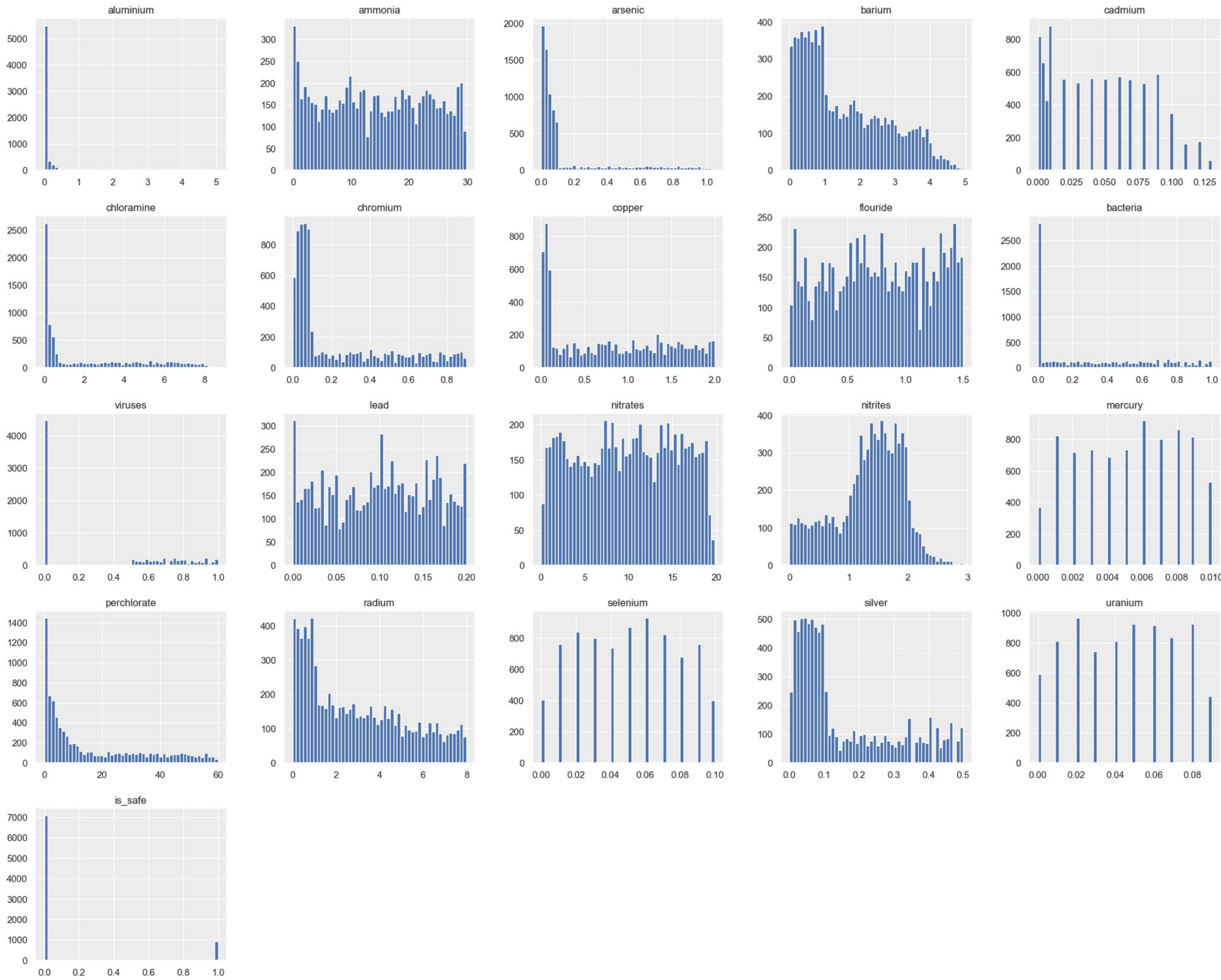
            radium     selenium       silver      uranium      is_safe
```

```
count  7996.000000  7996.000000  7996.000000  7996.000000  7996.000000
mean      2.920106     0.049684     0.147811     0.044672     0.114057
std       2.322805     0.028773     0.143569     0.026906     0.317900
min       0.000000     0.000000     0.000000     0.000000     0.000000
25%       0.820000     0.020000     0.040000     0.020000     0.000000
50%       2.410000     0.050000     0.080000     0.050000     0.000000
75%       4.670000     0.070000     0.240000     0.070000     0.000000
max       7.990000     0.100000     0.500000     0.090000     1.000000

[8 rows x 21 columns]
```

Visualization

```
# Viewing the histograms for each numerical feature
df.hist(bins=50, figsize=(25,20));
```

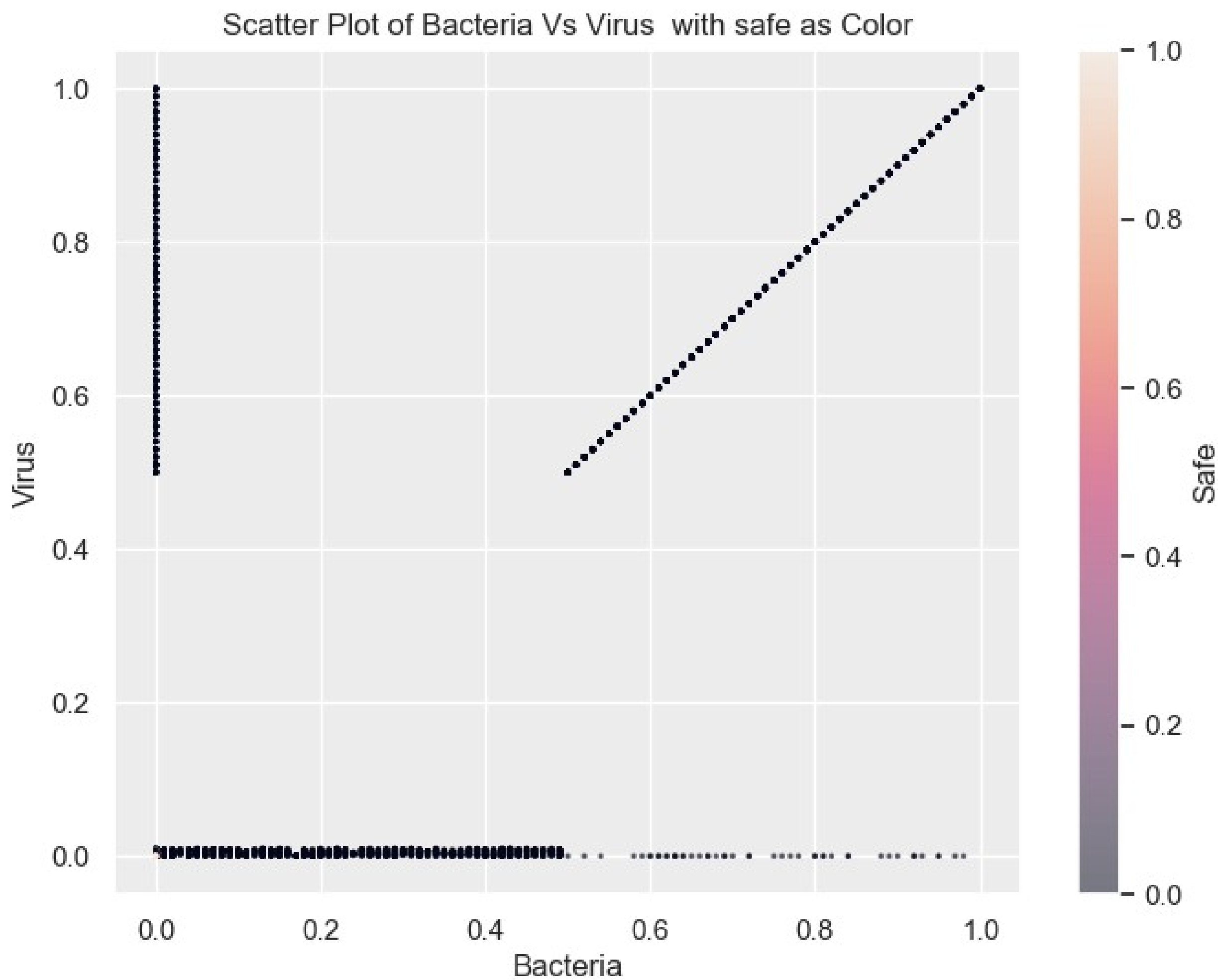



```
# Plotting Geographical data using Scatter Plot
plt.figure(figsize=(8, 6))
plt.scatter(df['bacteria'], df['viruses'], c=df['is_safe'],alpha=0.5,s
=2)

# Define color using median house value
plt.colorbar(label='Safe')

# Add labels and title
plt.xlabel('Bacteria')
plt.ylabel('Virus')
plt.title('Scatter Plot of Bacteria Vs Virus  with safe as Color')

# View the plot
plt.show()
```




```
# Identify the target variable
target = 'is_safe'

# Separate the independent variables
independent_vars = df.columns.difference([target])

palette = sns.color_palette("husl", len(independent_vars))

# Create box plots for all independent variables with different colors
for i, var in enumerate(independent_vars):
    plt.figure(figsize=(10, 6))
    sns.boxplot(x=target, y=var, data=df, palette=[palette[i]])
    plt.title(f'Box Plot of {var} vs {target}')
    plt.xlabel(target)
    plt.ylabel(var)
plt.show();

