

MEM680T - Homework Assignment 6: Machine Learning Application in Project Dataset

This dataset encompasses information intended for the assessment of obesity levels among individuals in the nations of Mexico, Peru, and Colombia.

The attributes related with eating habits are:

- 1. Frequent consumption of high caloric food (FAVC)
- 2. Frequency of consumption of vegetables (FCVC)
- 3. Number of main meals (NCP)
- 4. Consumption of food between meals (CAEC)
- 5. Consumption of water daily (CH20)
- 6. Consumption of alcohol (CALC)

The attributes related with the physical condition are:

- 1. Calories consumption monitoring (SCC)
- 2. Physical activity frequency (FAF)
- 3. Time using technology devices (TUE)
- 4. Transportation used (MTRANS)

other variables obtained were:

- 1. Gender
- 2. Age
- 3. Height
- 4. Weight
- 5. family history with overweight
- 6. SMOKE activity

Finally, all data was labeled and the class variable NObesity was created with the values of:

- a) Insufficient Weight
- b) Normal Weight
- c) Overweight Level I
- d) Overweight Level II
- e) Obesity Type I
- f) Obesity Type II
- g) Obesity Type III

```
In [ ]: import pandas as pd
from matplotlib import pyplot as plt
import seaborn as sns
import numpy as np
```

Displaying the dataset, examining the first few rows, and checking for any missing data or understanding the dataset's structure.

```
In [ ]: # importing dataset and initial assestment
df = pd.read_csv('/content/drive/MyDrive/HW4/ObesityDataSet.csv')
df_initial=df
df
```

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Final_Project

Out []:

	Gender	Age	Height	Weight	family_history_with_overweight	FAVC	FCVC	NCP	CAEC	SMOKE	CH2O	SCC	FAF	TU
0	Female	21.000000	1.620000	64.000000	yes	no	2.0	3.0	Sometimes	no	2.000000	no	0.000000	1.000000
1	Female	21.000000	1.520000	56.000000	yes	no	3.0	3.0	Sometimes	yes	3.000000	yes	3.000000	0.000000
2	Male	23.000000	1.800000	77.000000	yes	no	2.0	3.0	Sometimes	no	2.000000	no	2.000000	1.000000
3	Male	27.000000	1.800000	87.000000	no	no	3.0	3.0	Sometimes	no	2.000000	no	2.000000	0.000000
4	Male	22.000000	1.780000	89.800000	no	no	2.0	1.0	Sometimes	no	2.000000	no	0.000000	0.000000
...
2106	Female	20.976842	1.710730	131.408528	yes	yes	3.0	3.0	Sometimes	no	1.728139	no	1.676269	0.906240
2107	Female	21.982942	1.748584	133.742943	yes	yes	3.0	3.0	Sometimes	no	2.005130	no	1.341390	0.599270
2108	Female	22.524036	1.752206	133.689352	yes	yes	3.0	3.0	Sometimes	no	2.054193	no	1.414209	0.646280
2109	Female	24.361936	1.739450	133.346641	yes	yes	3.0	3.0	Sometimes	no	2.852339	no	1.139107	0.586030
2110	Female	23.664709	1.738836	133.472641	yes	yes	3.0	3.0	Sometimes	no	2.863513	no	1.026452	0.714130

2111 rows × 17 columns

◀

▶

Data cleaning To omit rows with missing values and keep only one occurrence of each set of duplicate rows.

Display information about the original and cleaned DataFrames. Omit rows with missing values. Remove duplicate rows. Optionally, save the cleaned DataFrame to a new file. Generate a report on missing values and duplicates. Print the number of rows that have been deleted during the cleaning process.

In []:

```
print("Original DataFrame Info:")
print(df.info())

# Count the number of rows before cleaning
original_rows = len(df)

# Omit rows with missing values
df_cleaned = df.dropna() # Drop rows with any missing values

# Remove duplicates, keeping the first occurrence
df_cleaned = df_cleaned.drop_duplicates()

# Count the number of rows after cleaning
cleaned_rows = len(df_cleaned)

# Display information about the cleaned DataFrame
print('-----')
print('-----')
print("\nCleaned DataFrame Info:")
print(df_cleaned.info())
print('-----')
print('-----')

# Print the number of rows deleted
rows_deleted = original_rows - cleaned_rows
print('-----')
print('-----')
print(f"\nNumber of Rows Deleted: {rows_deleted}")
print('-----')
print('-----')

# we can save the cleaned DataFrame to a new file
# df_cleaned.to_csv('cleaned_data.csv', index=False)

# Generate a report on missing values and duplicates
report = pd.DataFrame({
    'Column': df.columns,
    'Missing Values': df.isnull().sum(),
    'Unique Values': df.nunique(),
    'Duplicates': df.duplicated().sum()
})

print("\nReport on Missing Values and Duplicates:")
print(report)
print('-----')
print('The data is cleaned!')
print('-----')
df=df_cleaned
df = df.reset_index(drop=True)
df
```


CAEC	0	4	24
SMOKE	0	2	24
CH2O	0	1268	24
SCC	0	2	24
FAF	0	1190	24
TUE	0	1129	24
CALC	0	4	24
MTRANS	0	5	24
NObeyesdad	0	7	24

The data is cleaned!

Out[]:

	Gender	Age	Height	Weight	family_history_with_overweight	FAVC	FCVC	NCP	CAEC	SMOKE	CH2O	SCC	FAF	TU
0	Female	21.000000	1.620000	64.000000	yes	no	2.0	3.0	Sometimes	no	2.000000	no	0.000000	1.000000
1	Female	21.000000	1.520000	56.000000	yes	no	3.0	3.0	Sometimes	yes	3.000000	yes	3.000000	0.000000
2	Male	23.000000	1.800000	77.000000	yes	no	2.0	3.0	Sometimes	no	2.000000	no	2.000000	1.000000
3	Male	27.000000	1.800000	87.000000	no	no	3.0	3.0	Sometimes	no	2.000000	no	2.000000	0.000000
4	Male	22.000000	1.780000	89.800000	no	no	2.0	1.0	Sometimes	no	2.000000	no	0.000000	0.000000
...
2082	Female	20.976842	1.710730	131.408528	yes	yes	3.0	3.0	Sometimes	no	1.728139	no	1.676269	0.906241
2083	Female	21.982942	1.748584	133.742943	yes	yes	3.0	3.0	Sometimes	no	2.005130	no	1.341390	0.599271
2084	Female	22.524036	1.752206	133.689352	yes	yes	3.0	3.0	Sometimes	no	2.054193	no	1.414209	0.646281
2085	Female	24.361936	1.739450	133.346641	yes	yes	3.0	3.0	Sometimes	no	2.852339	no	1.139107	0.586031
2086	Female	23.664709	1.738836	133.472641	yes	yes	3.0	3.0	Sometimes	no	2.863513	no	1.026452	0.714131

2087 rows × 17 columns

In []:

```
# Report after cleaning
df.head() #Examination of dataset
df.info() #Check possibility of missing data for each column
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2087 entries, 0 to 2086
Data columns (total 17 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   Gender                                2087 non-null   object
1   Age                                   2087 non-null   float64
2   Height                               2087 non-null   float64
3   Weight                               2087 non-null   float64
4   family_history_with_overweight       2087 non-null   object
5   FAVC                                 2087 non-null   object
6   FCVC                                 2087 non-null   float64
7   NCP                                  2087 non-null   float64
8   CAEC                                 2087 non-null   object
9   SMOKE                                2087 non-null   object
10  CH2O                                 2087 non-null   float64
11  SCC                                  2087 non-null   object
12  FAF                                  2087 non-null   float64
13  TUE                                  2087 non-null   float64
14  CALC                                 2087 non-null   object
15  MTRANS                               2087 non-null   object
16  NObeyesdad                           2087 non-null   object
dtypes: float64(8), object(9)
memory usage: 277.3+ KB
```

Categorical Data

Identifying and analyzing categorical data, providing detailed insights for each category and graphically show each of them.

1. Text Explanation:

Column Information:

Column Name: The name of the categorical column being analyzed.

Number of Unique States: The total number of unique categories or states within the column.

States and Counts: A breakdown of each unique state along with the count of occurrences in the dataset.

2. Graphical Representation:

Type of Diagram: Bar Chart (specifically, sns.countplot is used).

X-Axis: Represents the unique states or categories within the column.

Y-Axis: Represents the count or frequency of each state.

Title: Indicates the distribution of the categorical variable.

```
In [ ]: # Identify categorical columns
categorical_cols = df.select_dtypes(include=['object']).columns

# Determine the number of rows needed for the subplots
num_rows = (len(categorical_cols) + 2) // 3 # Add 2 to round up to the nearest multiple of 3

# Create subplots with the determined number of rows
fig, axes = plt.subplots(nrows=num_rows, ncols=3, figsize=(15, 5 * num_rows))

for i, col in enumerate(categorical_cols):
    unique_states = df[col].unique()
    num_states = len(unique_states)
    states_count = df[col].value_counts()

    # Display results in text format
    text_result = f"\n{' '*30}\nColumn: {col}\n{' '*30}\nNumber of unique states: {num_states}\nStates and their counts:\n{states_count}"
    print(text_result)

    # Plot a bar chart for visual representation
    row_index, col_index = divmod(i, 3)
    sns.countplot(x=col, data=df, palette='viridis', ax=axes[row_index, col_index])
    axes[row_index, col_index].set_title(f'Distribution of {col}')
    axes[row_index, col_index].set_xlabel(col)
    axes[row_index, col_index].set_ylabel('Count')
    axes[row_index, col_index].tick_params(axis='x', rotation=45, labelrotation=45) # Fix rotation

# Adjust layout for better visualization
plt.tight_layout()
plt.show()
```

=====

Column: Gender

=====

Number of unique states: 2

States and their counts:

Male 1052

Female 1035

Name: Gender, dtype: int64

=====

Column: family_history_with_overweight

=====

Number of unique states: 2

States and their counts:

yes 1722

no 365

Name: family_history_with_overweight, dtype: int64

=====

Column: FAVC

=====

Number of unique states: 2

States and their counts:

yes 1844

no 243

Name: FAVC, dtype: int64

=====

Column: CAEC

=====

Number of unique states: 4

States and their counts:

Sometimes 1761

Frequently 236

Always 53

no 37

Name: CAEC, dtype: int64

=====

Column: SMOKE

=====

Number of unique states: 2

States and their counts:

no 2043

yes 44

Name: SMOKE, dtype: int64

=====

Column: SCC

=====

Number of unique states: 2

States and their counts:

no 1991

yes 96

Name: SCC, dtype: int64

=====

Column: CALC

=====

Number of unique states: 4

States and their counts:

Sometimes 1380

no 636

Frequently 70

Always 1

Name: CALC, dtype: int64

=====

Column: MTRANS

=====

Number of unique states: 5

States and their counts:

Public_Transportation 1558

Automobile 456

Walking 55

Motorbike 11

Bike 7

Name: MTRANS, dtype: int64

=====

Column: NObeyesdad

=====

Number of unique states: 7

States and their counts:

Obesity_Type_I 351

Obesity_Type_III 324

Obesity_Type_II 297

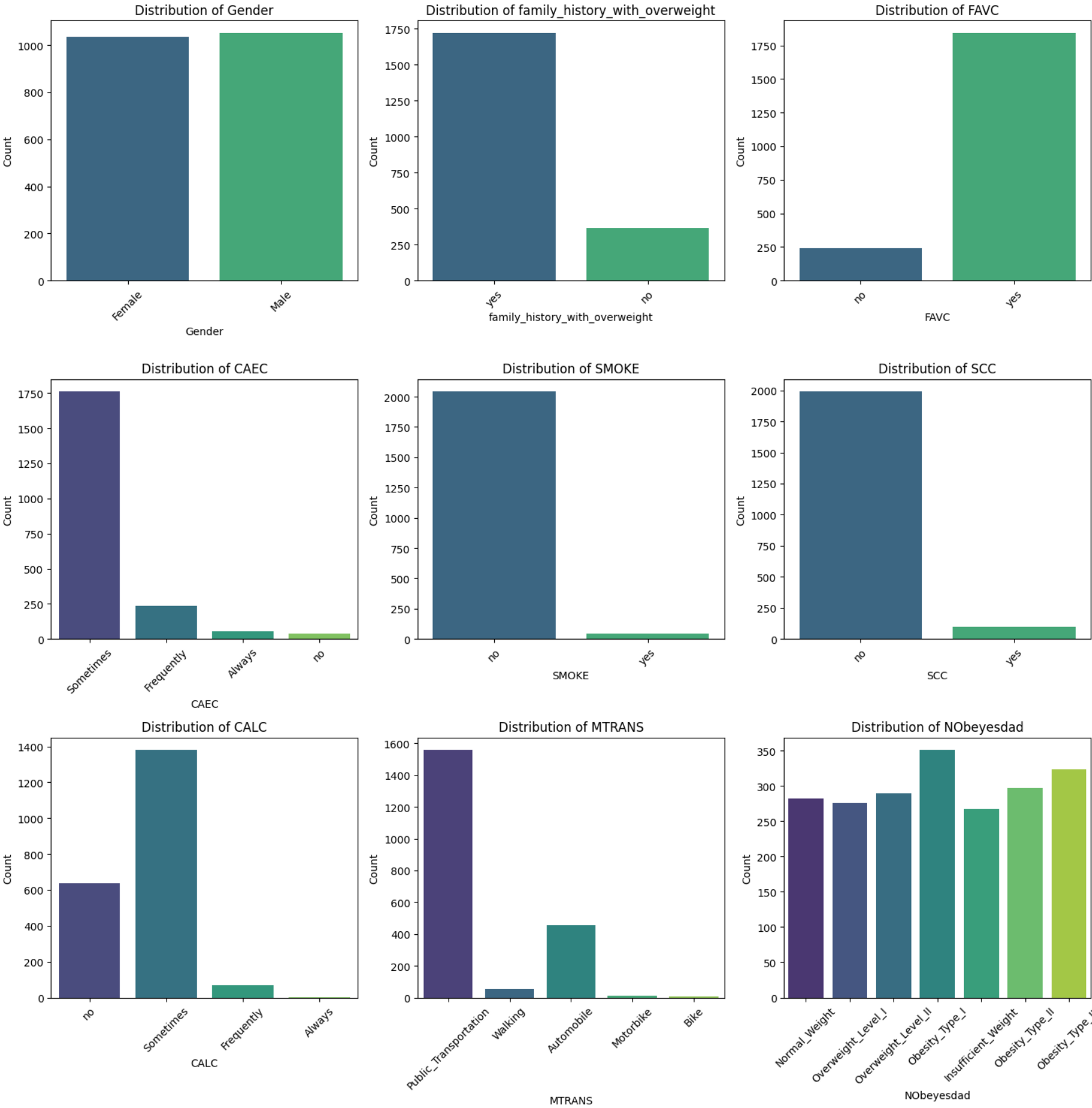
Overweight_Level_II 290

Normal_Weight 282

Overweight_Level_I 276

Insufficient_Weight 267

Name: NObeyesdad, dtype: int64



Non Categorical Data:-

1. Text Explanation:

Column Information: Column Name: The name of the non-categorical (numerical) column being analyzed.

Summary Statistics: Descriptive statistics, including count, mean, standard deviation, minimum, 25th percentile, median, 75th percentile, and maximum.

Minimum:

The smallest value in the dataset. It represents the floor or lower boundary of the dataset.

25th Percentile (First Quartile):

The value below which 25% of the data falls.

It is the first quartile and is also known as the lower quartile.

Median (50th Percentile or Second Quartile):

The middle value in the dataset when it is sorted in ascending order.

It represents the point below which 50% of the data falls.

In a symmetrical distribution, the median is the same as the mean.

75th Percentile (Third Quartile):

The value below which 75% of the data falls. It is the third quartile and is also known as the upper quartile.

2. Graphical Representation:

Type of Diagram: Histogram with Kernel Density Estimate (KDE) (specifically, sns.histplot is used).

X-Axis: Represents the numerical values within the column.

Y-Axis: Represents the frequency or density of values.

Title: Indicates the distribution of the numerical variable.

```
In [ ]: # Identify non-categorical columns (numerical)
numerical_cols = df.select_dtypes(include=['float64']).columns

# Determine the number of rows needed for the subplots
num_rows_numeric = (len(numerical_cols) + 2) // 3 # Add 2 to round up to the nearest multiple of 3

# Create subplots for non-categorical data
fig_numeric, axes_numeric = plt.subplots(nrows=num_rows_numeric, ncols=3, figsize=(15, 5 * num_rows_numeric))

# Initialize variables for tracking text results
text_results_numeric = []

for i, col in enumerate(numerical_cols):
    # Display results in text format
    text_result_numeric = f"\n{'='*30}\nColumn: {col}\n{'='*30}\n"
    text_result_numeric += f"Summary Statistics:\n{df[col].describe()}"
    text_results_numeric.append(text_result_numeric)
    #if not df[col].dropna().empty:
        # Plot a histogram for visual representation
    row_index, col_index = divmod(i, 3)
    sns.histplot(data=df, x=col, bins=20, kde=True, color='skyblue', ax=axes_numeric[row_index, col_index])
    axes_numeric[row_index, col_index].set_title(f'Distribution of {col}')
    axes_numeric[row_index, col_index].set_xlabel(col)
    axes_numeric[row_index, col_index].set_ylabel('Frequency')

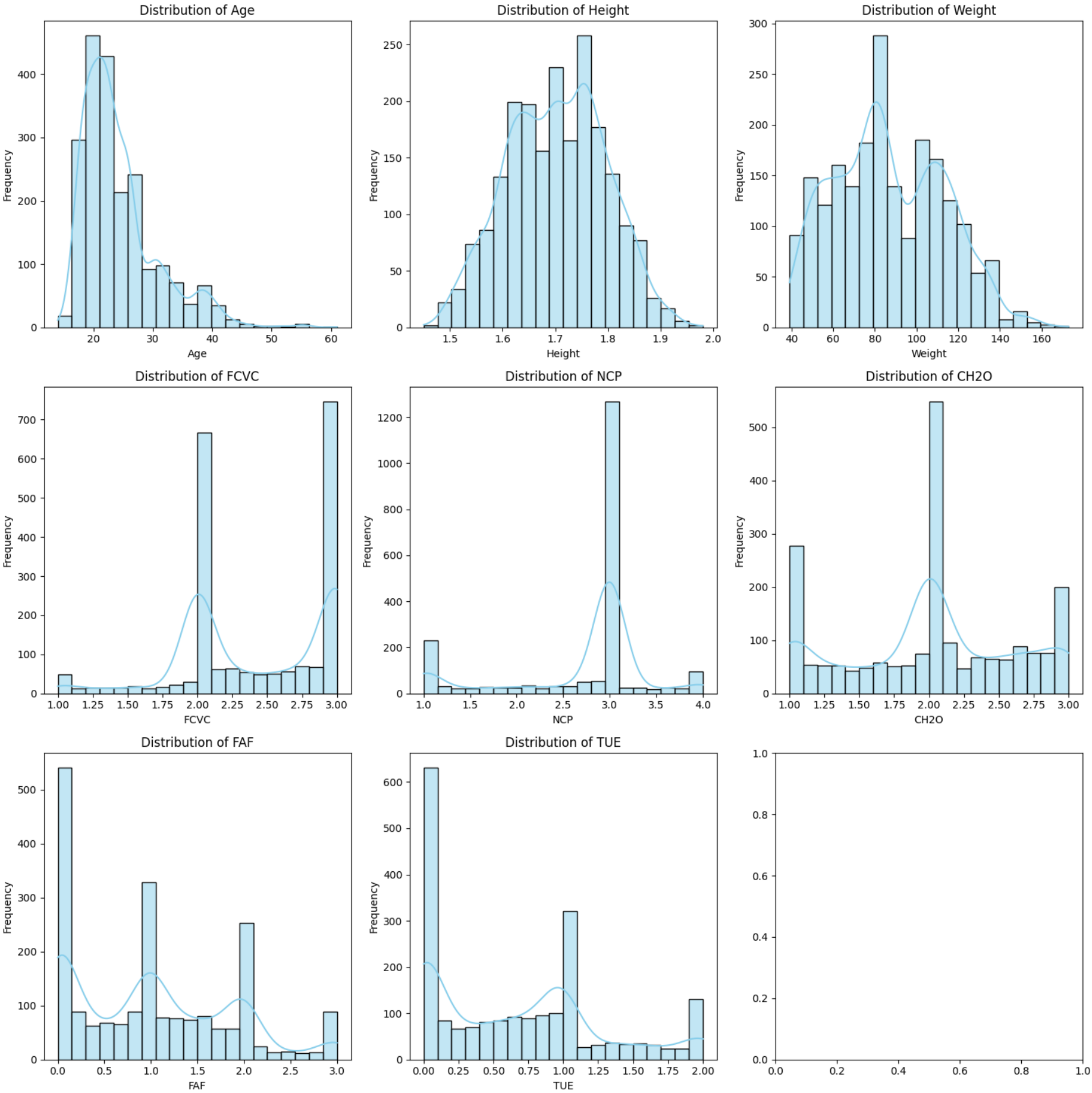
# Display text results for non-categorical data
text_results_numeric_str = ' '.join(text_results_numeric)
print(text_results_numeric_str)

# Adjust layout for better visualization
plt.tight_layout()
plt.show()
```



```
=====
Column: Age
=====
Summary Statistics:
count      2087.000000
mean       24.353090
std        6.368801
min        14.000000
25%        19.915937
50%        22.847618
75%        26.000000
max        61.000000
Name: Age, dtype: float64
=====
Column: Height
=====
Summary Statistics:
count      2087.000000
mean       1.702674
std        0.093186
min        1.450000
25%        1.630178
50%        1.701584
75%        1.769491
max        1.980000
Name: Height, dtype: float64
=====
Column: Weight
=====
Summary Statistics:
count      2087.000000
mean       86.858730
std        26.190847
min        39.000000
25%        66.000000
50%        83.101100
75%        108.015907
max        173.000000
Name: Weight, dtype: float64
=====
Column: FCVC
=====
Summary Statistics:
count      2087.000000
mean       2.421466
std        0.534737
min        1.000000
25%        2.000000
50%        2.396265
75%        3.000000
max        3.000000
Name: FCVC, dtype: float64
=====
Column: NCP
=====
Summary Statistics:
count      2087.000000
mean       2.701179
std        0.764614
min        1.000000
25%        2.697467
50%        3.000000
75%        3.000000
max        4.000000
Name: NCP, dtype: float64
=====
Column: CH2O
=====
Summary Statistics:
count      2087.000000
mean       2.004749
std        0.608284
min        1.000000
25%        1.590922
50%        2.000000
75%        2.466193
max        3.000000
Name: CH2O, dtype: float64
=====
Column: FAF
=====
Summary Statistics:
count      2087.000000
mean       1.012812
std        0.853475
min        0.000000
25%        0.124505
50%        1.000000
75%        1.678102
max        3.000000
Name: FAF, dtype: float64
=====
Column: TUE
```

```
=====
Summary Statistics:
count    2087.000000
mean      0.663035
std       0.608153
min       0.000000
25%      0.000000
50%      0.630866
75%      1.000000
max       2.000000
Name: TUE, dtype: float64
```



Transforming categorical variables into a suitable format for numerical computation.

Ordinal Categorical Variables: Ordinal variables are categorical variables with a natural order or ranking between the categories. The distances between the categories are not defined, but there is a clear order. Examples include education levels (e.g., high school, bachelor's, master's), economic status (e.g., low, medium, high), or customer satisfaction levels (e.g., low, medium, high). For our dataset:

- 1. Category of Obesity (NObesity)
- 2. Consumption of food between meals (CAEC)
- 3. Consumption of alcohol (CALC)

Handling in Machine Learning:

Ordinal variables are often encoded using label encoding, where each category is assigned a unique integer. The order of the integers reflects the order of the categories. Algorithms: Many machine learning algorithms can handle ordinal variables well. Decision trees and ensemble methods (e.g., Random Forests) are particularly suitable as they can naturally split data based on ordinal features.

Binary Variables: Binary variables take on only two possible values, often 0 and 1. These variables are a special case of categorical variables where there are only two categories. Examples include yes/no, true/false, or the presence/absence of a particular characteristic. For our dataset: ['Gender', 'family_history_with_overweight', 'FAVC', 'SCC', 'MTRANS', 'SMOKE']

1. Gender
2. family_history_with_overweight
3. Frequent consumption of high caloric food (FAVC)
4. Calories consumption monitoring (SCC)
5. Transportation used (MTRANS) ---> a. Walking/ Public_Transportation/ Automobile/ Motorbike/ Bike
6. SMOKE activity

Handling in Machine Learning:

One-Hot Encoding: While binary variables can be left as they are (0 or 1), they can also be one-hot encoded to represent them as two separate columns (e.g., presence = 1, absence = 0). Algorithms: Binary variables are well-suited for algorithms that work with binary data. Logistic Regression, Support Vector Machines (SVM), and certain decision tree variants (e.g., CART) are commonly used for binary classification tasks.

