Machine Learning Methology for Diagnosing Chronic Kidney Disease

All features

In [50]:
```
#import necessary library
import pandas as pd # for data analysis
import numpy as np # for numerical calculation
import matplotlib.pyplot as plt # for data visualization
import seaborn as sns #for interactive data visualization
# Ignore warnings
import warnings
warnings.filterwarnings('ignore')
pd.set_option('display.max_columns', None)  # or use a very large number like 1000
```

In [2]:
```
#load data set
df = pd.read_csv("kidney_disease.csv")
#see forward data
df.head(5)
```

Out[2]:

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	bu	sc	sod	p
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	121.0	36.0	1.2	NaN	Na
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	NaN	18.0	0.8	NaN	Na
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	423.0	53.0	1.8	NaN	Na
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	56.0	3.8	111.0	2
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	106.0	26.0	1.4	NaN	Na

In [3]:
```
# see data shape(number of rows and columns)
df.shape
```

Out[3]:
```
(400, 26)
```

In [4]:
```
#see columns
df.columns
```

Out[4]:
```
Index(['id', 'age', 'bp', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'bgr',
       'bu', 'sc', 'sod', 'pot', 'hemo', 'pcv', 'wc', 'rc', 'htn', 'dm', 'cad',
       'appet', 'pe', 'ane', 'classification'],
      dtype='object')
```

In [5]:
```
#droping id column
df.drop('id', axis = 1, inplace = True)
```

In [6]:
```
#rename columns name
df.columns = ['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar', 'red_bl
              'pus_cell_clumps', 'bacteria', 'blood_glucose_random', 'blood_urea', 'se
              'potassium', 'haemoglobin', 'packed_cell_volume', 'white_blood_cell_cour
              'hypertension', 'diabetes_mellitus', 'coronary_artery_disease', 'appetit
              'aanemia', 'class']
df.columns
```

Out[6]:
```
Index(['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar',
       'red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria',
       'blood_glucose_random', 'blood_urea', 'serum_creatinine', 'sodium',
       'potassium', 'haemoglobin', 'packed_cell_volume',
       'white_blood_cell_count', 'red_blood_cell_count', 'hypertension',
       'diabetes_mellitus', 'coronary_artery_disease', 'appetite',
       'peda_edema', 'aanemia', 'class'],
      dtype='object')
```

In [8]:
```
# Basic statistical measurements
df.describe().T
```

Out[8]:

	count	mean	std	min	25%	50%	75%	max
age	391.0	51.483376	17.169714	2.000	42.00	55.00	64.50	90.000
blood_pressure	388.0	76.469072	13.683637	50.000	70.00	80.00	80.00	180.000
specific_gravity	353.0	1.017408	0.005717	1.005	1.01	1.02	1.02	1.025
albumin	354.0	1.016949	1.352679	0.000	0.00	0.00	2.00	5.000
sugar	351.0	0.450142	1.099191	0.000	0.00	0.00	0.00	5.000
blood_glucose_random	356.0	148.036517	79.281714	22.000	99.00	121.00	163.00	490.000
blood_urea	381.0	57.425722	50.503006	1.500	27.00	42.00	66.00	391.000
serum_creatinine	383.0	3.072454	5.741126	0.400	0.90	1.30	2.80	76.000
sodium	313.0	137.528754	10.408752	4.500	135.00	138.00	142.00	163.000
potassium	312.0	4.627244	3.193904	2.500	3.80	4.40	4.90	47.000
haemoglobin	348.0	12.526437	2.912587	3.100	10.30	12.65	15.00	17.800

In [11]:
```
#see data info()
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 25 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   age                      391 non-null    float64
 1   blood_pressure           388 non-null    float64
 2   specific_gravity         353 non-null    float64
 3   albumin                  354 non-null    float64
 4   sugar                    351 non-null    float64
 5   red_blood_cells          248 non-null    object 
 6   pus_cell                 335 non-null    object 
 7   pus_cell_clumps          396 non-null    object 
 8   bacteria                 396 non-null    object 
 9   blood_glucose_random     356 non-null    float64
 10  blood_urea               381 non-null    float64
 11  serum_creatinine         383 non-null    float64
 12  sodium                   313 non-null    float64
 13  potassium                312 non-null    float64
 14  haemoglobin              348 non-null    float64
 15  packed_cell_volume       329 non-null    float64
 16  white_blood_cell_count   294 non-null    float64
 17  red_blood_cell_count     269 non-null    float64
 18  hypertension             398 non-null    object 
 19  diabetes_mellitus        398 non-null    object 
 20  coronary_artery_disease  398 non-null    object 
 21  appetite                 399 non-null    object 
 22  peda_edema               399 non-null    object 
 23  aanemia                  399 non-null    object 
 24  class                    400 non-null    object 
dtypes: float64(14), object(11)
memory usage: 78.2+ KB
```

In [10]:

```
# converting necessary columns to numerical type

df['packed_cell_volume'] = pd.to_numeric(df['packed_cell_volume'], errors='coerce')
df['white_blood_cell_count'] = pd.to_numeric(df['white_blood_cell_count'], errors='coe
df['red_blood_cell_count'] = pd.to_numeric(df['red_blood_cell_count'], errors='coerce'
```

In [12]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 25 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   age                      391 non-null    float64
 1   blood_pressure           388 non-null    float64
 2   specific_gravity         353 non-null    float64
 3   albumin                  354 non-null    float64
 4   sugar                    351 non-null    float64
 5   red_blood_cells          248 non-null    object 
 6   pus_cell                 335 non-null    object 
 7   pus_cell_clumps          396 non-null    object 
 8   bacteria                 396 non-null    object 
 9   blood_glucose_random     356 non-null    float64
 10  blood_urea               381 non-null    float64
 11  serum_creatinine         383 non-null    float64
 12  sodium                   313 non-null    float64
 13  potassium                312 non-null    float64
 14  haemoglobin              348 non-null    float64
 15  packed_cell_volume       329 non-null    float64
 16  white_blood_cell_count   294 non-null    float64
 17  red_blood_cell_count     269 non-null    float64
 18  hypertension             398 non-null    object 
 19  diabetes_mellitus        398 non-null    object 
 20  coronary_artery_disease  398 non-null    object 
 21  appetite                 399 non-null    object 
 22  peda_edema               399 non-null    object 
 23  aanemia                  399 non-null    object 
 24  class                    400 non-null    object 
dtypes: float64(14), object(11)
memory usage: 78.2+ KB
```

Data Preprocessing

In [19]:
```python
# Extract categorical columns (object types)
categorical_columns = df.select_dtypes(include=['object']).columns.tolist()
print(categorical_columns)
print(len(categorical_columns))
```

```
['red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria', 'hypertension', 'diabe
tes_mellitus', 'coronary_artery_disease', 'appetite', 'peda_edema', 'aanemia', 'clas
s']
11
```

In [18]:
```python
# Extract numerical columns (integer and float types)
numerical_columns = df.select_dtypes(include=['int64', 'float64']).columns.tolist()
print(numerical_columns)
print(len(numerical_columns))
```

```
['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar', 'blood_glucose_rand
om', 'blood_urea', 'serum_creatinine', 'sodium', 'potassium', 'haemoglobin', 'packed_
cell_volume', 'white_blood_cell_count', 'red_blood_cell_count']
14
```

In [20]:
```python
# Iterate through each categorical column
for column in categorical_columns:
    unique_values = df[column].unique()
    print(f"Unique values in '{column}': {unique_values}")
```

```
Unique values in 'red_blood_cells': [nan 'normal' 'abnormal']
Unique values in 'pus_cell': ['normal' 'abnormal' nan]
Unique values in 'pus_cell_clumps': ['notpresent' 'present' nan]
Unique values in 'bacteria': ['notpresent' 'present' nan]
Unique values in 'hypertension': ['yes' 'no' nan]
Unique values in 'diabetes_mellitus': ['yes' 'no' ' yes' '\tno' '\tyes' nan]
Unique values in 'coronary_artery_disease': ['no' 'yes' '\tno' nan]
Unique values in 'appetite': ['good' 'poor' nan]
Unique values in 'peda_edema': ['no' 'yes' nan]
Unique values in 'aanemia': ['no' 'yes' nan]
Unique values in 'class': ['ckd' 'ckd\t' 'notckd']
```

In [21]:

```
# replace incorrect values

df['diabetes_mellitus'].replace(to_replace = {'\tno':'no','\tyes':'yes',' yes':'yes'},

df['coronary_artery_disease'] = df['coronary_artery_disease'].replace(to_replace = '\t

df['class'] = df['class'].replace(to_replace = {'ckd\t': 'ckd', 'notckd': 'not ckd'})
```

In [22]:

```
df['class'] = df['class'].map({'ckd': 0, 'not ckd': 1})
df['class'] = pd.to_numeric(df['class'], errors='coerce')
cols = ['diabetes_mellitus', 'coronary_artery_disease', 'class']

for col in cols:
    print(f"{col} has {df[col].unique()} values\n")
```

```
diabetes_mellitus has ['yes' 'no' nan] values

coronary_artery_disease has ['no' 'yes' nan] values

class has [0 1] values
```

In [23]:

```
# Checking missing value
df.isnull().sum()
```

Out[23]:
```
age                         9
blood_pressure             12
specific_gravity           47
albumin                    46
sugar                      49
red_blood_cells           152
pus_cell                   65
pus_cell_clumps             4
bacteria                    4
blood_glucose_random       44
blood_urea                 19
serum_creatinine           17
sodium                     87
potassium                  88
haemoglobin                52
packed_cell_volume         71
white_blood_cell_count    106
red_blood_cell_count      131
hypertension                2
diabetes_mellitus           2
coronary_artery_disease     2
appetite                    1
peda_edema                  1
aanemia                     1
class                       0
dtype: int64
```

In [25]:
```python
# Checking missing values in numerical columns
numerical_columns = df.select_dtypes(include=['int64', 'float64']).columns.tolist()

for column in numerical_columns:
    missing_count = df[column].isnull().sum()
    print(f"Missing values in '{column}': {missing_count}")
```