C:\Users\IDZ\AppData\Local\Temp\ipykernel_14484\4172465249.py:12:
FutureWarning:
```

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`legend=False` for the same effect.

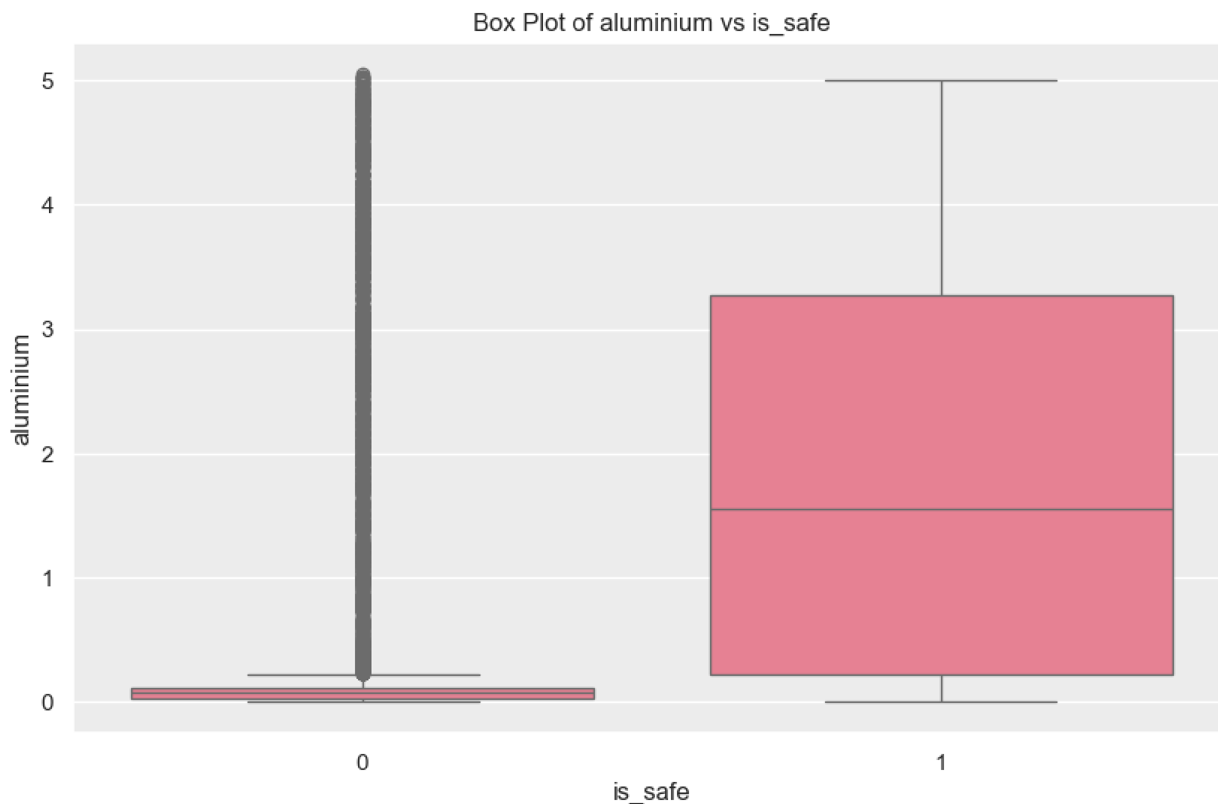
  sns.boxplot(x=target, y=var, data=df, palette=[palette[i]])
C:\Users\IDZ\AppData\Local\Temp\ipykernel_14484\4172465249.py:12:
UserWarning:
The palette list has fewer values (1) than needed (2) and will cycle,
which may produce an uninterpretable plot.
  sns.boxplot(x=target, y=var, data=df, palette=[palette[i]])
C:\Users\IDZ\AppData\Local\Temp\ipykernel_14484\4172465249.py:12:
FutureWarning:

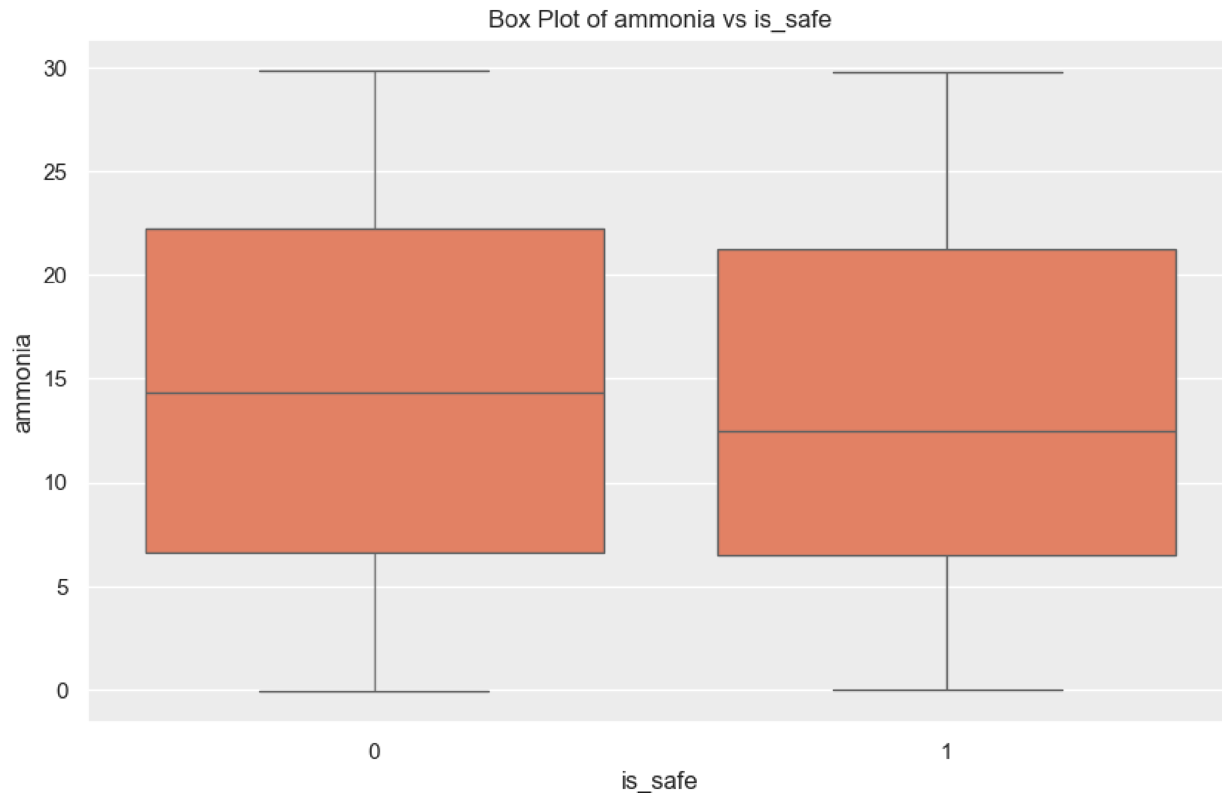
Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `x` variable to `hue` and set
`legend=False` for the same effect.

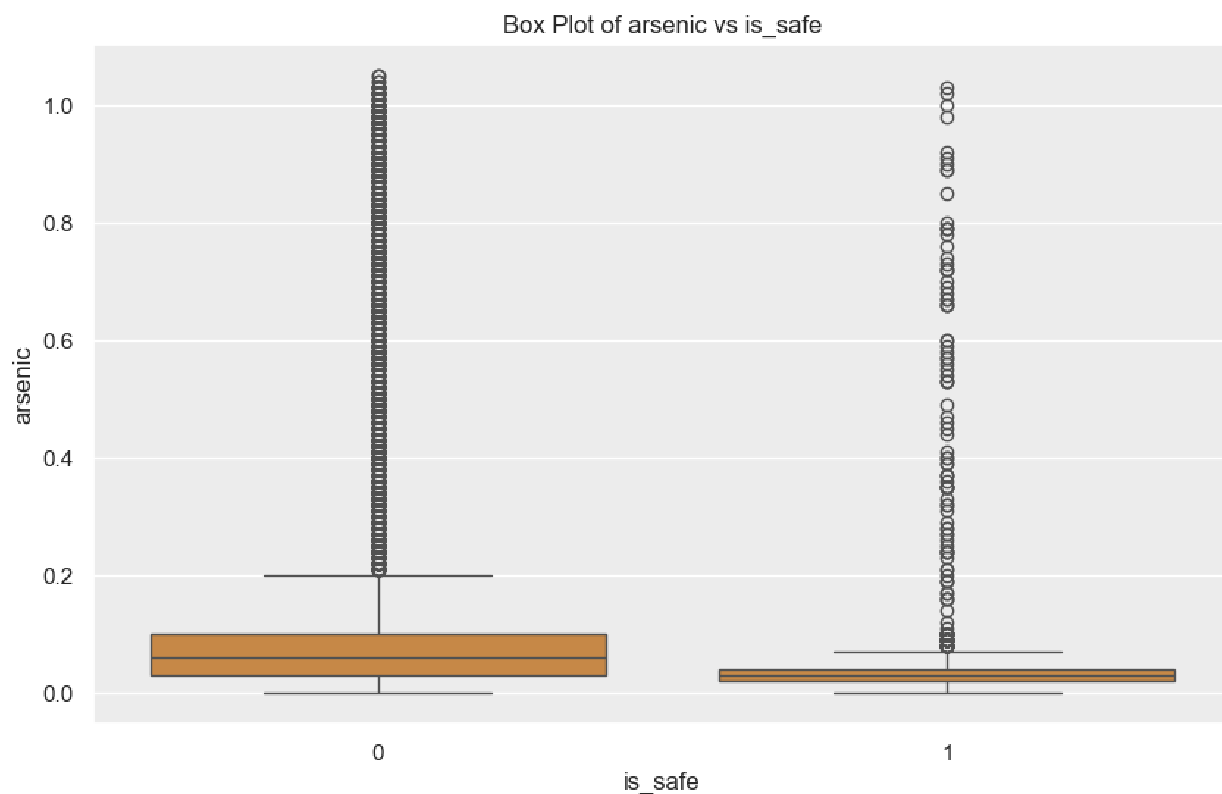
  sns.boxplot(x=target, y=var, data=df, palette=[palette[i]])
C:\Users\IDZ\AppData\Local\Temp\ipykernel_14484\4172465249.py:12:
UserWarning:
The palette list has fewer values (1) than needed (2) and will cycle,
which may produce an uninterpretable plot.
  sns.boxplot(x=target, y=var, data=df, palette=[palette[i]])
C:\Users\IDZ\AppData\Local\Temp\ipykernel_14484\4172465249.py:12:
FutureWarning:

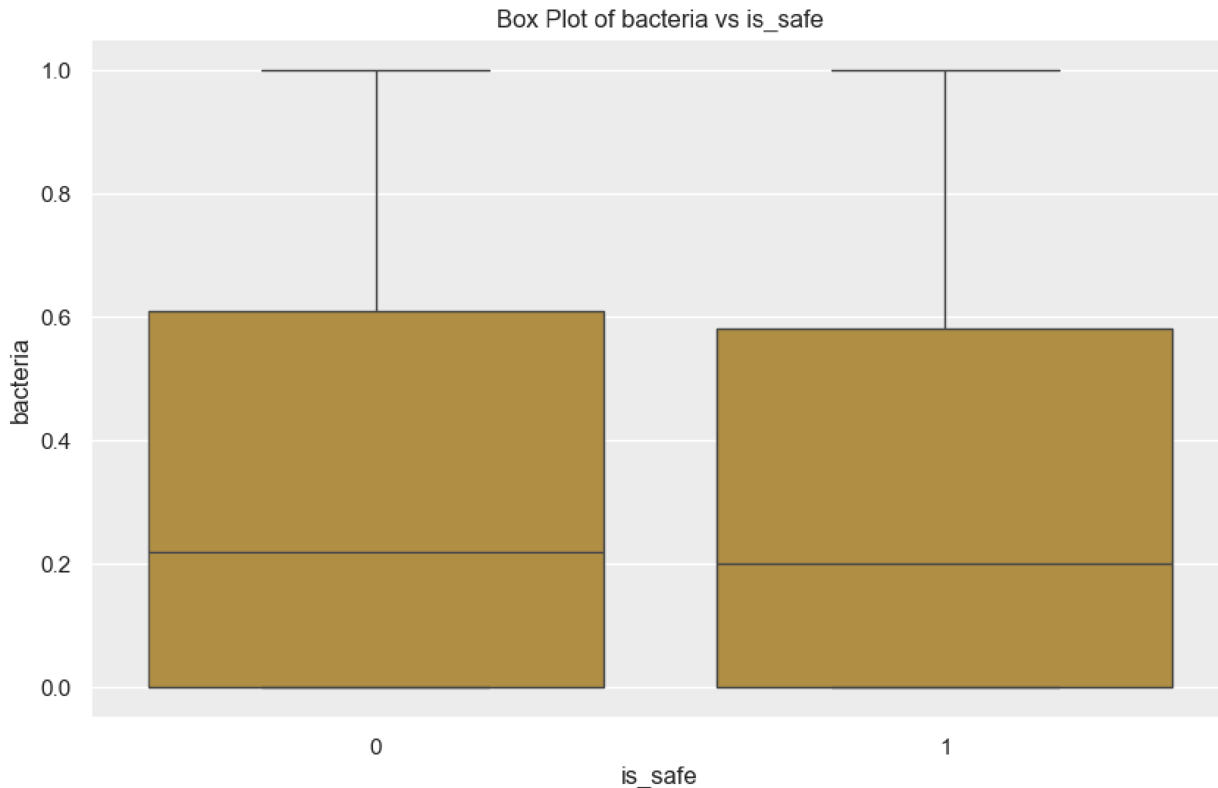
Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `x` variable to `hue` and set
`legend=False` for the same effect.
```

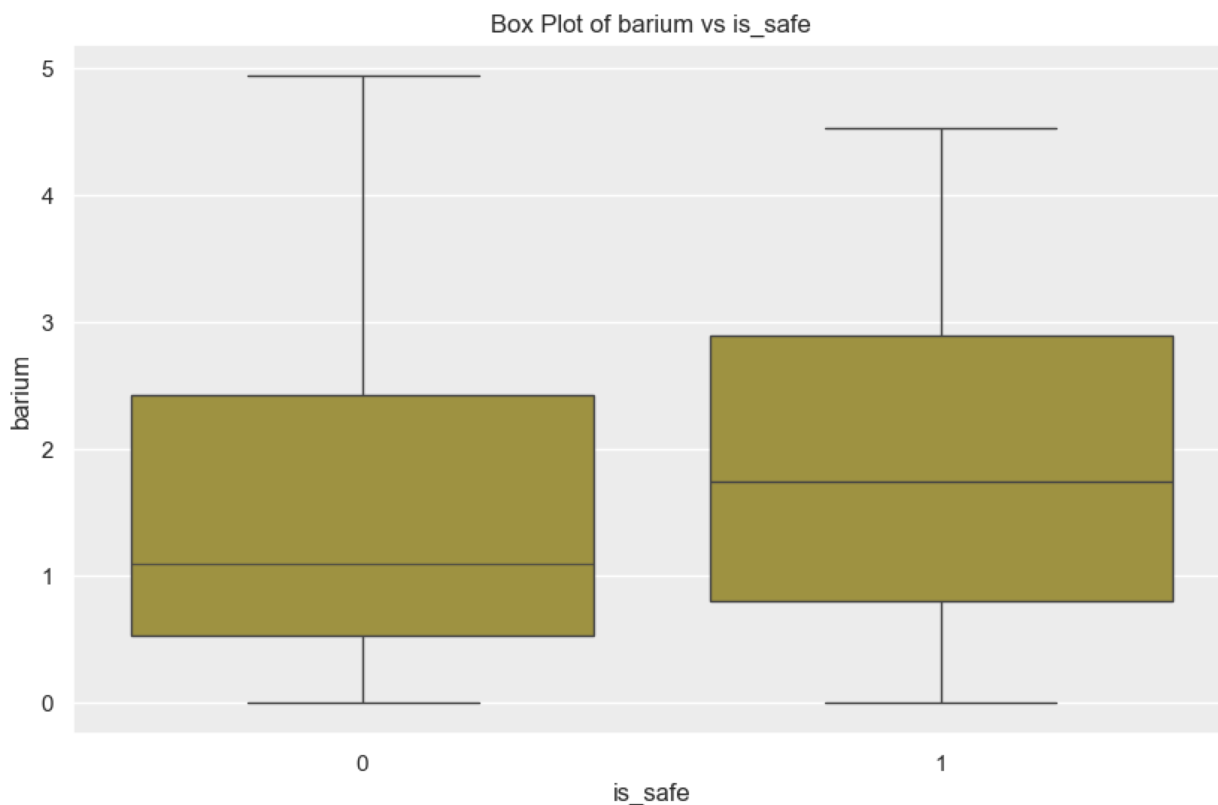
```
  sns.boxplot(x=target, y=var, data=df, palette=[palette[i]])
C:\Users\IDZ\AppData\Local\Temp\ipykernel_14484\4172465249.py:12: 
UserWarning: 
The palette list has fewer values (1) than needed (2) and will cycle, 
which may produce an uninterpretable plot.
  sns.boxplot(x=target, y=var, data=df, palette=[palette[i]])
```