In []:

```
from sklearn.preprocessing import OneHotEncoder, LabelEncoder

# Separate the data into numerical, non-ordinal categorical, and ordinal categorical columns
numerical_cols = ['Age', 'Height', 'Weight', 'FCVC', 'NCP', 'CH2O', 'FAF', 'TUE']
non_ordinal_categorical_cols = ['Gender', 'family_history_with_overweight', 'FAVC', 'SCC', 'MTRANS', 'SMOKE']
ordinal_categorical_col = ['CAEC', 'CALC', 'NObeyesdad']

# Separate the dataset into features (X) and target variable (y)
X = df[numerical_cols + non_ordinal_categorical_cols + ordinal_categorical_col]
y = df['NObeyesdad']

# One-Hot Encoding for non-ordinal categorical columns
encoder = OneHotEncoder(drop='first', sparse=False)
non_ordinal_categorical_encoded = encoder.fit_transform(X[non_ordinal_categorical_cols])

# Create a DataFrame for the One-Hot Encoded non-ordinal categorical columns
non_ordinal_categorical_encoded_df = pd.DataFrame(non_ordinal_categorical_encoded, columns=encoder.get_feature_names_out(non_ordinal_categorical_cols))

# Label Encoding for ordinal categorical columns
label_encoder = LabelEncoder()
for col in ordinal_categorical_col:
    X[col] = label_encoder.fit_transform(X[col])

# Concatenate the numerical columns, One-Hot Encoded non-ordinal categorical columns, and ordinal categorical columns
X_normalized_ctgric = pd.concat([X[numerical_cols], non_ordinal_categorical_encoded_df, X[ordinal_categorical_col]], axis=1)

# Display the normalized data
# print(X_normalized.head())
X_normalized_ctgric
```

/usr/local/lib/python3.10/dist-packages/sklearn/preprocessing/_encoders.py:868: FutureWarning: `sparse` was renamed to `sparse_output` in version 1.2 and will be removed in 1.4. `sparse_output` is ignored unless you leave `sparse` to its default value.
warnings.warn(

Out[]:

	Age	Height	Weight	FCVC	NCP	CH2O	FAF	TUE	Gender_Male	family_history_with_overweight_yes	FAVC_yes	SCC_yes	MTRANS
0	21.000000	1.620000	64.000000	2.0	3.0	2.000000	0.000000	1.000000	0.0	1.0	0.0	0.0	Walking
1	21.000000	1.520000	56.000000	3.0	3.0	3.000000	3.000000	0.000000	0.0	1.0	0.0	1.0	Walking
2	23.000000	1.800000	77.000000	2.0	3.0	2.000000	2.000000	1.000000	1.0	1.0	0.0	0.0	Walking
3	27.000000	1.800000	87.000000	3.0	3.0	2.000000	2.000000	0.000000	1.0	0.0	0.0	0.0	Walking
4	22.000000	1.780000	89.800000	2.0	1.0	2.000000	0.000000	0.000000	1.0	0.0	0.0	0.0	Walking
...
2082	20.976842	1.710730	131.408528	3.0	3.0	1.728139	1.676269	0.906247	0.0	1.0	1.0	0.0	Walking
2083	21.982942	1.748584	133.742943	3.0	3.0	2.005130	1.341390	0.599270	0.0	1.0	1.0	0.0	Walking
2084	22.524036	1.752206	133.689352	3.0	3.0	2.054193	1.414209	0.646288	0.0	1.0	1.0	0.0	Walking
2085	24.361936	1.739450	133.346641	3.0	3.0	2.852339	1.139107	0.586035	0.0	1.0	1.0	0.0	Walking
2086	23.664709	1.738836	133.472641	3.0	3.0	2.863513	1.026452	0.714137	0.0	1.0	1.0	0.0	Walking

2087 rows × 20 columns

Normalizing numerical Data

In the previous section Categorical data have been modified and in this section the Z_score and Min_Max methods have been used for normalizing numerical parameters.

Z-Score Normalization (Standardization):

['Age', 'Weight']

Pros:

Retains the shape of the original distribution. Sensitive to outliers, but doesn't overly amplify their impact.

Cons:

The resulting values may not be in a specific range.

Min-Max Normalization (Scaling):

['Height','Number of main meals (NCP)','Consumption of water daily (CH20)', 'Physical activity frequency (FAF)','Time using technology devices (TUE)']

Pros:

Scales the data to a specific range (commonly [0, 1]).

Simple and intuitive.

Cons: Sensitive to outliers, as extreme values can heavily influence the scaling.

```
In [ ]: from sklearn.preprocessing import StandardScaler, MinMaxScaler
numerical_columns = X_normalized_ctgric.select_dtypes(include=['float64', 'int64']).columns
# z_score_columns = []
# Separate columns based on normalization method
z_score_columns = ['Age', 'Weight']
#z_score_columns = ['Age']
exempt_catgr_data=['CAEC', 'CALC', 'NObeyesdad', 'Gender', 'family_history_with_overweight', 'Gender_Male', 'family_history_with_ove
min_max_columns = [col for col in numerical_columns if col not in z_score_columns if col not in exempt_catgr_data]

# Create a new DataFrame for normalized data
Normalized_df = X_normalized_ctgric.copy()

# Apply Z-score normalization to selected columns
scaler = StandardScaler()
if z_score_columns:
    Normalized_df[z_score_columns] = scaler.fit_transform(X_normalized_ctgric[z_score_columns])

# Apply Min-Max normalization to selected columns
min_max_scaler = MinMaxScaler()
Normalized_df[min_max_columns] = min_max_scaler.fit_transform(X_normalized_ctgric[min_max_columns])

# Print or use the Normalized_df DataFrame as needed
Normalized_df
```

Out []:

	Age	Height	Weight	FCVC	NCP	CH2O	FAF	TUE	Gender_Male	family_history_with_overweight_yes	FAVC_yes	SCC_yes
0	-0.526613	0.320755	-0.872985	0.5	0.666667	0.500000	0.000000	0.500000	0.0	1.0	0.0	0.0
1	-0.526613	0.132075	-1.178508	1.0	0.666667	1.000000	1.000000	0.000000	0.0	1.0	0.0	1.0
2	-0.212507	0.660377	-0.376509	0.5	0.666667	0.500000	0.666667	0.500000	1.0	1.0	0.0	0.0
3	0.415705	0.660377	0.005395	1.0	0.666667	0.500000	0.666667	0.000000	1.0	0.0	0.0	0.0
4	-0.369560	0.622642	0.112328	0.5	0.000000	0.500000	0.000000	0.000000	1.0	0.0	0.0	0.0
...
2082	-0.530250	0.491943	1.701376	1.0	0.666667	0.364070	0.558756	0.453124	0.0	1.0	1.0	0.0
2083	-0.372239	0.563366	1.790528	1.0	0.666667	0.502565	0.447130	0.299635	0.0	1.0	1.0	0.0
2084	-0.287258	0.570200	1.788482	1.0	0.666667	0.527097	0.471403	0.323144	0.0	1.0	1.0	0.0
2085	0.001389	0.546132	1.775393	1.0	0.666667	0.926170	0.379702	0.293017	0.0	1.0	1.0	0.0
2086	-0.108112	0.544974	1.780205	1.0	0.666667	0.931757	0.342151	0.357069	0.0	1.0	1.0	0.0

2087 rows × 13 columns



This section help us to follow the learning process by selecting the different dataset.

- 1. df: whitouth normalization (only data cleaning)
- 2. X_normalized_ctgric: Transforming categorical variables into a suitable format for numerical computation.
- 3. Normalized_df: all numerical data have been normalized

```
In [ ]: X_normalized= Normalized_df          # all numerical data have been normalized and categorical data have been converted
# X_normalized= X_normalized_ctgric      # only categorical data have been converted
#X_normalized=df                        # whitouth normalization

# separation Inputs and output
X=X_normalized.iloc[:, :-1]            # all Inputs
```

```
Y=X_normalized.iloc[:,-1] # output
X
# y
```

Out []:

	Age	Height	Weight	FCVC	NCP	CH2O	FAF	TUE	Gender_Male	family_history_with_overweight_yes	FAVC_yes	SCC_yes
0	-0.526613	0.320755	-0.872985	0.5	0.666667	0.500000	0.000000	0.500000	0.0	1.0	0.0	0.0
1	-0.526613	0.132075	-1.178508	1.0	0.666667	1.000000	1.000000	0.000000	0.0	1.0	0.0	1.0
2	-0.212507	0.660377	-0.376509	0.5	0.666667	0.500000	0.666667	0.500000	1.0	1.0	0.0	0.0
3	0.415705	0.660377	0.005395	1.0	0.666667	0.500000	0.666667	0.000000	1.0	0.0	0.0	0.0
4	-0.369560	0.622642	0.112328	0.5	0.000000	0.500000	0.000000	0.000000	1.0	0.0	0.0	0.0
...
2082	-0.530250	0.491943	1.701376	1.0	0.666667	0.364070	0.558756	0.453124	0.0	1.0	1.0	0.0
2083	-0.372239	0.563366	1.790528	1.0	0.666667	0.502565	0.447130	0.299635	0.0	1.0	1.0	0.0
2084	-0.287258	0.570200	1.788482	1.0	0.666667	0.527097	0.471403	0.323144	0.0	1.0	1.0	0.0
2085	0.001389	0.546132	1.775393	1.0	0.666667	0.926170	0.379702	0.293017	0.0	1.0	1.0	0.0
2086	-0.108112	0.544974	1.780205	1.0	0.666667	0.931757	0.342151	0.357069	0.0	1.0	1.0	0.0

2087 rows × 19 columns

Before and after of Normalizing

Graphically show the initial and modified dataset by using different plots.

```
In [ ]: # Assuming X and df are your dataframes, and 'NObesesdad' is a column in df
categories = ['Insufficient Weight', 'Normal Weight', 'Overweight Level I', 'Overweight Level II', 'Obesity Type I', 'Obesity Type II', 'Obesity Type III']

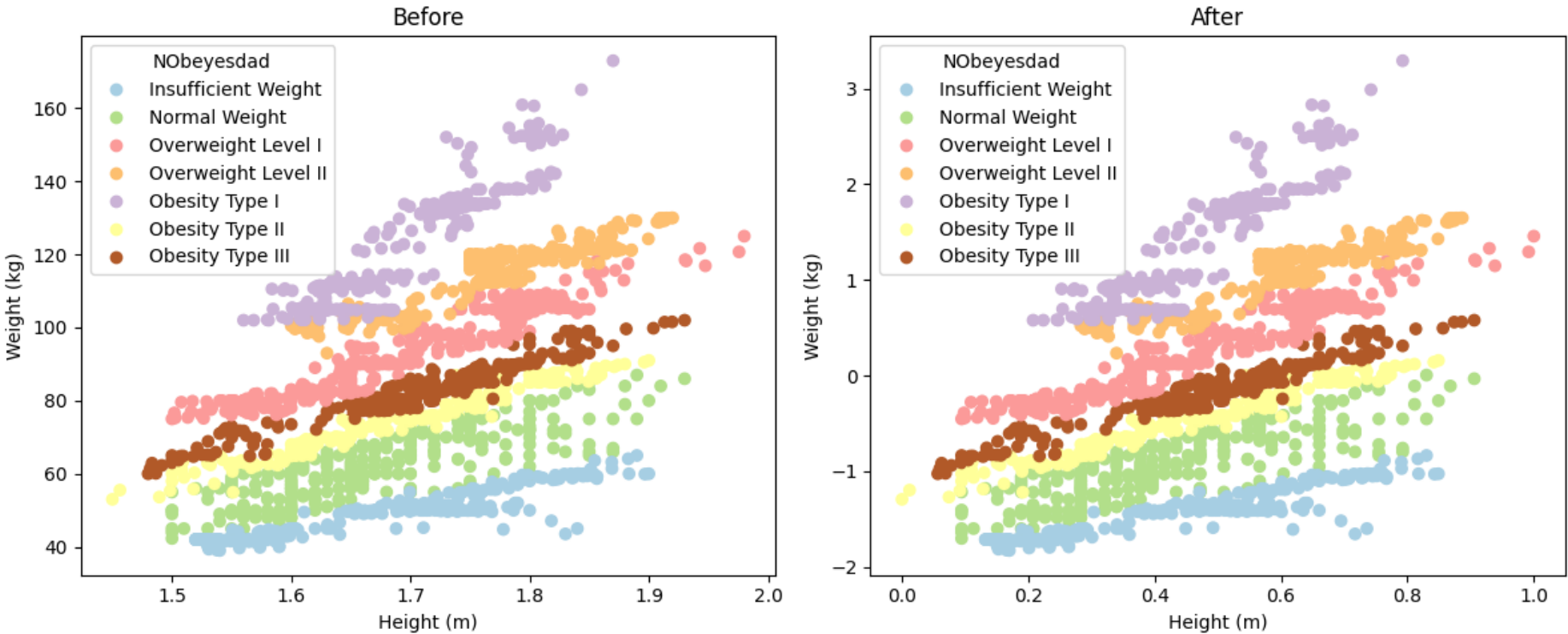
# Create a subplot grid with 1 row and 2 columns
fig, axs = plt.subplots(1, 2, figsize=(12, 5))

# Plot for the right side
scatter_plot_right = axs[1].scatter(x=X['Height'], y=X['Weight'], c=df['NObesesdad'].astype('category').cat.codes, cmap='Paired')
legend_right = axs[1].legend(handles=scatter_plot_right.legend_elements()[0], title='NObesesdad', labels=categories)
axs[1].set_xlabel('Height (m)')
axs[1].set_ylabel('Weight (kg)')
axs[1].set_title('After')

# Plot for the left side
scatter_plot_left = axs[0].scatter(x=df_initial['Height'], y=df_initial['Weight'], c=df_initial['NObesesdad'].astype('category').cat.codes, cmap='Paired')
legend_left = axs[0].legend(handles=scatter_plot_left.legend_elements()[0], title='NObesesdad', labels=categories)
axs[0].set_xlabel('Height (m)')
axs[0].set_ylabel('Weight (kg)')
axs[0].set_title('Before')

# Adjust layout to prevent clipping of the Legend
plt.tight_layout()

# Display the plots
plt.show()
```



```
In [ ]: # Assuming X and df are your dataframes, and 'NObesesdad' is a column in df
categories = ['Male', 'Female']

# Create a subplot grid with 1 row and 2 columns
fig, axs = plt.subplots(1, 2, figsize=(12, 5))

# Plot for the right side
```

```

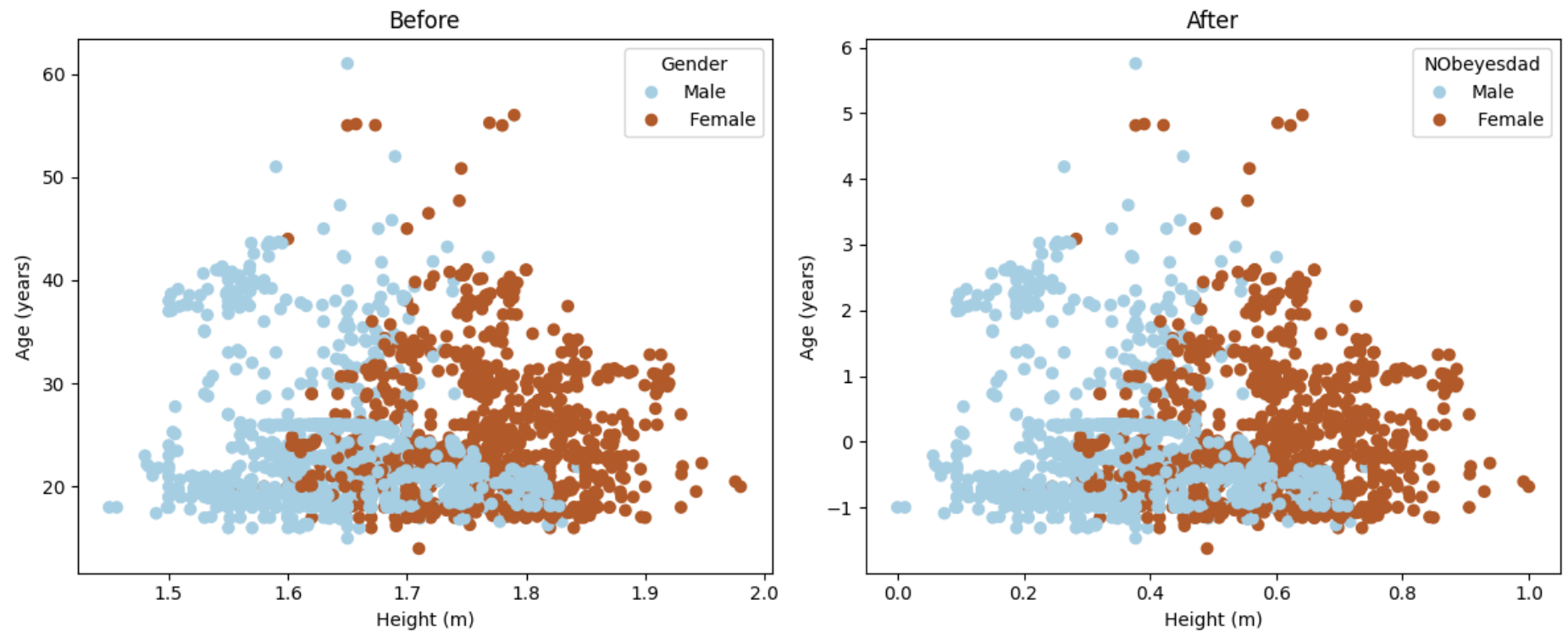
scatter_plot_right = axs[1].scatter(x=X['Height'], y=X['Age'], c=df['Gender'].astype('category').cat.codes, cmap='Paired')
legend_right = axs[1].legend(handles=scatter_plot_right.legend_elements()[0], title='NObeyesdad', labels=categories)
axs[1].set_xlabel('Height (m)')
axs[1].set_ylabel('Age (years)')
axs[1].set_title('After')

# Plot for the left side
scatter_plot_left = axs[0].scatter(x=df_initial['Height'], y=df_initial['Age'], c=df_initial['Gender'].astype('category').cat.codes, cmap='Paired')
legend_left = axs[0].legend(handles=scatter_plot_left.legend_elements()[0], title='Gender', labels=categories)
axs[0].set_xlabel('Height (m)')
axs[0].set_ylabel('Age (years)')
axs[0].set_title('Before')

# Adjust layout to prevent clipping of the Legend
plt.tight_layout()

# Display the plots
plt.show()

```



```

In [ ]: left_palette = 'Set2'
right_palette = 'Set1'

# First set of box plots
numerical_columns = ['Age', 'Height', 'Weight', 'FCVC', 'NCP', 'CH20', 'FAF', 'TUE']
num_plots = len(numerical_columns)
num_cols = min(num_plots, 2)
num_rows = -(-num_plots // num_cols) * 2 # Twice the number of rows for each variable

fig, axes = plt.subplots(nrows=num_rows, ncols=num_cols, figsize=(16, 4 * num_rows))
axes = axes.flatten()

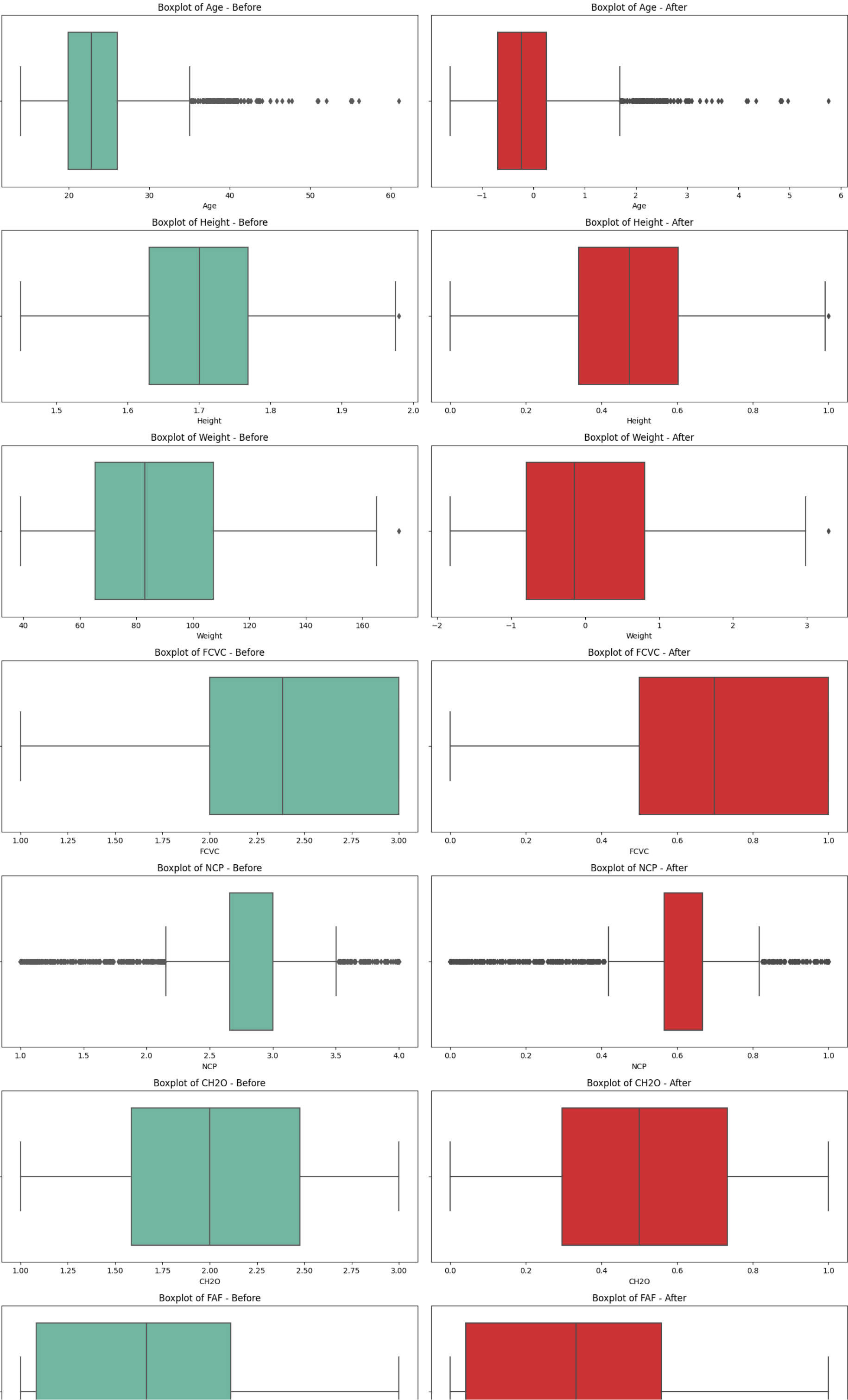
for i, column in enumerate(numerical_columns):
    sns.boxplot(x=df_initial[column], ax=axes[i * 2], palette=left_palette)
    axes[i * 2].set_title(f'Boxplot of {column} - Before')

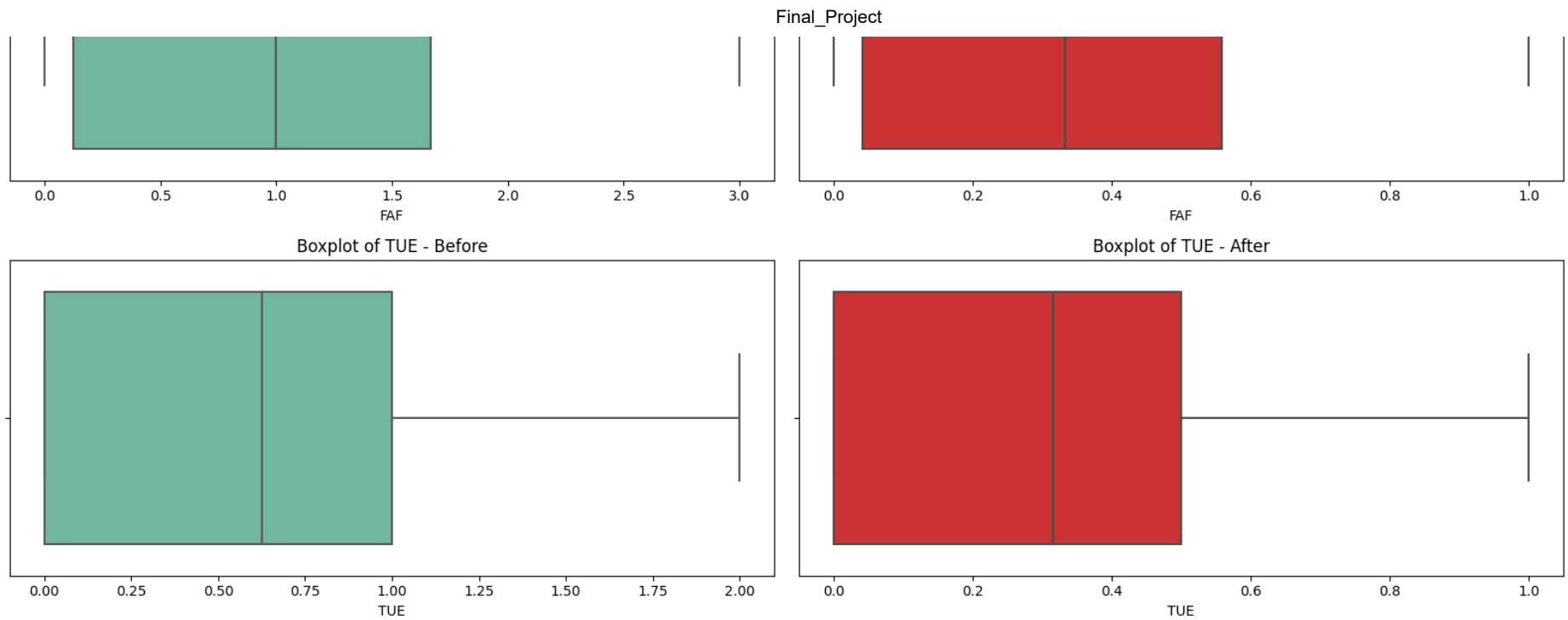
    sns.boxplot(x=X[column], ax=axes[i * 2 + 1], palette=right_palette)
    axes[i * 2 + 1].set_title(f'Boxplot of {column} - After')

for j in range(num_plots * 2, len(axes)):
    fig.delaxes(axes[j])

plt.tight_layout()
plt.show()