```
Missing values in 'age': 9
Missing values in 'blood_pressure': 12
Missing values in 'specific_gravity': 47
Missing values in 'albumin': 46
Missing values in 'sugar': 49
Missing values in 'blood_glucose_random': 44
Missing values in 'blood_urea': 19
Missing values in 'serum_creatinine': 17
Missing values in 'sodium': 87
Missing values in 'potassium': 88
Missing values in 'haemoglobin': 52
Missing values in 'packed_cell_volume': 71
Missing values in 'white_blood_cell_count': 106
Missing values in 'red_blood_cell_count': 131
Missing values in 'class': 0
```

In [26]:
```python
# Checking missing values in categorical column
categorical_columns= df.select_dtypes(include=['object']).columns.tolist()

for column in categorical_columns:
    missing_count = df[column].isnull().sum()
    print(f"Missing values in '{column}': {missing_count}")
```

```
Missing values in 'red_blood_cells': 152
Missing values in 'pus_cell': 65
Missing values in 'pus_cell_clumps': 4
Missing values in 'bacteria': 4
Missing values in 'hypertension': 2
Missing values in 'diabetes_mellitus': 2
Missing values in 'coronary_artery_disease': 2
Missing values in 'appetite': 1
Missing values in 'peda_edema': 1
Missing values in 'aanemia': 1
```

Handing Missing Value with KNNImputer

In [31]:

```python
from sklearn.impute import KNNImputer

# List of categorical and numerical columns
cat_cols = ['red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria', 'hypertensio
num_cols = ['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar', 'blood_gl

# Initialize KNNImputer
knn_imputer = KNNImputer(n_neighbors=5)  # You can adjust the number of neighbors

# Filling missing values for numerical columns
df[num_cols] = knn_imputer.fit_transform(df[num_cols])

# Filling missing values for categorical columns
df[cat_cols] = df[cat_cols].apply(lambda col: col.fillna(col.value_counts().idxmax()))

# Verify that missing values are filled
print(df.isnull().sum())
```

```
age                        0
blood_pressure             0
specific_gravity           0
albumin                    0
sugar                      0
red_blood_cells            0
pus_cell                   0
pus_cell_clumps            0
bacteria                   0
blood_glucose_random       0
blood_urea                 0
serum_creatinine           0
sodium                     0
potassium                  0
haemoglobin                0
packed_cell_volume         0
white_blood_cell_count     0
red_blood_cell_count       0
hypertension               0
diabetes_mellitus          0
coronary_artery_disease    0
appetite                   0
peda_edema                 0
aanemia                    0
class                      0
dtype: int64
```

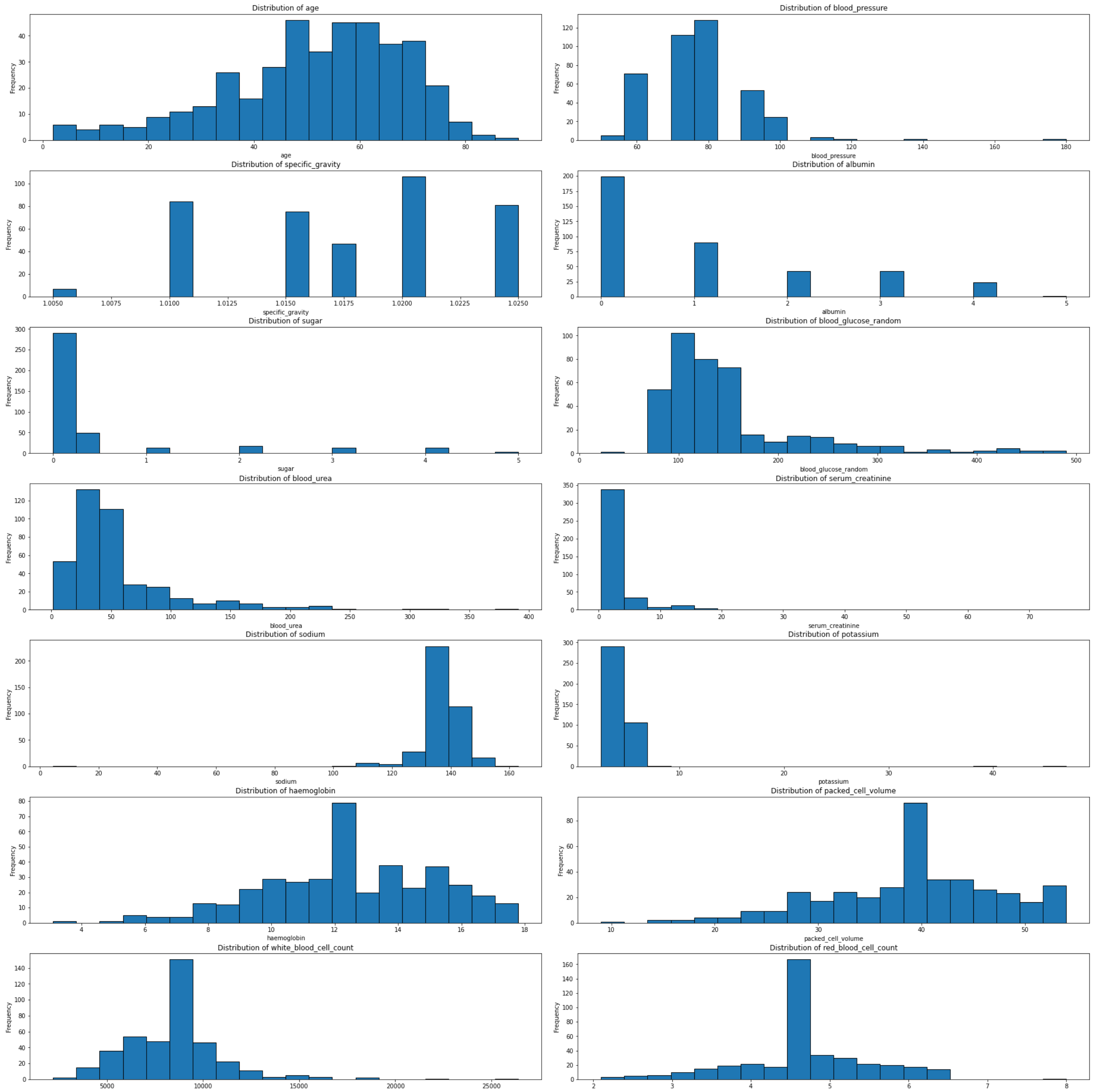
In [ ]:

Exploratory data analysis

Numerical columns analysis

In [35]:

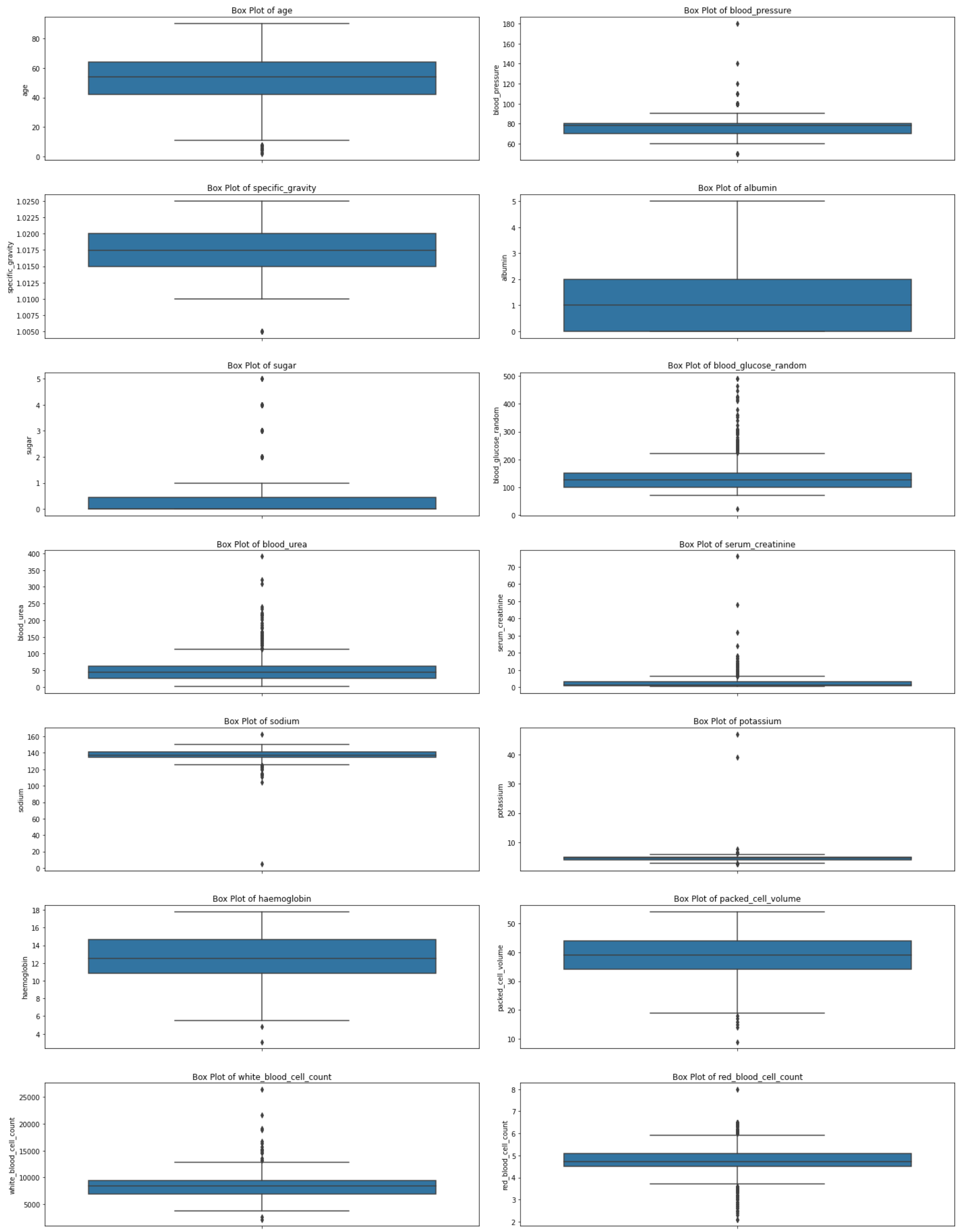
```
import matplotlib.pyplot as plt