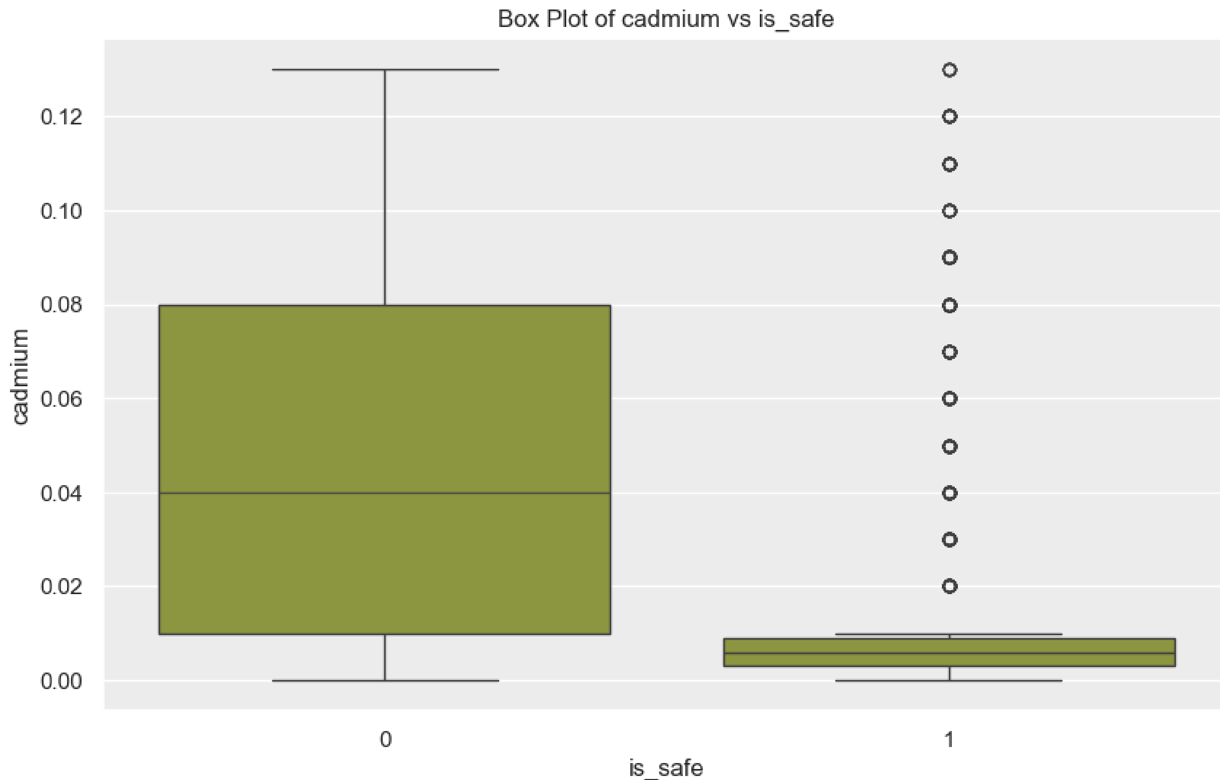


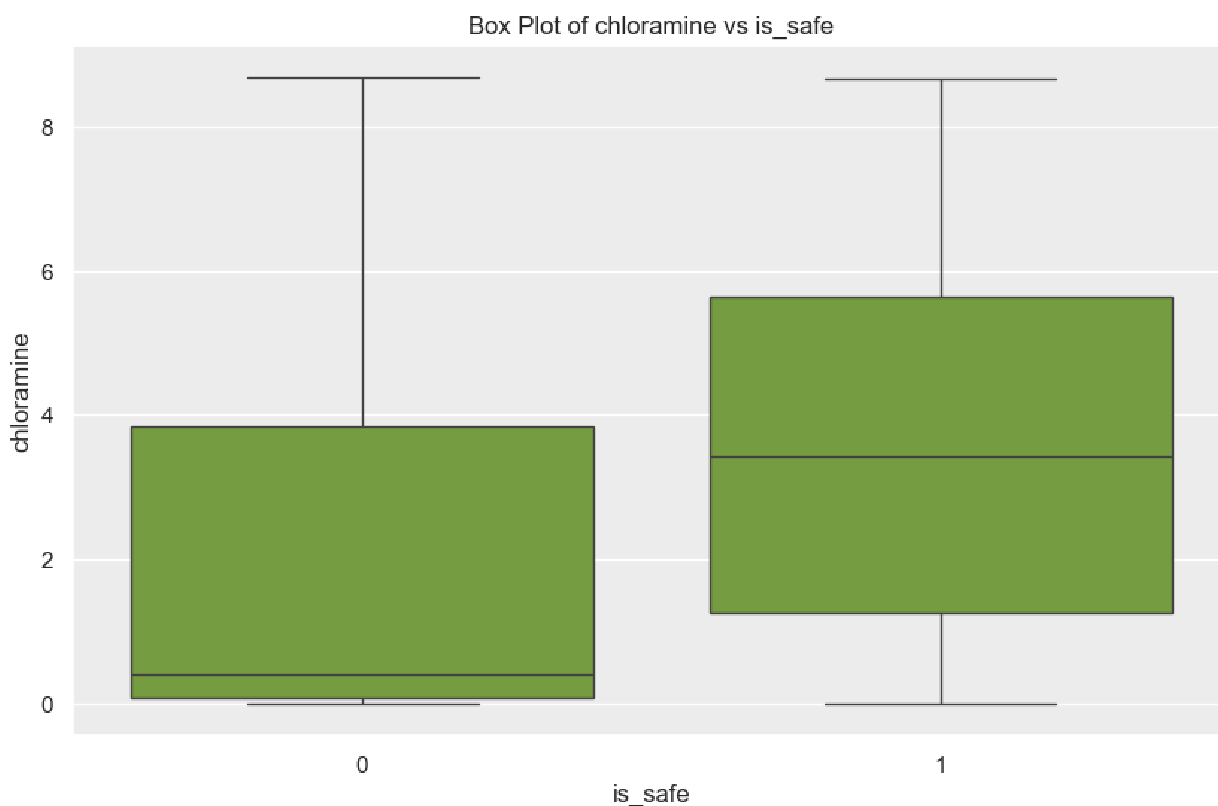

Box Plot of ammonia vs is_safe
30
25
20
15
10
5
0
ammonia
0
1
is_safe

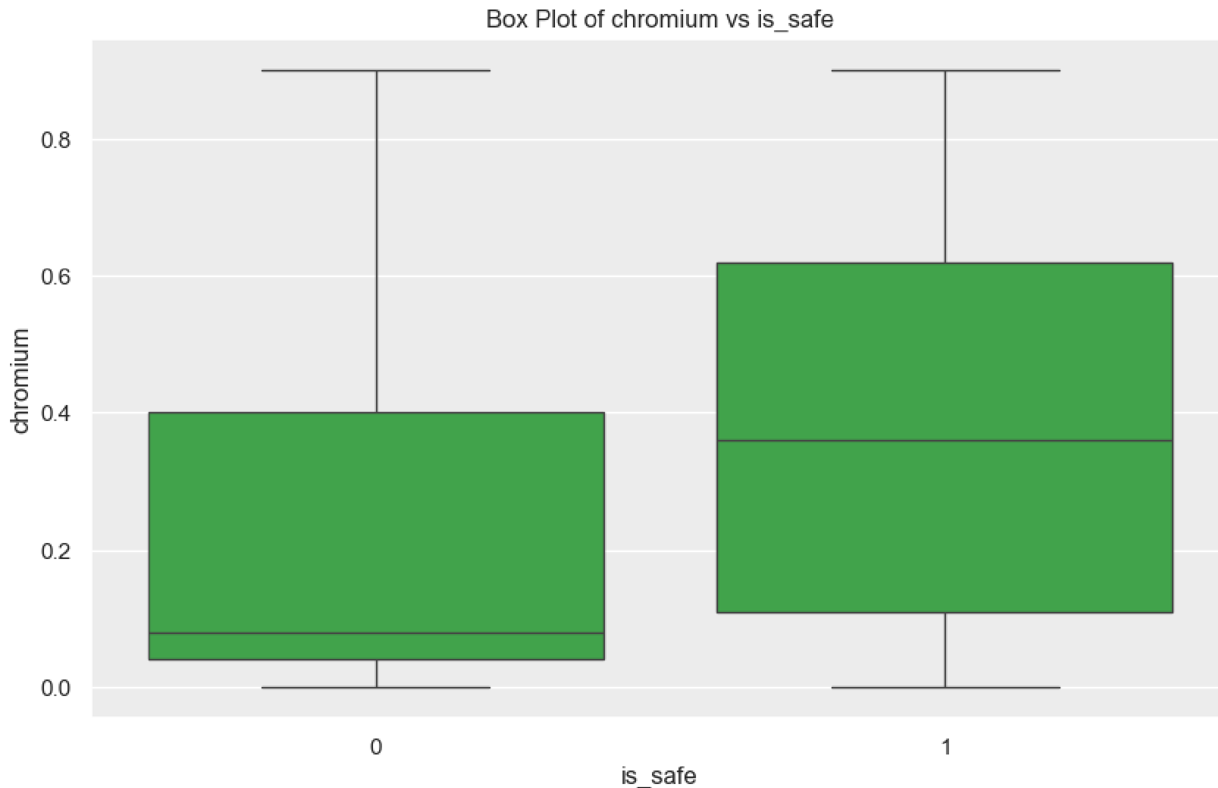

Box Plot of arsenic vs is_safe
1.0
0.8
0.6
0.4
0.2
0.0
arsenic
0
1
is_safe

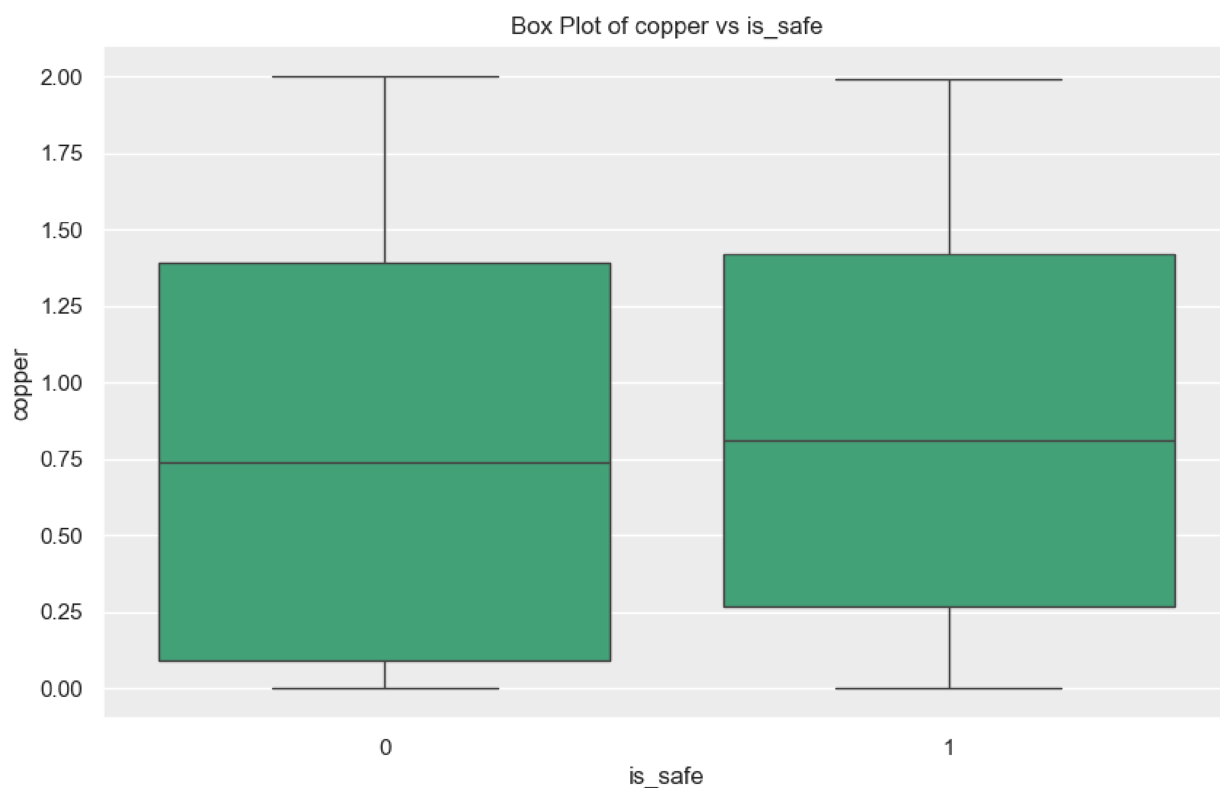

Box Plot of bacteria vs is_safe
1.0
0.8
0.6
0.4
0.2
0.0
bacteria
0
1
is_safe

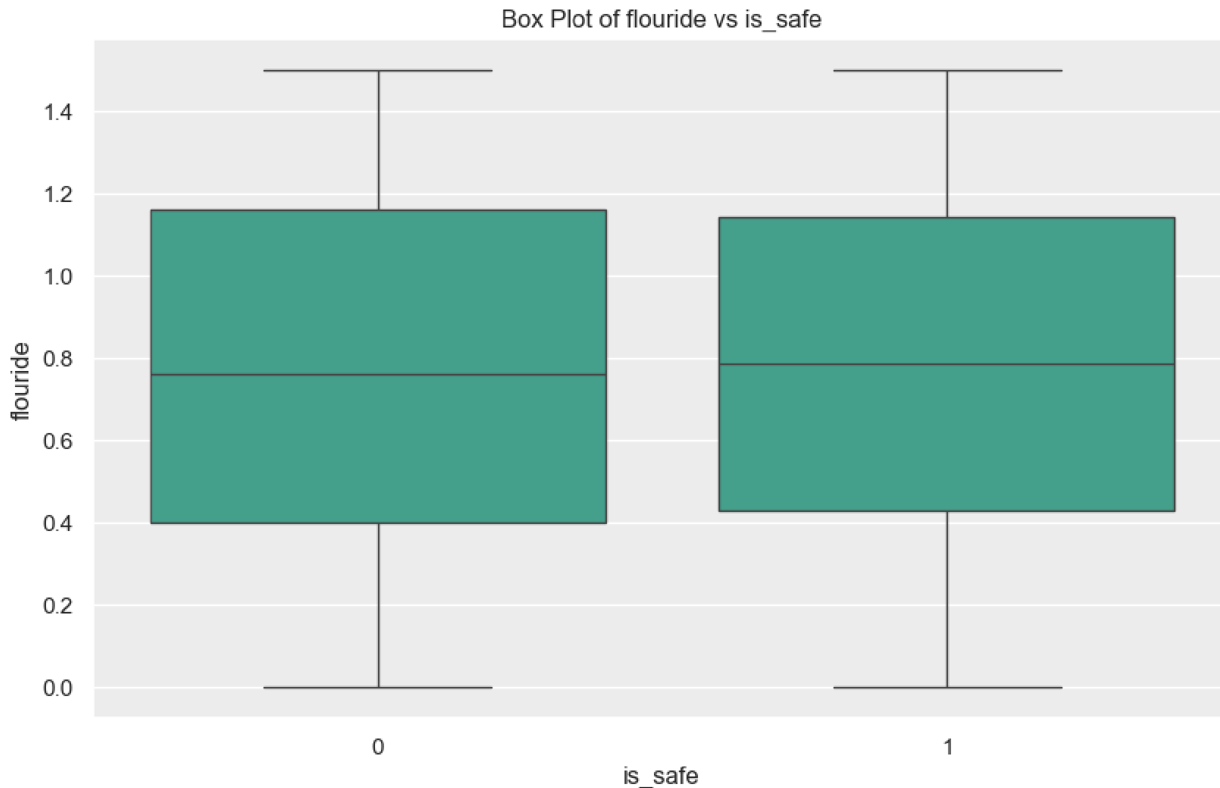

Box Plot of barium vs is_safe