```





```
In [ ]: # Set custom colors for the left and right violin plots
left_palette = 'Set2'
right_palette = 'Set1'

# First set of violin plots
numerical_columns = ['Age', 'Height', 'Weight', 'FCVC', 'NCP', 'CH20', 'FAF', 'TUE']
num_plots = len(numerical_columns)
num_cols = min(num_plots, 2)
num_rows = -(-num_plots // num_cols) * 2 # Twice the number of rows for each variable

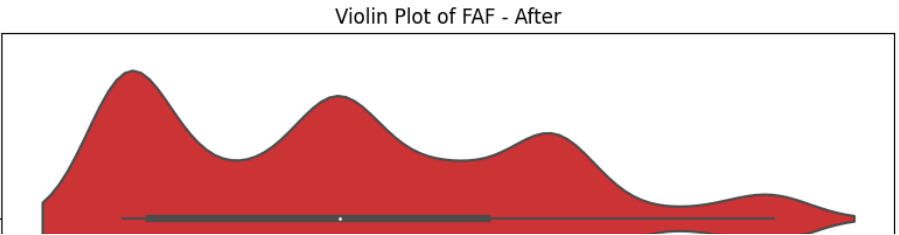
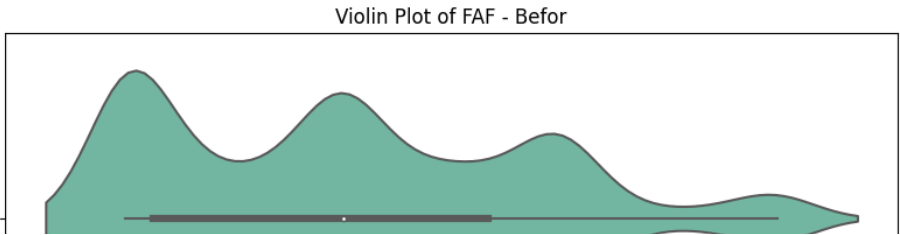
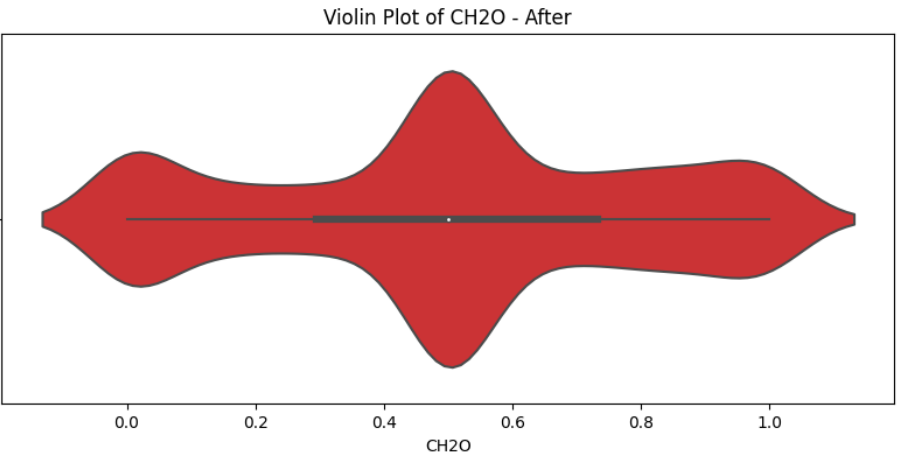
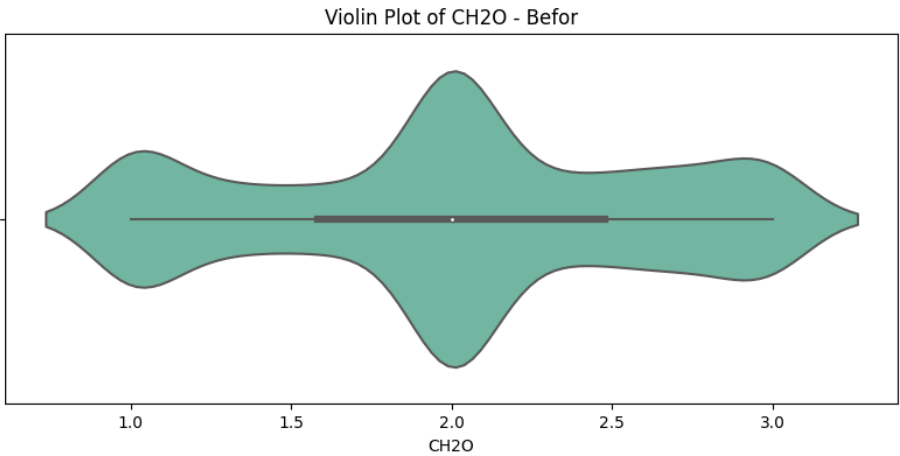
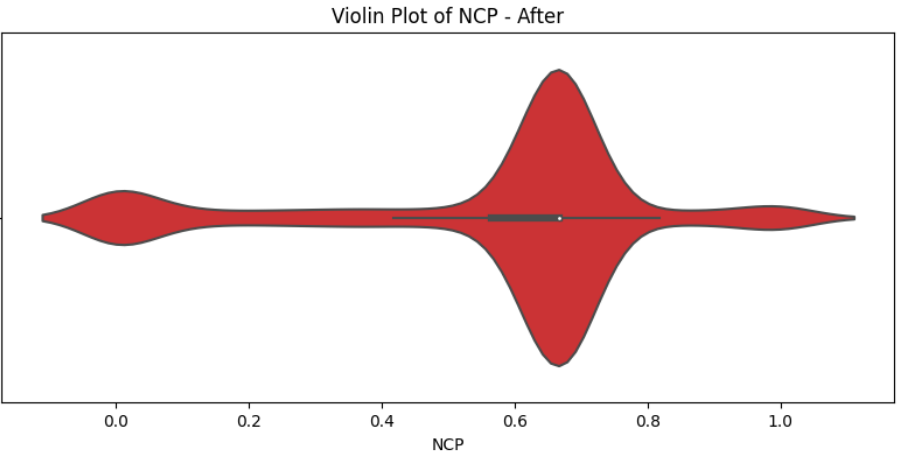
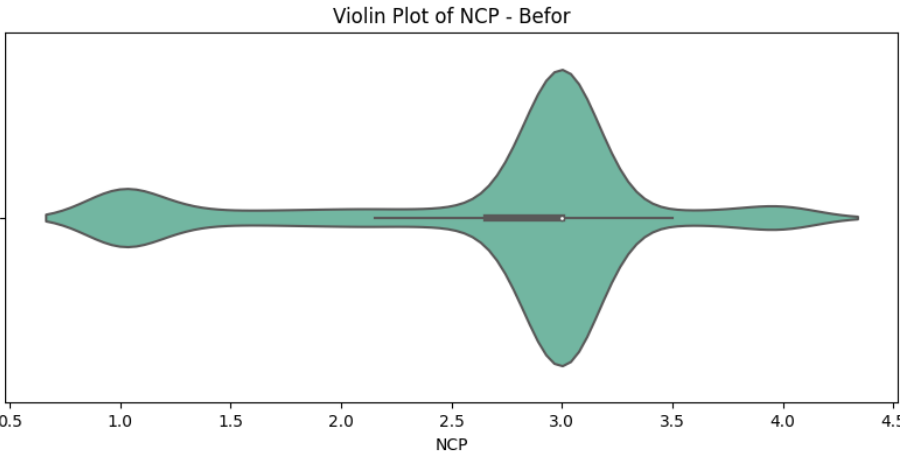
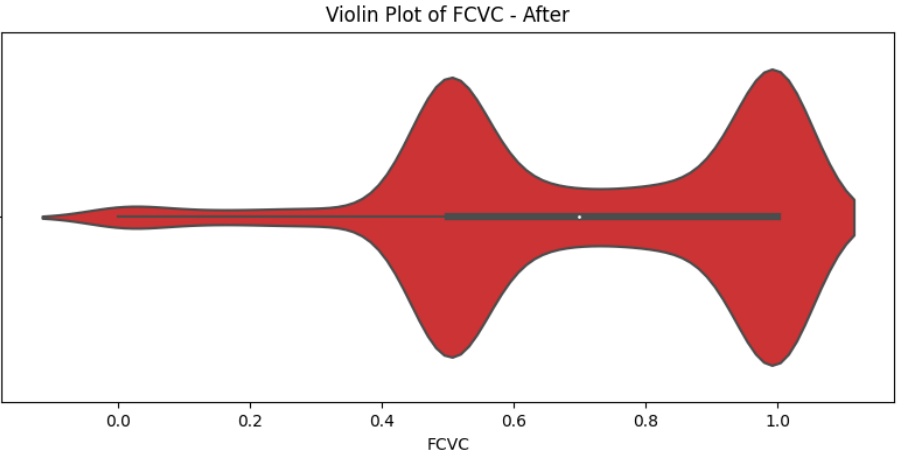
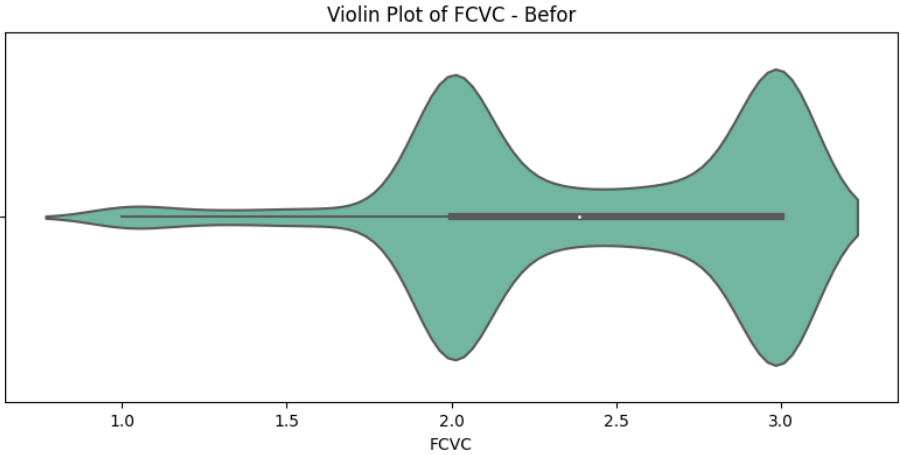
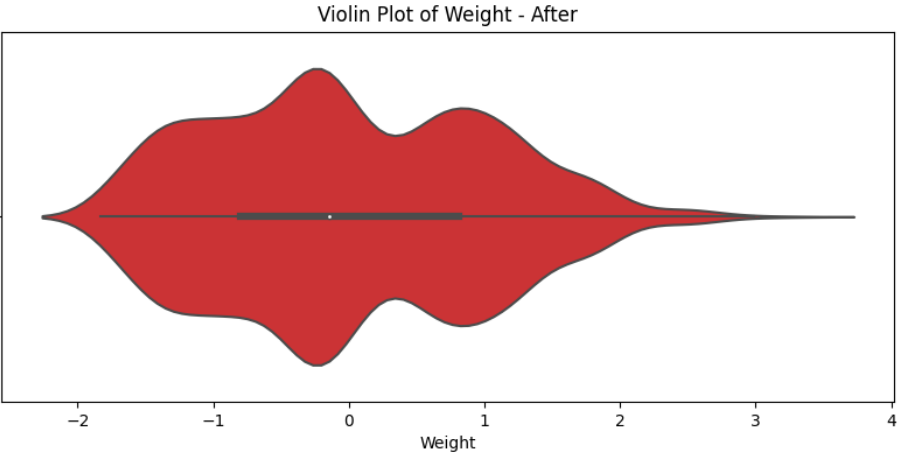
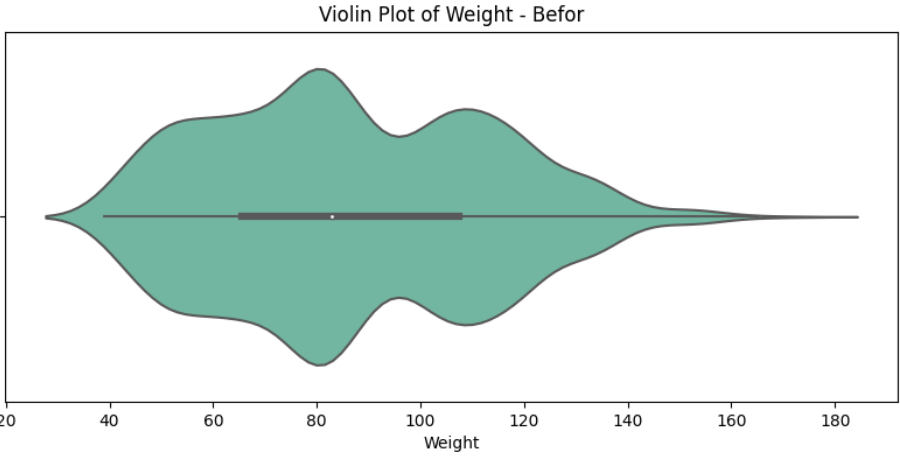
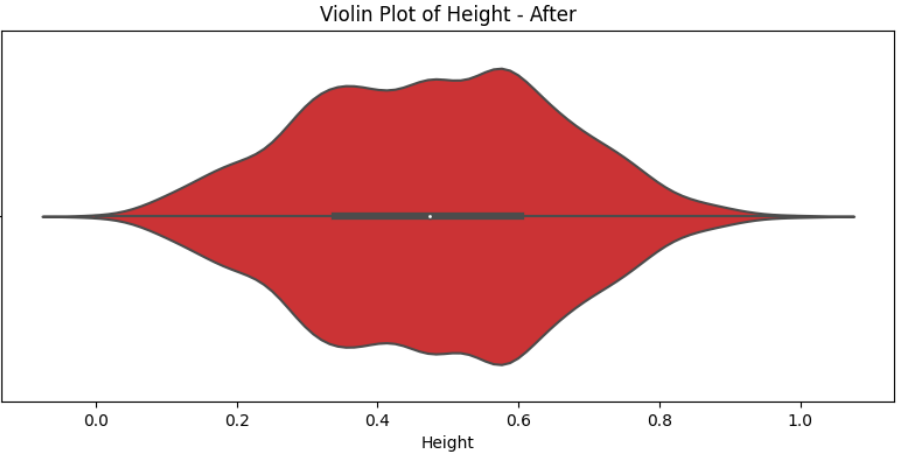
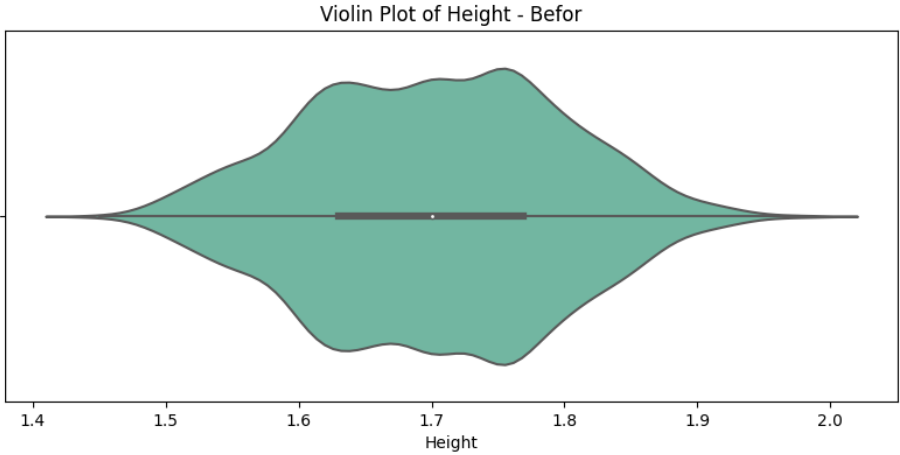
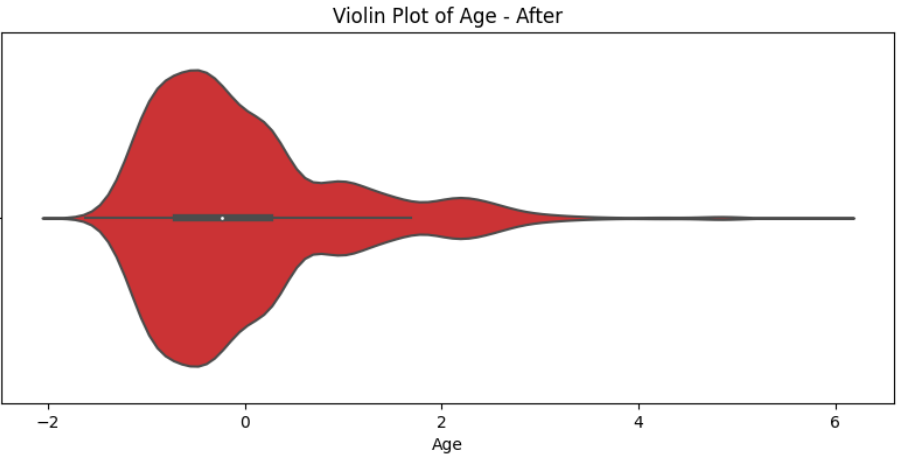
fig, axes = plt.subplots(nrows=num_rows, ncols=num_cols, figsize=(16, 4 * num_rows))
axes = axes.flatten()

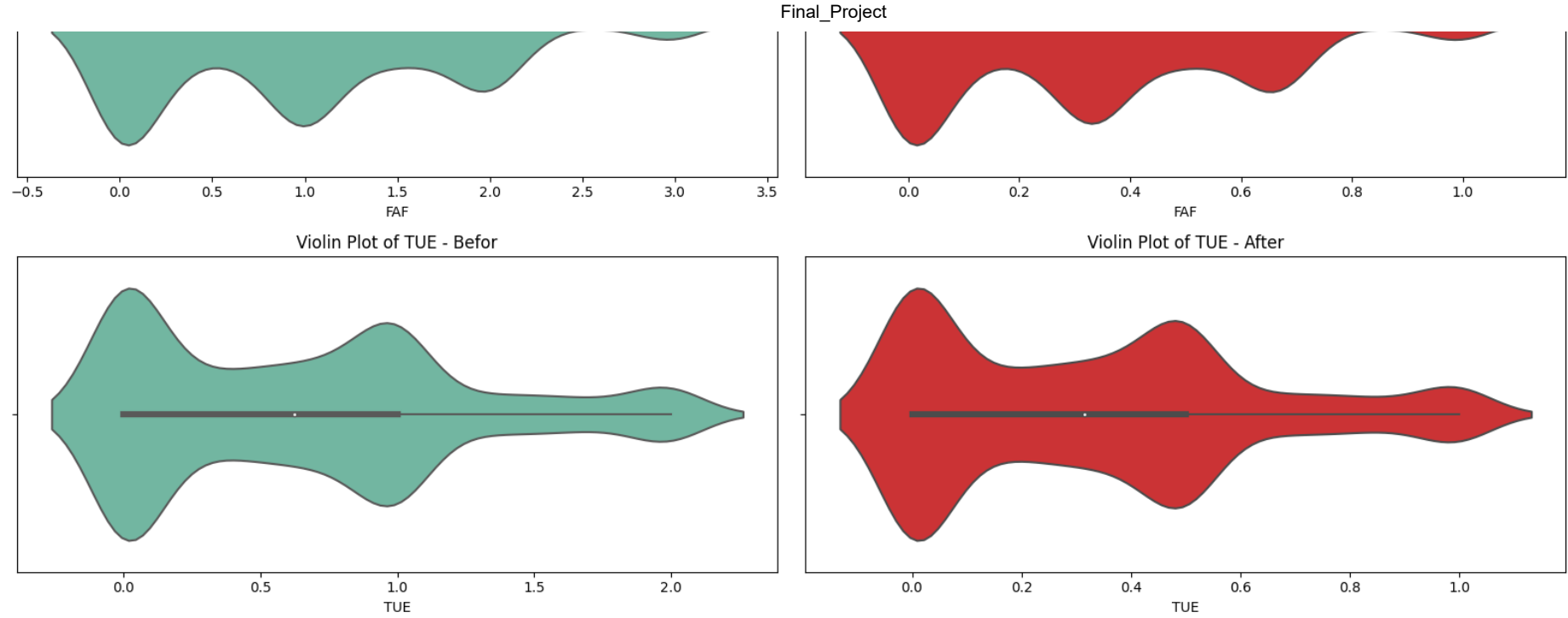
for i, column in enumerate(numerical_columns):
    sns.violinplot(x=df_initial[column], ax=axes[i * 2], palette=left_palette)
    axes[i * 2].set_title(f'Violin Plot of {column} - Befor')

    sns.violinplot(x=X[column], ax=axes[i * 2 + 1], palette=right_palette)
    axes[i * 2 + 1].set_title(f'Violin Plot of {column} - After')

for j in range(num_plots * 2, len(axes)):
    fig.delaxes(axes[j])

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



Performing Principal Component Analysis (PCA)

Goal:

PCA (Principal Component Analysis) aims to simplify complex data by finding a new set of features, called principal components, that capture the most important information.

High-Dimensional Data:

Imagine you have data with many features (dimensions). PCA helps reduce this high-dimensional data to a smaller number of dimensions while retaining as much relevant information as possible.

Variance Matters:

PCA looks for directions in the data where the variance (spread) is maximum. These directions are the principal components.

Eigenvalues and Eigenvectors:

PCA uses math concepts called eigenvalues and eigenvectors to find these principal components. Eigenvalues represent the amount of variance in each direction, and eigenvectors are the corresponding directions.