# Calculate the number of rows and columns needed for the grid
num_rows = len(num_cols) // 2 + len(num_cols) % 2
num_cols_per_row = 2

fig, axes = plt.subplots(num_rows, num_cols_per_row, figsize=(26, 26))
fig.tight_layout(pad=3.0)  # Adjust the spacing between plots

for i, column in enumerate(num_cols):
    row = i // num_cols_per_row
    col = i % num_cols_per_row

    axes[row, col].hist(df[column], bins=20, edgecolor='k')
    axes[row, col].set_title(f'Distribution of {column}')
    axes[row, col].set_xlabel(column)
    axes[row, col].set_ylabel('Frequency')

# Hide any empty subplots
for i in range(len(num_cols), num_rows * num_cols_per_row):
    row = i // num_cols_per_row
    col = i % num_cols_per_row
    axes[row, col].axis('off')

plt.show()
```



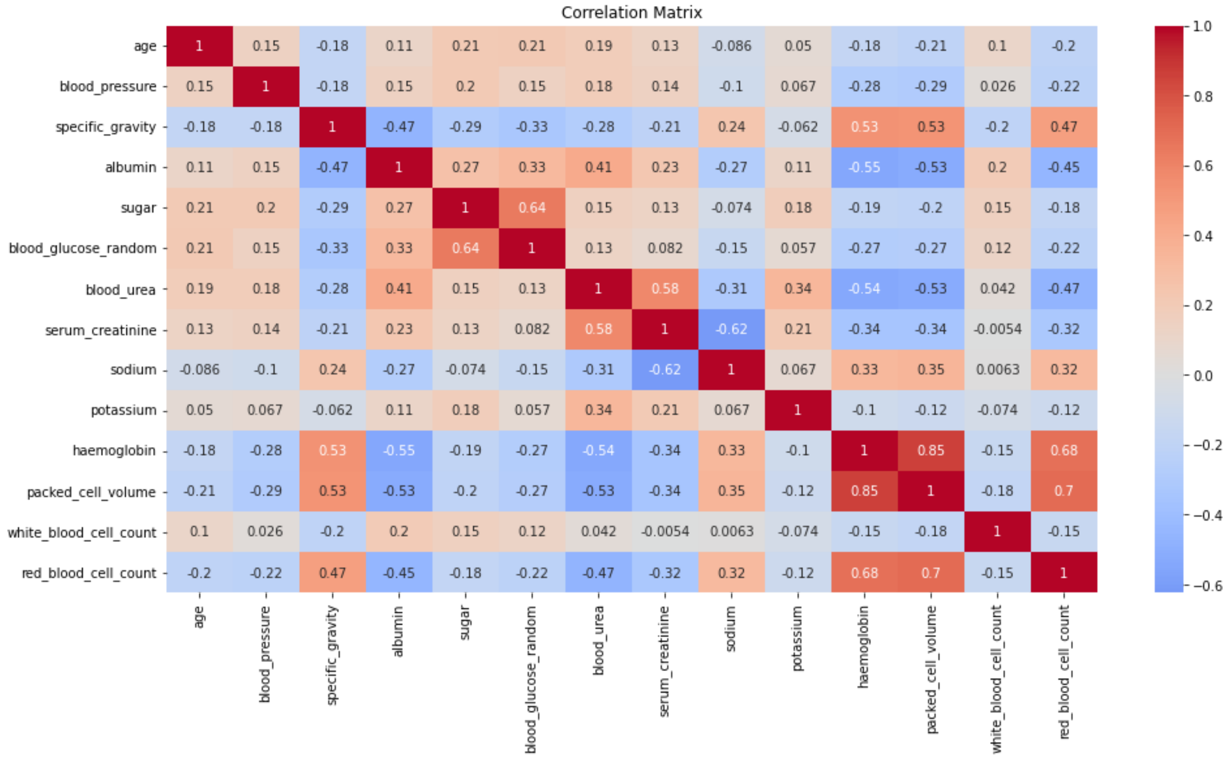
In [39]:

```
# Calculate the number of rows and columns needed for the grid
num_rows = len(num_cols) // 2 + len(num_cols) % 2
num_cols_per_row = 2

fig, axes = plt.subplots(num_rows, num_cols_per_row, figsize=(20, 26))
fig.tight_layout(pad=3.0)  # Adjust the spacing between plots

for i, column in enumerate(num_cols):
    row = i // num_cols_per_row
    col = i % num_cols_per_row

    sns.boxplot(data=df, y=column, ax=axes[row, col])
    axes[row, col].set_title(f'Box Plot of {column}')
    axes[row, col].set_ylabel(column)

# Hide any empty subplots
for i in range(len(num_cols), num_rows * num_cols_per_row):
    row = i // num_cols_per_row
    col = i % num_cols_per_row
    axes[row, col].axis('off')
```

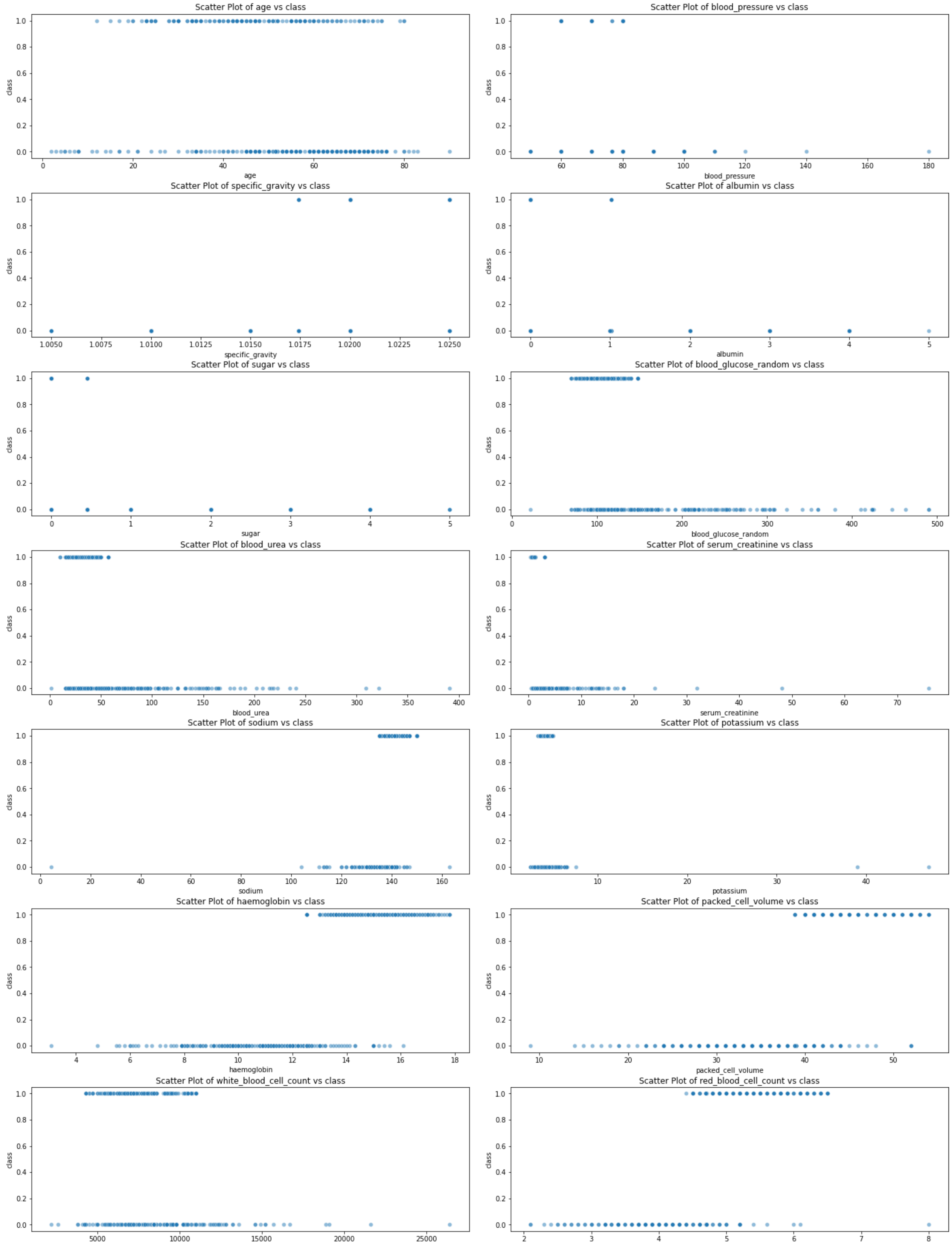
```
plt.show()
```



In [41]:
```
correlation_matrix = df[num_cols].corr()
plt.figure(figsize=(16, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', center=0)
plt.title('Correlation Matrix')
plt.show()
```



In [44]:
```python
target_col = 'class'  # target variable

# Calculate the number of rows and columns needed for the grid
num_rows = len(num_cols) // 2 + len(num_cols) % 2
num_cols_per_row = 2

fig, axes = plt.subplots(num_rows, num_cols_per_row, figsize=(20, 26))
fig.tight_layout(pad=3.0)  # Adjust the spacing between plots

for i, column in enumerate(num_cols):
    row = i // num_cols_per_row
    col = i % num_cols_per_row

    sns.scatterplot(data=df, x=column, y=target_col, alpha=0.5, ax=axes[row, col])
    axes[row, col].set_title(f'Scatter Plot of {column} vs {target_col}')
    axes[row, col].set_xlabel(column)
    axes[row, col].set_ylabel(target_col)

# Hide any empty subplots
for i in range(len(num_cols), num_rows * num_cols_per_row):
    row = i // num_cols_per_row
    col = i % num_cols_per_row
    axes[row, col].axis('off')

plt.show()
```



In [ ]:

In [ ]:

In [ ]:

Feature Enginnering

In [53]:
```
cat_col_unique_counts = {}

for col in cat_cols:
    unique_count = df[col].nunique()
    cat_col_unique_counts[col] = unique_count
    print(f"{col} has: {unique_count} categories\n")
```