5
4
3
2
1
0
barium
0
1
is_safe


Box Plot of cadmium vs is_safe
0.12
0.10
0.08
0.06
0.04
0.02
0.00
cadmium
0
1
is_safe

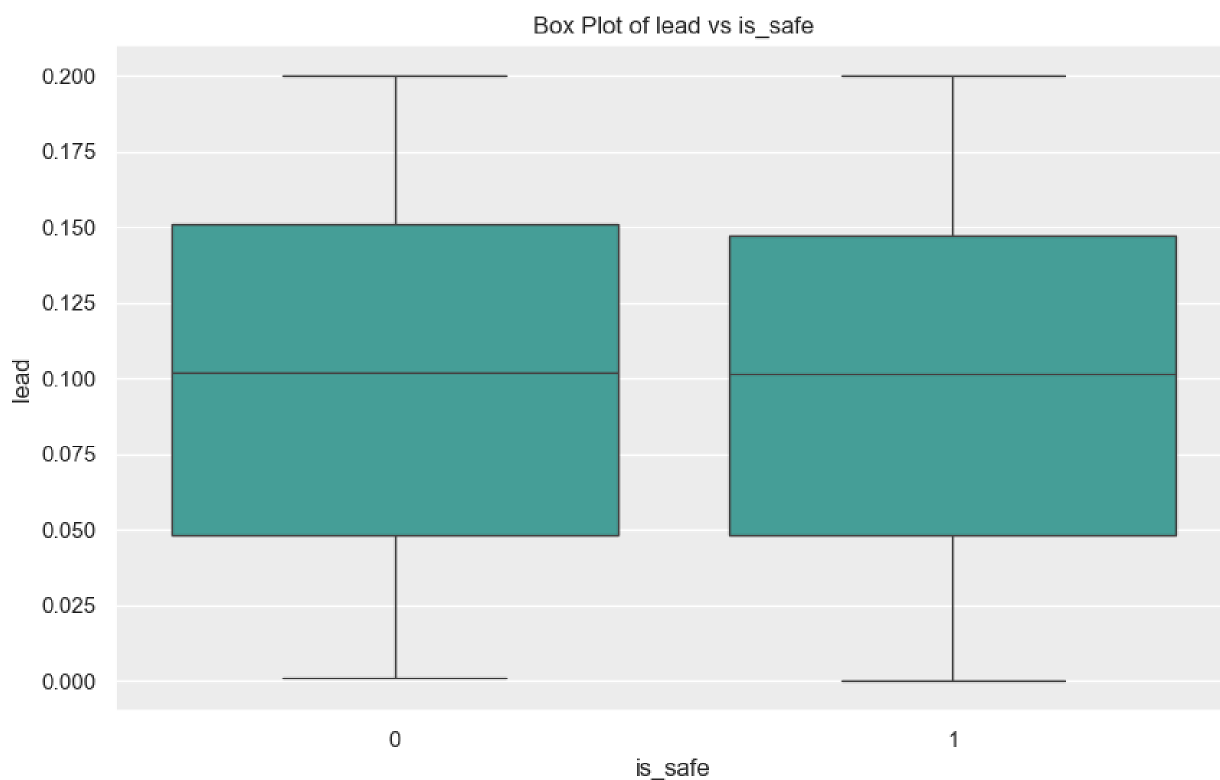

Box Plot of chloramine vs is_safe
8
6
4
2
0
chloramine
0
1
is_safe


Box Plot of chromium vs is_safe
chromium
0.0
0.2
0.4
0.6
0.8
0
1
is_safe

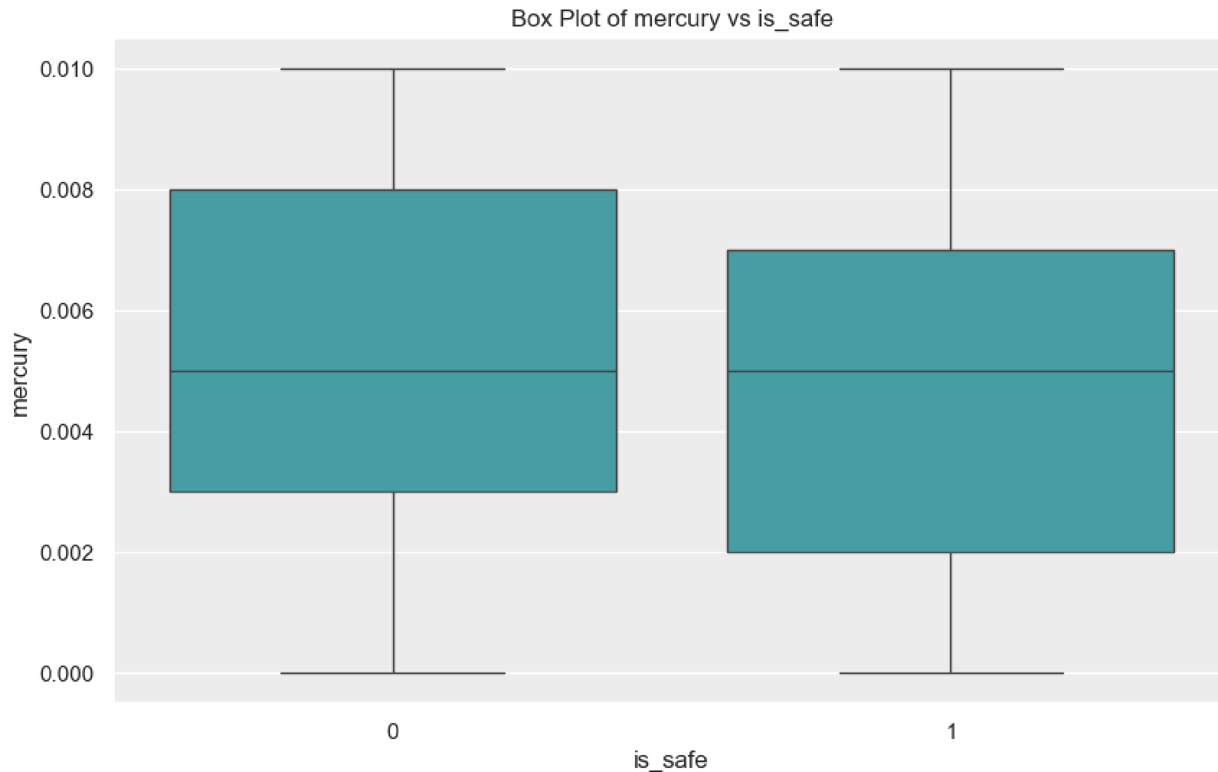

Box Plot of copper vs is_safe
copper
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00
0
1
is_safe

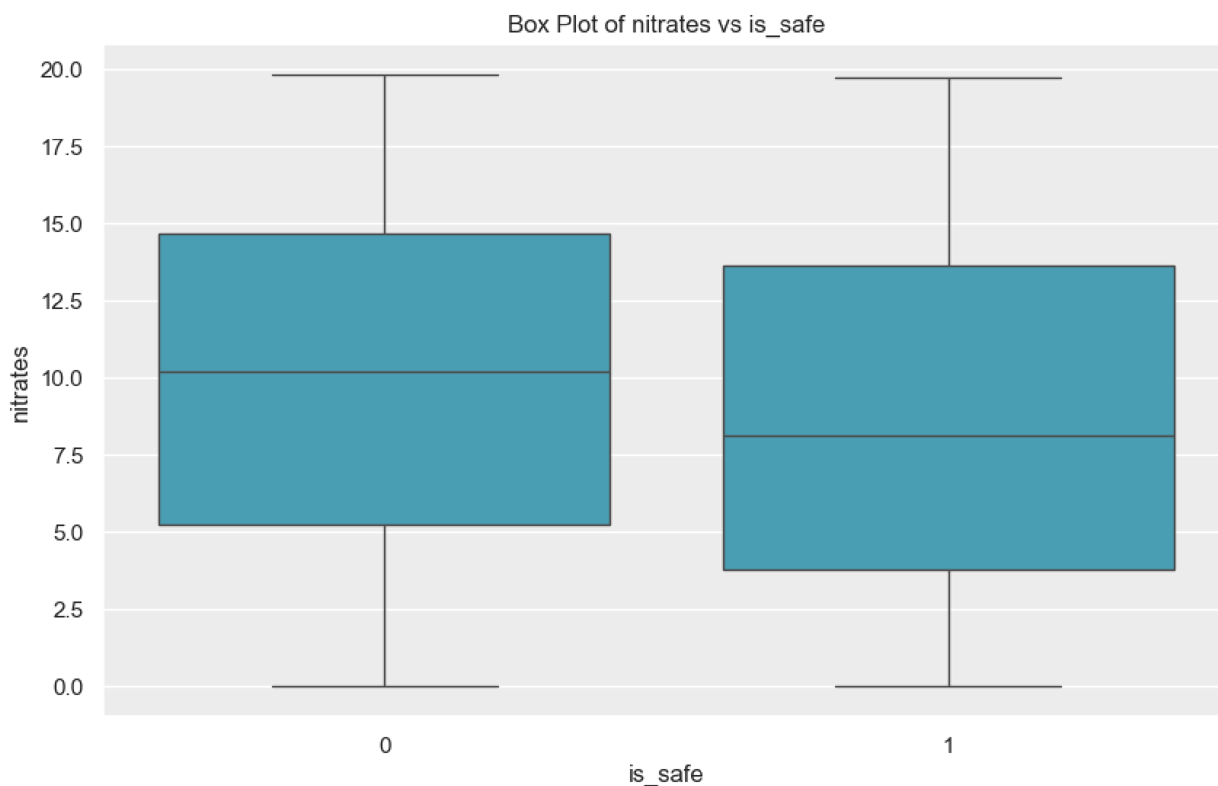


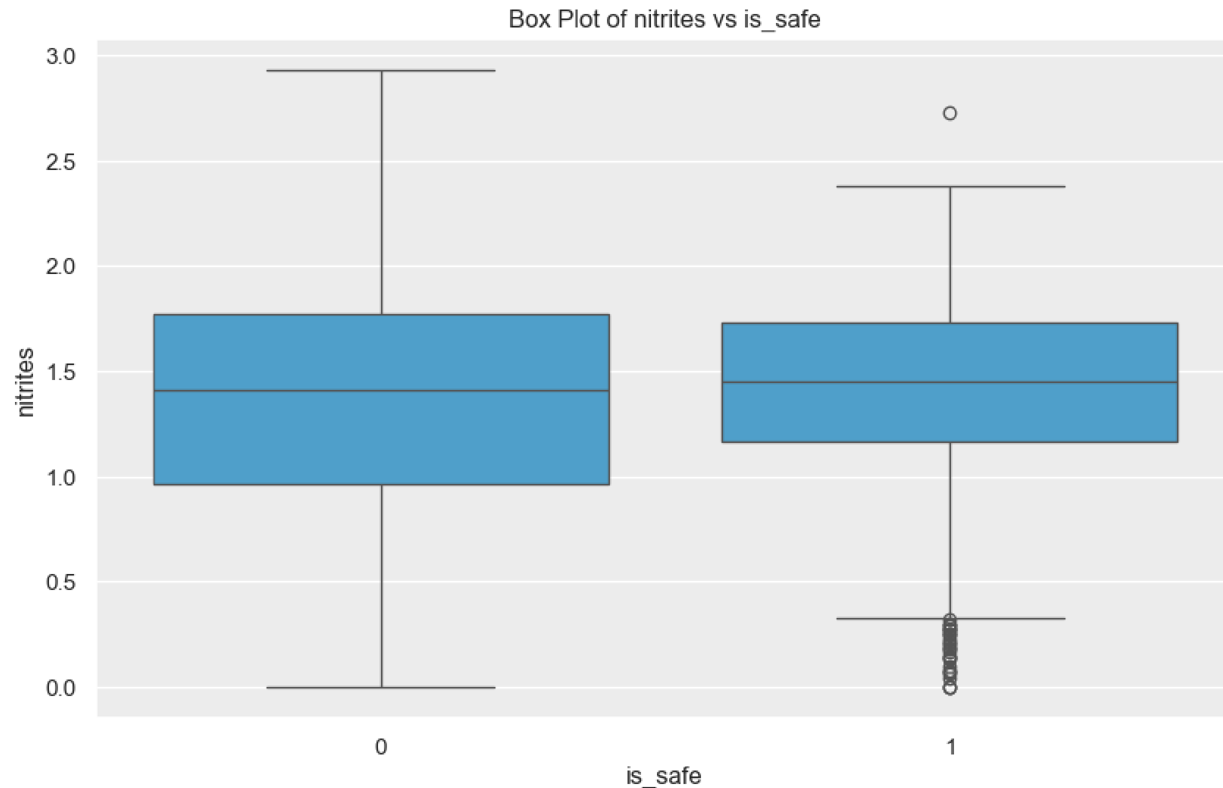
Box Plot of flouride vs is_safe
flouride
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
1
is_safe

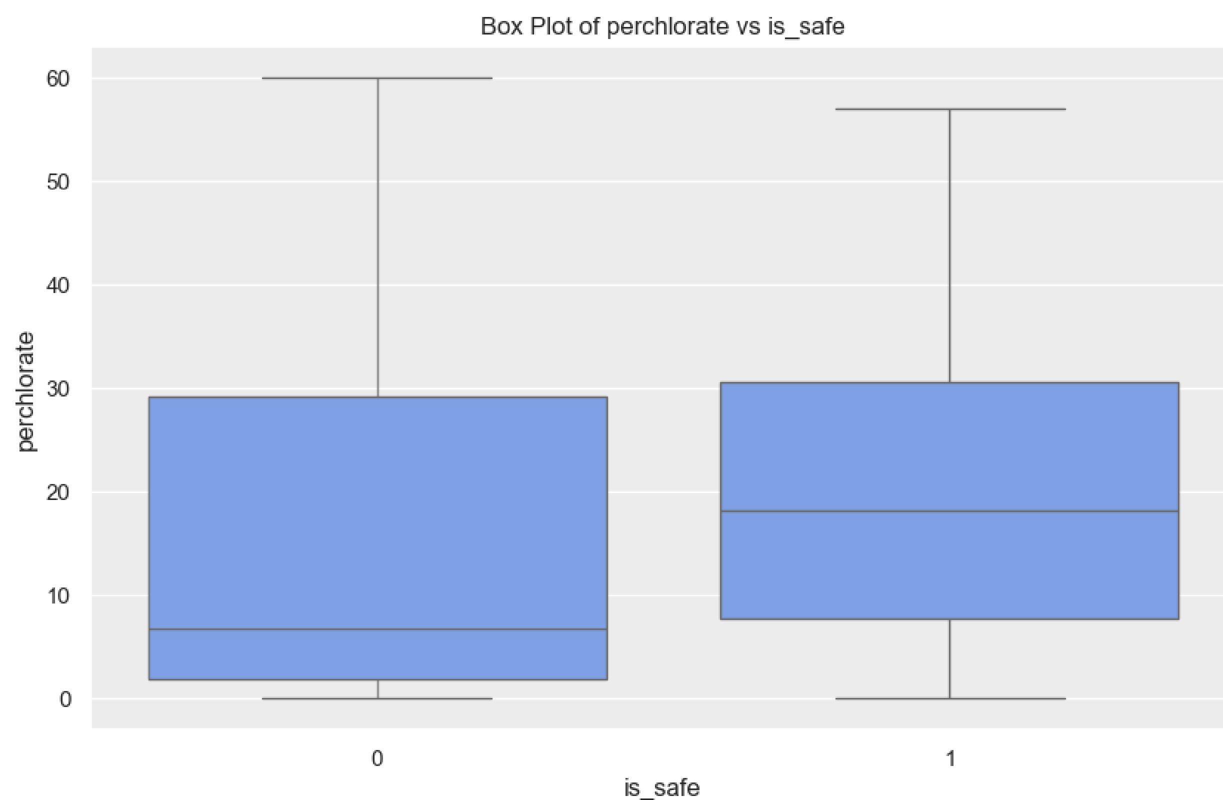


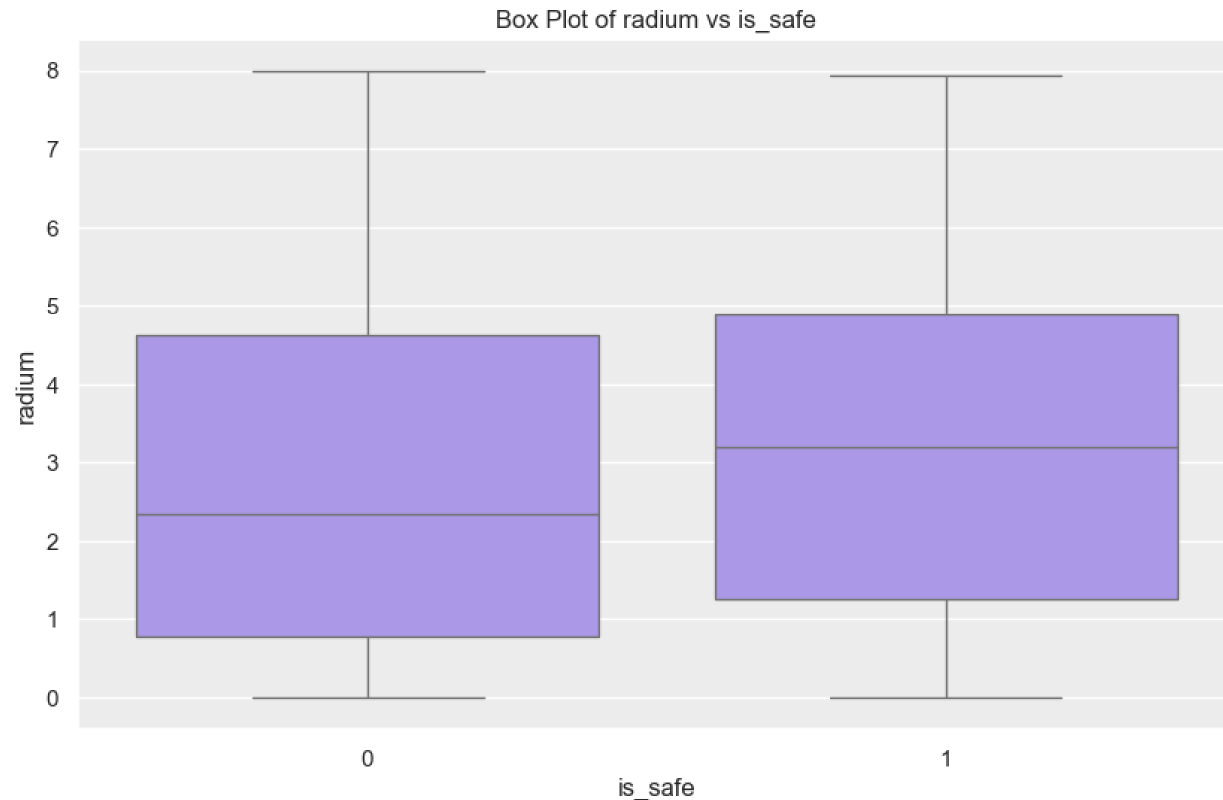
Box Plot of lead vs is_safe
lead
0.200
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
0
1
is_safe

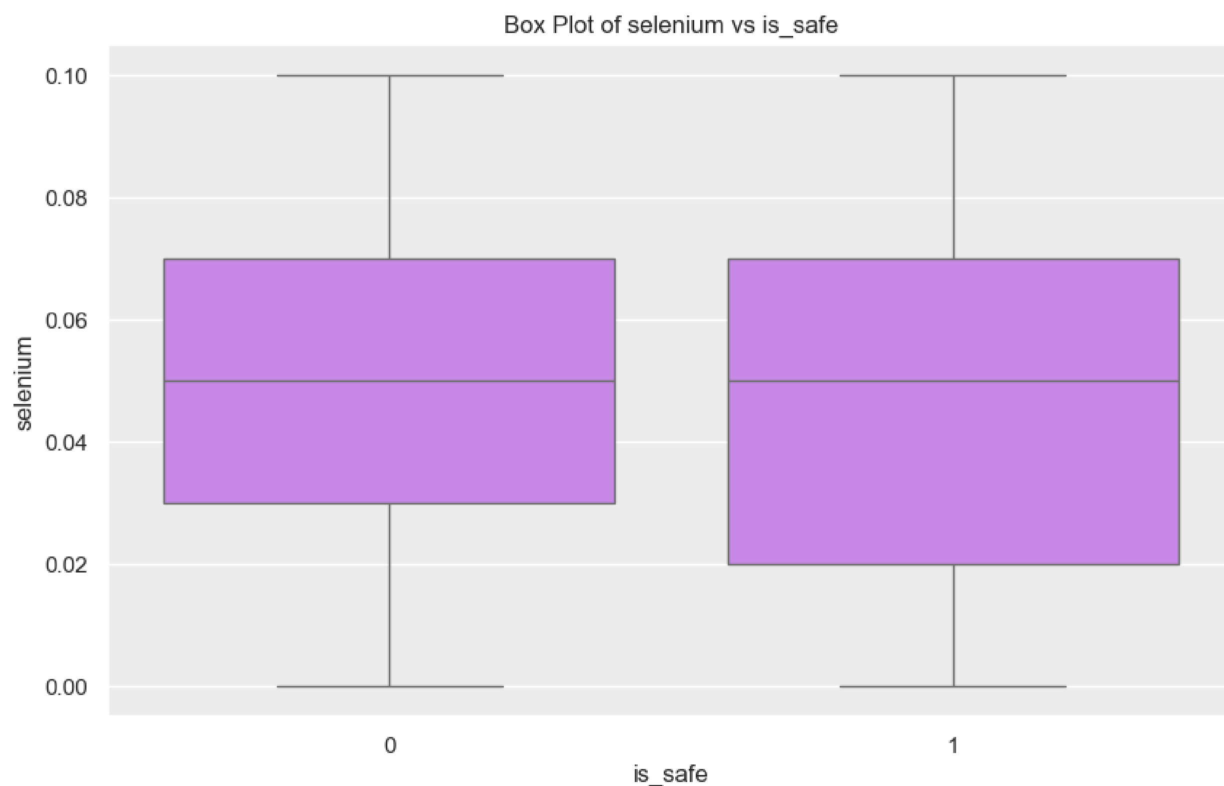

Box Plot of mercury vs is_safe
0.010
0.008
0.006
0.004
0.002
0.000
mercury
0
1
is_safe

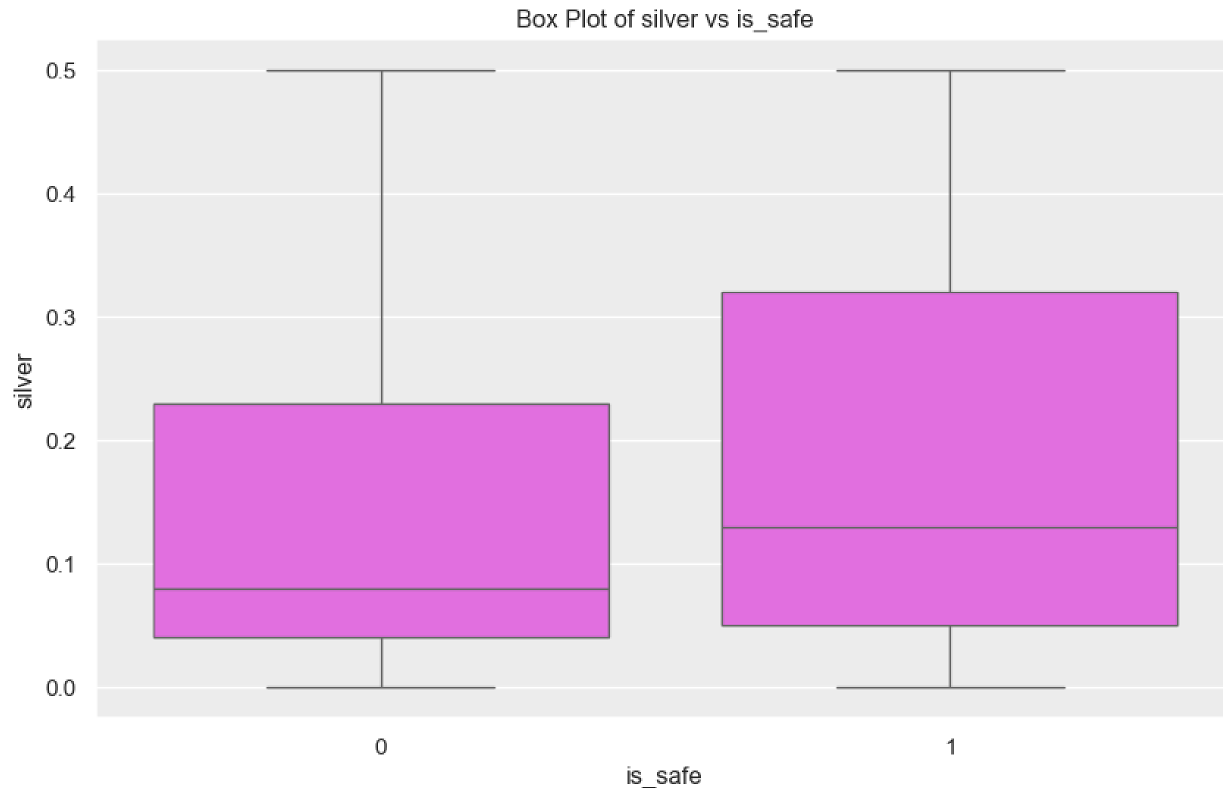

Box Plot of nitrates vs is_safe
20.0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
nitrates
0
1
is_safe

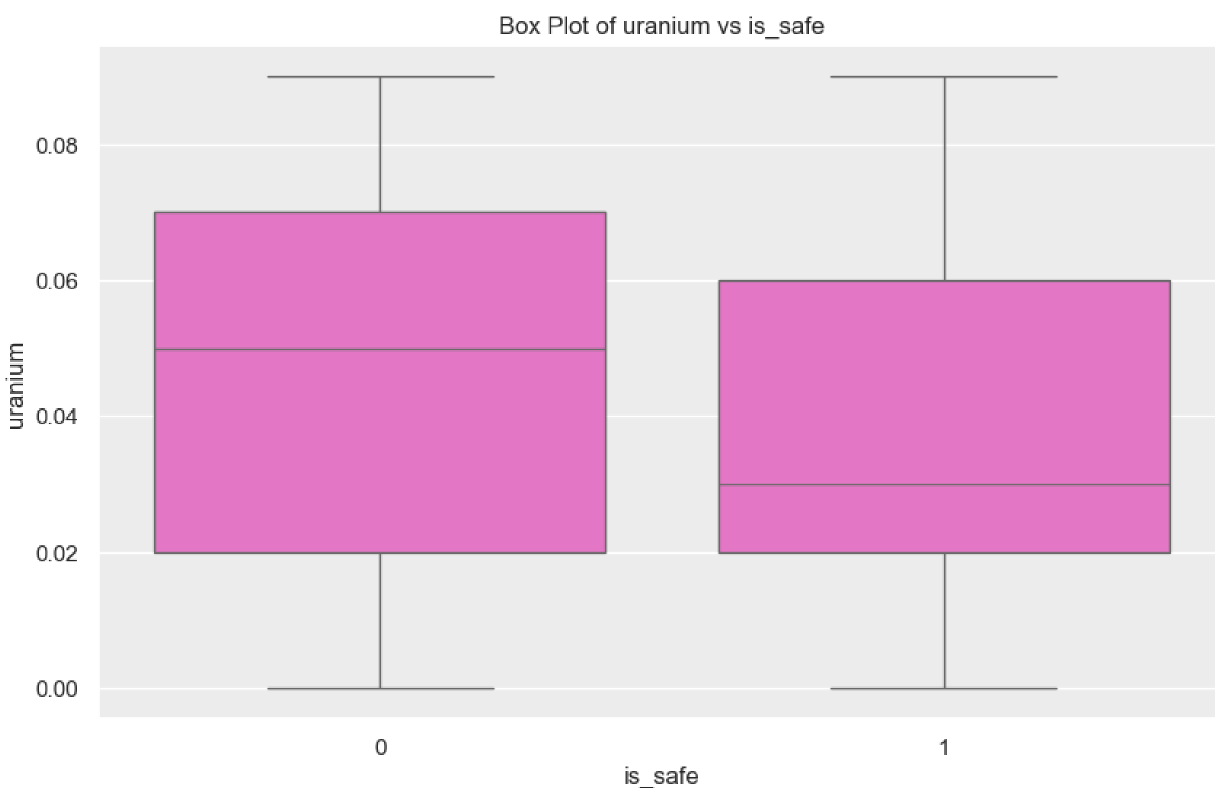

Box Plot of nitrites vs is_safe
nitrites
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
1
is_safe

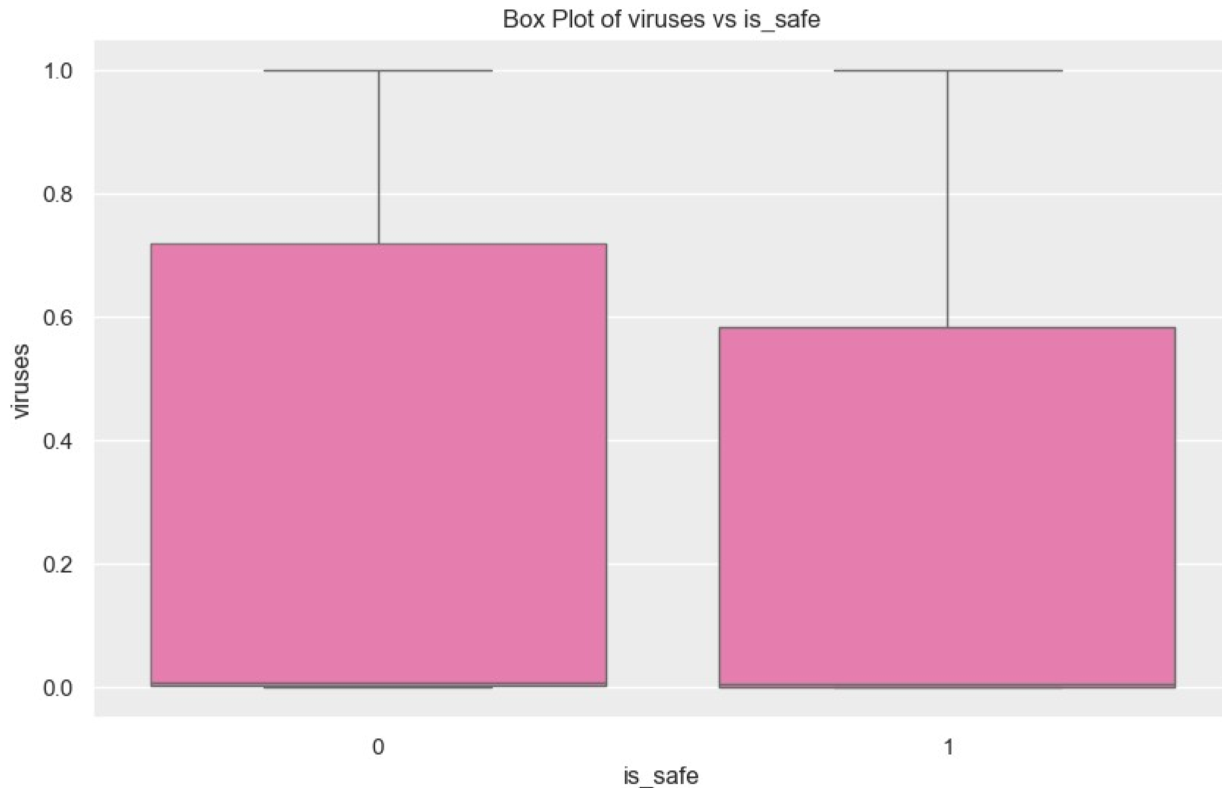

Box Plot of perchlorate vs is_safe
perchlorate
60
50
40
30
20
10
0
0
1
is_safe


Box Plot of radium vs is_safe
radium
8
7
6
5
4
3
2
1
0
0
1
is_safe

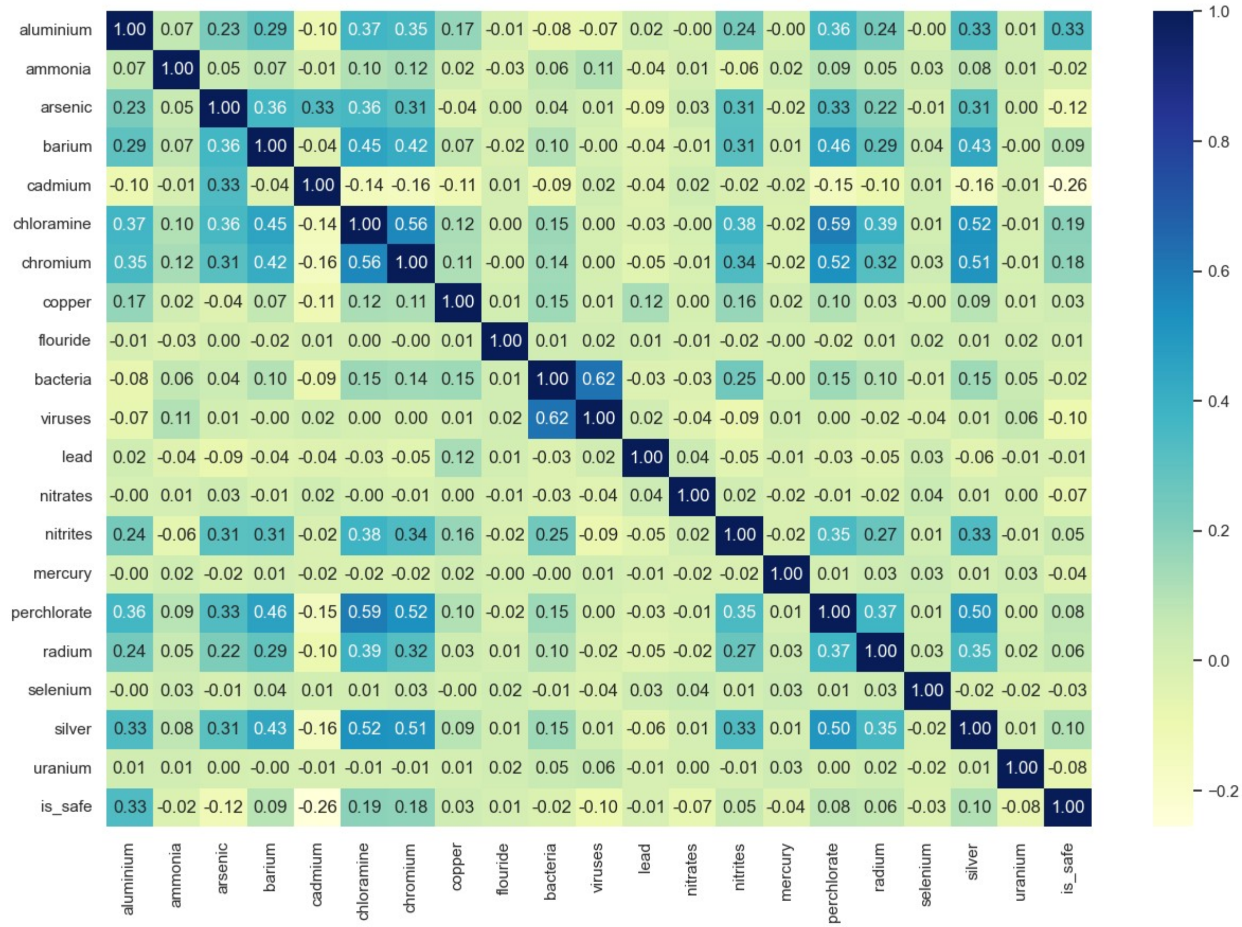

Box Plot of selenium vs is_safe
selenium
0.10
0.08
0.06
0.04
0.02
0.00
0
1
is_safe


Box Plot of silver vs is_safe
0.5
0.4
0.3
0.2
0.1
0.0
silver
0
1
is_safe


Box Plot of uranium vs is_safe
0.08
0.06
0.04
0.02
0.00
uranium
0
1
is_safe

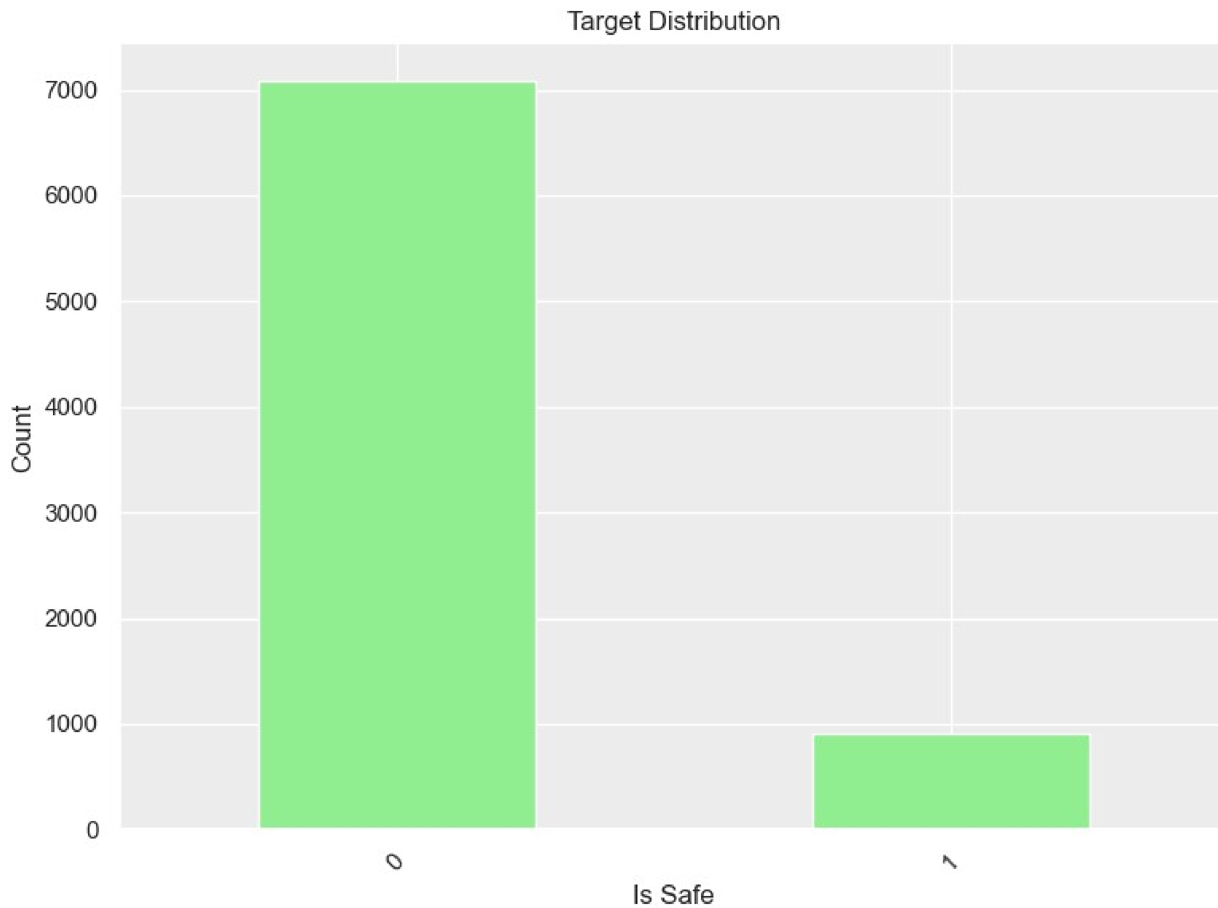



```
# Plotting heatmap
plt.figure(figsize = (15, 10))
df_corr = df.corr()
sns.heatmap(df_corr, fmt = ".2f", annot = True, cmap = "YlGnBu")
plt.show()
```




```
is_safe = df['is_safe'].value_counts()

# Plotting the bar plot
plt.figure(figsize=(8, 6))
is_safe.plot(kind='bar', color='lightgreen')
plt.title('Target Distribution')
plt.xlabel('Is Safe')
plt.ylabel('Count')
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```



Model Building

```
X = np.array(df)
features = X[:,0:19]
target = X[:,-1]

# Splitting data for Model Building
X_train, X_test, y_train, y_test = train_test_split(features, target,
test_size=0.2, random_state=42)

# Fitting the model

model = KNeighborsClassifier()
model.fit(X_train,y_train)

# Predicting for training set
train_pred = model.predict(X_train)

# Calculating training accuracy
train_accuracy = accuracy_score(y_train,train_pred)
print("Training accuracy is : " + str(train_accuracy))

# Getting confusion matrix and classification report
```

```
print("Confusion Matrix:")
print(confusion_matrix(y_train, train_pred))
print("Classification Report:")
print(classification_report(y_train, train_pred))
```

```
Training accuracy is : 0.9111944965603502
Confusion Matrix:
[[5620   64]
 [ 504  208]]
Classification Report:
              precision    recall  f1-score   support

         0.0       0.92      0.99      0.95      5684
         1.0       0.76      0.29      0.42       712

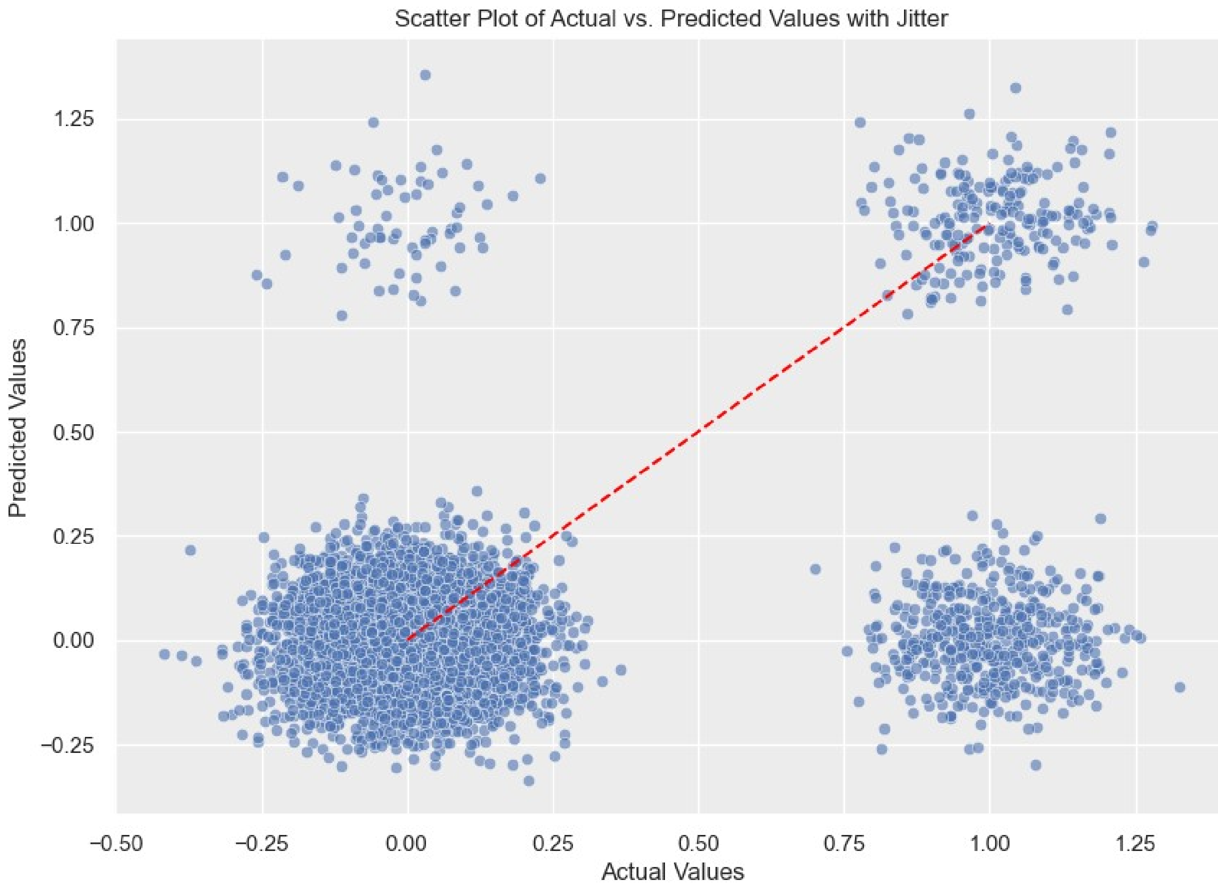
    accuracy                           0.91      6396
   macro avg       0.84      0.64      0.69      6396
weighted avg       0.90      0.91      0.89      6396
```

```
# Adding jitter to avoid overlap in scatter plot
def add_jitter(arr, jitter_strength=0.1):
    stdev = jitter_strength * (max(arr) - min(arr))
    return arr + np.random.randn(len(arr)) * stdev

# Plotting the scatter plot for actual vs predicted values
plt.figure(figsize=(10, 7))
sns.scatterplot(x=add_jitter(y_train), y=add_jitter(train_pred),
marker='o', alpha=0.6)

# Adding a diagonal line to show perfect prediction
plt.plot([min(y_train), max(y_train)], [min(y_train), max(y_train)],
color='red', linestyle='--')

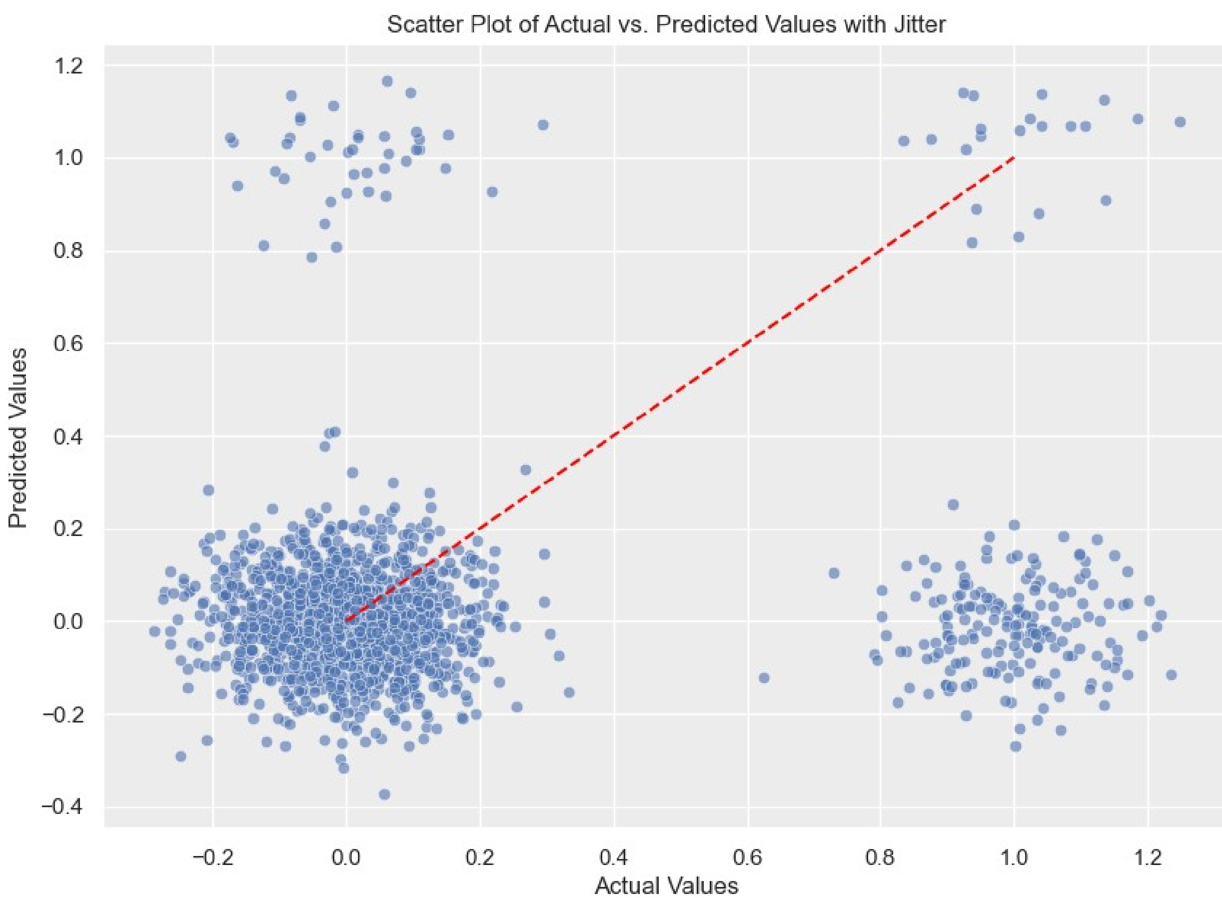
plt.xlabel('Actual Values')
plt.ylabel('Predicted Values')
plt.title('Scatter Plot of Actual vs. Predicted Values with Jitter')
plt.show()
```




```python
# Predicting for testing set
test_pred = model.predict(X_test)

# Calculating testing accuracy
test_accuracy = accuracy_score(y_test,test_pred)
print("Training accuracy is : " + str(test_accuracy))

# Getting confusion matrix and classification report
print("Confusion Matrix:")
print(confusion_matrix(y_test,test_pred))
print("Classification Report:")
print(classification_report(y_test,test_pred))
```

```
Training accuracy is : 0.8625
Confusion Matrix:
[[1359   41]
 [ 179   21]]
Classification Report:
              precision    recall  f1-score   support

         0.0       0.88      0.97      0.93      1400
         1.0       0.34      0.10      0.16       200
```

```
   accuracy                           0.86      1600
  macro avg       0.61      0.54      0.54      1600
weighted avg       0.82      0.86      0.83      1600


# Plotting the scatter plot for actual vs predicted values
plt.figure(figsize=(10, 7))
sns.scatterplot(x=add_jitter(y_test), y=add_jitter(test_pred),
marker='o', alpha=0.6)

# Adding a diagonal line to show perfect prediction
plt.plot([min(y_test), max(y_test)], [min(y_test), max(y_test)],
color='red', linestyle='--')

plt.xlabel('Actual Values')
plt.ylabel('Predicted Values')
plt.title('Scatter Plot of Actual vs. Predicted Values with Jitter')
plt.show()
```



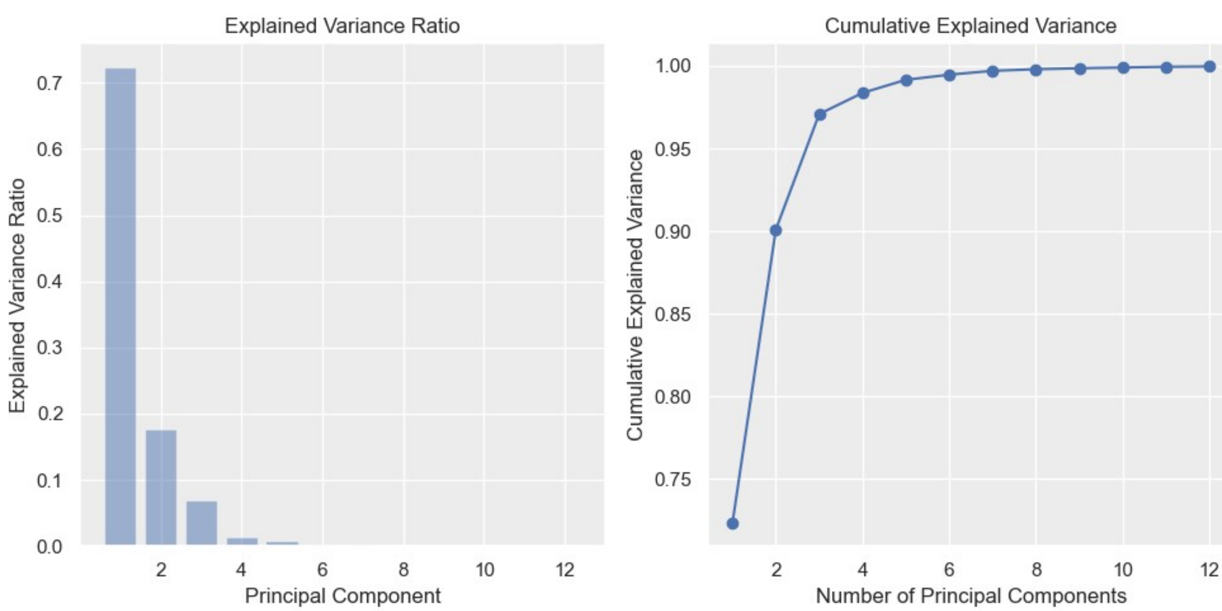
Model Improvement

```
n_components = 12
```

```python
# Importing PCA
from sklearn.decomposition import PCA

# Let's say, components = 2
pca = PCA(n_components=12)
pca.fit(X)
x_pca = pca.transform(X)

# Create the dataframe
df_pca1 = pd.DataFrame(x_pca,columns=['PC{}'.format(i+1) for i in
range(n_components)])
print(df_pca1)
```

```
            PC1        PC2       PC3       PC4       PC5       PC6
PC7  \
0     20.875094   6.460591  6.377741 -0.075213 -4.468788  1.176144
0.683676
1     16.518599  -5.860612 -7.776526  1.008795  1.832076  1.220882
0.589493
2     33.872073   2.291372  4.502261  0.868194 -2.580851 -1.195053 -
1.749896
3     -6.982723   2.501815 -8.403896  3.420961  5.031750  0.321890
0.619224
4      1.035591  -9.979904 -3.154869 -0.397186  0.542414 -0.216626 -
1.444306
...         ...        ...       ...       ...       ...       ...
...
7991 -13.441977   5.673185  4.448488 -0.555633 -0.545002  0.212029
0.908805
7992 -14.563406 -10.827515  0.293340 -1.299944  0.241330 -0.217025 -
0.346170
7993 -15.619716   6.448067  6.054763  1.461705 -2.448939 -0.271492 -
0.401118
7994 -16.733170   3.333144 -9.856313 -0.688998  2.457217 -0.059811
0.824874
7995 -15.618424   6.448248  6.054627  1.466486 -2.445993 -0.290451 -
0.302166

           PC8       PC9      PC10      PC11      PC12
0    -0.786923 -0.261715 -0.484511  0.542568  0.956504
1    -0.233650  0.323953  0.420361  0.016980  0.811942
2    -0.955396 -0.284386 -0.207000 -0.329719 -0.045636
3     0.624846 -0.557999  0.482380 -0.032048  0.675337
4    -0.354707  0.007436 -0.437549 -0.049879  0.839236
...        ...       ...       ...       ...       ...
7991 -0.772219 -0.173152 -0.049259 -0.699844  0.889071
7992 -0.757892  0.083607 -0.073058 -0.863743  0.860983
7993 -0.756346 -0.107219 -0.241161 -0.262259  0.881928
7994 -1.028636 -0.996383 -0.697608  0.583452  0.748330
7995 -0.742315 -0.124202 -0.206084 -0.344706  0.879444
```

```
[7996 rows x 12 columns]

explained_variance = pca.explained_variance_
explained_variance_ratio = pca.explained_variance_ratio_
cumulative_explained_variance = np.cumsum(explained_variance_ratio)

# Plot the explained variance ratio and cumulative explained variance
plt.figure(figsize=(10, 5))

# Plot explained variance ratio
plt.subplot(1, 2, 1)
plt.bar(range(1, len(explained_variance_ratio) + 1),
explained_variance_ratio, alpha=0.5, align='center')
plt.xlabel('Principal Component')
plt.ylabel('Explained Variance Ratio')
plt.title('Explained Variance Ratio')

# Plot cumulative explained variance
plt.subplot(1, 2, 2)
plt.plot(range(1, len(cumulative_explained_variance) + 1),
cumulative_explained_variance, marker='o', linestyle='-')
plt.xlabel('Number of Principal Components')
plt.ylabel('Cumulative Explained Variance')
plt.title('Cumulative Explained Variance')

plt.tight_layout()
plt.show()
```




```
target=X[:,-1]
```

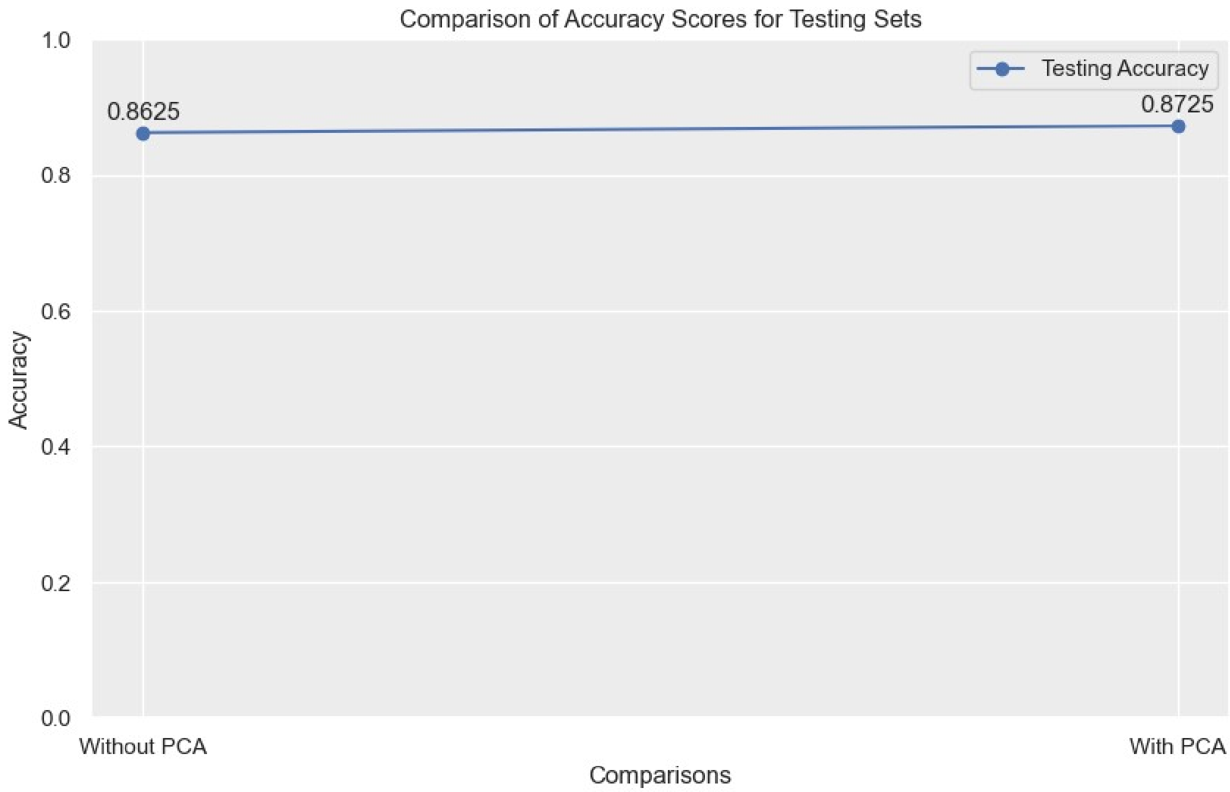
```python
# Splitting data for model building
im_X_train, im_X_test, im_y_train, im_y_test =
train_test_split(df_pca1, target, test_size=0.2, random_state=42)

# Fitting the model
model = KNeighborsClassifier()
model.fit(im_X_train,im_y_train)

# Predicting for training set
im_train_pred = model.predict(im_X_train)

# Calculating training accuracy
im_train_accuracy = accuracy_score(im_y_train,im_train_pred)
print("Training accuracy is: " + str(im_train_accuracy))

# Getting confusion matrix and Classification report
print("Confusion Matrix: ")
print(confusion_matrix(im_y_train,im_train_pred))

print("Classification Report: ")
print(classification_report(im_y_train,im_train_pred))
```

```
Training accuracy is: 0.9177611006879299
Confusion Matrix:
[[5632   52]
 [ 474  238]]
Classification Report:
              precision    recall  f1-score   support

         0.0       0.92      0.99      0.96      5684
         1.0       0.82      0.33      0.48       712

    accuracy                           0.92      6396
   macro avg       0.87      0.66      0.72      6396
weighted avg       0.91      0.92      0.90      6396
```

```python
# Predicting for testing set
im_test_pred = model.predict(im_X_test)

# Calculating testing accuracy
im_test_accuracy = accuracy_score(im_y_test,im_test_pred)
print("Training accuracy is: " + str(im_test_accuracy))

# Getting confusion matrix and Classification report
print("Confusion Matrix: ")
print(confusion_matrix(im_y_test,im_test_pred))

print("Classification Report: ")
print(classification_report(im_y_test,im_test_pred))
```

```
Training accuracy is: 0.8725
Confusion Matrix:
[[1369   31]
 [ 173   27]]
Classification Report:
              precision    recall  f1-score   support

         0.0       0.89      0.98      0.93      1400
         1.0       0.47      0.14      0.21       200

    accuracy                           0.87      1600
   macro avg       0.68      0.56      0.57      1600
weighted avg       0.84      0.87      0.84      1600
```

```
comparisions = ['Without PCA' , 'With PCA']
accuracies = [test_accuracy, im_test_accuracy]

plt.figure(figsize=(10, 6))
plt.plot(comparisions, accuracies, marker='o', linestyle='-',
color='b', label='Testing Accuracy')
plt.ylim(0, 1)
plt.xlabel('Comparisons')
plt.ylabel('Accuracy')
plt.title('Comparison of Accuracy Scores for Testing Sets')
plt.legend()
for i, acc in enumerate(accuracies):
    plt.text(i, acc + 0.02, round(acc, 4), ha='center')
plt.show()
```



Hyperparameter Tuning

```
# create numpy array for future K value
neighbors = np.arange(1, 40)
train_accuracy = np.empty(len(neighbors))
test_accuracy = np.empty(len(neighbors))

# Code Help taken from :
https://www.kaggle.com/code/elisthefox/ultimate-guide-to-k-nearest-
neighbors-k-nn#4.-Results-of-K-NN-implementation-after-preparation-of-
data

# Loop over different values of k
for i, k in enumerate(neighbors):
    # Setup a k-NN Classifier with k neighbors: knn
    knn = KNeighborsClassifier(n_neighbors=k)

    # Fit the classifier to the training data
    knn.fit(im_X_train, im_y_train)

    #Compute accuracy on the training set
    train_accuracy[i] = knn.score(im_X_train, im_y_train)

    #Compute accuracy on the testing set
    test_accuracy[i] = knn.score(im_X_test,im_y_test)
```

```
# Generate plot
sns.set(rc={'axes.facecolor':'#ECECEC'}) #background color of all
plots
plt.figure(figsize=(12,6.5))
plt.title(label='K-NN: Varying Number of Neighbors', fontsize=15,
fontweight='bold', fontname='Verdana', ha='center')
plt.plot(neighbors, test_accuracy, label = 'Testing Accuracy',
color='#E68753')
plt.plot(neighbors, train_accuracy, label = 'Training Accuracy', color
= '#409996')
plt.legend()
plt.xlabel('Number of Neighbors')
plt.ylabel('Accuracy')
plt.show();
```