```
In [ ]: from sklearn.decomposition import PCA

# List to store singular values for each number of components
List_pca = []

# Loop through different numbers of components
for i in range(19):
    # Fit PCA model with the current number of components
    pca = PCA(n_components=i).fit(X)

    # Store the singular values in the list
    lambda_ = pca.singular_values_
    List_pca.append(pca.singular_values_)

# Generate x-axis values for the plot
Xplt = np.arange(1, 19)

# Plot singular values against the number of components
plt.plot(Xplt, lambda_, linewidth=3, color='g')
plt.xlabel("Number of components", fontsize=10)
plt.ylabel("Singular Values", fontsize=10)
plt.title("Choosing Optimal Reduction", fontsize=10)
plt.xlim(0, 20)
plt.show()

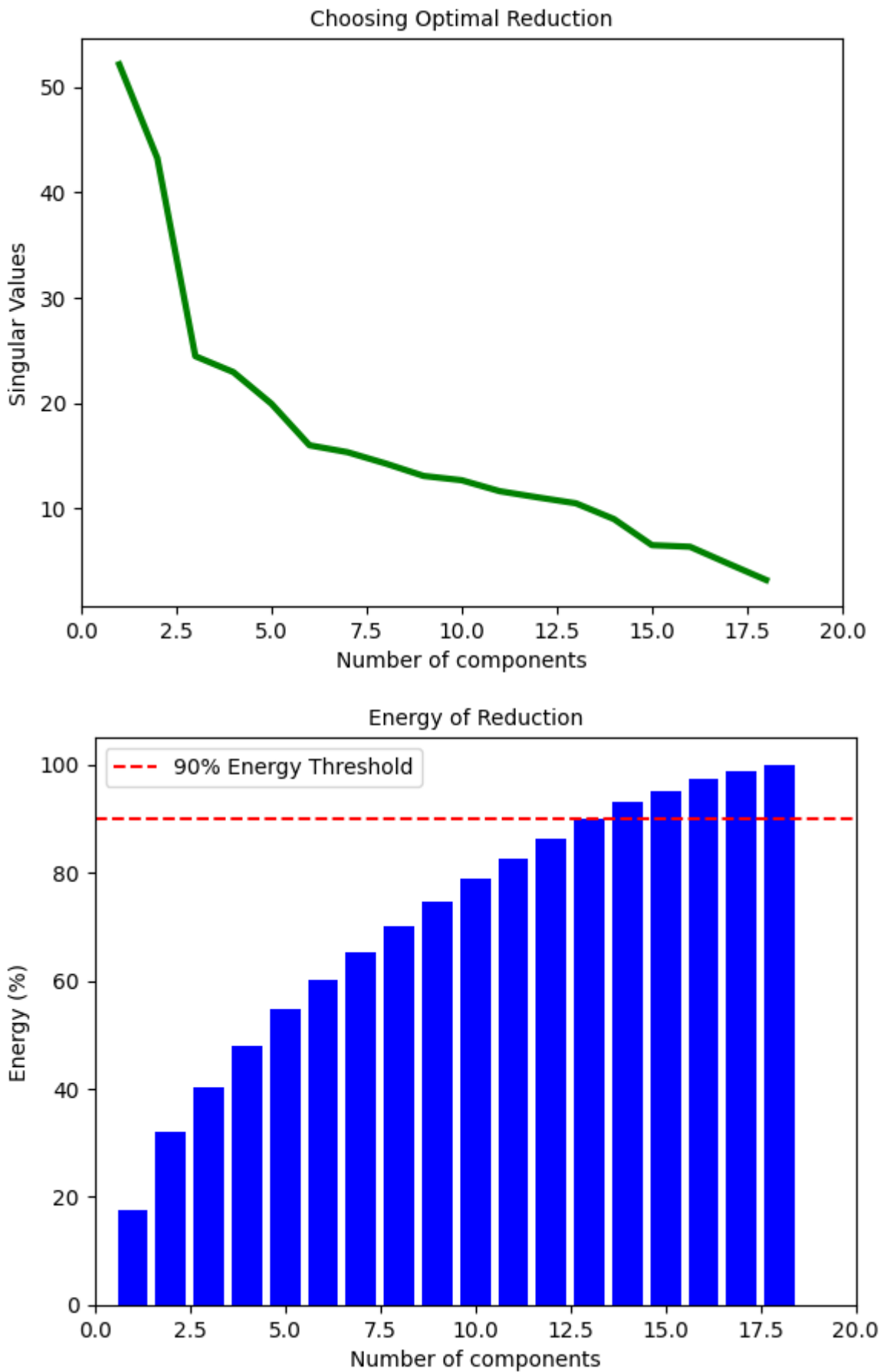
# Calculate cumulative sum of singular values to represent energy
lambda_sum = []
a = 0
for i in range(len(lambda_)):
    a += lambda_[i]
    lambda_sum.append(a)

# Calculate the percentage of energy explained by each number of components
filter1 = (lambda_sum / lambda_sum[-1]) * 100
Energy = np.array([filter1]).reshape(18,)

# Print and plot the energy of PCA
# print("Energy of PCA:", Energy)

# Plot a bar diagram for the energy of each number of components
plt.bar(Xplt, Energy, color='blue')
plt.xlabel("Number of components", fontsize=10)
plt.ylabel("Energy (%)", fontsize=10)
plt.xlim(0, 20)
plt.title("Energy of Reduction", fontsize=10)
```

```
# Highlight the area where energy is more than 90%
plt.axhline(y=90, color='red', linestyle='--', label='90% Energy Threshold')
plt.legend()
plt.show()
```



Choosing Optimal Reduction:

The first plot, titled "Choosing Optimal Reduction," displays the singular values of the principal components against the number of components. Singular values represent the amount of variance captured by each principal component. In PCA, these singular values are also called the eigenvalues.

Interpretation:

The higher the singular value, the more variance the corresponding principal component captures. By looking at the plot, you can observe the rate at which the singular values decrease. The point where the values start to level off or become very small is a potential indicator of the optimal number of components. A significant drop in singular values may suggest that adding more components doesn't provide much additional information.

Selection Criteria:

Choose the number of components at the "elbow" or the point where the rate of decrease in singular values slows down.

Energy of Reduction:

The second plot, titled "Energy of Reduction," represents the cumulative energy (variance) captured by the principal components.

Interpretation:

Each bar in the plot represents the cumulative sum of singular values up to a certain number of components. The height of the bar at a specific number of components indicates the percentage of total variance explained by those components. The cumulative sum essentially tells you how

much of the total variance in the data is retained as you increase the number of components.

Selection Criteria:

We can use a threshold, such as 90%, to decide how much energy (variance) you want to retain. The point where the bar crosses the threshold line (e.g., 90%) can be considered a good choice for the number of components to retain.

Putting it Together:

Ideally, we want to find a balance where we retain enough information to describe the data well while reducing dimensionality. Consider both plots together. A common approach is to choose the number of components at the elbow in the "Choosing Optimal Reduction" plot, and then verify that it retains a sufficient amount of energy in the "Energy of Reduction" plot.

By examining these plots, we can make an informed decision about the number of principal components to retain in your PCA analysis.

In the following section, we can determine the number of components for reducing the dataset based on the PCA analysis results. The reduced dataset will then be saved for future use in comparing results.

```
In [ ]: # Decision on the number of components based on the analysis
n_components=12
# Perform PCA with the chosen number of components
Main_pca = PCA(n_components).fit(X)
Xreduc = Main_pca.transform(X)
Xreduc=pd.DataFrame(Xreduc)
# X=Xreduc
```

Unsupervised learning algorithm

Using clustering algorithms (MiniBatchKMeans and AgglomerativeClustering) for unsupervised learning and evaluating their performance using the silhouette score and a confusion matrix.

Features of the Code:

Cross-Validation: The code uses k-fold cross-validation (KFold) with 5 splits.

Clustering Models: Two clustering models are used: MiniBatchKMeans with 7 clusters. AgglomerativeClustering with 7 clusters. These models are trained on the training data and used to predict cluster assignments for the test data.

Evaluation Metrics: The silhouette score is calculated for each model, providing a measure of how well-separated the clusters are. Higher silhouette scores indicate better-defined clusters. Confusion matrices are used to visualize the performance of the best-performing model.

Visualization: Bar plots show the average silhouette scores for each model. A confusion matrix is plotted for the best-performing model.

```
In [ ]: from sklearn.cluster import MiniBatchKMeans, AgglomerativeClustering
from sklearn.model_selection import KFold
from sklearn.metrics import silhouette_score, confusion_matrix
from sklearn.preprocessing import LabelEncoder
import seaborn as sns
X_input = X
Y_encoded = Y

# Number of folds for cross-validation
k = 5
kf = KFold(n_splits=k, shuffle=True, random_state=42)

# Initialize clustering models
kmeans_model = MiniBatchKMeans(n_clusters=7, random_state=42) # Adjust the number of clusters
agglomerative_model = AgglomerativeClustering(n_clusters=7)

models = [kmeans_model, agglomerative_model] # Add more models as needed
model_names = ['MiniBatchKMeans', 'Agglomerative'] # Add corresponding model names

# Lists to store results for each model
silhouette_scores = []
cluster_assignments = []

# Bar plots for each model's silhouette score across folds
for model, model_name in zip(models, model_names):
    fold_silhouette_scores = []
    fold_cluster_assignments = []

    for train_index, test_index in kf.split(X_input):
        X_train, X_test = X_input.iloc[train_index], X_input.iloc[test_index]

        # Fit the model
        model.fit(X_train)

        # Predict cluster assignments
        predictions = model.fit_predict(X_test)

        # Calculate silhouette score
        silhouette = silhouette_score(X_test, predictions)
        fold_silhouette_scores.append(silhouette)
```

```

        # Store cluster assignments
        fold_cluster_assignments.append(predictions)

    # Store the cluster assignments to the List
    cluster_assignments.append(fold_cluster_assignments)

    # Print average silhouette score for the model
    avg_silhouette = np.mean(fold_silhouette_scores)
    silhouette_scores.append(avg_silhouette)
    print(f"Average Silhouette Score for {model_name}: {avg_silhouette:.4f}\n")

# Plot bar plot for the average silhouette score of each model
plt.figure(figsize=(8, 4))
plt.bar(model_names, silhouette_scores, color=['blue', 'green']) # Adjust colors accordingly
plt.title('Model Comparison - Average Silhouette Score')
plt.xlabel('Model')
plt.ylabel('Average Silhouette Score')
plt.ylim(0, 1)
plt.show()

# Find the best-performing model
best_model_index = np.argmax(silhouette_scores)
best_model_name = model_names[best_model_index]
best_cluster_assignments = cluster_assignments[best_model_index][-1]

# Plot confusion matrix for the best-performing model
plt.figure(figsize=(8, 6))
cm = confusion_matrix(Y_encoded[test_index], best_cluster_assignments)
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=label_encoder.classes_,
            yticklabels=label_encoder.classes_)
plt.title(f'Confusion Matrix for Best Model - {best_model_name}')
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.show()

```

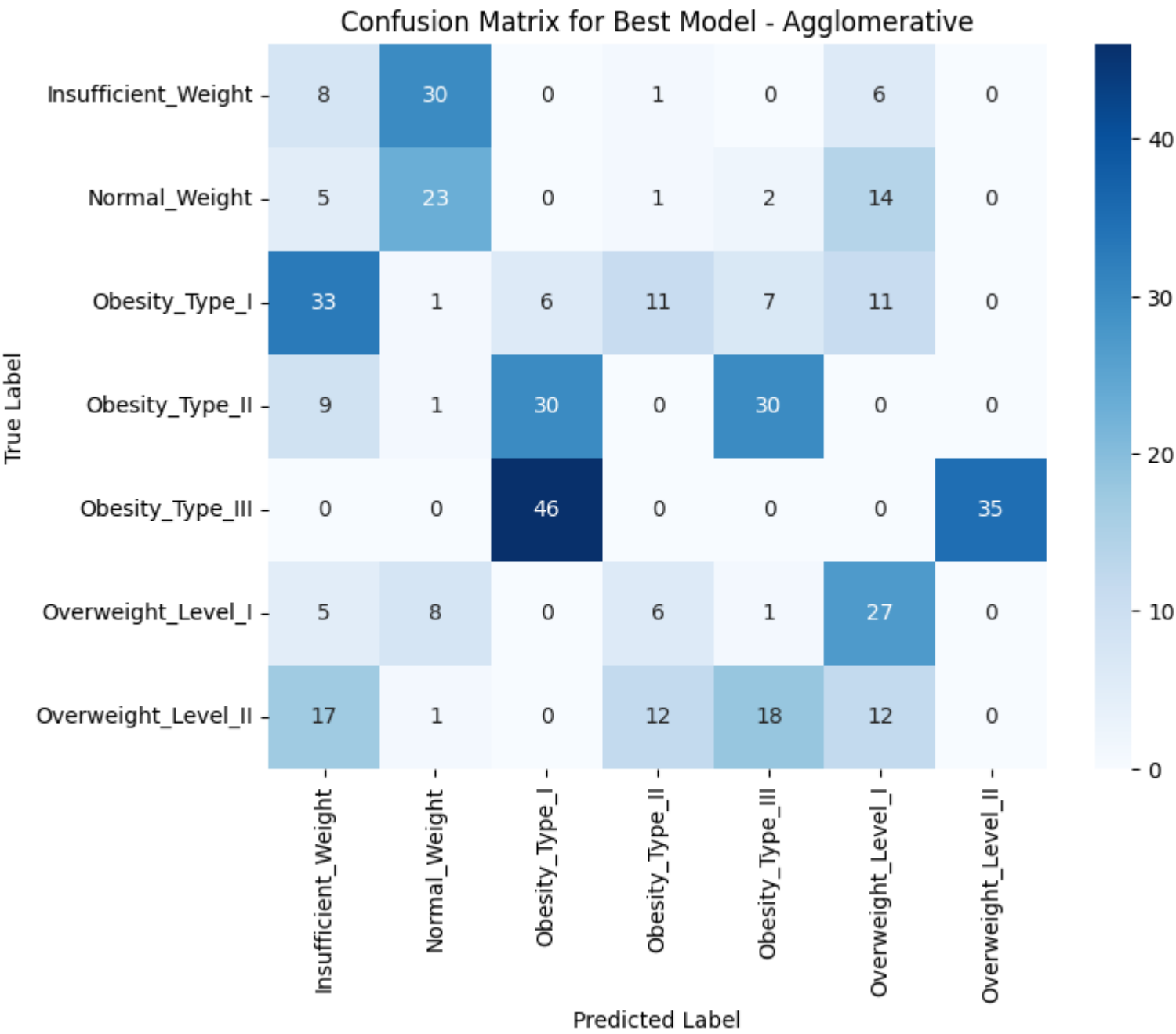
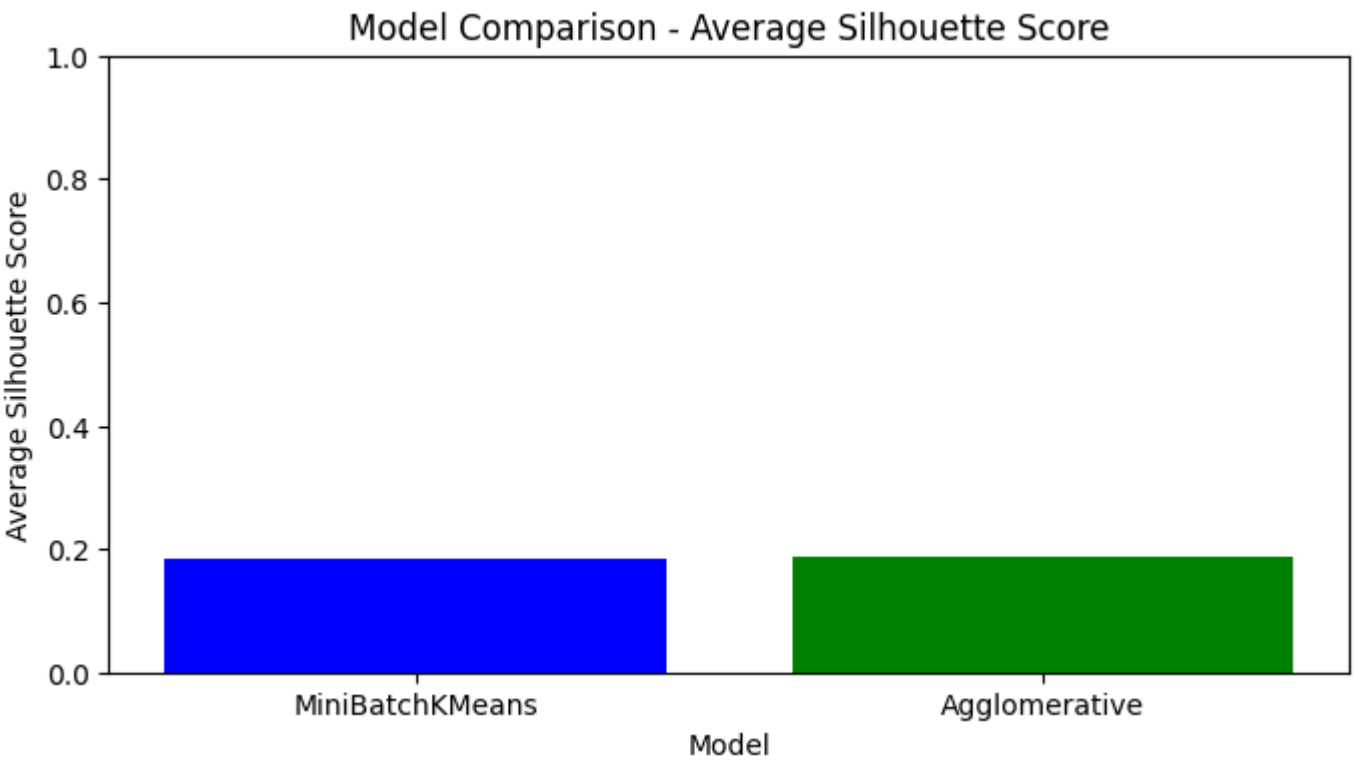
```

/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change
from 3 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
    warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change
from 3 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
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/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change
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/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change
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/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change
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    warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change
from 3 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
    warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change
from 3 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
    warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change
from 3 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
    warnings.warn(

```

Average Silhouette Score for MiniBatchKMeans: 0.1854

Average Silhouette Score for Agglomerative: 0.1875



K-Fold Cross-Validation: (Supervised learning algorithm)

Concept: K-Fold Cross-Validation is a technique used to assess the performance of a machine learning model. The dataset is split into 'k' folds, and the model is trained and tested 'k' times, each time using a different fold for testing and the remaining folds for training. Usage in Code: The `perform_kfold` function implements K-Fold Cross-Validation, splitting the dataset into 'k' folds.

Pipeline:

Concept: A pipeline is used to streamline a lot of the routine processes, providing a simple way to keep everything organized. In the context of scikit-learn, a pipeline bundles preprocessing and modeling steps into a single object. Usage in Code: The `Pipeline` class is used to create a pipeline for each classification model, including the classifier and, if applicable, preprocessing steps.

GridSearchCV:

Concept: GridSearchCV is a method for systematically working through multiple combinations of hyperparameter values, tuning them to find the best performance for a model. Usage in Code: The `GridSearchCV` function is used to perform hyperparameter tuning for each model. It searches through the hyperparameter grid defined for each model and performs cross-validated grid search.

Hyperparameter Tuning:

Concept: Hyperparameters are parameters that are not learned from the data but set prior to the training process. Tuning these hyperparameters is crucial for improving model performance. Usage in Code: Hyperparameter tuning is performed using GridSearchCV for the 'Logistic Regression' and 'Decision Tree' models. The hyperparameter grids (param_grids) define the range of values to search.

Bar Plots with Matplotlib:

Concept: Bar plots are used to visually represent the accuracy of each model on different folds or the average accuracy across folds. Usage in Code: Matplotlib is used to create bar plots. Each bar represents the accuracy of a model on a specific fold, and comparisons are made between models.

Model Evaluation - Accuracy:

Concept: Accuracy is a common metric for classification problems, representing the ratio of correctly predicted instances to the total instances. Usage in Code: The accuracy_score function from scikit-learn is used to evaluate the accuracy of the models.

```
In [ ]: from sklearn.model_selection import KFold, GridSearchCV
from sklearn.metrics import accuracy_score, confusion_matrix
from sklearn.pipeline import Pipeline
from sklearn import linear_model
from sklearn.svm import LinearSVC
from sklearn.naive_bayes import GaussianNB
from sklearn.tree import DecisionTreeClassifier
from sklearn.linear_model import SGDClassifier
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np

# Function to perform k-fold cross-validation and return data for each fold

def perform_kfold(X1, Y1, k1):
    kfold = KFold(k1, random_state=None, shuffle=True)
    folds = []
    for train_index, test_index in kfold.split(X1):
        X_train, X_test = X1.iloc[train_index], X1.iloc[test_index]
        Y_train, Y_test = Y1.iloc[train_index], Y1.iloc[test_index]
        folds.append([X_train, X_test, Y_train, Y_test])
    return folds

# Function to train and evaluate a model on a given fold and return confusion matrix
def train_and_evaluate_model_confusion_matrix(model, X_train, X_test, Y_train, Y_test):
    model.fit(X_train, Y_train)
    Y_pred = model.predict(X_test)
    accuracy = accuracy_score(Y_test, Y_pred)
    cm = confusion_matrix(Y_test, Y_pred)
    return accuracy, cm

# List of classification models with pipelines
models = {
    'Logistic Regression': Pipeline([
        ('classifier', linear_model.LogisticRegression(solver='saga', max_iter=100))
    ]),
    'Naive Bayes': Pipeline([
        ('classifier', GaussianNB())
    ]),
    'Perceptron': Pipeline([
        ('classifier', linear_model.Perceptron())
    ]),
    'SVM': Pipeline([
        ('classifier', LinearSVC(max_iter=10))
    ]),
    'Decision Tree': Pipeline([
        ('classifier', DecisionTreeClassifier(random_state=0))
    ]),
    'SGD': Pipeline([
        ('classifier', SGDClassifier(loss="hinge", max_iter=50))
    ])
}

# Hyperparameter grids for each model
param_grids = {
    'Logistic Regression': {'classifier__C': [0.0001, 0.01, 0.1, 1, 10, 100, 1000, 10000]},
    'Naive Bayes': {}, # No hyperparameters to tune for Naive Bayes
    'Perceptron': {}, # No hyperparameters to tune for Perceptron
    'SVM': {'classifier__C': [0.001, 0.01, 0.1, 1, 10, 100, 10000]},
    'Decision Tree': {'classifier__max_depth': [None, 0.01, 0.1, 1, 10, 20, 30, 40, 100]},
    'SGD': {'classifier__alpha': [0.000001, 0.001, 0.01, 0.1, 1, 10]}
}

# Number of folds for cross-validation
k = 5
# Assuming X is defined earlier

# Perform k-fold cross-validation
folds = perform_kfold(X_input, Y, k)

# Lists to store accuracies and best hyperparameters for each model
accuracies_with_hp = {model_name: [] for model_name in models}
accuracies_without_hp = {model_name: [] for model_name in models}
```

```

best_params = {model_name: [] for model_name in models}

# Train and evaluate each model on each fold with hyperparameter tuning
best_accuracy_models = {model_name: {'accuracy': 0, 'method': 'None', 'confusion_matrix': None} for model_name in models}

for model_name, model_pipeline in models.items():
    param_grid = param_grids.get(model_name, {}) # Get hyperparameter grid for the model
    grid_search = GridSearchCV(model_pipeline, param_grid, cv=k, scoring='accuracy', n_jobs=-1)

    for fold_data in folds:
        grid_search.fit(fold_data[0], fold_data[2])
        accuracy, cm = train_and_evaluate_model_confusion_matrix(grid_search, *fold_data[0:4])
        accuracies_with_hp[model_name].append(accuracy)
        best_params[model_name].append(grid_search.best_params_)

    # Update best accuracy models
    if accuracy > best_accuracy_models[model_name]['accuracy']:
        best_accuracy_models[model_name]['accuracy'] = accuracy
        best_accuracy_models[model_name]['method'] = 'With Hyperparameter Tuning'
        best_accuracy_models[model_name]['confusion_matrix'] = cm

# Train and evaluate each model on each fold without hyperparameter tuning
for model_name, model_pipeline in models.items():
    for fold_data in folds:
        accuracy, cm = train_and_evaluate_model_confusion_matrix(model_pipeline, *fold_data[0:4])
        accuracies_without_hp[model_name].append(accuracy)

    # Update best accuracy models
    if accuracy > best_accuracy_models[model_name]['accuracy']:
        best_accuracy_models[model_name]['accuracy'] = accuracy
        best_accuracy_models[model_name]['method'] = 'Without Hyperparameter Tuning'
        best_accuracy_models[model_name]['confusion_matrix'] = cm

# Bar plots for each model's accuracy with and without hyperparameter tuning
for model_name, model_accuracies_with_hp in accuracies_with_hp.items():
    model_accuracies_without_hp = accuracies_without_hp[model_name]
    best_param = best_params[model_name][0]

    # Plot with hyperparameter tuning
    plt.figure(figsize=(12, 6))
    plt.bar(np.arange(len(folds)) - 0.2, model_accuracies_with_hp, width=0.4, label='With Hyperparameter Tuning', color='skyblue')

    # Plot without hyperparameter tuning
    plt.bar(np.arange(len(folds)) + 0.2, model_accuracies_without_hp, width=0.4, label='Without Hyperparameter Tuning', color='lightcoral')

    plt.xlabel("Fold", fontsize=12)
    plt.ylabel("Accuracy", fontsize=12)
    plt.title(f"{model_name} - With and Without Hyperparameter Tuning", fontsize=14)
    plt.ylim(0, 1)
    plt.legend()
    plt.show()

# Print confusion matrix for the best accuracy
for model_name, details in best_accuracy_models.items():
    print(f"\n{model_name}:")
    print(f"    Best Accuracy: {details['accuracy']:.2f}% using {details['method']}")
    print(f"    Best Hyperparameters: {best_params[model_name][0]}")
    print(f"    Confusion Matrix:")
    print(details['confusion_matrix'])

    # Plot the confusion matrix
    plt.figure(figsize=(8, 6))
    sns.heatmap(details['confusion_matrix'], annot=True, fmt='d', cmap='Blues', xticklabels=label_encoder.classes_, yticklabels=label_encoder.classes_)
    #sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=label_encoder.classes_, yticklabels=label_encoder.classes_)
    plt.title(f"Confusion Matrix for {model_name} - Best Accuracy")
    plt.xlabel('Predicted')
    plt.ylabel('True')
    plt.show()

# Comparison plot for all methods with and without hyperparameter tuning
plt.figure(figsize=(15, 8.5))
average_accuracies_with_hp = [np.mean(accuracies_with_hp[model_name]) for model_name in models]
average_accuracies_without_hp = [np.mean(accuracies_without_hp[model_name]) for model_name in models]

plt.bar(np.arange(len(models)) - 0.2, average_accuracies_with_hp, width=0.4, label='With Hyperparameter Tuning', color='skyblue')
plt.bar(np.arange(len(models)) + 0.2, average_accuracies_without_hp, width=0.4, label='Without Hyperparameter Tuning', color='lightcoral')

plt.xlabel("Model", fontsize=12)
plt.ylabel("Average Accuracy", fontsize=12)
plt.title("Comparison of Average Accuracy for All Models with and without Hyperparameter Tuning", fontsize=14)
plt.xticks(np.arange(len(models)), list(models.keys()))
plt.ylim(0, 1)
plt.legend()
plt.show()

# Display accuracy and best hyperparameters of each model at the end
print("\nResults:")
print("-----")
for model_name in models.keys():
    avg_accuracy_with_hp = np.mean(accuracies_with_hp[model_name]) * 100
    avg_accuracy_without_hp = np.mean(accuracies_without_hp[model_name]) * 100
    print(f"\n{model_name}:")
    print(f"    Average Accuracy with Hyperparameter Tuning: {avg_accuracy_with_hp:.2f}%")

```



```
print(f"  Average Accuracy without Hyperparameter Tuning: {avg_accuracy_without_hp:.2f}%")

if best_params[model_name]:
    print(f"  Best Hyperparameters: {best_params[model_name][0]}")
else:
    print(f"  Best Hyperparameters: No hyperparameters tuned.")
print("-----")
```



```

    super().fit(
File "/usr/local/lib/python3.10/dist-packages/sklearn/tree/_classes.py", line 177, in fit
    self._validate_params()
File "/usr/local/lib/python3.10/dist-packages/sklearn/base.py", line 600, in _validate_params
    validate_parameter_constraints(
File "/usr/local/lib/python3.10/dist-packages/sklearn/utils/_param_validation.py", line 97, in validate_parameter_constraints
    raise InvalidParameterError(
sklearn.utils._param_validation.InvalidParameterError: The 'max_depth' parameter of DecisionTreeClassifier must be an int in the
range [1, inf) or None. Got 0.1 instead.

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```

    warnings.warn(some_fits_failed_message, FitFailedWarning)
/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_search.py:952: UserWarning: One or more of the test scores are
non-finite: [0.91014008      nan      nan 0.29718401 0.91313589 0.91014008
0.91014008 0.91014008 0.91014008]
    warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_validation.py:378: FitFailedWarning:
10 fits failed out of a total of 45.
The score on these train-test partitions for these parameters will be set to nan.
If these failures are not expected, you can try to debug them by setting error_score='raise'.

```

Below are more details about the failures:

```

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5 fits failed with the following error:
Traceback (most recent call last):
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    estimator.fit(X_train, y_train, **fit_params)
  File "/usr/local/lib/python3.10/dist-packages/sklearn/pipeline.py", line 405, in fit
    self._final_estimator.fit(Xt, y, **fit_params_last_step)
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  File "/usr/local/lib/python3.10/dist-packages/sklearn/utils/_param_validation.py", line 97, in validate_parameter_constraints
    raise InvalidParameterError(
sklearn.utils._param_validation.InvalidParameterError: The 'max_depth' parameter of DecisionTreeClassifier must be an int in the
range [1, inf) or None. Got 0.01 instead.

```

```

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    validate_parameter_constraints(
  File "/usr/local/lib/python3.10/dist-packages/sklearn/utils/_param_validation.py", line 97, in validate_parameter_constraints
    raise InvalidParameterError(
sklearn.utils._param_validation.InvalidParameterError: The 'max_depth' parameter of DecisionTreeClassifier must be an int in the
range [1, inf) or None. Got 0.1 instead.

```

```

    warnings.warn(some_fits_failed_message, FitFailedWarning)
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  File "/usr/local/lib/python3.10/dist-packages/sklearn/utils/_param_validation.py", line 97, in validate_parameter_constraints
    raise InvalidParameterError(
sklearn.utils._param_validation.InvalidParameterError: The 'max_depth' parameter of DecisionTreeClassifier must be an int in the
range [1, inf) or None. Got 0.01 instead.

```

```

-----
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  File "/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_validation.py", line 686, in _fit_and_score
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File "/usr/local/lib/python3.10/dist-packages/sklearn/utils/_param_validation.py", line 97, in validate_parameter_constraints
    raise InvalidParameterError(
sklearn.utils._param_validation.InvalidParameterError: The 'max_depth' parameter of DecisionTreeClassifier must be an int in the range [1, inf) or None. Got 0.1 instead.
```

```
warnings.warn(some_fits_failed_message, FitFailedWarning)
/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_search.py:952: UserWarning: One or more of the test scores are non-finite: [0.91254248      nan      nan 0.28639837 0.90654906 0.91254248
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  File "/usr/local/lib/python3.10/dist-packages/sklearn/utils/_param_validation.py", line 97, in validate_parameter_constraints
    raise InvalidParameterError(
sklearn.utils._param_validation.InvalidParameterError: The 'max_depth' parameter of DecisionTreeClassifier must be an int in the range [1, inf) or None. Got 0.01 instead.
```

```
-----
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Traceback (most recent call last):
  File "/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_validation.py", line 686, in _fit_and_score
    estimator.fit(X_train, y_train, **fit_params)
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```

```
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    raise InvalidParameterError(
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0.90778443 0.90778443 0.90778443]
warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_validation.py:378: FitFailedWarning:
10 fits failed out of a total of 45.
The score on these train-test partitions for these parameters will be set to nan.
If these failures are not expected, you can try to debug them by setting error_score='raise'.

```

Below are more details about the failures:

```

-----
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```

```

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```

```

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/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_search.py:952: UserWarning: One or more of the test scores are
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```

```

-----
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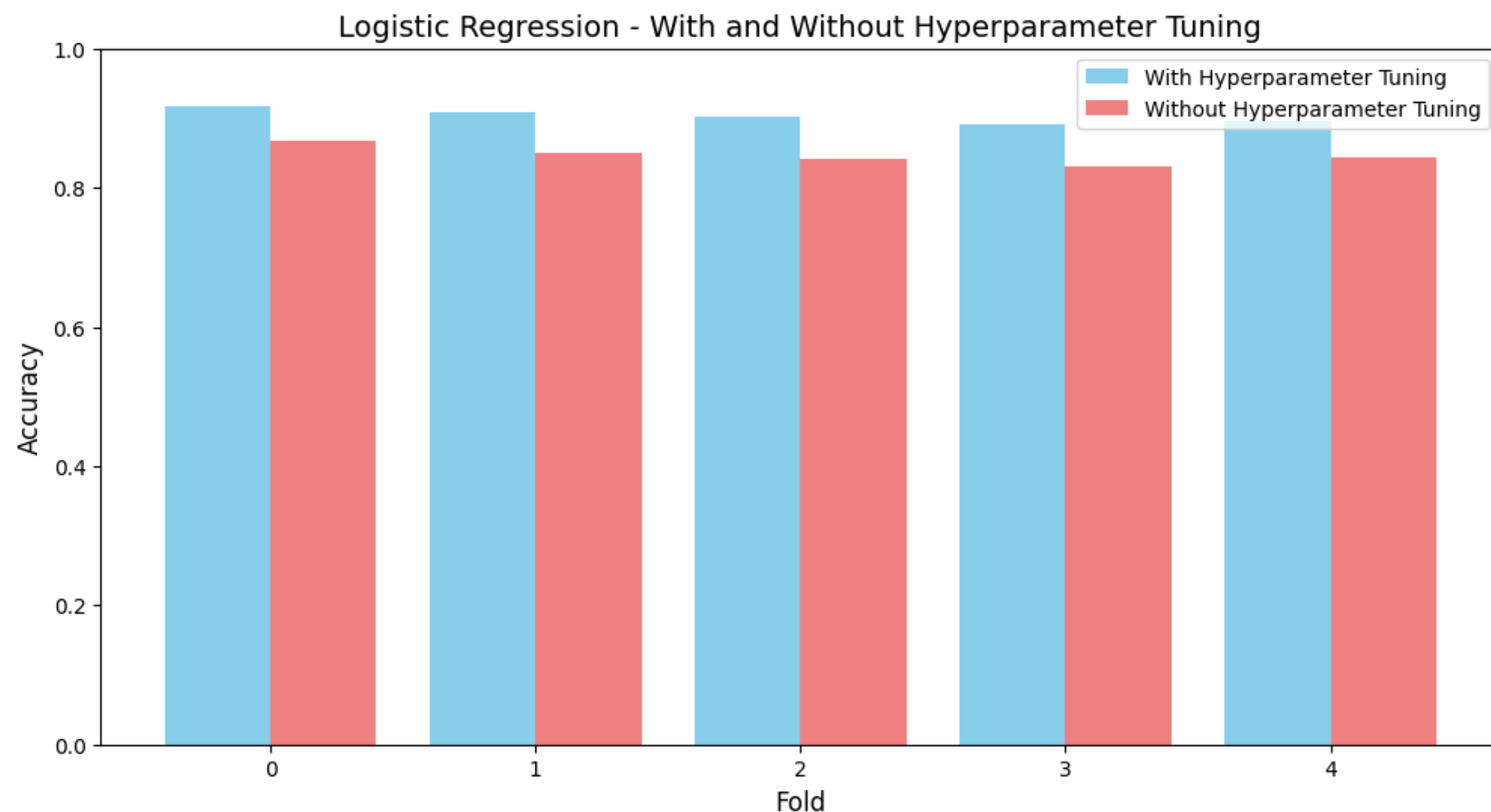
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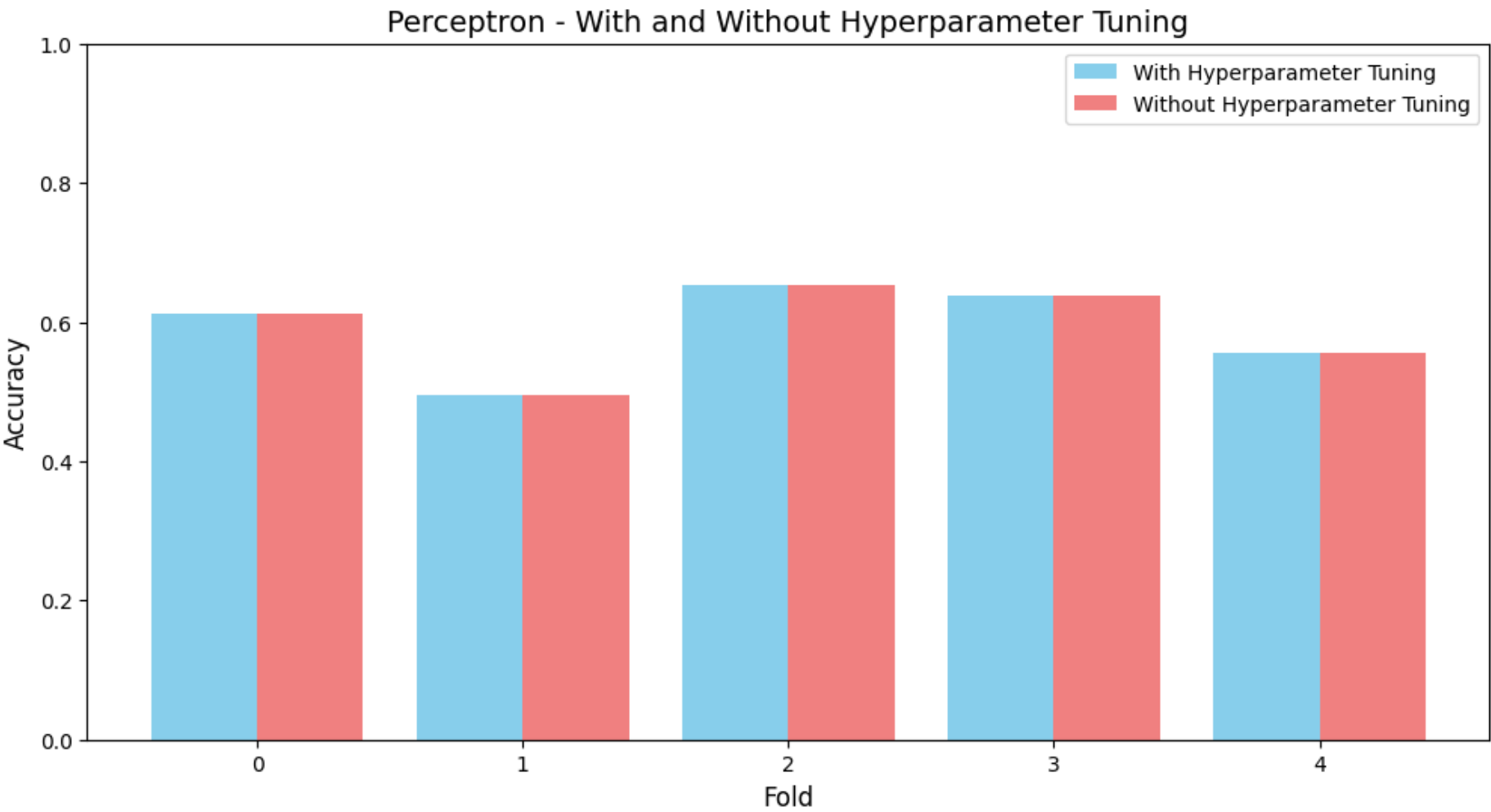
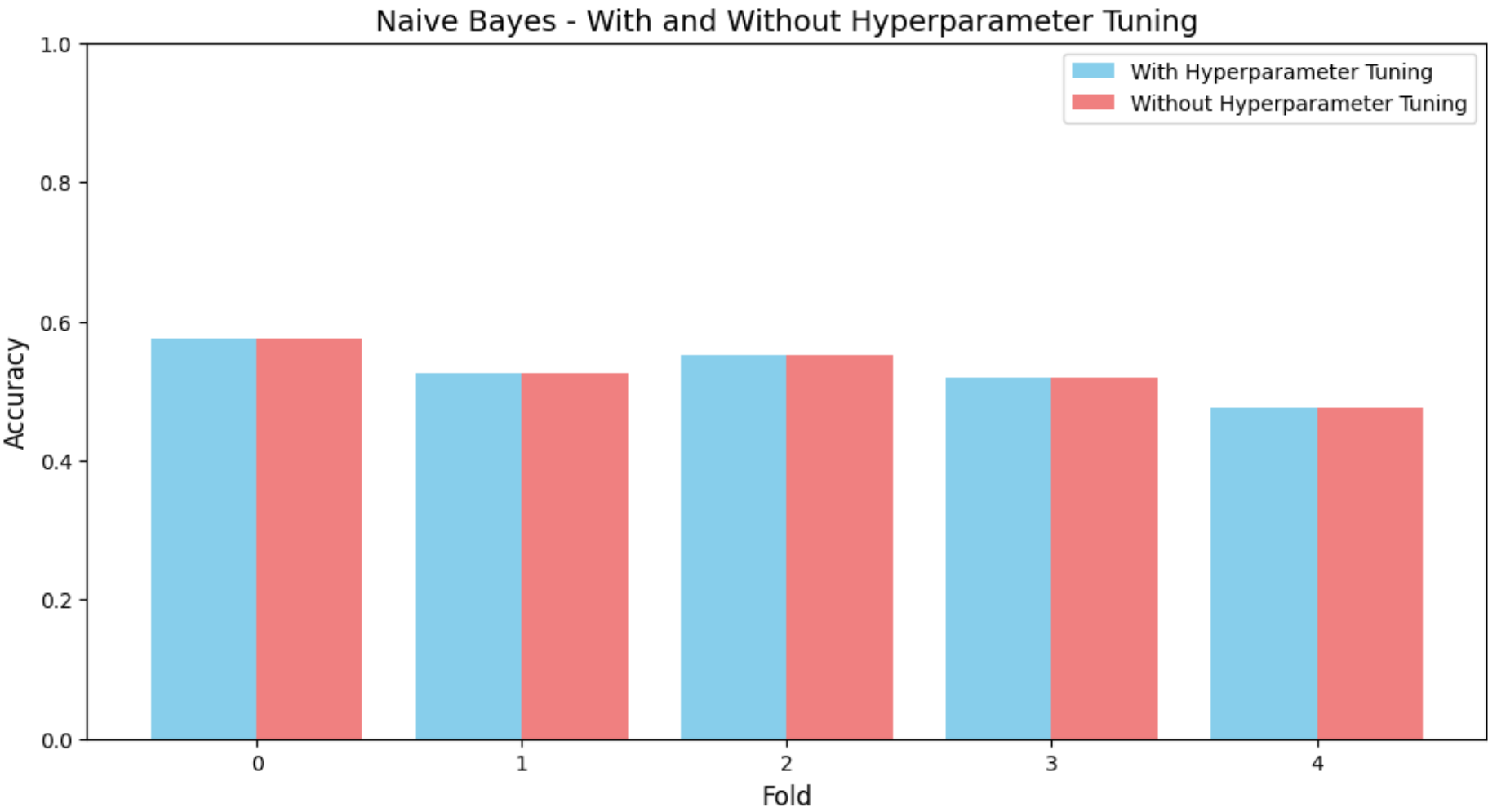
```

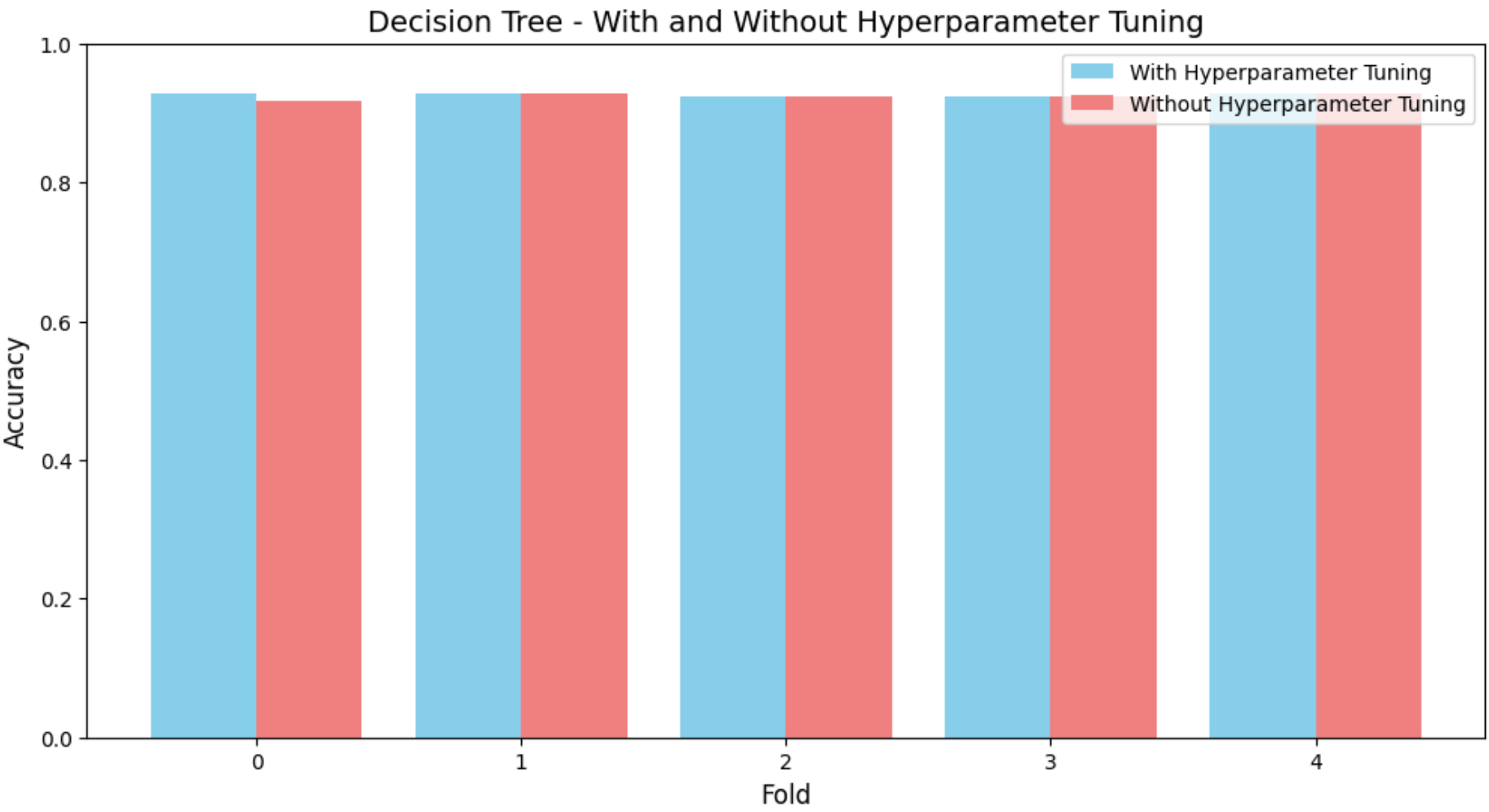
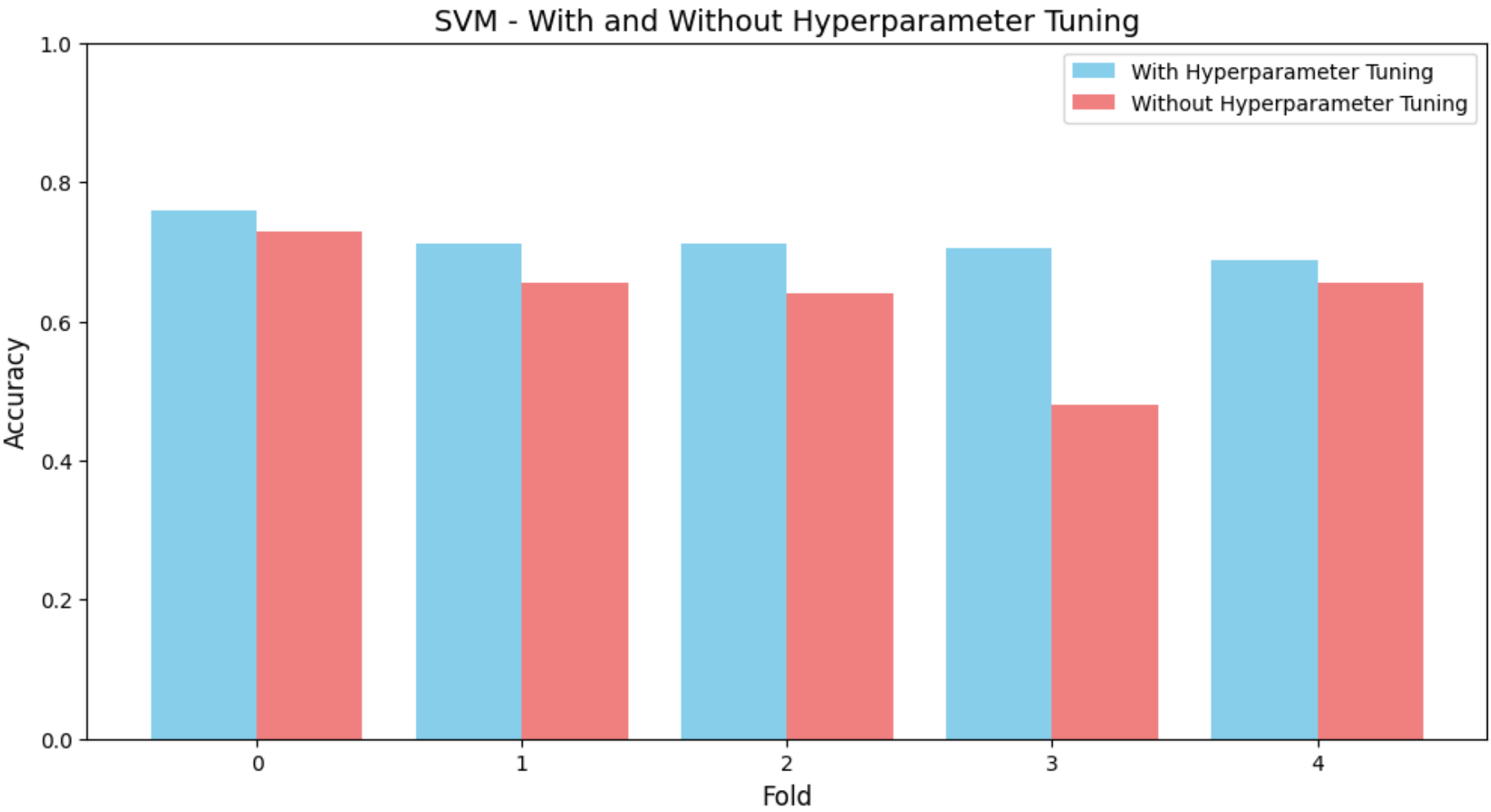
```

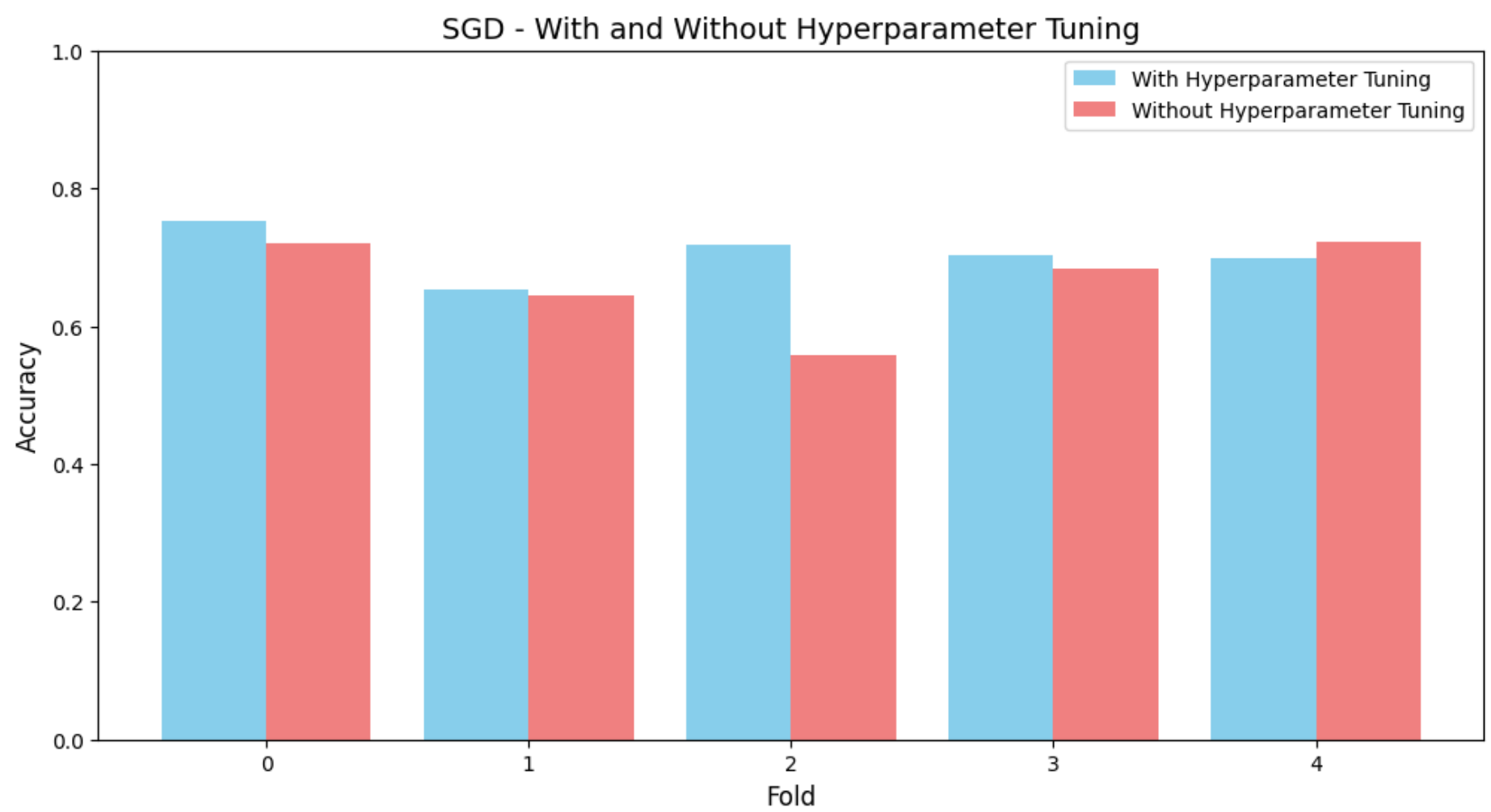
/usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_sag.py:350: ConvergenceWarning: The max_iter was reached which means the coef_ did not converge
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```









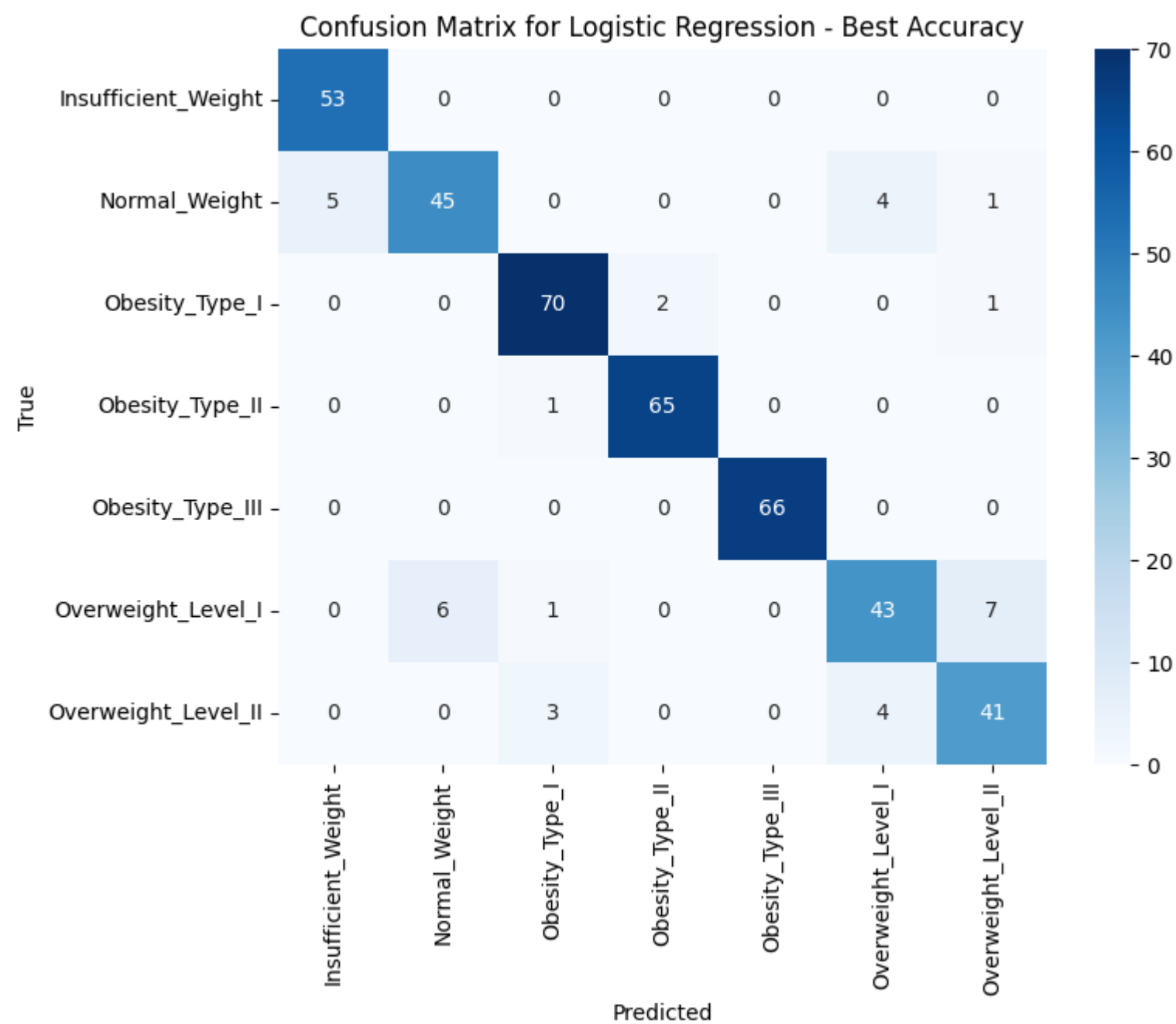
Logistic Regression:

Best Accuracy: 0.92% using With Hyperparameter Tuning

Best Hyperparameters: {'classifier__C': 100}

Confusion Matrix:

```
[[53  0  0  0  0  0  0]
 [ 5 45  0  0  0  4  1]
 [ 0  0 70  2  0  0  1]
 [ 0  0  1 65  0  0  0]
 [ 0  0  0  0 66  0  0]
 [ 0  6  1  0  0 43  7]
 [ 0  0  3  0  0  4 41]]
```



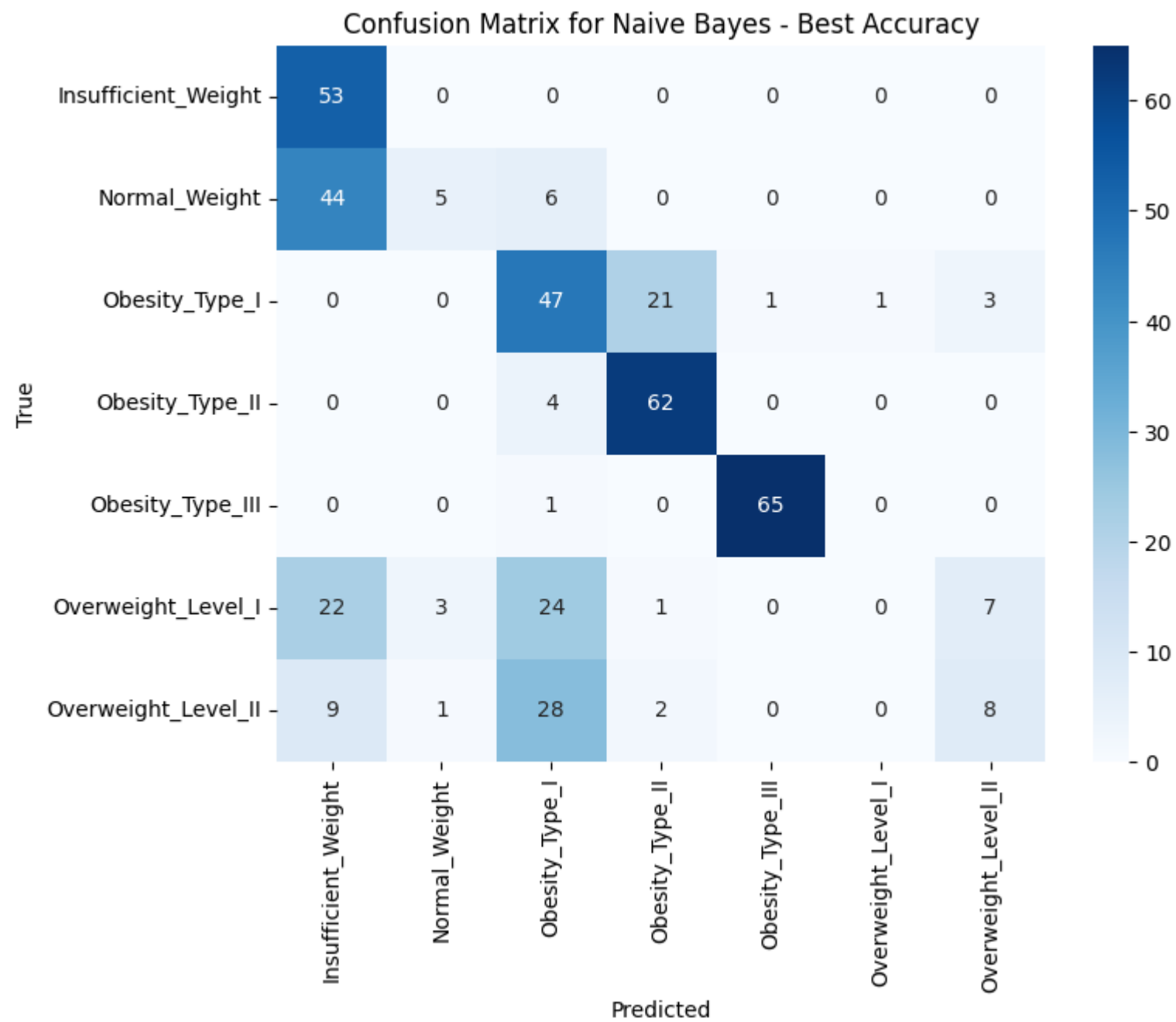
Naive Bayes:

Best Accuracy: 0.57% using With Hyperparameter Tuning

Best Hyperparameters: {}

Confusion Matrix:

```
[[53  0  0  0  0  0  0]
 [44  5  6  0  0  0  0]
 [ 0  0 47 21  1  1  3]
 [ 0  0  4 62  0  0  0]
 [ 0  0  1  0 65  0  0]
 [22  3 24  1  0  0  7]
 [ 9  1 28  2  0  0  8]]
```



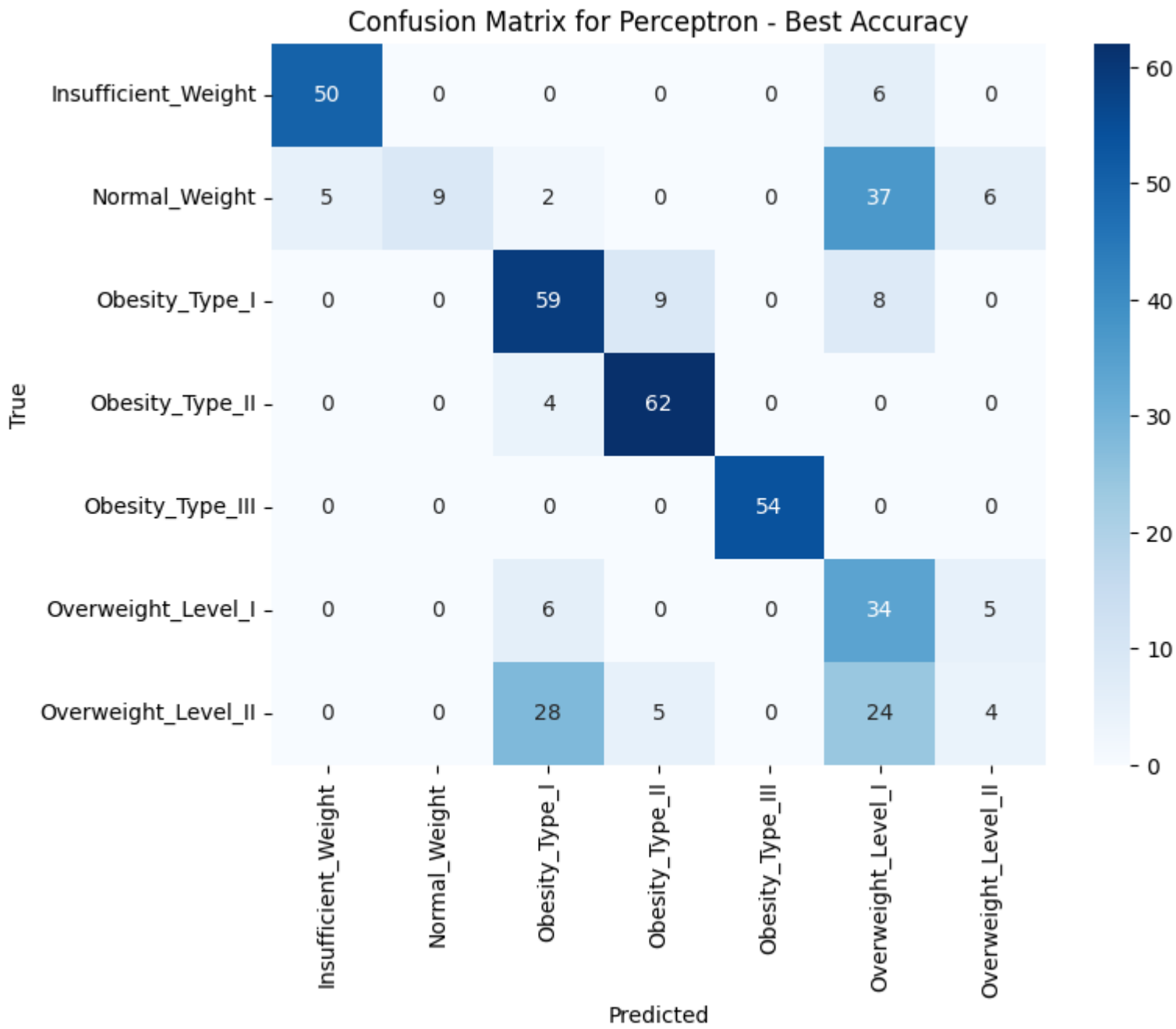
Perceptron:

Best Accuracy: 0.65% using With Hyperparameter Tuning

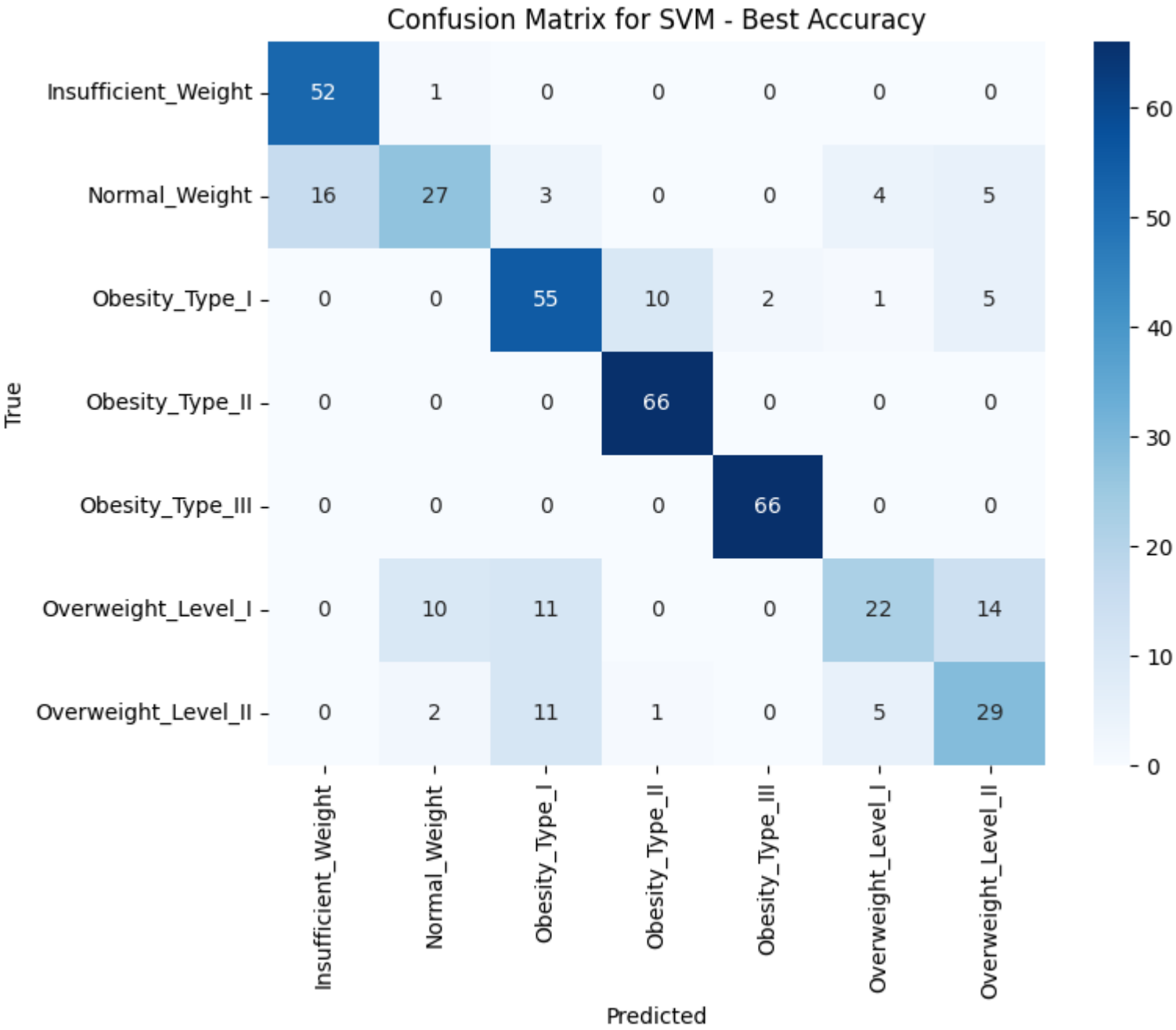
Best Hyperparameters: {}

Confusion Matrix:

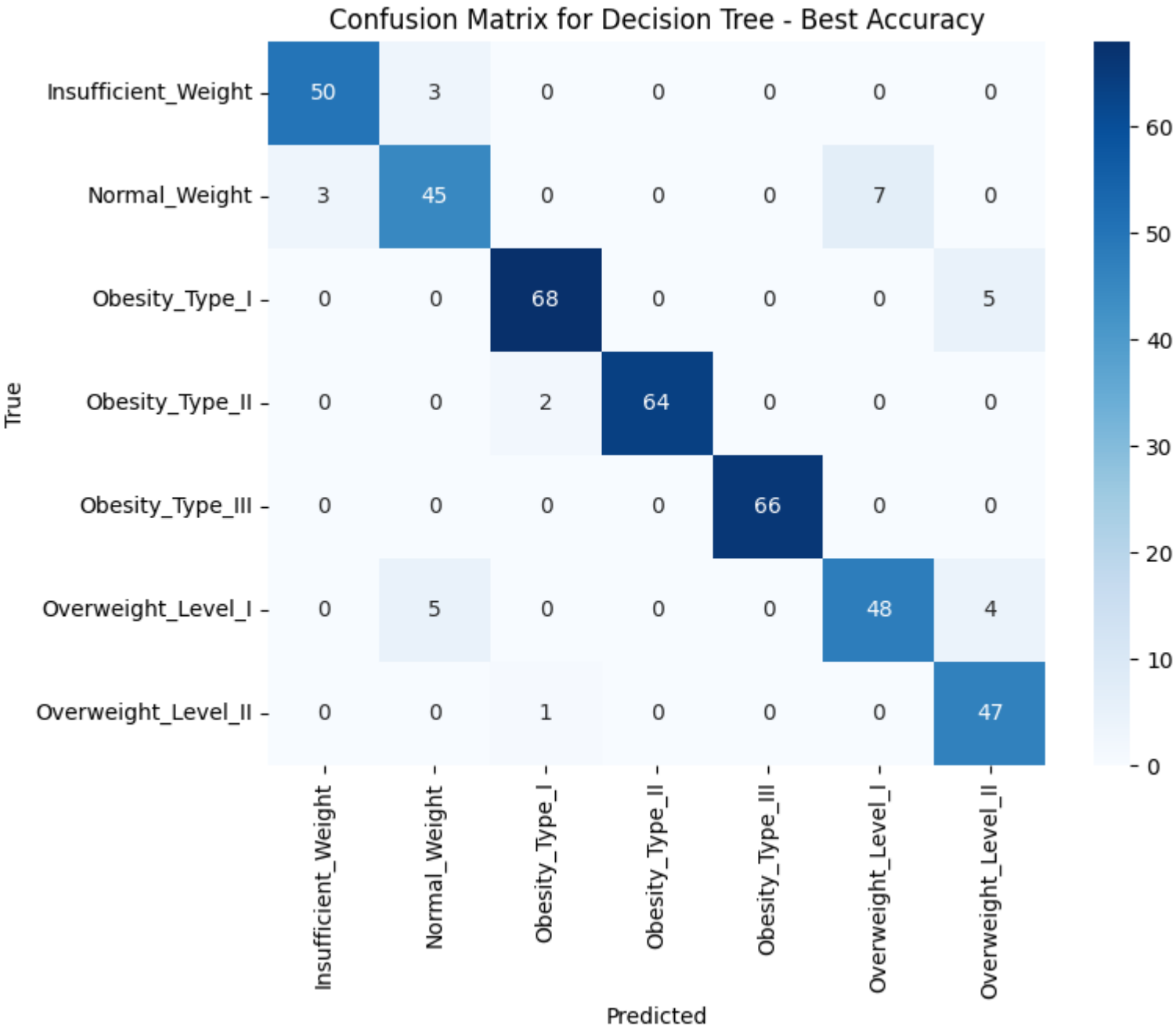
```
[[50  0  0  0  0  6  0]
 [ 5  9  2  0  0 37  6]
 [ 0  0 59  9  0  8  0]
 [ 0  0  4 62  0  0  0]
 [ 0  0  0  0 54  0  0]
 [ 0  0  6  0  0 34  5]
 [ 0  0 28  5  0 24  4]]
```



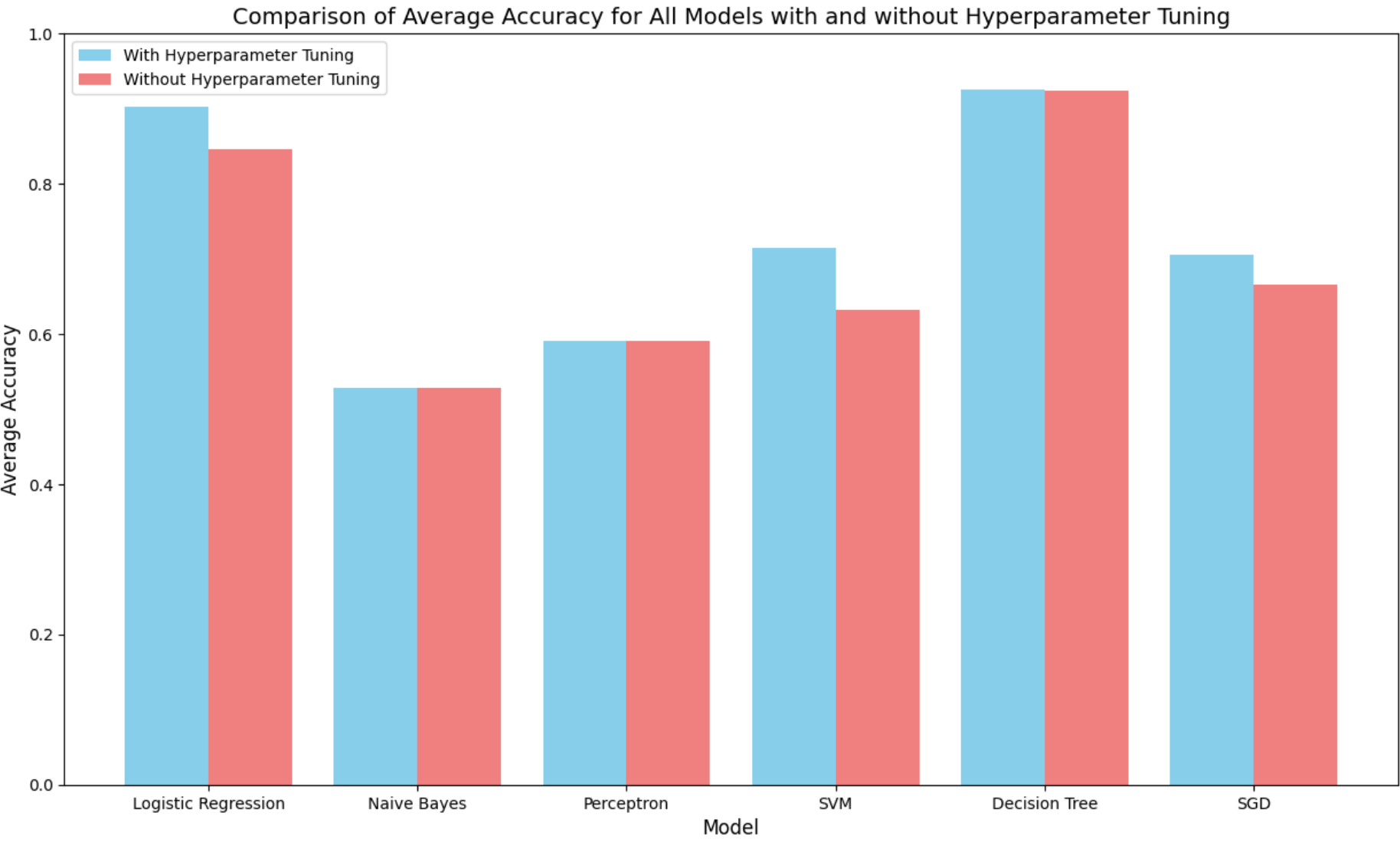
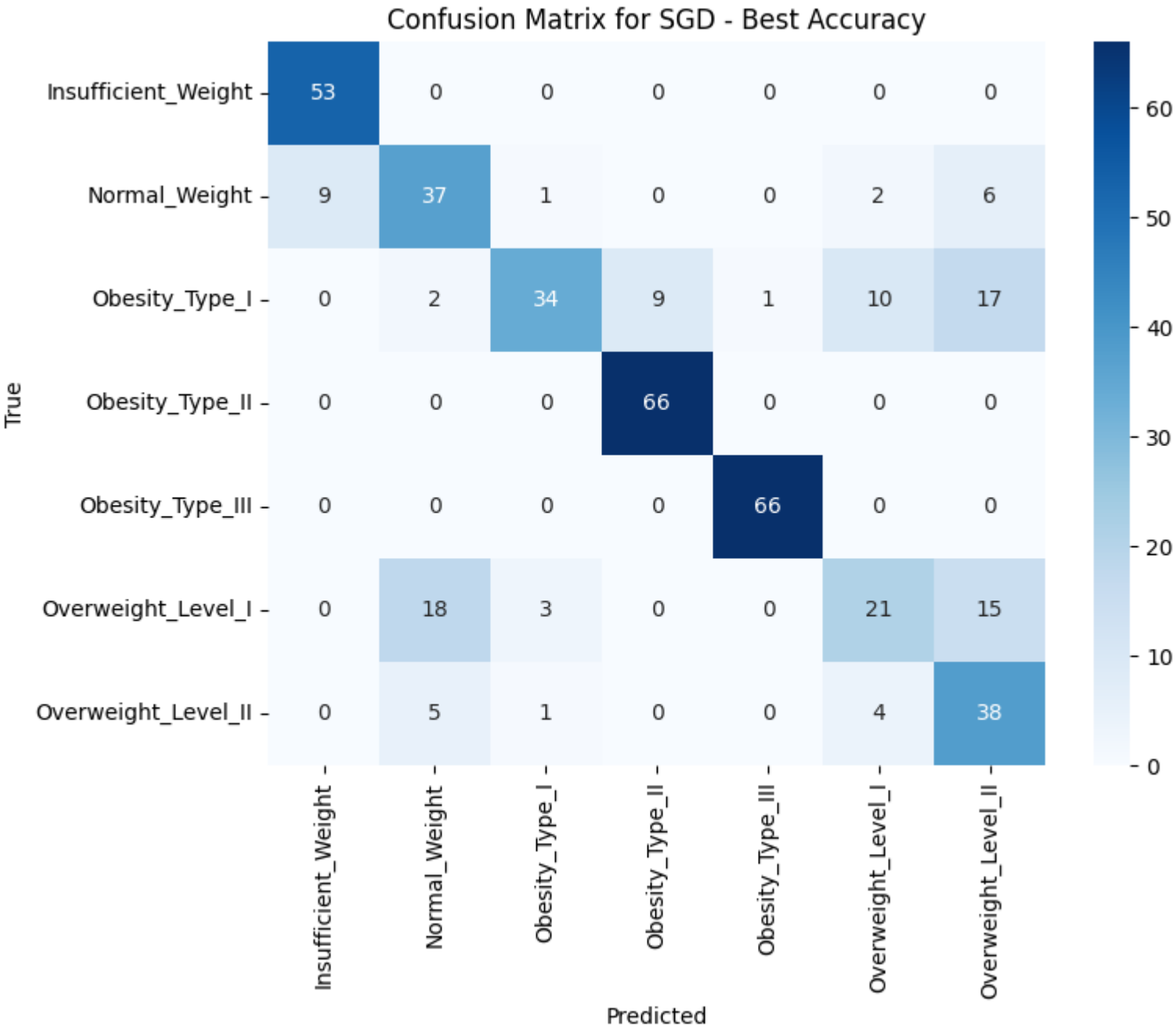
SVM:
Best Accuracy: 0.76% using With Hyperparameter Tuning
Best Hyperparameters: {'classifier_C': 0.1}
Confusion Matrix:
[[52 1 0 0 0 0 0]
[16 27 3 0 0 4 5]
[0 0 55 10 2 1 5]
[0 0 0 66 0 0 0]
[0 0 0 0 66 0 0]
[0 10 11 0 0 22 14]
[0 2 11 1 0 5 29]]



```
Decision Tree:
Best Accuracy: 0.93% using With Hyperparameter Tuning
Best Hyperparameters: {'classifier__max_depth': 10}
Confusion Matrix:
[[50  3  0  0  0  0  0]
 [ 3 45  0  0  0  7  0]
 [ 0  0 68  0  0  0  5]
 [ 0  0  2 64  0  0  0]
 [ 0  0  0  0 66  0  0]
 [ 0  5  0  0  0 48  4]
 [ 0  0  1  0  0  0 47]]
```



```
SGD:
Best Accuracy: 0.75% using With Hyperparameter Tuning
Best Hyperparameters: {'classifier__alpha': 0.001}
Confusion Matrix:
[[53  0  0  0  0  0  0]
 [ 9 37  1  0  0  2  6]
 [ 0  2 34  9  1 10 17]
 [ 0  0  0 66  0  0  0]
 [ 0  0  0  0 66  0  0]
 [ 0 18  3  0  0 21 15]
 [ 0  5  1  0  0  4 38]]
```



Results:

Logistic Regression:

Average Accuracy with Hyperparameter Tuning: 90.27%
Average Accuracy without Hyperparameter Tuning: 84.67%
Best Hyperparameters: {'classifier__C': 100}

Naive Bayes:

Average Accuracy with Hyperparameter Tuning: 52.90%
Average Accuracy without Hyperparameter Tuning: 52.90%
Best Hyperparameters: {}

Perceptron:

Average Accuracy with Hyperparameter Tuning: 59.08%
Average Accuracy without Hyperparameter Tuning: 59.08%
Best Hyperparameters: {}

SVM:

Average Accuracy with Hyperparameter Tuning: 71.49%
Average Accuracy without Hyperparameter Tuning: 63.19%
Best Hyperparameters: {'classifier__C': 0.1}

Decision Tree:

Average Accuracy with Hyperparameter Tuning: 92.62%
Average Accuracy without Hyperparameter Tuning: 92.38%
Best Hyperparameters: {'classifier__max_depth': 10}

SGD:

Average Accuracy with Hyperparameter Tuning: 70.48%
Average Accuracy without Hyperparameter Tuning: 66.55%
Best Hyperparameters: {'classifier__alpha': 0.001}

I have achieved an accuracy of nearly 93% using supervised methods, specifically employing the Decision Tree method for prediction. However, the results obtained from unsupervised methods are less satisfactory. Suggestions to enhance the accuracy of the classification problem using ChatGPT 3.5 are as follows:

1. Consider introducing additional features or engaging in feature engineering to improve the separability of clusters.
2. Explore Alternative Clustering Algorithms: Experiment with clustering algorithms beyond MiniBatchKMeans and AgglomerativeClustering, such as DBSCAN or hierarchical clustering.
3. Hyperparameter Tuning: If applicable, delve into the exploration and tuning of hyperparameters for clustering algorithms to optimize their performance.
4. Explore Other Methods and Algorithms: Consider the utilization of alternative methods and algorithms, including deep learning approaches, to further enhance classification accuracy.

In []: `pip install keras`

Requirement already satisfied: keras in /usr/local/lib/python3.10/dist-packages (2.14.0)

The following code builds and trains a neural network for multi-class classification, using regularization techniques and adaptive learning rates. It evaluates the model with accuracy, confusion matrix, ROC curve, and a detailed classification report, providing a comprehensive analysis of performance on the test set.

```
In [ ]: from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import train_test_split
from keras.models import Sequential
from keras.layers import Dense, Dropout, BatchNormalization
from keras.optimizers import Adam
from keras.callbacks import EarlyStopping, ReduceLROnPlateau
from keras.regularizers import l2
from keras.utils import to_categorical
from sklearn.metrics import classification_report
from sklearn.metrics import roc_curve, auc
import numpy as np

# Encode labels into numerical values
label_encoder = LabelEncoder()
Y_encoded = label_encoder.fit_transform(Y)

# Convert labels to one-hot encoding
Y_encoded_onehot = to_categorical(Y_encoded)

# Split the data into training and testing sets
X_train, X_test, Y_train, Y_test = train_test_split(X, Y_encoded_onehot, test_size=0.2, random_state=42)

# Build a neural network model
model = Sequential()
model.add(Dense(128, input_dim=X_train.shape[1], activation='relu', kernel_regularizer=l2(0.001)))
model.add(BatchNormalization())
model.add(Dropout(0.4))
model.add(Dense(64, activation='relu', kernel_regularizer=l2(0.001)))
model.add(BatchNormalization())
model.add(Dropout(0.4))
model.add(Dense(32, activation='relu', kernel_regularizer=l2(0.001)))
```

```

model.add(Dense(7, activation='softmax'))

# Compile the model with Adam optimizer and a smaller learning rate
model.compile(loss='categorical_crossentropy', optimizer=Adam(lr=0.02), metrics=['accuracy'])

# Train the model with early stopping and learning rate reduction on plateau
early_stopping = EarlyStopping(monitor='val_loss', patience=20, restore_best_weights=True)
reduce_lr = ReduceLROnPlateau(monitor='val_loss', factor=0.2, patience=5, min_lr=0.001)

history = model.fit(
    X_train, Y_train,
    epochs=100,
    batch_size=32,
    validation_split=0.2,
    verbose=1,
    callbacks=[early_stopping, reduce_lr]
)

# Evaluate the model on the test set
accuracy = model.evaluate(X_test, Y_test)[1]
print(f"Accuracy of the deep learning model: {accuracy * 100:.2f}%")

# Plot training history
plt.figure(figsize=(12, 6))
plt.plot(history.history['accuracy'], label='Training Accuracy')
plt.plot(history.history['val_accuracy'], label='Validation Accuracy')
plt.xlabel('Epochs')
plt.ylabel('Accuracy')
plt.title('Training and Validation Accuracy Over Epochs')
plt.legend()
plt.show()

# Get predicted probabilities for each class
Y_prob = model.predict(X_test)

# Predicted classes
Y_pred = np.argmax(Y_prob, axis=1)

# Confusion Matrix
conf_mat = confusion_matrix(np.argmax(Y_test, axis=1), Y_pred)

# Plot confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(conf_mat, annot=True, fmt='d', cmap='Blues', xticklabels=label_encoder.classes_, yticklabels=label_encoder.classes_)

plt.title("Confusion Matrix for Deep Learning Model")
plt.xlabel('Predicted')
plt.ylabel('True')
plt.show()

# ROC Curve
plt.figure(figsize=(12, 8))
for i in range(len(label_encoder.classes_)):
    fpr, tpr, _ = roc_curve(Y_test[:, i], Y_prob[:, i])
    roc_auc = auc(fpr, tpr)
    plt.plot(fpr, tpr, label=f'{label_encoder.classes_[i]} (AUC = {roc_auc:.2f})')

plt.plot([0, 1], [0, 1], color='navy', linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend()
plt.show()

# Print classification report
class_names = list(map(str, label_encoder.classes_))
print("Classification Report:")
print(classification_report(np.argmax(Y_test, axis=1), Y_pred, target_names=class_names))

```

WARNING:abs1:'lr' is deprecated in Keras optimizer, please use 'learning_rate' or use the legacy optimizer, e.g.,tf.keras.optimizers.legacy.Adam.

Epoch 1/100
42/42 [=====] - 5s 22ms/step - loss: 2.2068 - accuracy: 0.2996 - val_loss: 1.9171 - val_accuracy: 0.5749 - lr: 0.0010

Epoch 2/100
42/42 [=====] - 0s 9ms/step - loss: 1.5455 - accuracy: 0.4637 - val_loss: 1.6988 - val_accuracy: 0.5569 - lr: 0.0010

Epoch 3/100
42/42 [=====] - 0s 10ms/step - loss: 1.2536 - accuracy: 0.5775 - val_loss: 1.4386 - val_accuracy: 0.6677 - lr: 0.0010

Epoch 4/100
42/42 [=====] - 0s 10ms/step - loss: 1.1349 - accuracy: 0.6180 - val_loss: 1.2151 - val_accuracy: 0.7156 - lr: 0.0010

Epoch 5/100
42/42 [=====] - 0s 11ms/step - loss: 1.0331 - accuracy: 0.6584 - val_loss: 1.0328 - val_accuracy: 0.7425 - lr: 0.0010

Epoch 6/100
42/42 [=====] - 0s 6ms/step - loss: 0.9482 - accuracy: 0.6749 - val_loss: 0.8802 - val_accuracy: 0.8054 - lr: 0.0010

Epoch 7/100
42/42 [=====] - 0s 11ms/step - loss: 0.9337 - accuracy: 0.6816 - val_loss: 0.7616 - val_accuracy: 0.8323 - lr: 0.0010

Epoch 8/100
42/42 [=====] - 1s 13ms/step - loss: 0.8359 - accuracy: 0.7206 - val_loss: 0.6667 - val_accuracy: 0.8743 - lr: 0.0010

Epoch 9/100
42/42 [=====] - 1s 17ms/step - loss: 0.7978 - accuracy: 0.7461 - val_loss: 0.5958 - val_accuracy: 0.8952 - lr: 0.0010

Epoch 10/100
42/42 [=====] - 1s 17ms/step - loss: 0.7985 - accuracy: 0.7378 - val_loss: 0.5559 - val_accuracy: 0.8922 - lr: 0.0010

Epoch 11/100
42/42 [=====] - 1s 20ms/step - loss: 0.7104 - accuracy: 0.7700 - val_loss: 0.4947 - val_accuracy: 0.8982 - lr: 0.0010

Epoch 12/100
42/42 [=====] - 1s 14ms/step - loss: 0.7460 - accuracy: 0.7498 - val_loss: 0.4857 - val_accuracy: 0.9012 - lr: 0.0010

Epoch 13/100
42/42 [=====] - 0s 11ms/step - loss: 0.7453 - accuracy: 0.7506 - val_loss: 0.4659 - val_accuracy: 0.8922 - lr: 0.0010

Epoch 14/100
42/42 [=====] - 1s 16ms/step - loss: 0.7055 - accuracy: 0.7693 - val_loss: 0.4541 - val_accuracy: 0.9042 - lr: 0.0010

Epoch 15/100
42/42 [=====] - 1s 15ms/step - loss: 0.6324 - accuracy: 0.8030 - val_loss: 0.4280 - val_accuracy: 0.8982 - lr: 0.0010

Epoch 16/100
42/42 [=====] - 1s 13ms/step - loss: 0.6746 - accuracy: 0.7858 - val_loss: 0.4319 - val_accuracy: 0.9102 - lr: 0.0010

Epoch 17/100
42/42 [=====] - 1s 14ms/step - loss: 0.6347 - accuracy: 0.8007 - val_loss: 0.4096 - val_accuracy: 0.9042 - lr: 0.0010

Epoch 18/100
42/42 [=====] - 1s 17ms/step - loss: 0.6131 - accuracy: 0.8172 - val_loss: 0.4065 - val_accuracy: 0.9162 - lr: 0.0010

Epoch 19/100
42/42 [=====] - 1s 20ms/step - loss: 0.6137 - accuracy: 0.8052 - val_loss: 0.4139 - val_accuracy: 0.9132 - lr: 0.0010

Epoch 20/100
42/42 [=====] - 1s 17ms/step - loss: 0.6188 - accuracy: 0.8120 - val_loss: 0.3931 - val_accuracy: 0.9132 - lr: 0.0010

Epoch 21/100
42/42 [=====] - 1s 17ms/step - loss: 0.6061 - accuracy: 0.8067 - val_loss: 0.3831 - val_accuracy: 0.9072 - lr: 0.0010

Epoch 22/100
42/42 [=====] - 0s 10ms/step - loss: 0.5935 - accuracy: 0.8217 - val_loss: 0.3757 - val_accuracy: 0.9162 - lr: 0.0010

Epoch 23/100
42/42 [=====] - 1s 13ms/step - loss: 0.5719 - accuracy: 0.8255 - val_loss: 0.3683 - val_accuracy: 0.9102 - lr: 0.0010

Epoch 24/100
42/42 [=====] - 1s 15ms/step - loss: 0.5682 - accuracy: 0.8180 - val_loss: 0.3965 - val_accuracy: 0.9042 - lr: 0.0010

Epoch 25/100
42/42 [=====] - 0s 12ms/step - loss: 0.5532 - accuracy: 0.8240 - val_loss: 0.3572 - val_accuracy: 0.9251 - lr: 0.0010

Epoch 26/100
42/42 [=====] - 0s 10ms/step - loss: 0.5385 - accuracy: 0.8322 - val_loss: 0.3548 - val_accuracy: 0.9162 - lr: 0.0010

Epoch 27/100
42/42 [=====] - 0s 10ms/step - loss: 0.5523 - accuracy: 0.8337 - val_loss: 0.3536 - val_accuracy: 0.9072 - lr: 0.0010

Epoch 28/100
42/42 [=====] - 0s 9ms/step - loss: 0.5732 - accuracy: 0.8240 - val_loss: 0.3420 - val_accuracy: 0.9162 - lr: 0.0010

Epoch 29/100
42/42 [=====] - 0s 8ms/step - loss: 0.5189 - accuracy: 0.8509 - val_loss: 0.3547 - val_accuracy: 0.9222 - lr: 0.0010

Epoch 30/100
42/42 [=====] - 0s 10ms/step - loss: 0.5128 - accuracy: 0.8509 - val_loss: 0.3318 - val_accuracy: 0.9162 - lr: 0.0010

Epoch 31/100
42/42 [=====] - 0s 10ms/step - loss: 0.5165 - accuracy: 0.8434 - val_loss: 0.3438 - val_accuracy: 0.9162 - lr: 0.0010

Epoch 32/100
42/42 [=====] - 0s 11ms/step - loss: 0.5166 - accuracy: 0.8412 - val_loss: 0.3181 - val_accuracy: 0.9341 - lr: 0.0010

Epoch 33/100
42/42 [=====] - 0s 9ms/step - loss: 0.5036 - accuracy: 0.8569 - val_loss: 0.3329 - val_accuracy: 0.9311 - lr: 0.0010

Epoch 34/100
42/42 [=====] - 1s 13ms/step - loss: 0.4641 - accuracy: 0.8644 - val_loss: 0.3060 - val_accuracy: 0.9341 - lr: 0.0010

Epoch 35/100
42/42 [=====] - 0s 7ms/step - loss: 0.4839 - accuracy: 0.8629 - val_loss: 0.3139 - val_accuracy: 0.9401 - lr: 0.0010

Epoch 36/100
42/42 [=====] - 0s 7ms/step - loss: 0.4597 - accuracy: 0.8742 - val_loss: 0.3320 - val_accuracy: 0.9311 - lr: 0.0010

Epoch 37/100
42/42 [=====] - 0s 9ms/step - loss: 0.4773 - accuracy: 0.8622 - val_loss: 0.3054 - val_accuracy: 0.9311 - lr: 0.0010

Epoch 38/100
42/42 [=====] - 1s 13ms/step - loss: 0.4849 - accuracy: 0.8569 - val_loss: 0.3095 - val_accuracy: 0.9222 - lr: 0.0010

Epoch 39/100
42/42 [=====] - 0s 9ms/step - loss: 0.4424 - accuracy: 0.8764 - val_loss: 0.3422 - val_accuracy: 0.9222 - lr: 0.0010

Epoch 40/100
42/42 [=====] - 0s 6ms/step - loss: 0.4539 - accuracy: 0.8667 - val_loss: 0.2945 - val_accuracy: 0.9431 - lr: 0.0010

Epoch 41/100
42/42 [=====] - 0s 7ms/step - loss: 0.4946 - accuracy: 0.8554 - val_loss: 0.3081 - val_accuracy: 0.9162 - lr: 0.0010

Epoch 42/100
42/42 [=====] - 0s 12ms/step - loss: 0.4335 - accuracy: 0.8824 - val_loss: 0.3248 - val_accuracy: 0.9222 - lr: 0.0010

Epoch 43/100
42/42 [=====] - 0s 10ms/step - loss: 0.4421 - accuracy: 0.8742 - val_loss: 0.3867 - val_accuracy: 0.8982 - lr: 0.0010

Epoch 44/100
42/42 [=====] - 0s 11ms/step - loss: 0.4480 - accuracy: 0.8801 - val_loss: 0.2895 - val_accuracy: 0.9491 - lr: 0.0010

Epoch 45/100
42/42 [=====] - 1s 16ms/step - loss: 0.4572 - accuracy: 0.8682 - val_loss: 0.2907 - val_accuracy: 0.9341 - lr: 0.0010

Epoch 46/100
42/42 [=====] - 1s 16ms/step - loss: 0.3985 - accuracy: 0.8944 - val_loss: 0.2894 - val_accuracy: 0.9491 - lr: 0.0010

Epoch 47/100
42/42 [=====] - 1s 14ms/step - loss: 0.4421 - accuracy: 0.8704 - val_loss: 0.2878 - val_accuracy: 0.9431 - lr: 0.0010

Epoch 48/100
42/42 [=====] - 1s 14ms/step - loss: 0.4424 - accuracy: 0.8824 - val_loss: 0.2952 - val_accuracy: 0.9311 - lr: 0.0010

Epoch 49/100
42/42 [=====] - 1s 14ms/step - loss: 0.4234 - accuracy: 0.8794 - val_loss: 0.2936 - val_accuracy: 0.9401 - lr: 0.0010