```
red_blood_cells has: 2 categories

pus_cell has: 2 categories

pus_cell_clumps has: 2 categories

bacteria has: 2 categories

hypertension has: 2 categories

diabetes_mellitus has: 2 categories

coronary_artery_disease has: 2 categories

appetite has: 2 categories

peda_edema has: 2 categories

aanemia has: 2 categories

class has: 2 categories
```

In [54]:
```
# LebelEncoding
from sklearn.preprocessing import LabelEncoder

label_encoder = LabelEncoder()

for col in cat_cols:
    df[col] = label_encoder.fit_transform(df[col])
```

In [55]:
```
df.head(10)
```

Out[55]:

	age	blood_pressure	specific_gravity	albumin	sugar	red_blood_cells	pus_cell	pus_cell_clumps	b
0	48.0	80.000000	1.020	1.0	0.0	1	1	0	
1	7.0	50.000000	1.020	4.0	0.0	1	1	0	
2	62.0	80.000000	1.010	2.0	3.0	1	1	0	
3	48.0	70.000000	1.005	4.0	0.0	1	0	1	
4	51.0	80.000000	1.010	2.0	0.0	1	1	0	
5	60.0	90.000000	1.015	3.0	0.0	1	1	0	
6	68.0	70.000000	1.010	0.0	0.0	1	1	0	
7	24.0	76.469072	1.015	2.0	4.0	1	0	0	
8	52.0	100.000000	1.015	3.0	0.0	1	0	1	
9	53.0	90.000000	1.020	2.0	0.0	0	0	1	

In [56]:

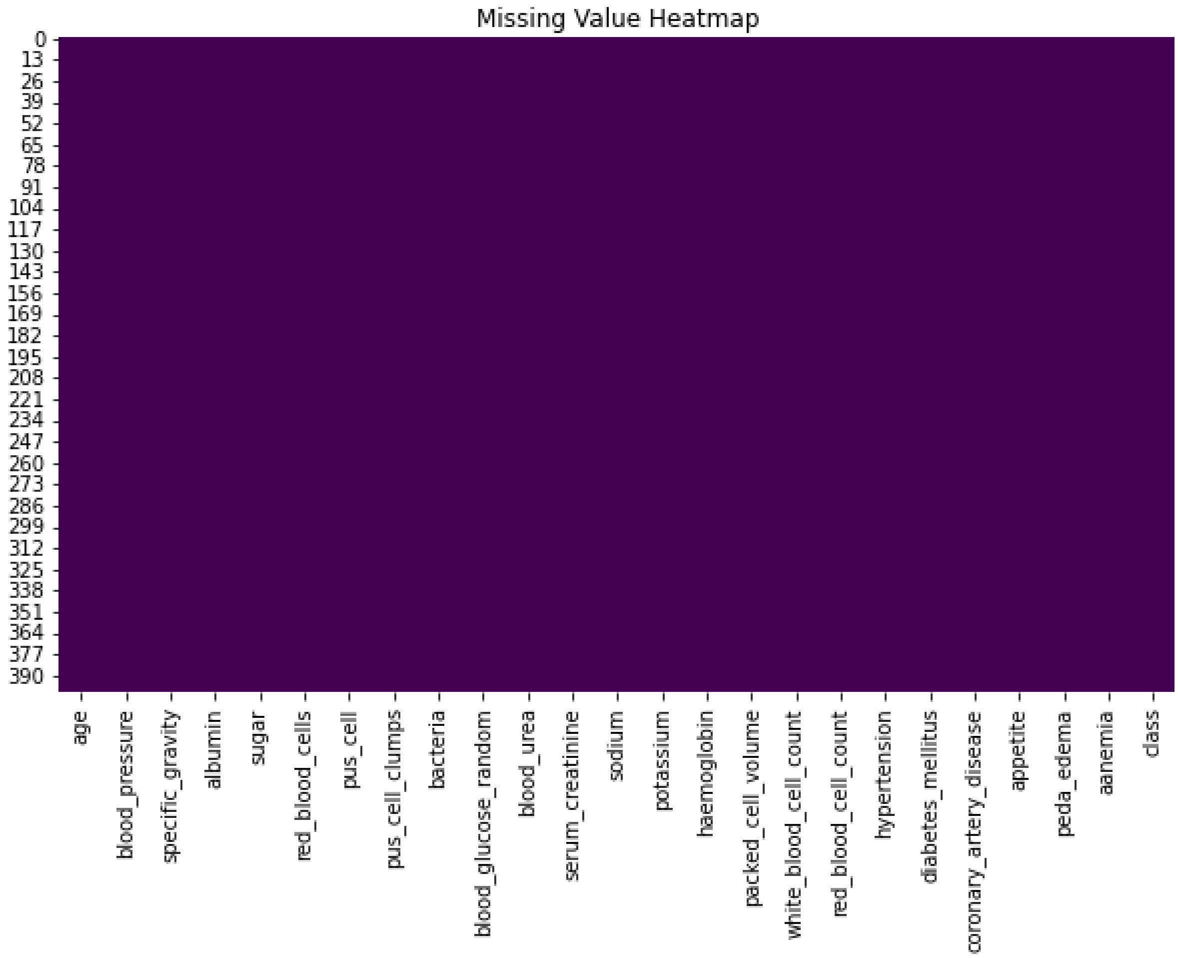
```
df.isnull().sum()
```

Out[56]:

```
age                        0
blood_pressure             0
specific_gravity           0
albumin                    0
sugar                      0
red_blood_cells            0
pus_cell                   0
pus_cell_clumps            0
bacteria                   0
blood_glucose_random       0
blood_urea                 0
serum_creatinine           0
sodium                     0
potassium                  0
haemoglobin                0
packed_cell_volume         0
white_blood_cell_count     0
red_blood_cell_count       0
hypertension               0
diabetes_mellitus          0
coronary_artery_disease    0
appetite                   0
peda_edema                 0
aanemia                    0
class                      0
dtype: int64
```

In [57]:

```
plt.figure(figsize=(10, 6))
sns.heatmap(df.isnull(), cmap='viridis', cbar=False)
plt.title('Missing Value Heatmap')
plt.show()
```



In [ ]:

MODEL BUILDING

In [ ]:

Train Test split and Normalization

In [58]:

```
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.model_selection import train_test_split

# Splitting the data into features (X) and target variable (y)
X = df.drop('class', axis=1)  # Features
y = df['class']               # Target variable

# Splitting the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=

# Create a pipeline with StandardScaler
pipeline_standard = Pipeline([
    ('scaler', StandardScaler())  # Step 1: StandardScaler for normalization
])

# Create a pipeline with MinMaxScaler
```

```
pipeline_minmax = Pipeline([
    ('scaler', MinMaxScaler())  # Step 1: MinMaxScaler for normalization
])

# Fit and transform using the pipeline with StandardScaler
X_train_standard = pipeline_standard.fit_transform(X_train)

# Fit and transform using the pipeline with MinMaxScaler
X_train_minmax = pipeline_minmax.fit_transform(X_train)
```

In [73]:

```
print("X shape:", X_train.shape)

print("y shape:", y_train.shape)
```

```
X shape: (320, 24)
y shape: (320,)
```

Model building

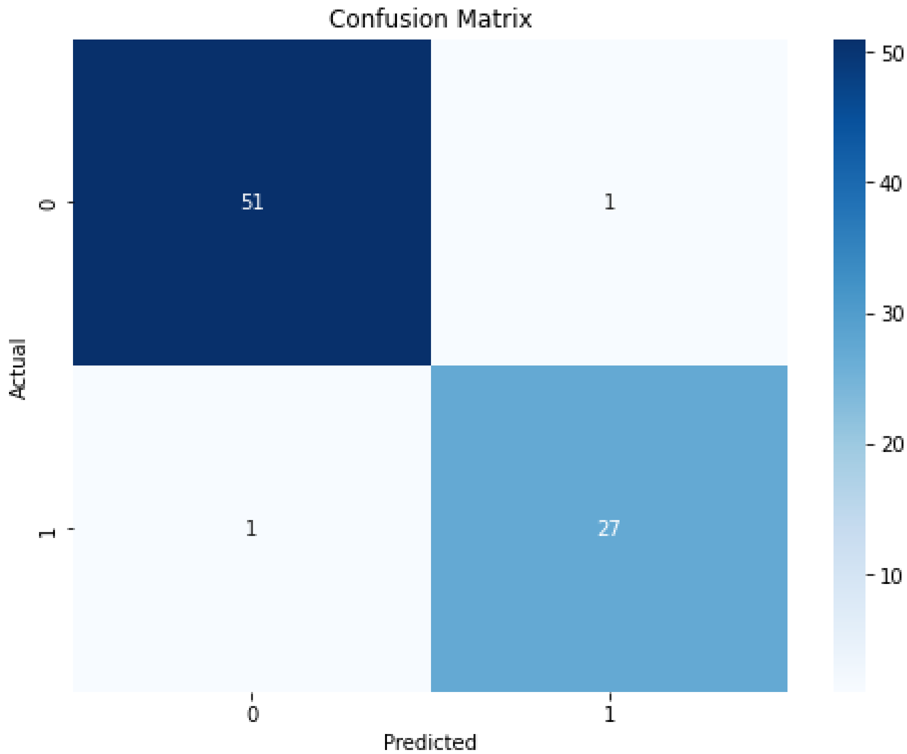
Logistic Regression

In [82]:

```
from sklearn.model_selection import GridSearchCV, train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

param_grid = {
    'solver': ['newton-cg', 'lbfgs', 'liblinear'],
    'penalty': ['l2'],  # 'none', 'l1', 'l2', 'elasticnet'
    'C': np.logspace(-5, 2, num=10)
}

grid = GridSearchCV(LogisticRegression(max_iter=1000), param_grid, refit=True, verbose
grid.fit(X_train, y_train)

# Access the best model and its parameters
best_model = grid.best_estimator_
best_params = grid.best_params_
print(f"Best params: {best_params}")

# Evaluate the best model
y_train_pred = best_model.predict(X_train)
y_test_pred = best_model.predict(X_test)

train_accuracy = accuracy_score(y_train, y_train_pred)
test_accuracy = accuracy_score(y_test, y_test_pred)

print(f"Train Accuracy: {train_accuracy:.4f}")
print(f"Test Accuracy: {test_accuracy:.4f}")


# Visualize confusion matrix
conf_matrix = confusion_matrix(y_test, y_test_pred)
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues')
plt.title('Confusion Matrix')
plt.xlabel('Predicted')
```

```
plt.ylabel('Actual')
plt.show()

# Print classification report
print(f"Classification Report :- \n {classification_report(y_test, y_test_pred)}")
```

```
Fitting 5 folds for each of 30 candidates, totalling 150 fits
Best params: {'C': 16.68100537200059, 'penalty': 'l2', 'solver': 'liblinear'}
Train Accuracy: 0.9906
Test Accuracy: 0.9750
```