Epoch 50/100
42/42 [=====] - 0s 10ms/step - loss: 0.4311 - accuracy: 0.8749 - val_loss: 0.2885 - val_accuracy: 0.9431 - lr: 0.0010

Epoch 51/100
42/42 [=====] - 1s 12ms/step - loss: 0.4276 - accuracy: 0.8899 - val_loss: 0.2996 - val_accuracy: 0.9401 - lr: 0.0010

Epoch 52/100
42/42 [=====] - 1s 26ms/step - loss: 0.4181 - accuracy: 0.8787 - val_loss: 0.2866 - val_accuracy: 0.9341 - lr: 0.0010

Epoch 53/100
42/42 [=====] - 1s 28ms/step - loss: 0.4106 - accuracy: 0.8906 - val_loss: 0.2868 - val_accuracy: 0.9401 - lr: 0.0010

Epoch 54/100
42/42 [=====] - 1s 15ms/step - loss: 0.3839 - accuracy: 0.8974 - val_loss: 0.2731 - val_accuracy: 0.9401 - lr: 0.0010

Epoch 55/100
42/42 [=====] - 1s 14ms/step - loss: 0.4030 - accuracy: 0.8959 - val_loss: 0.2622 - val_accuracy: 0.9461 - lr: 0.0010

Epoch 56/100
42/42 [=====] - 1s 13ms/step - loss: 0.3643 - accuracy: 0.9056 - val_loss: 0.2882 - val_accuracy: 0.9341 - lr: 0.0010

Epoch 57/100
42/42 [=====] - 0s 10ms/step - loss: 0.3691 - accuracy: 0.9041 - val_loss: 0.2957 - val_accuracy: 0.9311 - lr: 0.0010

Epoch 58/100
42/42 [=====] - 1s 16ms/step - loss: 0.3680 - accuracy: 0.8921 - val_loss: 0.2987 - val_accuracy: 0.9281 - lr: 0.0010

Epoch 59/100
42/42 [=====] - 0s 6ms/step - loss: 0.3435 - accuracy: 0.9131 - val_loss: 0.2830 - val_accuracy: 0.9461 - lr: 0.0010

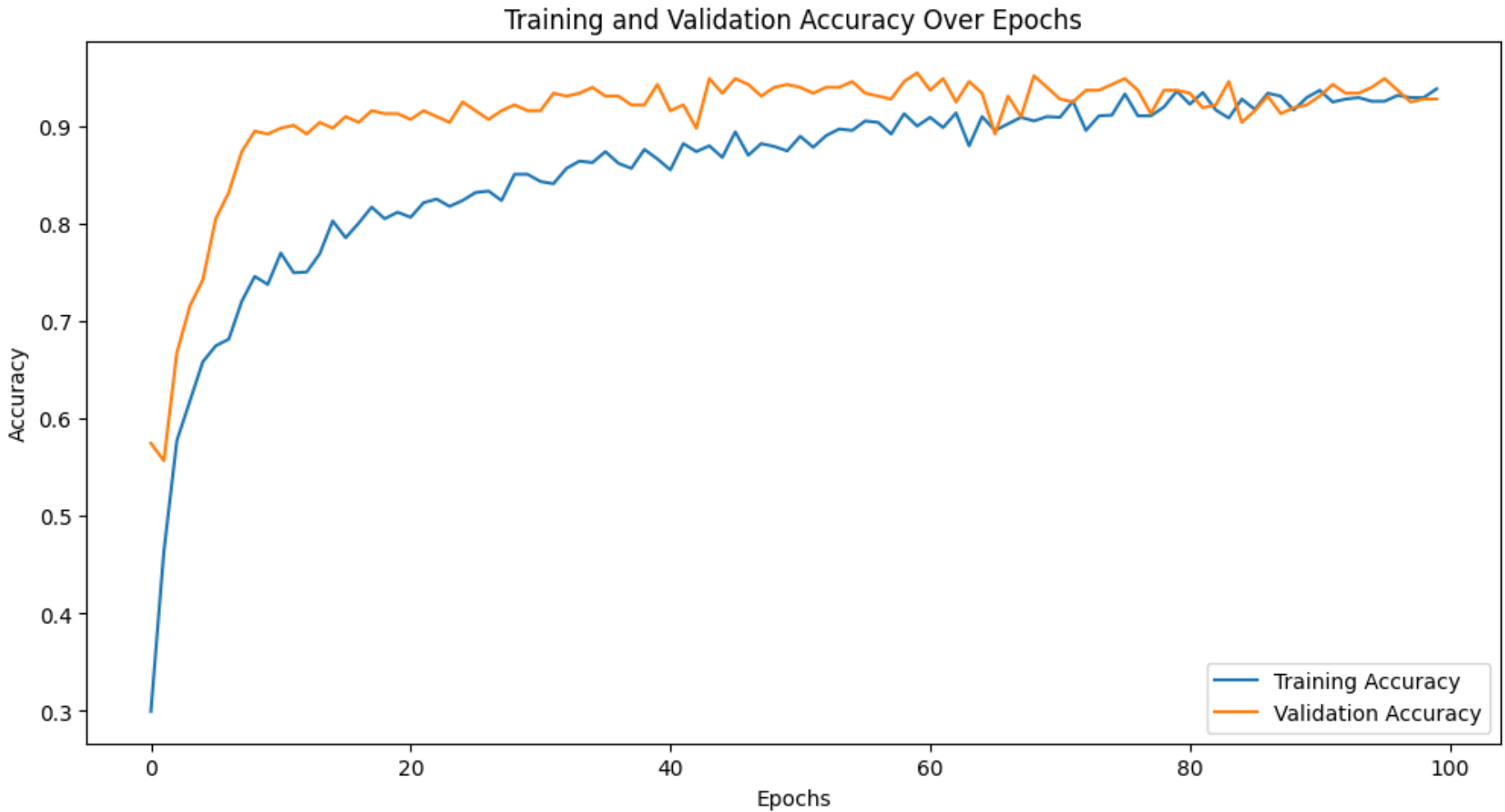
Epoch 60/100
42/42 [=====] - 0s 7ms/step - loss: 0.3635 - accuracy: 0.9004 - val_loss: 0.2634 - val_accuracy: 0.9551 - lr: 0.0010

Epoch 61/100
42/42 [=====] - 0s 8ms/step - loss: 0.3583 - accuracy: 0.9094 - val_loss: 0.2800 - val_accuracy: 0.9371 - lr: 0.0010

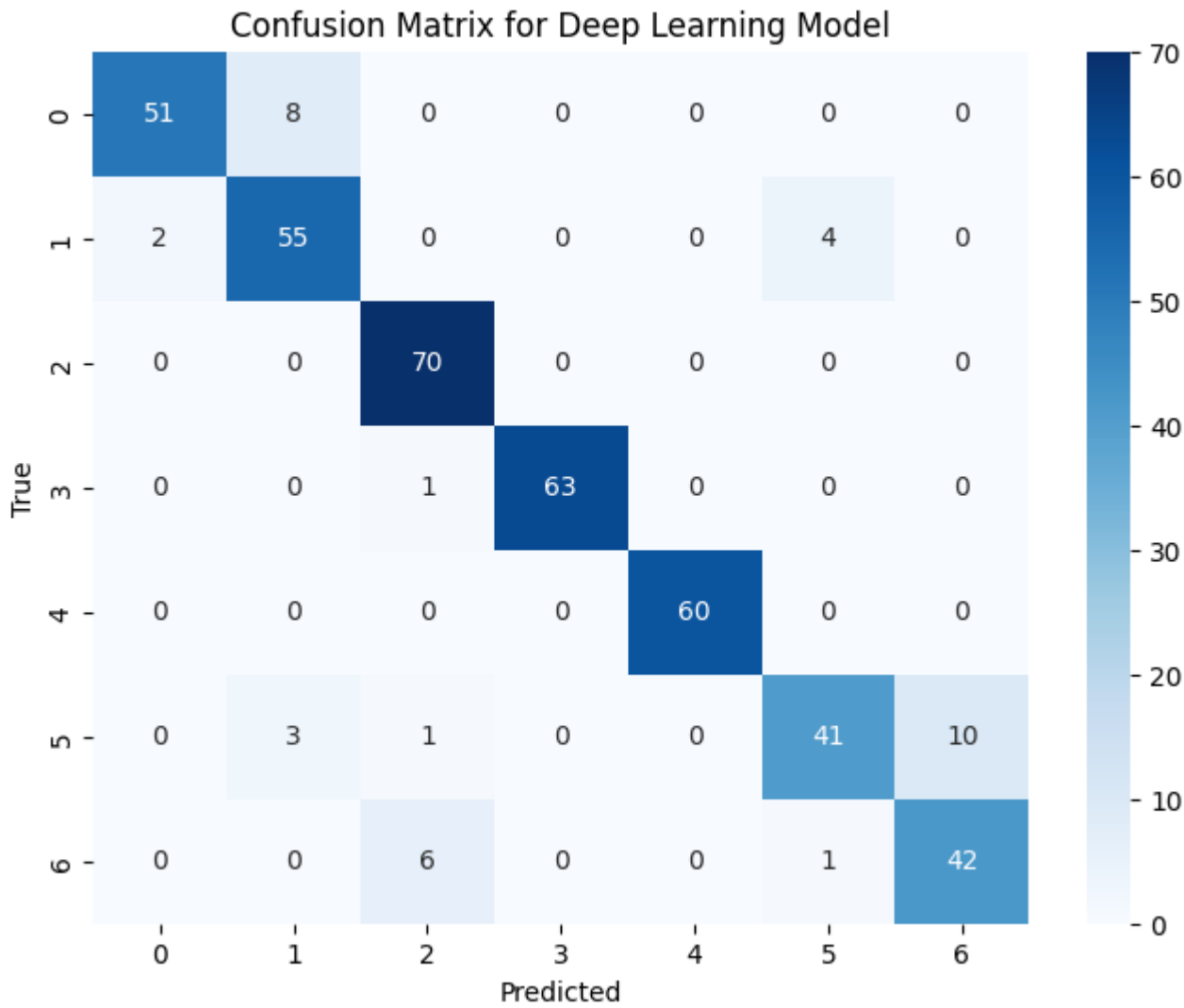
Epoch 62/100
42/42 [=====] - 0s 8ms/step - loss: 0.3583 - accuracy: 0.8989 - val_loss: 0.2711 - val_accuracy: 0.9491 - lr: 0.0010

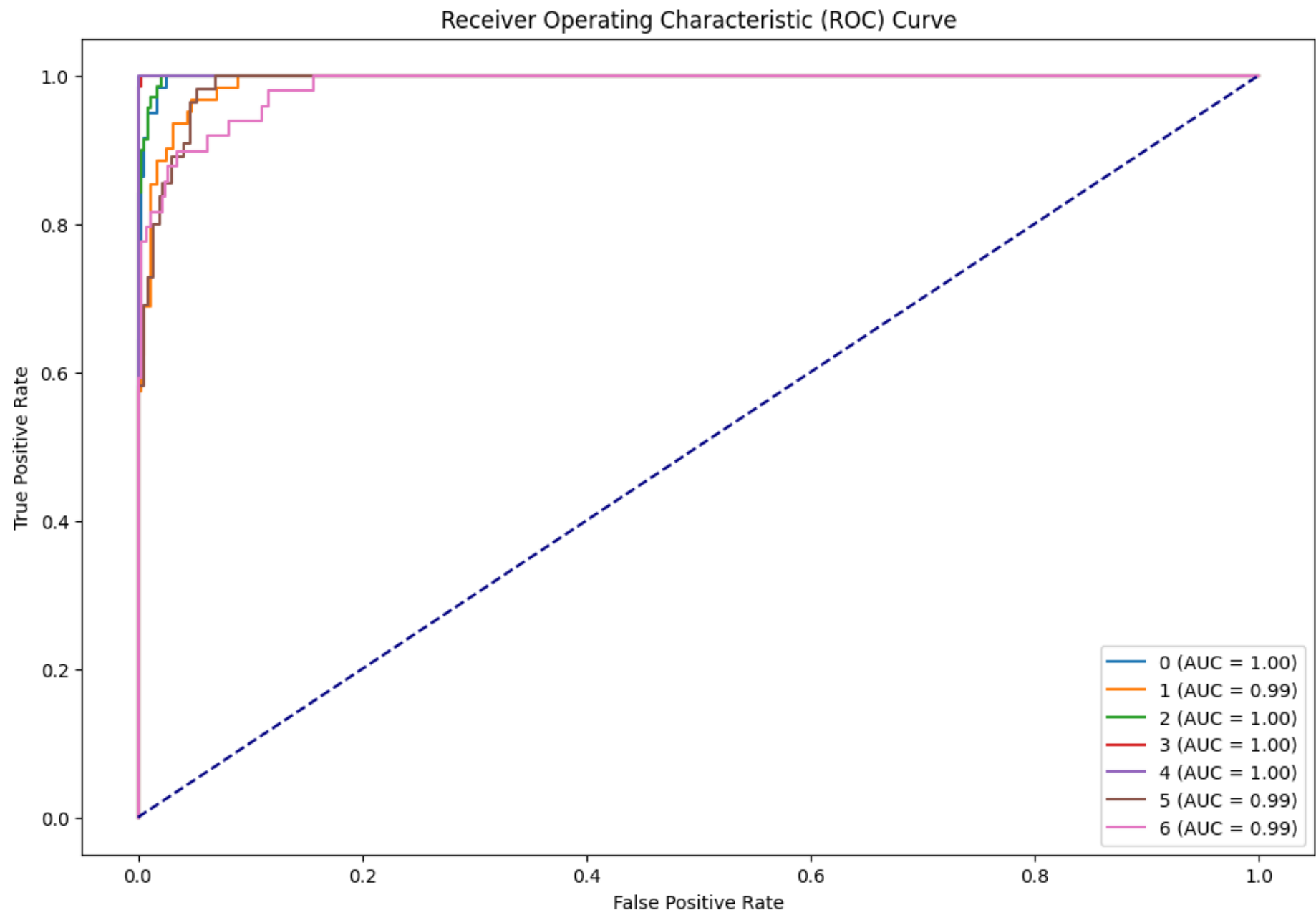
Epoch 63/100
42/42 [=====] - 0s 7ms/step - loss: 0.3357 - accuracy: 0.9139 - val_loss: 0.2935 - val_accuracy: 0.9251
- lr: 0.0010
Epoch 64/100
42/42 [=====] - 0s 7ms/step - loss: 0.4290 - accuracy: 0.8801 - val_loss: 0.2669 - val_accuracy: 0.9461
- lr: 0.0010
Epoch 65/100
42/42 [=====] - 0s 7ms/step - loss: 0.3422 - accuracy: 0.9101 - val_loss: 0.2681 - val_accuracy: 0.9341
- lr: 0.0010
Epoch 66/100
42/42 [=====] - 0s 8ms/step - loss: 0.3775 - accuracy: 0.8959 - val_loss: 0.3651 - val_accuracy: 0.8922
- lr: 0.0010
Epoch 67/100
42/42 [=====] - 0s 7ms/step - loss: 0.3558 - accuracy: 0.9026 - val_loss: 0.2841 - val_accuracy: 0.9311
- lr: 0.0010
Epoch 68/100
42/42 [=====] - 0s 7ms/step - loss: 0.3502 - accuracy: 0.9094 - val_loss: 0.3070 - val_accuracy: 0.9102
- lr: 0.0010
Epoch 69/100
42/42 [=====] - 0s 7ms/step - loss: 0.3511 - accuracy: 0.9056 - val_loss: 0.2557 - val_accuracy: 0.9521
- lr: 0.0010
Epoch 70/100
42/42 [=====] - 0s 8ms/step - loss: 0.3216 - accuracy: 0.9101 - val_loss: 0.2837 - val_accuracy: 0.9401
- lr: 0.0010
Epoch 71/100
42/42 [=====] - 0s 7ms/step - loss: 0.3227 - accuracy: 0.9094 - val_loss: 0.2759 - val_accuracy: 0.9281
- lr: 0.0010
Epoch 72/100
42/42 [=====] - 0s 7ms/step - loss: 0.3169 - accuracy: 0.9258 - val_loss: 0.2849 - val_accuracy: 0.9251
- lr: 0.0010
Epoch 73/100
42/42 [=====] - 0s 9ms/step - loss: 0.3656 - accuracy: 0.8959 - val_loss: 0.2599 - val_accuracy: 0.9371
- lr: 0.0010
Epoch 74/100
42/42 [=====] - 0s 11ms/step - loss: 0.3491 - accuracy: 0.9109 - val_loss: 0.2570 - val_accuracy: 0.937
1 - lr: 0.0010
Epoch 75/100
42/42 [=====] - 0s 4ms/step - loss: 0.3286 - accuracy: 0.9116 - val_loss: 0.2505 - val_accuracy: 0.9431
- lr: 0.0010
Epoch 76/100
42/42 [=====] - 0s 4ms/step - loss: 0.2938 - accuracy: 0.9333 - val_loss: 0.2412 - val_accuracy: 0.9491
- lr: 0.0010
Epoch 77/100
42/42 [=====] - 0s 4ms/step - loss: 0.3416 - accuracy: 0.9109 - val_loss: 0.2431 - val_accuracy: 0.9371
- lr: 0.0010
Epoch 78/100
42/42 [=====] - 0s 4ms/step - loss: 0.3382 - accuracy: 0.9109 - val_loss: 0.3058 - val_accuracy: 0.9132
- lr: 0.0010
Epoch 79/100
42/42 [=====] - 0s 4ms/step - loss: 0.3240 - accuracy: 0.9199 - val_loss: 0.2799 - val_accuracy: 0.9371
- lr: 0.0010
Epoch 80/100
42/42 [=====] - 0s 4ms/step - loss: 0.3004 - accuracy: 0.9363 - val_loss: 0.2709 - val_accuracy: 0.9371
- lr: 0.0010
Epoch 81/100
42/42 [=====] - 0s 4ms/step - loss: 0.2960 - accuracy: 0.9228 - val_loss: 0.2635 - val_accuracy: 0.9341
- lr: 0.0010
Epoch 82/100
42/42 [=====] - 0s 4ms/step - loss: 0.2974 - accuracy: 0.9348 - val_loss: 0.3076 - val_accuracy: 0.9192
- lr: 0.0010
Epoch 83/100
42/42 [=====] - 0s 4ms/step - loss: 0.3147 - accuracy: 0.9169 - val_loss: 0.2767 - val_accuracy: 0.9222
- lr: 0.0010
Epoch 84/100
42/42 [=====] - 0s 4ms/step - loss: 0.3196 - accuracy: 0.9086 - val_loss: 0.2560 - val_accuracy: 0.9461
- lr: 0.0010
Epoch 85/100
42/42 [=====] - 0s 4ms/step - loss: 0.3092 - accuracy: 0.9281 - val_loss: 0.2912 - val_accuracy: 0.9042
- lr: 0.0010
Epoch 86/100
42/42 [=====] - 0s 4ms/step - loss: 0.3309 - accuracy: 0.9176 - val_loss: 0.2858 - val_accuracy: 0.9162
- lr: 0.0010
Epoch 87/100
42/42 [=====] - 0s 4ms/step - loss: 0.2844 - accuracy: 0.9341 - val_loss: 0.2725 - val_accuracy: 0.9311
- lr: 0.0010
Epoch 88/100
42/42 [=====] - 0s 4ms/step - loss: 0.2803 - accuracy: 0.9311 - val_loss: 0.2934 - val_accuracy: 0.9132
- lr: 0.0010
Epoch 89/100
42/42 [=====] - 0s 4ms/step - loss: 0.2871 - accuracy: 0.9169 - val_loss: 0.3058 - val_accuracy: 0.9192
- lr: 0.0010
Epoch 90/100
42/42 [=====] - 0s 5ms/step - loss: 0.2836 - accuracy: 0.9296 - val_loss: 0.3064 - val_accuracy: 0.9222
- lr: 0.0010
Epoch 91/100
42/42 [=====] - 0s 4ms/step - loss: 0.2762 - accuracy: 0.9371 - val_loss: 0.2843 - val_accuracy: 0.9311
- lr: 0.0010
Epoch 92/100
42/42 [=====] - 0s 4ms/step - loss: 0.3047 - accuracy: 0.9251 - val_loss: 0.2660 - val_accuracy: 0.9431
- lr: 0.0010
Epoch 93/100
42/42 [=====] - 0s 4ms/step - loss: 0.3016 - accuracy: 0.9281 - val_loss: 0.2724 - val_accuracy: 0.9341
- lr: 0.0010

```
Epoch 94/100
42/42 [=====] - 0s 4ms/step - loss: 0.2902 - accuracy: 0.9296 - val_loss: 0.2856 - val_accuracy: 0.9341
- lr: 0.0010
Epoch 95/100
42/42 [=====] - 0s 4ms/step - loss: 0.2635 - accuracy: 0.9258 - val_loss: 0.2819 - val_accuracy: 0.9401
- lr: 0.0010
Epoch 96/100
42/42 [=====] - 0s 4ms/step - loss: 0.2960 - accuracy: 0.9258 - val_loss: 0.2327 - val_accuracy: 0.9491
- lr: 0.0010
Epoch 97/100
42/42 [=====] - 0s 4ms/step - loss: 0.2798 - accuracy: 0.9318 - val_loss: 0.2708 - val_accuracy: 0.9371
- lr: 0.0010
Epoch 98/100
42/42 [=====] - 0s 4ms/step - loss: 0.2951 - accuracy: 0.9296 - val_loss: 0.2715 - val_accuracy: 0.9251
- lr: 0.0010
Epoch 99/100
42/42 [=====] - 0s 5ms/step - loss: 0.2952 - accuracy: 0.9296 - val_loss: 0.2725 - val_accuracy: 0.9281
- lr: 0.0010
Epoch 100/100
42/42 [=====] - 0s 6ms/step - loss: 0.2665 - accuracy: 0.9386 - val_loss: 0.3064 - val_accuracy: 0.9281
- lr: 0.0010
14/14 [=====] - 0s 3ms/step - loss: 0.3017 - accuracy: 0.9139
Accuracy of the deep learning model: 91.39%
```



```
14/14 [=====] - 0s 2ms/step
```





Classification Report:

	precision	recall	f1-score	support
0	0.96	0.86	0.91	59
1	0.83	0.90	0.87	61
2	0.90	1.00	0.95	70
3	1.00	0.98	0.99	64
4	1.00	1.00	1.00	60
5	0.89	0.75	0.81	55
6	0.81	0.86	0.83	49
accuracy			0.91	418
macro avg	0.91	0.91	0.91	418
weighted avg	0.92	0.91	0.91	418

Neural Network Model:

A sequential neural network model is built using Keras with three dense layers. Batch normalization is applied after each dense layer to improve training stability. Dropout layers are added to reduce overfitting.

Model Compilation: The model is compiled using the Adam optimizer with a specified learning rate. Categorical cross-entropy is used as the loss function, and accuracy is chosen as the metric.

Training with Early Stopping and Learning Rate Reduction: The model is trained using the training set. Early stopping is implemented to prevent overfitting, and learning rate reduction on plateau is used for adaptive learning rates.

Evaluation and Plotting: The code evaluates the model on the test set and prints the accuracy. It plots the training and validation accuracy over epochs, the confusion matrix, and the ROC curve.

Classification Report: The code generates a classification report, including precision, recall, and F1-score for each class.

Methods Used:

Neural Network: The neural network architecture consists of fully connected dense layers with ReLU activation functions. Batch normalization and dropout are used for regularization.

Optimization Algorithm: The Adam optimizer is employed for model optimization.

Regularization: L2 regularization is applied to the weights of the dense layers to prevent overfitting.

Callbacks: Early stopping is implemented to halt training when the validation loss plateaus. Learning rate reduction on plateau adjusts the learning rate dynamically during training.

Evaluation Metrics: Accuracy is used as the primary evaluation metric. Additional metrics such as the confusion matrix, ROC curve, and classification report provide insights into model performance.

Results:

Accuracy: The code reports the accuracy of the deep learning model on the test set. The training history plot shows the training and validation accuracy trends over epochs.

Confusion Matrix: A heatmap of the confusion matrix is plotted, visualizing the model's performance in predicting each class.

ROC Curve: The ROC curve is plotted to evaluate the trade-off between true positive rate and false positive rate for different thresholds.

Classification Report: The classification report provides detailed metrics for each class, including precision, recall, and F1-score.

Potential Improvements (GPT 3.5):

Hyperparameter Tuning: Further exploration of hyperparameters like batch size, dropout rates, and regularization strength may lead to better results.

Advanced Architectures: Consider experimenting with more complex architectures, such as convolutional neural networks (CNNs) or recurrent neural networks (RNNs), depending on the nature of the data.

Ensemble Methods: Implement ensemble methods by combining predictions from multiple models.

Data Augmentation: If the dataset is limited, applying data augmentation techniques during training could be beneficial.

The project has been done by Mahdi Baniyadi.

December_2023