```
Classification Report :-
               precision    recall  f1-score   support

           0       0.98      0.98      0.98        52
           1       0.96      0.96      0.96        28

    accuracy                           0.97        80
   macro avg       0.97      0.97      0.97        80
weighted avg       0.97      0.97      0.97        80
```

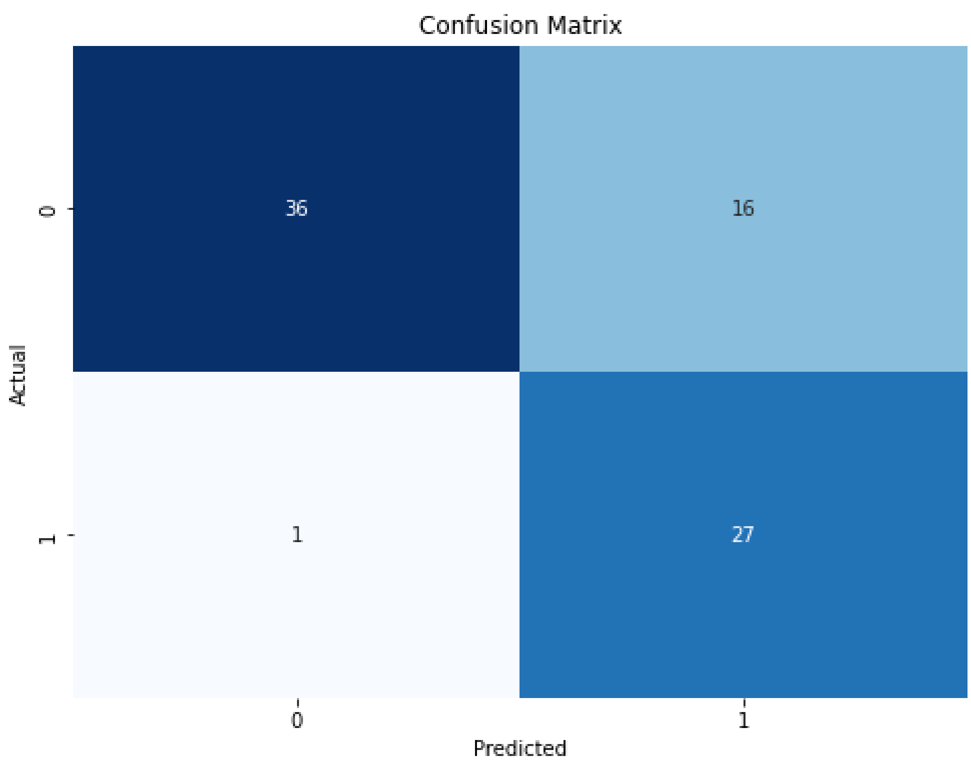
KNN

In [89]:

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

param_grid = {
    'n_neighbors': [3, 5, 7, 9, 11],
    'weights': ['uniform', 'distance'],
    'metric': ['euclidean', 'manhattan']
}

grid = GridSearchCV(KNeighborsClassifier(), param_grid, refit=True, verbose=1, cv=5)
model = grid.fit(X_train, y_train).best_estimator_
```

```
best_params = grid.best_params_
print(f"Best params: {best_params}")

y_train_pred = model.predict(X_train)
y_test_pred = model.predict(X_test)

# Define a function to print scores
def print_score(model, X_train, y_train, X_test, y_test):
    print("Training Result:\n")
    acc_train = accuracy_score(y_train, model.predict(X_train))
    print(f"Training Accuracy Score: {acc_train:.4f}\n")
    conf_matrix_train = confusion_matrix(y_train, model.predict(X_train))

    print("Testing Result:\n")
    acc_test = accuracy_score(y_test, model.predict(X_test))
    print(f"Testing Accuracy Score: {acc_test:.4f}\n")
    conf_matrix_test = confusion_matrix(y_test, model.predict(X_test))

    print(f"Confusion Matrix (Training):\n{conf_matrix_train}\n")
    print(f"Confusion Matrix (Testing):\n{conf_matrix_test}\n")
    print(f"Classification Report (Testing):\n{classification_report(y_test, model.pre

print_score(model, X_train, y_train, X_test, y_test)

# Visualize the confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(confusion_matrix(y_test, y_test_pred), annot=True, fmt='d', cmap='Blues',
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix')
plt.show()
```

```
Fitting 5 folds for each of 20 candidates, totalling 100 fits
Best params: {'metric': 'manhattan', 'n_neighbors': 3, 'weights': 'distance'}
Training Result:

Training Accuracy Score: 1.0000

Testing Result:

Testing Accuracy Score: 0.7875

Confusion Matrix (Training):
[[198   0]
 [  0 122]]

Confusion Matrix (Testing):
[[36 16]
 [ 1 27]]

Classification Report (Testing):
              precision    recall  f1-score   support

           0       0.97      0.69      0.81        52
           1       0.63      0.96      0.76        28

    accuracy                           0.79        80
   macro avg       0.80      0.83      0.78        80
weighted avg       0.85      0.79      0.79        80
```

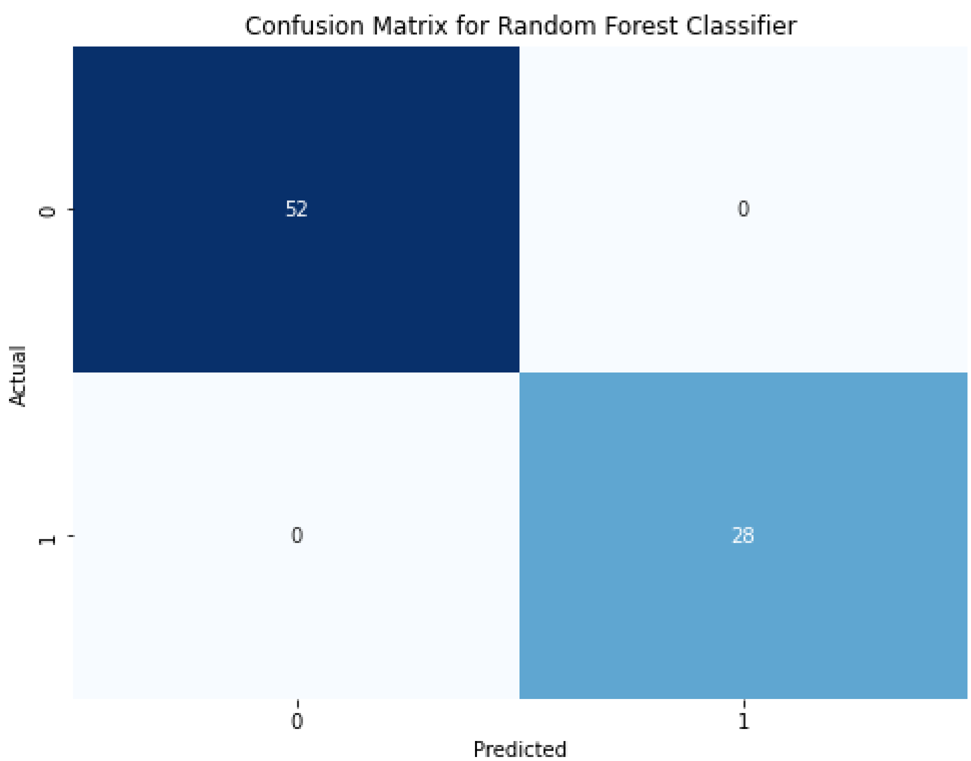


Random Forest

In [97]:
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

rd_clf = RandomForestClassifier(criterion='entropy', max_depth=11, max_features='auto'
```

```
rd_clf.fit(X_train, y_train)

# Accuracy score, confusion matrix and classification report of random forest
rd_clf_acc = accuracy_score(y_test, rd_clf.predict(X_test))

print(f"Training Accuracy of Random Forest Classifier is {accuracy_score(y_train, rd_c
print(f"Test Accuracy of Random Forest Classifier is {rd_clf_acc} \n")

#conf_matrix_rf = confusion_matrix(y_test, rd_clf.predict(X_test))
# Visualize the confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix_rf, annot=True, fmt='d', cmap='Blues', cbar=False)
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix for Random Forest Classifier')
plt.show()

#print(f"Confusion Matrix :- \n{conf_matrix_rf}\n")
print(f"Classification Report :- \n {classification_report(y_test, rd_clf.predict(X_te
```

```
Training Accuracy of Random Forest Classifier is 1.0
Test Accuracy of Random Forest Classifier is 0.9875
```

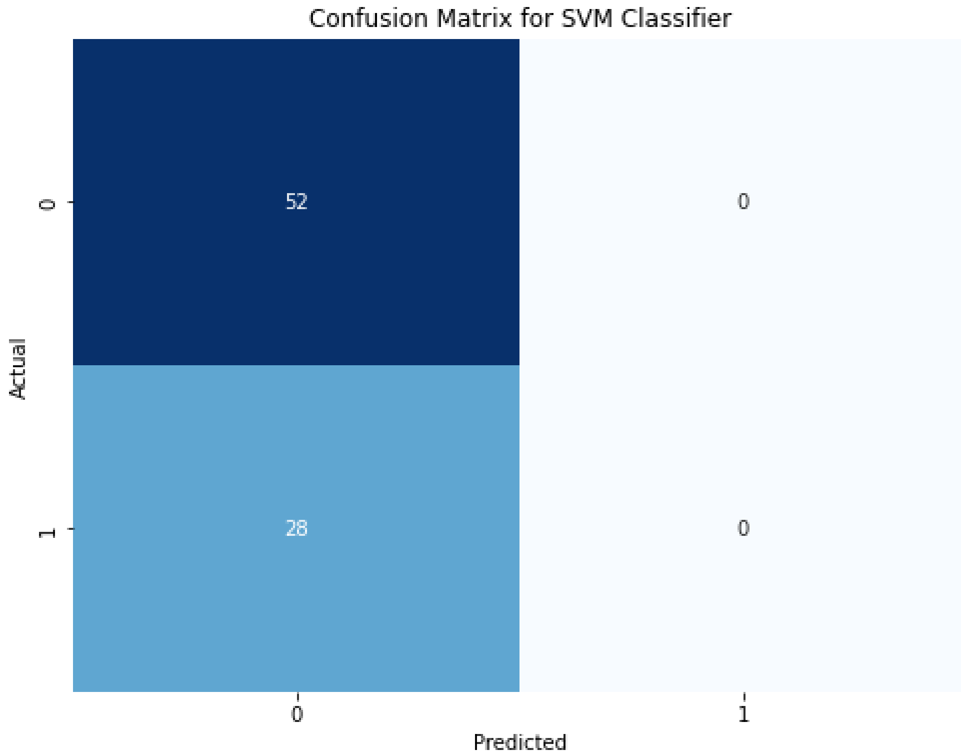



```
Classification Report :-
               precision    recall  f1-score   support

           0       1.00      0.98      0.99        52
           1       0.97      1.00      0.98        28

    accuracy                           0.99        80
   macro avg       0.98      0.99      0.99        80
weighted avg       0.99      0.99      0.99        80
```

SVM

In [96]:
```
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

# Create an instance of the SVM classifier
svm_clf = SVC(kernel='rbf', C=1, gamma='auto')

# Train the SVM model
svm_clf.fit(X_train, y_train)

# Make predictions
y_train_pred = svm_clf.predict(X_train)
y_test_pred = svm_clf.predict(X_test)

# Calculate accuracy scores
svm_train_acc = accuracy_score(y_train, y_train_pred)
svm_test_acc = accuracy_score(y_test, y_test_pred)

print(f"Training Accuracy of SVM Classifier: {svm_train_acc:.4f}")
print(f"Test Accuracy of SVM Classifier: {svm_test_acc:.4f}")

# Calculate confusion matrix
#conf_matrix_svm = confusion_matrix(y_test, y_test_pred)

# Visualize the confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix_svm, annot=True, fmt='d', cmap='Blues', cbar=False)
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix for SVM Classifier')
plt.show()

#print(f"Confusion Matrix:\n{conf_matrix_svm}")
print(f"Classification Report:\n{classification_report(y_test, y_test_pred)}")
```

```
Training Accuracy of SVM Classifier: 1.0000
Test Accuracy of SVM Classifier: 0.6500
```




```
Classification Report:
              precision    recall  f1-score   support

           0       0.65      1.00      0.79        52
           1       0.00      0.00      0.00        28

    accuracy                           0.65        80
   macro avg       0.33      0.50      0.39        80
weighted avg       0.42      0.65      0.51        80
```

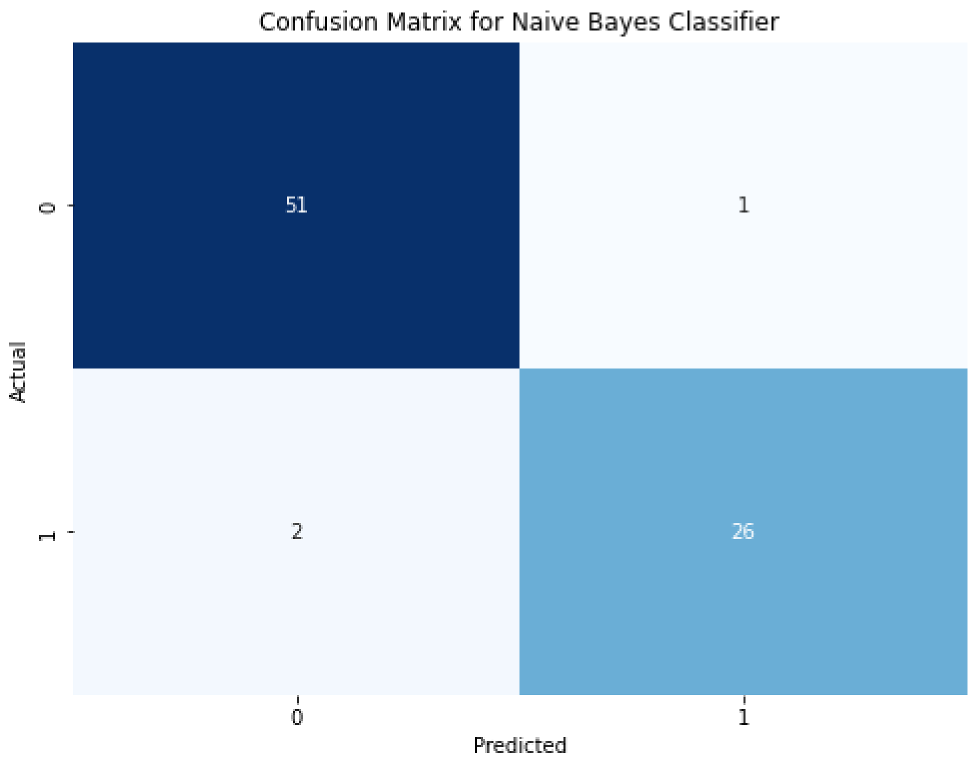
Naive Biyes

In [100…

```
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
import matplotlib.pyplot as plt
import seaborn as sns

# Create an instance of the Naive Bayes classifier
nb_clf = GaussianNB()

# Train the Naive Bayes model
nb_clf.fit(X_train, y_train)

# Make predictions
y_train_pred = nb_clf.predict(X_train)
y_test_pred = nb_clf.predict(X_test)

# Calculate accuracy scores
nb_train_acc = accuracy_score(y_train, y_train_pred)
nb_test_acc = accuracy_score(y_test, y_test_pred)

print(f"Training Accuracy of Naive Bayes Classifier: {nb_train_acc:.4f}")
print(f"Test Accuracy of Naive Bayes Classifier: {nb_test_acc:.4f}")
```

```
# Calculate confusion matrix
conf_matrix_nb = confusion_matrix(y_test, y_test_pred)

print(f"Confusion Matrix:\n{conf_matrix_nb}")

# Visualize the confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix_nb, annot=True, fmt='d', cmap='Blues', cbar=False)
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix for Naive Bayes Classifier')
plt.show()

print(f"Classification Report:\n{classification_report(y_test, y_test_pred)}")
```

```
Training Accuracy of Naive Bayes Classifier: 0.9625
Test Accuracy of Naive Bayes Classifier: 0.9625
Confusion Matrix:
[[51  1]
 [ 2 26]]
```




```
Classification Report:
              precision    recall  f1-score   support

           0       0.96      0.98      0.97        52
           1       0.96      0.93      0.95        28

    accuracy                           0.96        80
   macro avg       0.96      0.95      0.96        80
weighted avg       0.96      0.96      0.96        80
```

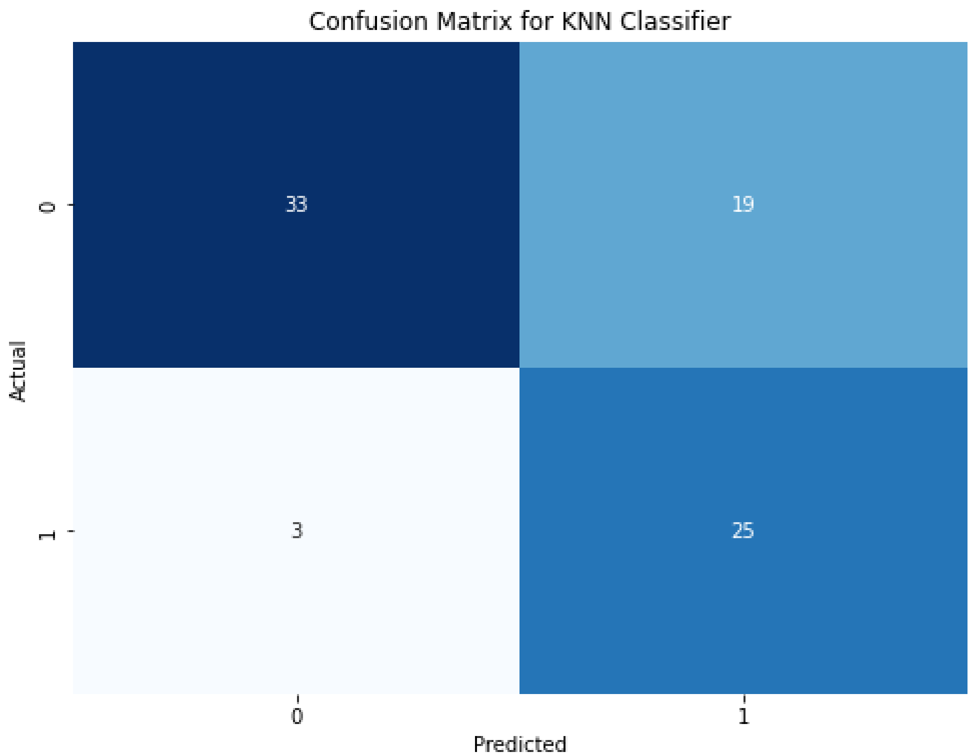
KNN

In [102…

```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
```

```
# Create an instance of the KNN classifier
knn_clf = KNeighborsClassifier(n_neighbors=5)  # You can adjust the number of neighbor

# Train the KNN model
knn_clf.fit(X_train, y_train)

# Make predictions
y_train_pred = knn_clf.predict(X_train)
y_test_pred = knn_clf.predict(X_test)

# Calculate accuracy scores
knn_train_acc = accuracy_score(y_train, y_train_pred)
knn_test_acc = accuracy_score(y_test, y_test_pred)

print(f"Training Accuracy of KNN Classifier: {knn_train_acc:.4f}")
print(f"Test Accuracy of KNN Classifier: {knn_test_acc:.4f}")

# Calculate confusion matrix
conf_matrix_knn = confusion_matrix(y_test, y_test_pred)

print(f"Confusion Matrix:\n{conf_matrix_knn}")
# Visualize the confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix_knn, annot=True, fmt='d', cmap='Blues', cbar=False)
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix for KNN Classifier')
plt.show()

print(f"Classification Report:\n{classification_report(y_test, y_test_pred)}")
```

```
Training Accuracy of KNN Classifier: 0.8531
Test Accuracy of KNN Classifier: 0.7250
Confusion Matrix:
[[33 19]
 [ 3 25]]
```




```
Classification Report:
              precision    recall  f1-score   support

           0       0.92      0.63      0.75        52
           1       0.57      0.89      0.69        28

    accuracy                           0.73        80
   macro avg       0.74      0.76      0.72        80
weighted avg       0.79      0.72      0.73        80
```

In [107…

```
from sklearn.model_selection import GridSearchCV

param_grid = {
    'n_neighbors': [3, 5, 7, 9, 11],
    'weights': ['uniform', 'distance'],
    'metric': ['euclidean', 'manhattan']
}

grid = GridSearchCV(KNeighborsClassifier(), param_grid, refit=True, verbose=1, cv=5)
best_knn_model = grid.fit(X_train, y_train).best_estimator_
from sklearn.metrics import accuracy_score

# Predicting on the test set
y_test_pred = best_knn_model.predict(X_test)

# Calculating accuracy
knn_accuracy = accuracy_score(y_test, y_test_pred)
print(f"Test Accuracy of the Best KNN Model: {knn_accuracy:.4f}")
```

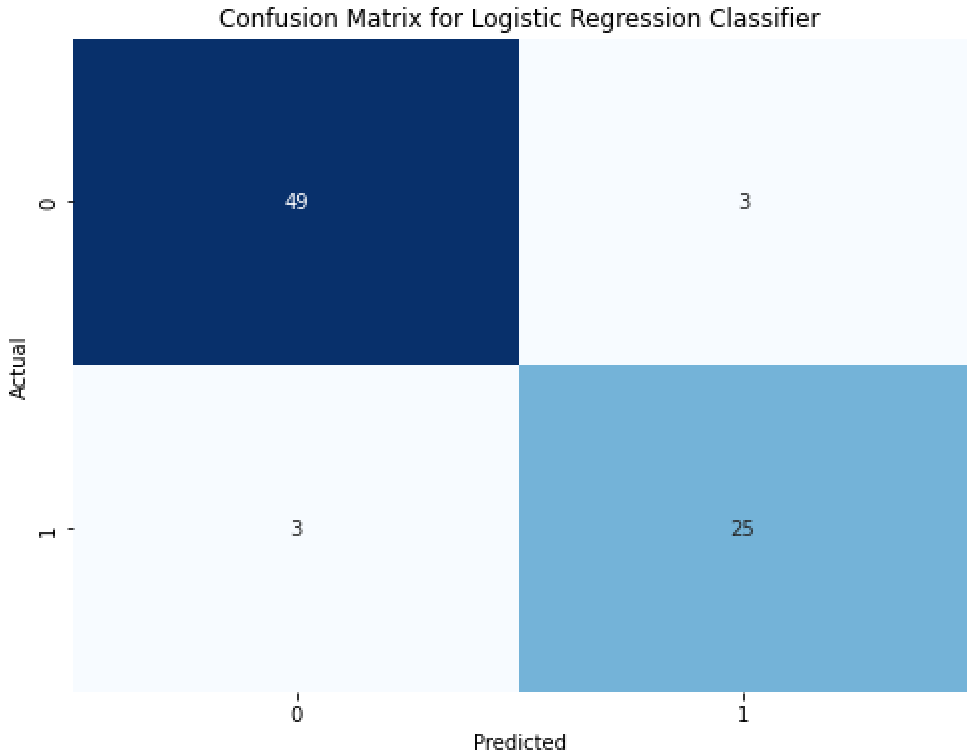
```
Fitting 5 folds for each of 20 candidates, totalling 100 fits
Test Accuracy of the Best KNN Model: 0.7875
```

Logistic Regression

In [104…

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

# Create an instance of the Logistic Regression classifier
logreg_clf = LogisticRegression()

# Train the Logistic Regression model
logreg_clf.fit(X_train, y_train)

# Make predictions
y_train_pred = logreg_clf.predict(X_train)
y_test_pred = logreg_clf.predict(X_test)

# Calculate accuracy scores
logreg_train_acc = accuracy_score(y_train, y_train_pred)
logreg_test_acc = accuracy_score(y_test, y_test_pred)

print(f"Training Accuracy of Logistic Regression Classifier: {logreg_train_acc:.4f}")
print(f"Test Accuracy of Logistic Regression Classifier: {logreg_test_acc:.4f}")

# Calculate confusion matrix
conf_matrix_logreg = confusion_matrix(y_test, y_test_pred)

print(f"Confusion Matrix:\n{conf_matrix_logreg}")
# Visualize the confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix_logreg, annot=True, fmt='d', cmap='Blues', cbar=False)
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix for Logistic Regression Classifier')
plt.show()

print(f"Classification Report:\n{classification_report(y_test, y_test_pred)}")
```

```
Training Accuracy of Logistic Regression Classifier: 0.9187
Test Accuracy of Logistic Regression Classifier: 0.9250
Confusion Matrix:
[[49  3]
 [ 3 25]]
```




```
Classification Report:
              precision    recall  f1-score   support

           0       0.94      0.94      0.94        52
           1       0.89      0.89      0.89        28

    accuracy                           0.93        80
   macro avg       0.92      0.92      0.92        80
weighted avg       0.93      0.93      0.93        80
```

In [105…

```python
from sklearn.model_selection import GridSearchCV

param_grid = {
    'C': [0.001, 0.01, 0.1, 1, 10, 100],
    'penalty': ['l1', 'l2'],
    'solver': ['liblinear', 'saga']
}

grid_search = GridSearchCV(LogisticRegression(), param_grid, cv=5)
grid_search.fit(X_train, y_train)

best_params = grid_search.best_params_
best_model = grid_search.best_estimator_

print("Best Hyperparameters:", best_params)

# Evaluate the best model
y_test_pred = best_model.predict(X_test)
logreg_test_acc = accuracy_score(y_test, y_test_pred)

print(f"Test Accuracy of Best Logistic Regression Classifier: {logreg_test_acc:.4f}")
```

```
Best Hyperparameters: {'C': 100, 'penalty': 'l2', 'solver': 'liblinear'}
Test Accuracy of Best Logistic Regression Classifier: 0.9750
```

Forward Nural Network

In [109…
```
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from keras.models import Sequential
from keras.layers import Dense
```

In [110…
```
# Splitting the data into features (X) and target variable (y)
X = df.drop('class', axis=1)  # Features
y = df['class']               # Target variable

# Splitting the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=

# Standardize the features
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

In [111…
```
model = Sequential()
model.add(Dense(64, activation='relu', input_dim=X_train_scaled.shape[1]))
model.add(Dense(32, activation='relu'))
model.add(Dense(1, activation='sigmoid'))
```

In [112…
```
model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
```

In [113…
```
history = model.fit(X_train_scaled, y_train, epochs=10, batch_size=32, validation_spli
```

```
Epoch 1/10
8/8 [==============================] - 1s 39ms/step - loss: 0.5139 - accuracy: 0.7109
- val_loss: 0.4125 - val_accuracy: 0.9062
Epoch 2/10
8/8 [==============================] - 0s 6ms/step - loss: 0.3431 - accuracy: 0.9766
- val_loss: 0.2877 - val_accuracy: 0.9844
Epoch 3/10
8/8 [==============================] - 0s 5ms/step - loss: 0.2475 - accuracy: 0.9844
- val_loss: 0.2118 - val_accuracy: 0.9844
Epoch 4/10
8/8 [==============================] - 0s 5ms/step - loss: 0.1837 - accuracy: 0.9844
- val_loss: 0.1592 - val_accuracy: 0.9688
Epoch 5/10
8/8 [==============================] - 0s 6ms/step - loss: 0.1360 - accuracy: 0.9883
- val_loss: 0.1230 - val_accuracy: 0.9844
Epoch 6/10
8/8 [==============================] - 0s 5ms/step - loss: 0.1014 - accuracy: 0.9922
- val_loss: 0.0979 - val_accuracy: 1.0000
Epoch 7/10
8/8 [==============================] - 0s 5ms/step - loss: 0.0778 - accuracy: 0.9961
- val_loss: 0.0800 - val_accuracy: 1.0000
Epoch 8/10
8/8 [==============================] - 0s 5ms/step - loss: 0.0608 - accuracy: 0.9961
- val_loss: 0.0672 - val_accuracy: 1.0000
Epoch 9/10
8/8 [==============================] - 0s 5ms/step - loss: 0.0486 - accuracy: 0.9961
- val_loss: 0.0578 - val_accuracy: 1.0000
Epoch 10/10
8/8 [==============================] - 0s 5ms/step - loss: 0.0390 - accuracy: 0.9961
- val_loss: 0.0511 - val_accuracy: 1.0000
```

In [114…

```
test_loss, test_accuracy = model.evaluate(X_test_scaled, y_test)
print(f"Test Loss: {test_loss:.4f}")
print(f"Test Accuracy: {test_accuracy:.4f}")
```

```
3/3 [==============================] - 0s 2ms/step - loss: 0.0431 - accuracy: 0.9875
Test Loss: 0.0431
Test Accuracy: 0.9875
```

In [ ]:

model evaluation

In [120…

```
from sklearn.linear_model import LogisticRegression

# Create and train a Logistic Regression model
lr_model = LogisticRegression()
lr_model.fit(X_train, y_train)

# Evaluate Logistic Regression
lr_pred = lr_model.predict(X_test)
print_metrics("Logistic Regression", y_test, lr_pred)
```

```
Logistic Regression Metrics:
Accuracy: 0.9250
Precision: 0.8929
Recall: 0.8929
F1-score: 0.8929
ROC AUC: 0.9176
```

In [123…

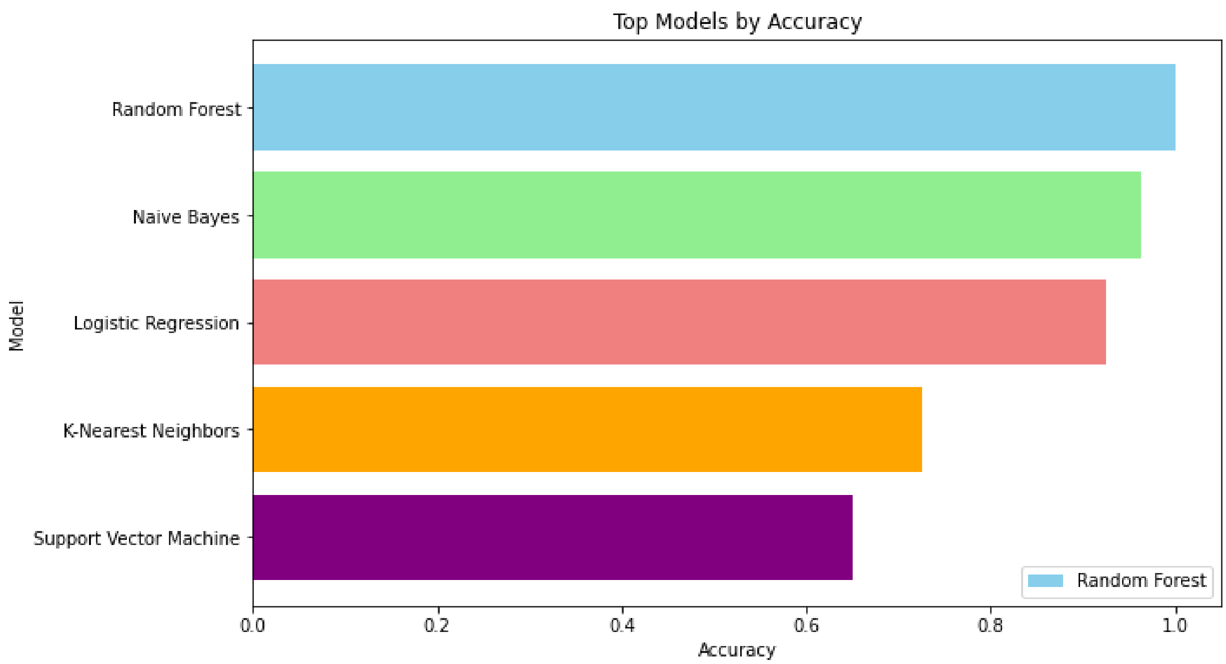
```
#from sklearn.linear_model import LogisticRegression
#from sklearn.ensemble import RandomForestClassifier
#from sklearn.svm import SVC
#from sklearn.naive_bayes import GaussianNB
#from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score, r

# Create an empty DataFrame to store results
results_df = pd.DataFrame(columns=['Model', 'Accuracy', 'Precision', 'Recall', 'F1 Sco

# List of models
models = [
    ('Logistic Regression', LogisticRegression()),
    ('Random Forest', RandomForestClassifier()),
    ('Support Vector Machine', SVC()),
    ('Naive Bayes', GaussianNB()),
    ('K-Nearest Neighbors', KNeighborsClassifier())
]

# Iterate through each model
for name, model in models:
    model.fit(X_train, y_train)  # Train the model
    y_pred = model.predict(X_test)  # Predict on the test set

    accuracy = accuracy_score(y_test, y_pred)
    precision = precision_score(y_test, y_pred)
    recall = recall_score(y_test, y_pred)
    f1 = f1_score(y_test, y_pred)
    roc_auc = roc_auc_score(y_test, y_pred)

    results_df = results_df.append({
        'Model': name,
        'Accuracy': accuracy,
        'Precision': precision,
        'Recall': recall,
        'F1 Score': f1,
        'ROC AUC': roc_auc
    }, ignore_index=True)

# Display the results DataFrame
print(results_df)
```

```
                    Model  Accuracy  Precision  Recall  F1 Score  ROC AUC
0     Logistic Regression    0.9250     0.8929  0.8929    0.8929   0.9176
1           Random Forest    1.0000     1.0000  1.0000    1.0000   1.0000
2  Support Vector Machine    0.6500     0.0000  0.0000    0.0000   0.5000
3             Naive Bayes    0.9625     0.9630  0.9286    0.9455   0.9547
4     K-Nearest Neighbors    0.7250     0.5682  0.8929    0.6944   0.7637
```

In [125…

```
#import matplotlib.pyplot as plt

# Define colors for each model
```

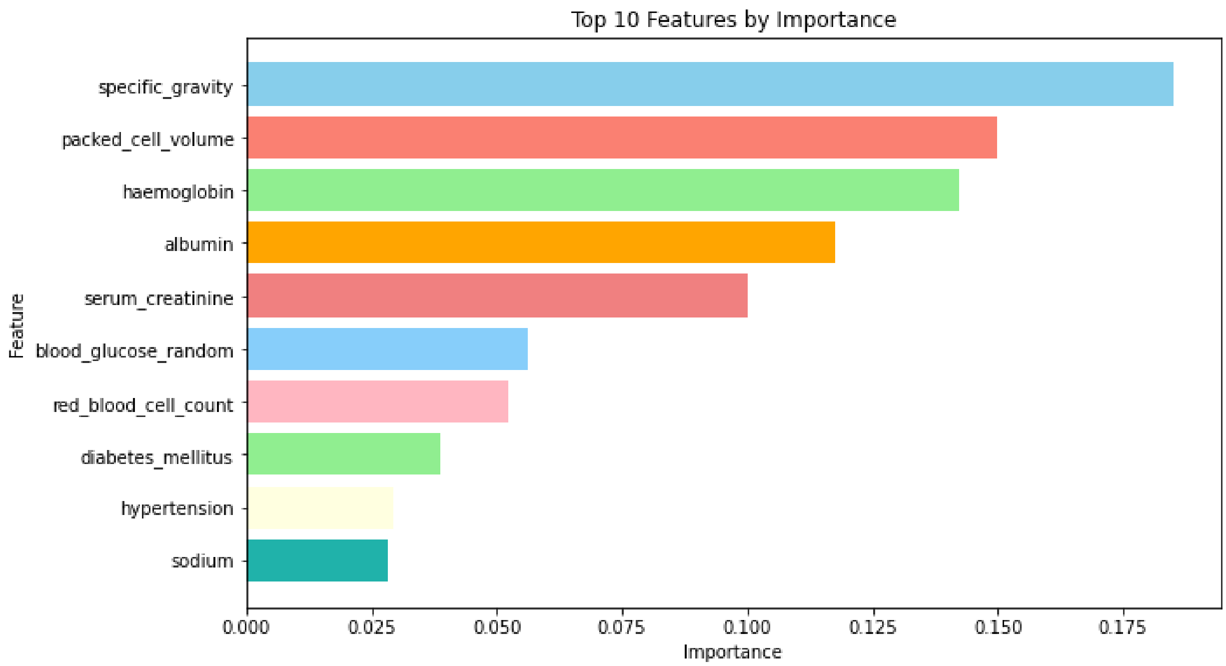
```
colors = ['skyblue', 'lightgreen', 'lightcoral', 'orange', 'purple']

# Sort the results DataFrame by Accuracy Score in descending order
results_df_sorted = results_df.sort_values(by='Accuracy', ascending=False)

# Create a bar chart with custom colors
plt.figure(figsize=(10, 6))
plt.barh(results_df_sorted['Model'], results_df_sorted['Accuracy'], color=colors)
plt.xlabel('Accuracy')
plt.ylabel('Model')
plt.title('Top Models by Accuracy')
plt.gca().invert_yaxis()  # Invert y-axis to have the highest accuracy on top

# Add a legend with model names and corresponding colors
plt.legend(results_df_sorted['Model'], loc='lower right')

plt.show()
```



In [127…

```
# eady trained the Random Forest model
rd_clf.fit(X_train, y_train)

# Get feature importances from the trained Random Forest model
feature_importances = rd_clf.feature_importances_

# Create a DataFrame with feature names and their corresponding importances
feature_importance_df = pd.DataFrame({'Feature': X.columns, 'Importance': feature_impo

# Sort the DataFrame by importance in descending order
feature_importance_df_sorted = feature_importance_df.sort_values(by='Importance', asce

# Choose different colors for the bars
colors = ['skyblue', 'salmon', 'lightgreen', 'orange', 'lightcoral', 'lightskyblue', '

# Plot the top N features and their importances with different colors
top_n = 10  # Number of top features to display
plt.figure(figsize=(10, 6))
plt.barh(feature_importance_df_sorted['Feature'][:top_n], feature_importance_df_sorted
plt.xlabel('Importance')
```

```
plt.ylabel('Feature')
plt.title(f'Top {top_n} Features by Importance')
plt.gca().invert_yaxis()  # Invert y-axis to have the highest importance on top

plt.show()
```



Model Save

In [130…

```
import joblib

# List of models
models = [
    ('Logistic Regression', LogisticRegression()),
    ('Random Forest', RandomForestClassifier()),
    ('Support Vector Machine', SVC()),
    ('Naive Bayes', GaussianNB()),
    ('K-Nearest Neighbors', KNeighborsClassifier())
]
# Save each model
for name, model in models:
    model_filename = f'{name.lower().replace(" ", "_")}_model.joblib'
    joblib.dump(model, model_filename)
    print(f"Model '{name}' saved as '{model_filename}'")
```

```
Model 'Logistic Regression' saved as 'logistic_regression_model.joblib'
Model 'Random Forest' saved as 'random_forest_model.joblib'
Model 'Support Vector Machine' saved as 'support_vector_machine_model.joblib'
Model 'Naive Bayes' saved as 'naive_bayes_model.joblib'
Model 'K-Nearest Neighbors' saved as 'k-nearest_neighbors_model.joblib'
```

In [131…

```
import pickle

# List of models
models = [
    ('Logistic Regression', LogisticRegression()),
    ('Random Forest', RandomForestClassifier()),
    ('Support Vector Machine', SVC()),
```

```
    ('Naive Bayes', GaussianNB()),
    ('K-Nearest Neighbors', KNeighborsClassifier())
]
# Save each model
for name, model in models:
    model_filename = f'{name.lower().replace(" ", "_")}_model.pkl'
    with open(model_filename, 'wb') as file:
        pickle.dump(model, file)
    print(f"Model '{name}' saved as '{model_filename}'")
```

```
Model 'Logistic Regression' saved as 'logistic_regression_model.pkl'
Model 'Random Forest' saved as 'random_forest_model.pkl'
Model 'Support Vector Machine' saved as 'support_vector_machine_model.pkl'
Model 'Naive Bayes' saved as 'naive_bayes_model.pkl'
Model 'K-Nearest Neighbors' saved as 'k-nearest_neighbors_model.pkl'
```

In [132…

```
import pickle

# Create a dictionary to store the models
all_models = {}
for name, model in models:
    all_models[name] = model

# Save the dictionary of models
with open('all_models.pkl', 'wb') as file:
    pickle.dump(all_models, file)

print("All models saved as 'all_models.pkl'")
```

```
All models saved as 'all_models.pkl'
```

In [ ]: