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    # This Python 3 environment comes with many helpful analytics
    libraries installed
    # It is defined by the kaggle/python Docker image:
    https://github.com/kaggle/docker-python
    # For example, here's several helpful packages to load

import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)

# Input data files are available in the read-only "../input/"
# directory
# For example, running this (by clicking run or pressing Shift+Enter)
# will list all files under the input directory

import os
    for dirname, _, filenames in os.walk('/kaggle/input'):
        for filename in filenames:
            print(os.path.join(dirname, filename))

# You can write up to 20GB to the current directory (/kaggle/working/)
# that gets preserved as output when you create a version using "Save &
# Run All"
# You can also write temporary files to /kaggle/temp/, but they won't
# be saved outside of the current session

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```

(2)/PPG_Dataset/Figures/fig_07_0003.jpg
/kaggle/input/ppg-signal-with-blood-sugar-level-data/archive
(2)/PPG_Dataset/Figures/fig_20_0002.jpg
/kaggle/input/ppg-signal-with-blood-sugar-level-data/archive
(2)/PPG_Dataset/Figures/fig_22_0002.jpg
/kaggle/input/ppg-signal-with-blood-sugar-level-data/archive
(2)/PPG_Dataset/Figures/fig_08_0001.jpg
/kaggle/input/ppg-signal-with-blood-sugar-level-data/archive
(2)/PPG_Dataset/Figures/fig_06_0001.jpg
/kaggle/input/ppg-signal-with-blood-sugar-level-data/archive
(2)/PPG_Dataset/Figures/fig_10_0002.jpg
/kaggle/input/ppg-signal-with-blood-sugar-level-data/archive
(2)/PPG_Dataset/Figures/fig_11_0003.jpg

```

```

import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

```

```

df=pd.read_csv('/kaggle/input/ppg-signal-with-blood-sugar-level-data/
clean-dataset.csv')

```

```
df.dtypes
```

```

PPG_Signal      int64
Patient_Id      int64
Heart_Rate      float64
Systolic_Peak   float64
Diastolic_Peak   float64
Pulse_Area      float64
index          int64
Gender          int64
Age            int64
Glucose_level   int64
Height         int64
Weight         int64
pl            int64
dtype: object

```

```
df
```

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0
505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0

```

505.0
...
...
...
844941      513      23      83.0      516.0
510.0
844942      513      23      83.0      516.0
510.0
844943      513      23      83.0      516.0
510.0
844944      513      23      83.0      516.0
510.0
844945      513      23      83.0      516.0
510.0

```

	Pulse_Area	index	Gender	Age	Glucose_level	Height	Weight
pl							
0	393.0	0	1	38	99	180	53
1							
1	393.0	1	1	38	102	180	53
2							
2	393.0	2	1	38	103	180	53
3							
3	393.0	3	1	38	128	180	53
4							
4	393.0	4	1	38	130	180	53
5							
...	...	...	...	...	...	...	...
...							
844941	366.0	43	1	27	108	173	57
1463368							
844942	366.0	42	1	27	100	173	57
1463369							
844943	366.0	43	1	27	108	173	57
1463370							
844944	366.0	42	1	27	100	173	57
1463371							
844945	366.0	43	1	27	108	173	57
1463372							

```
[844946 rows x 13 columns]
```

```
# Check for missing values in each column
```

```
missing_values = df.isnull().sum()
```

```
# Print the count of missing values for each column
```

```
print("Missing Values in Each Column:")
```

```
print(missing_values)
```

```
#if we have missing values, can lead to inaccuracies in the model training portion
```



Missing Values in Each Column:

PPG_Signal	0
Patient_Id	0
Heart_Rate	0
Systolic_Peak	0
Diastolic_Peak	0
Pulse_Area	0
index	0
Gender	0
Age	0
Glucose_level	0
Height	0
Weight	0
pl	0

dtype: int64

*#Loop through each column and print the unique values*

```
for column in df.columns:
    unique_values = df[column].unique()
    count_values = len(df[column].unique())
    print(f"Column: {column}")
    print(f"Unique Values: {unique_values}\n")
    print(f"total count unique values : {count_values}\n")
```

Column: PPG\_Signal

Unique Values: [511 512 513 514 515 516 517 510 509 508 507 506]

total count unique values : 12

Column: Patient\_Id

Unique Values: [ 1 2 3 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19  
20 21 22 23]

total count unique values : 22

Column: Heart\_Rate

Unique Values: [77. 75. 80. 79. 81. 76. 83. 65. 61. 63. 70. 85. 84.  
88. 86. 89. 93. 87.  
90. 78. 82. 64. 67. 68. 66. 74. 73. 71. 91. 62. 72. 92.]

total count unique values : 32

Column: Systolic\_Peak

Unique Values: [522. 520. 521. 518. 519. 524. 523. 526. 525. 527. 528.  
516. 514. 515.  
517. 529.]

total count unique values : 16

Column: Diastolic\_Peak

Unique Values: [505. 507. 508. 506. 509. 504. 511. 510. 512.]

total count unique values : 9

Column: Pulse\_Area

Unique Values: [393. 406. 383. 385. 386. 375. 394. 380. 376.  
396. 399. 369.  
468. 481.5 467. 438. 434. 355. 398. 365. 347. 356. 353.  
379.  
345. 363. 367. 364. 378. 312. 370. 349. 377. 366. 321.  
324.  
338. 390. 388. 374. 381. 362. 373. 405. 384. 480. 455.  
446.  
466. 459. 389. 412. 410. 309.5 400. 477. 465. 354. 417.  
433.  
426. 322. 313. 475. 335. 402. 401. 334. 427. 395. 428.  
404.  
416. 432. 479. 421. 422. 408. 343. 323. 450. 391. 423.  
392.  
342. 431. 333. 346. 357. 403. 424. 397. ]

total count unique values : 92

Column: index

Unique Values: [ 0 1 2 3 4 5 6 31 32 33 44 45 51 52 53 54 55 56  
57 58 59 60 61 62  
63 64 65 66 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25  
26  
27 28 30 29 34 35 36 38 37 39 40 41 42 43]

total count unique values : 62

Column: Gender

Unique Values: [1 0]

total count unique values : 2

Column: Age

Unique Values: [38 25 33 23 31 39 37 22 61 50 51 45 24 26 48 27]

total count unique values : 16

Column: Glucose\_level

Unique Values: [ 99 102 103 128 130 134 136 108 111 118 120 127 94  
96 106 110 129 88  
146 124 100 113 95 115 183 139 112 140]

total count unique values : 28

Column: Height

```
Unique Values: [180 187 175 165 179 172 182 161 178 157 169 170 154 173]
```

```
total count unique values : 14
```

```
Column: Weight
```

```
Unique Values: [ 53  75 103  56  60  93  63  90  62  61  96  83  89 55 42 88 50 57]
```

```
total count unique values : 18
```

```
Column: pl
```

```
Unique Values: [      1      2      3 ... 1463370 1463371 1463372]
```

```
total count unique values : 844946
```

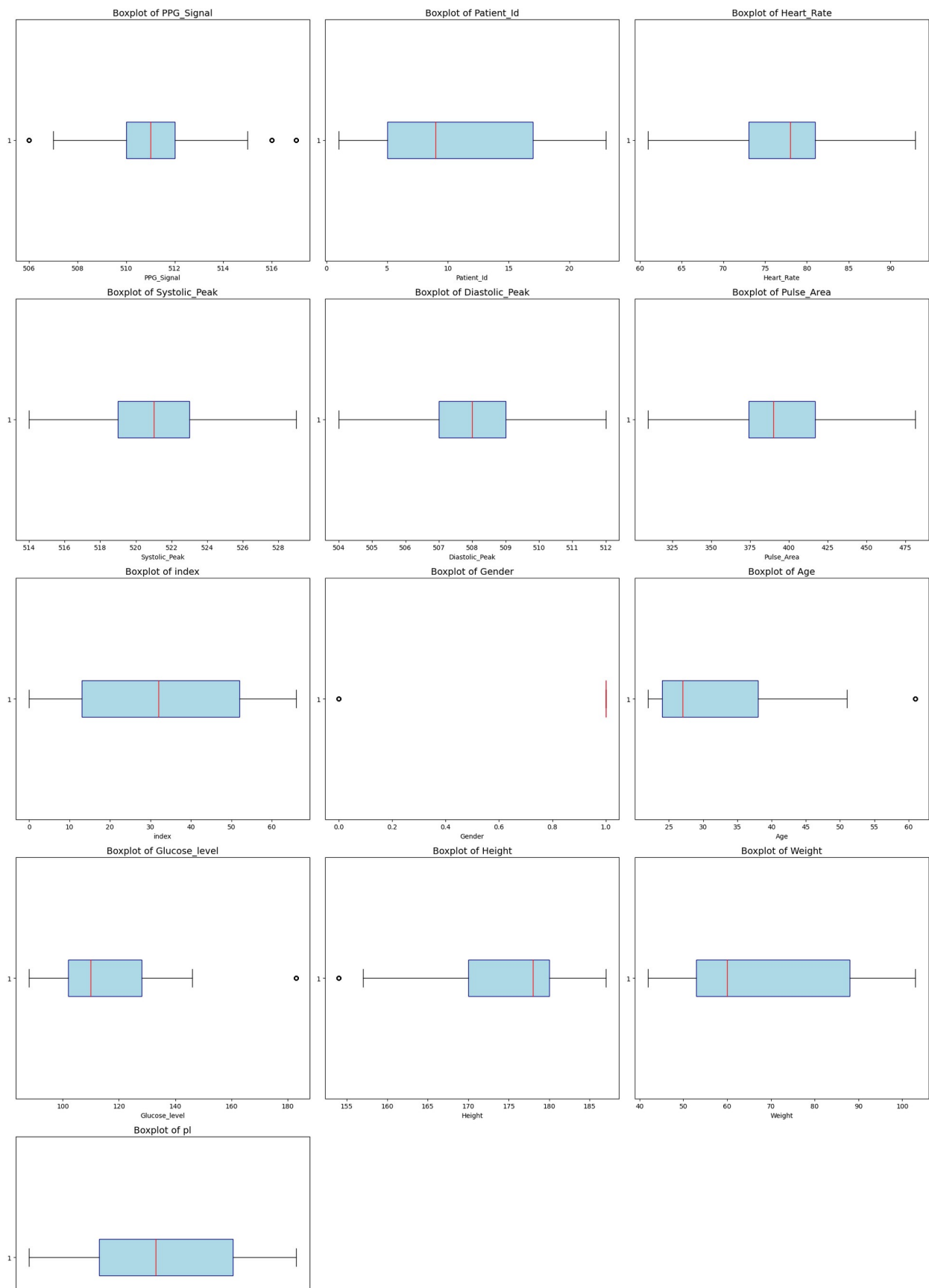
```
def plot_boxplots_alternative(df):
    num_columns = df.select_dtypes(include='number').columns
    num_features = len(num_columns)
    rows = (num_features // 3) + 1
    cols = min(num_features, 3)
    fig, axes = plt.subplots(rows, cols, figsize=(20, rows * 6))
    axes = axes.flatten()  # Flatten in case of more subplots

    for i, col in enumerate(num_columns):
        axes[i].boxplot(df[col], vert=False, patch_artist=True,
                        boxprops=dict(facecolor='lightblue',
color='navy'),
                        medianprops=dict(color='red'))
        axes[i].set_title(f'Boxplot of {col}', fontsize=14)
        axes[i].set_xlabel(col)

    for j in range(i + 1, len(axes)):
        fig.delaxes(axes[j])

    plt.tight_layout()
    plt.show()

plot_boxplots_alternative(df)
```



df

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0
505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				
844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0
510.0				
844945	513	23	83.0	516.0
510.0				

	Pulse_Area	index	Gender	Age	Glucose_level	Height	Weight
pl							
0	393.0	0	1	38	99	180	53
1							
1	393.0	1	1	38	102	180	53
2							
2	393.0	2	1	38	103	180	53
3							
3	393.0	3	1	38	128	180	53
4							
4	393.0	4	1	38	130	180	53
5							
...	...	...	...	...	...	...	...
...							
844941	366.0	43	1	27	108	173	57
1463368							
844942	366.0	42	1	27	100	173	57
1463369							
844943	366.0	43	1	27	108	173	57
1463370							
844944	366.0	42	1	27	100	173	57
1463371							
844945	366.0	43	1	27	108	173	57

1463372

[844946 rows x 13 columns]

```
import pandas as pd
```

```
# Define the bins (age ranges) and the corresponding labels
```

```
bins = [20, 30, 40, 50, 60, 70] # Age ranges (e.g., 0-20, 21-30, etc.)
```

```
labels = [1, 2, 3, 4, 5] # Corresponding labels
```

```
# Create a new column 'Age Range' based on the age values
```

```
df['Age Range'] = pd.cut(df['Age'], bins=bins, labels=labels,  
right=False)
```

```
# Display the DataFrame with the new 'Age Range' column
```

```
print(df)
```

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0
505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				
844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0
510.0				
844945	513	23	83.0	516.0
510.0				

	Pulse_Area	index	Gender	Age	Glucose_level	Height	Weight
\							
0	393.0	0	1	38	99	180	53
1	393.0	1	1	38	102	180	53
2	393.0	2	1	38	103	180	53

3	393.0	3	1	38	128	180	53
4	393.0	4	1	38	130	180	53
...	...	...	...	...	...	...	...
844941	366.0	43	1	27	108	173	57
844942	366.0	42	1	27	100	173	57
844943	366.0	43	1	27	108	173	57
844944	366.0	42	1	27	100	173	57
844945	366.0	43	1	27	108	173	57
	pl	Age	Range				
0	1		2				
1	2		2				
2	3		2				
3	4		2				
4	5		2				
...	...		...				
844941	1463368		1				
844942	1463369		1				
844943	1463370		1				
844944	1463371		1				
844945	1463372		1				
[844946 rows x 14 columns]							
df							
	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak			
Diastolic_Peak \							
0	511	1	77.0	522.0			
505.0							
1	511	1	77.0	522.0			
505.0							
2	511	1	77.0	522.0			
505.0							
3	511	1	77.0	522.0			
505.0							
4	511	1	77.0	522.0			
505.0							
...	...	...	...	...			
...							
844941	513	23	83.0	516.0			
510.0							
844942	513	23	83.0	516.0			

```

510.0
844943      513      23      83.0      516.0
510.0
844944      513      23      83.0      516.0
510.0
844945      513      23      83.0      516.0
510.0

```

```

      Pulse_Area  index  Gender  Age  Glucose_level  Height  Weight
\
0      393.0      0      1    38      99      180      53
1      393.0      1      1    38     102      180      53
2      393.0      2      1    38     103      180      53
3      393.0      3      1    38     128      180      53
4      393.0      4      1    38     130      180      53
...      ...      ...      ...  ...      ...      ...      ...
844941    366.0     43      1    27     108      173      57
844942    366.0     42      1    27     100      173      57
844943    366.0     43      1    27     108      173      57
844944    366.0     42      1    27     100      173      57
844945    366.0     43      1    27     108      173      57

```

```

      pl Age Range
0      1      2
1      2      2
2      3      2
3      4      2
4      5      2
...      ...      ...
844941 1463368      1
844942 1463369      1
844943 1463370      1
844944 1463371      1
844945 1463372      1

```

```
[844946 rows x 14 columns]
```

```

# Drop columns without modifying the original DataFrame
df = df.drop(columns=['Age'])

```



```
# Check the result
```

```
df.head()
```

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak	Diastolic_Peak
0	511	1	77.0	522.0	505.0
1	511	1	77.0	522.0	505.0
2	511	1	77.0	522.0	505.0
3	511	1	77.0	522.0	505.0
4	511	1	77.0	522.0	505.0

	Pulse_Area	index	Gender	Glucose_level	Height	Weight	pl	Age
0	393.0	0	1	99	180	53	1	
2								
1	393.0	1	1	102	180	53	2	
2								
2	393.0	2	1	103	180	53	3	
2								
3	393.0	3	1	128	180	53	4	
2								
4	393.0	4	1	130	180	53	5	
2								

```
df.columns
```

```
Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',  
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender',  
      'Glucose_level',  
      'Height', 'Weight', 'pl', 'Age Range'],  
      dtype='object')
```

## Remove Outlier in dataset

```
import pandas as pd  
import matplotlib.pyplot as plt  
import seaborn as sns  
import numpy as np
```

```
# Create a synthetic dataset (replace with your actual dataset)
```

```
np.random.seed(42)
```

```
# Print available columns to verify if 'Signal' is present
```

```
#print("Columns in the dataset:", df.columns)
```

```
# List of columns to handle outliers (in this case, just the 'Signal'
```

```

column)
columns_with_outliers = ['PPG_Signal']

# Create a boxplot for the 'Signal' column before handling outliers
plt.figure(figsize=(8, 5))
sns.boxplot(y=df['PPG_Signal'])
plt.title('Boxplot of Signal (Before Outlier Removal)')
plt.tight_layout()
plt.show()

# Define a function to handle outliers using the IQR method
def find_outliers(df, column, iqr_multiplier=1.5):
    Q1 = df[column].quantile(0.25)
    Q3 = df[column].quantile(0.75)
    IQR = Q3 - Q1
    lower_bound = Q1 - iqr_multiplier * IQR
    upper_bound = Q3 + iqr_multiplier * IQR

    # Identify the indices of rows that are outliers
    outlier_indices = df[(df[column] < lower_bound) | (df[column] >
upper_bound)].index
    return outlier_indices

# Find the outliers in the 'Signal' column
outlier_indices = find_outliers(df, 'PPG_Signal')

# Show the dataset rows that contain outliers
print("Outliers Found at Indices:")
print(outlier_indices)

# Show dataset rows containing the outliers
print("\nRows containing outliers:")
print(df.loc[outlier_indices])

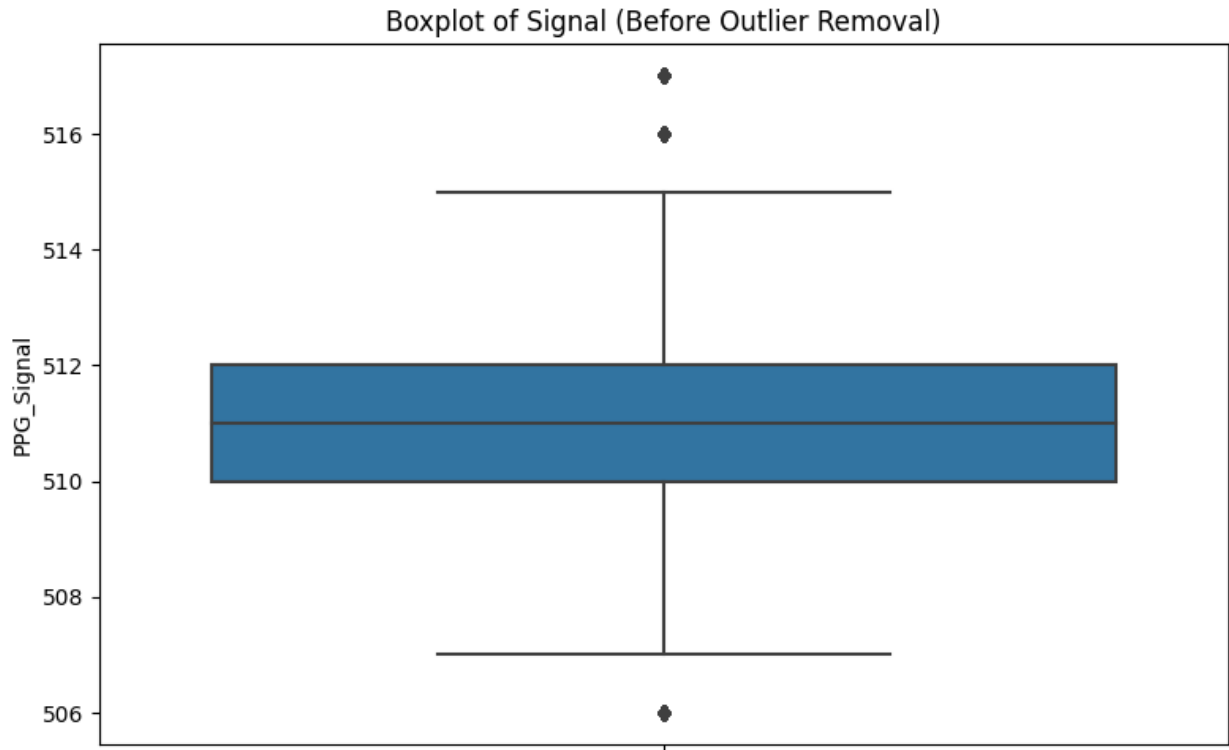
# Remove outliers from the dataset
df = df.drop(outlier_indices)

# Print the size of the dataset after removing outliers
print("\nDataset size after removing outliers:", df.shape)

# Create a boxplot for the 'Signal' column after handling outliers
plt.figure(figsize=(8, 5))
sns.boxplot(y=df['PPG_Signal'])
plt.title('Boxplot of PPG Signal (After Outlier Removal)')
plt.tight_layout()
plt.show()

# Optional: Save the cleaned data to a new CSV
# df_no_outliers.to_csv('/mnt/data/cleaned_data.csv', index=False)

```



```
Outliers Found at Indices:
Index([ 769, 770, 771, 772, 773, 774, 775, 776,
       777,
       778,
       ...
       814354, 814355, 814356, 814357, 814358, 814359, 814360, 814361,
       814362,
       814363]),
      dtype='int64', length=48385)
```

```
Rows containing outliers:
      PPG_Signal  Patient_Id  Heart_Rate  Systolic_Peak
Diastolic_Peak \
769             516          1         77.0          522.0
505.0
770             516          1         77.0          522.0
505.0
771             516          1         77.0          522.0
505.0
772             516          1         77.0          522.0
505.0
773             516          1         77.0          522.0
505.0
...             ...          ...          ...          ...
...
814359          506         22         73.0          528.0
```

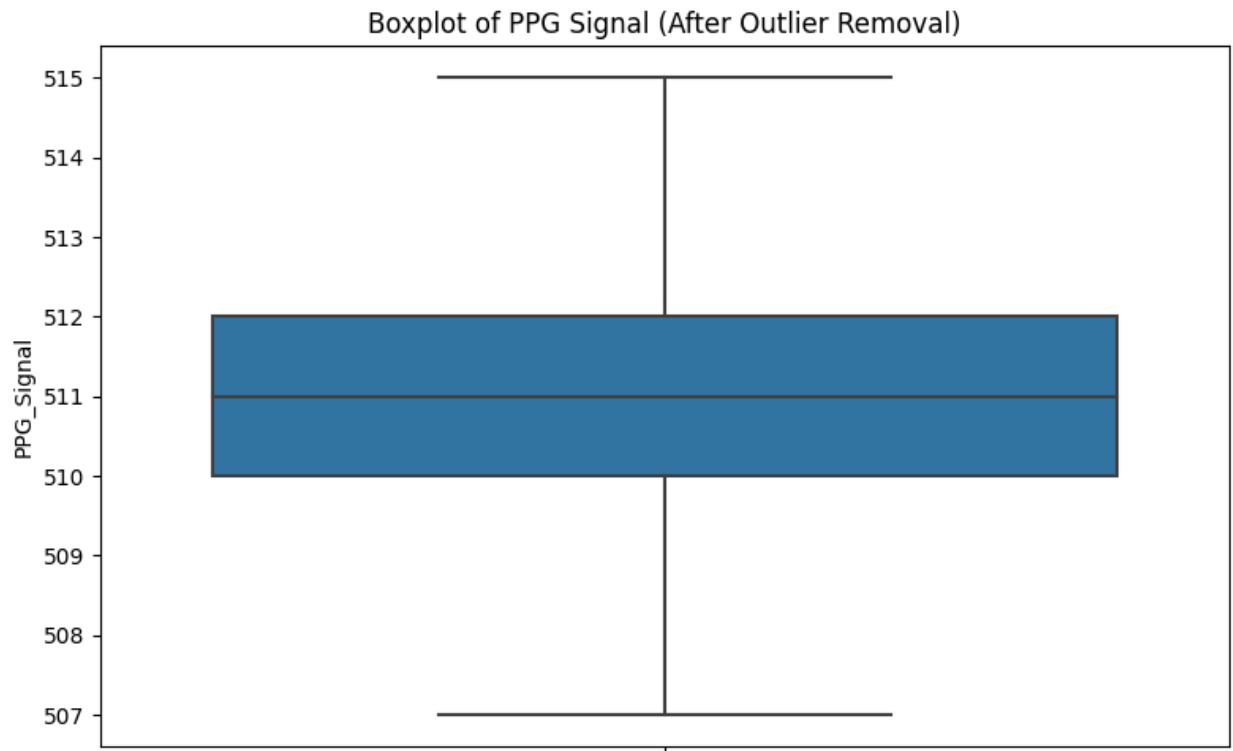
508.0				
814360	506	22	73.0	528.0
508.0				
814361	506	22	73.0	528.0
508.0				
814362	506	22	73.0	528.0
508.0				
814363	506	22	73.0	528.0
508.0				

	Pulse_Area	index	Gender	Glucose_level	Height	Weight
pl \						
769	393.0	6	1	136	180	53
770						
770	393.0	0	1	99	180	53
771						
771	393.0	1	1	102	180	53
772						
772	393.0	2	1	103	180	53
773						
773	393.0	3	1	128	180	53
774						
...	...	...	...	...	...	...
...						
814359	412.0	39	0	88	170	50
1423279						
814360	412.0	40	0	108	170	50
1423280						
814361	412.0	41	0	124	170	50
1423281						
814362	412.0	39	0	88	170	50
1423282						
814363	412.0	40	0	108	170	50
1423283						

	Age Range
769	2
770	2
771	2
772	2
773	2
...	...
814359	1
814360	1
814361	1
814362	1
814363	1

[48385 rows x 13 columns]

Dataset size after removing outliers: (796561, 13)



df				
	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0
505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				
844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0

```

510.0
844945      513      23      83.0      516.0
510.0

```

```

      Pulse_Area  index  Gender  Glucose_level  Height  Weight
pl  \
0      393.0      0      1      99      180      53
1
1      393.0      1      1      102      180      53
2
2      393.0      2      1      103      180      53
3
3      393.0      3      1      128      180      53
4
4      393.0      4      1      130      180      53
5
...      ...      ...      ...      ...      ...      ...
...
844941      366.0      43      1      108      173      57
1463368
844942      366.0      42      1      100      173      57
1463369
844943      366.0      43      1      108      173      57
1463370
844944      366.0      42      1      100      173      57
1463371
844945      366.0      43      1      108      173      57
1463372

```

```

      Age Range
0      2
1      2
2      2
3      2
4      2
...      ...
844941      1
844942      1
844943      1
844944      1
844945      1

```

```

[796561 rows x 13 columns]

```

```

df.columns

```

```

Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender',
      'Glucose_level',

```

```

        'Height', 'Weight', 'pl', 'Age Range'],
        dtype='object')

import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np

# Create a synthetic dataset (replace with your actual dataset)
np.random.seed(42)

# Print available columns to verify if 'Signal' is present
#print("Columns in the dataset:", df.columns)

# List of columns to handle outliers (in this case, just the 'Signal'
column)
columns_with_outliers = ['Height']

# Create a boxplot for the 'Signal' column before handling outliers
plt.figure(figsize=(8, 5))
sns.boxplot(y=df['Height'])
plt.title('Boxplot of height (Before Outlier Removal)')
plt.tight_layout()
plt.show()

# Define a function to handle outliers using the IQR method
def find_outliers(df, column, iqr_multiplier=1.5):
    Q1 = df[column].quantile(0.25)
    Q3 = df[column].quantile(0.75)
    IQR = Q3 - Q1
    lower_bound = Q1 - iqr_multiplier * IQR
    upper_bound = Q3 + iqr_multiplier * IQR

    # Identify the indices of rows that are outliers
    outlier_indices = df[(df[column] < lower_bound) | (df[column] >
upper_bound)].index
    return outlier_indices

# Find the outliers in the 'Signal' column
outlier_indices = find_outliers(df, 'Height')

# Show the dataset rows that contain outliers
print("Outliers Found at Indices:")
print(outlier_indices)

# Show dataset rows containing the outliers
print("\nRows containing outliers:")
print(df.loc[outlier_indices])

# Remove outliers from the dataset

```

```

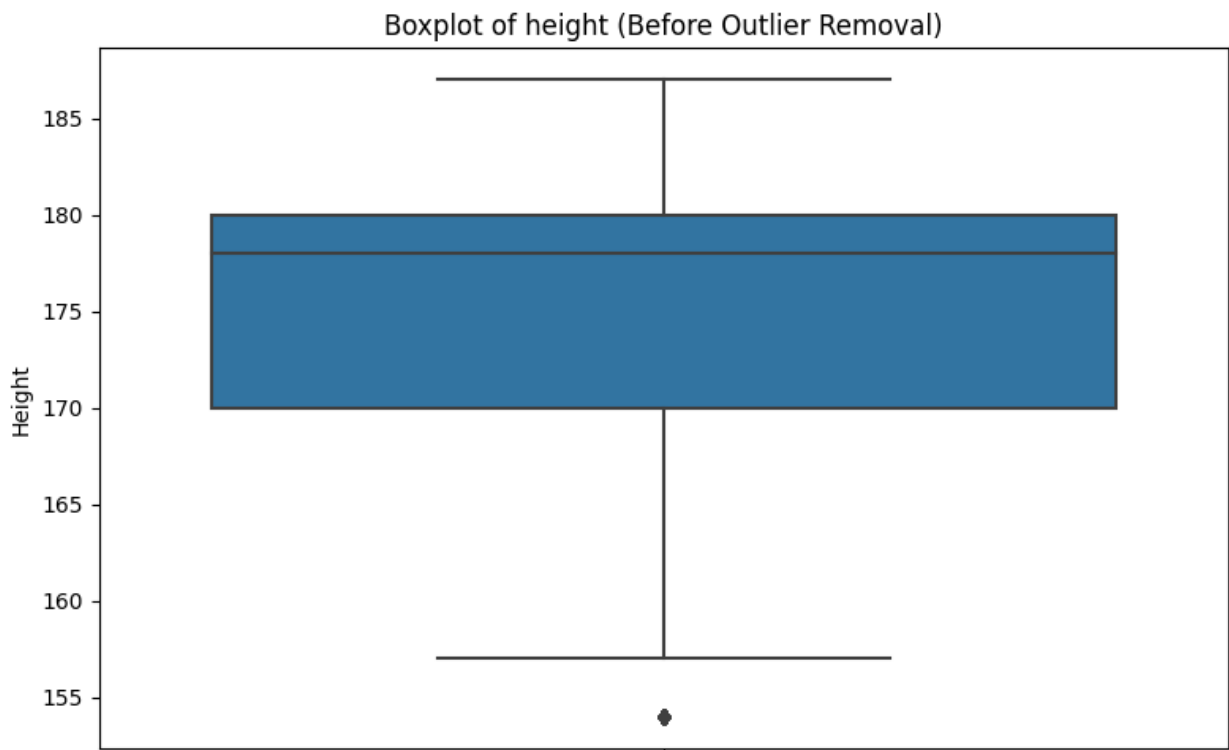
df = df.drop(outlier_indices)

# Print the size of the dataset after removing outliers
print("\nDataset size after removing outliers:", df.shape)

# Create a boxplot for the 'Signal' column after handling outliers
plt.figure(figsize=(8, 5))
sns.boxplot(y=df['Height'])
plt.title('Boxplot of Height (After Outlier Removal)')
plt.tight_layout()
plt.show()

# Optional: Save the cleaned data to a new CSV
# df_no_outliers.to_csv('/mnt/data/cleaned_data.csv', index=False)

```



```

Outliers Found at Indices:
Index([704505, 704506, 704507, 704508, 704509, 704510, 704511, 704512,
       704513,
       704514,
       ...,
       731761, 731762, 731763, 731764, 731765, 731766, 731767, 731768,
       731769,
       731770],
      dtype='int64', length=24985)

```

Rows containing outliers:

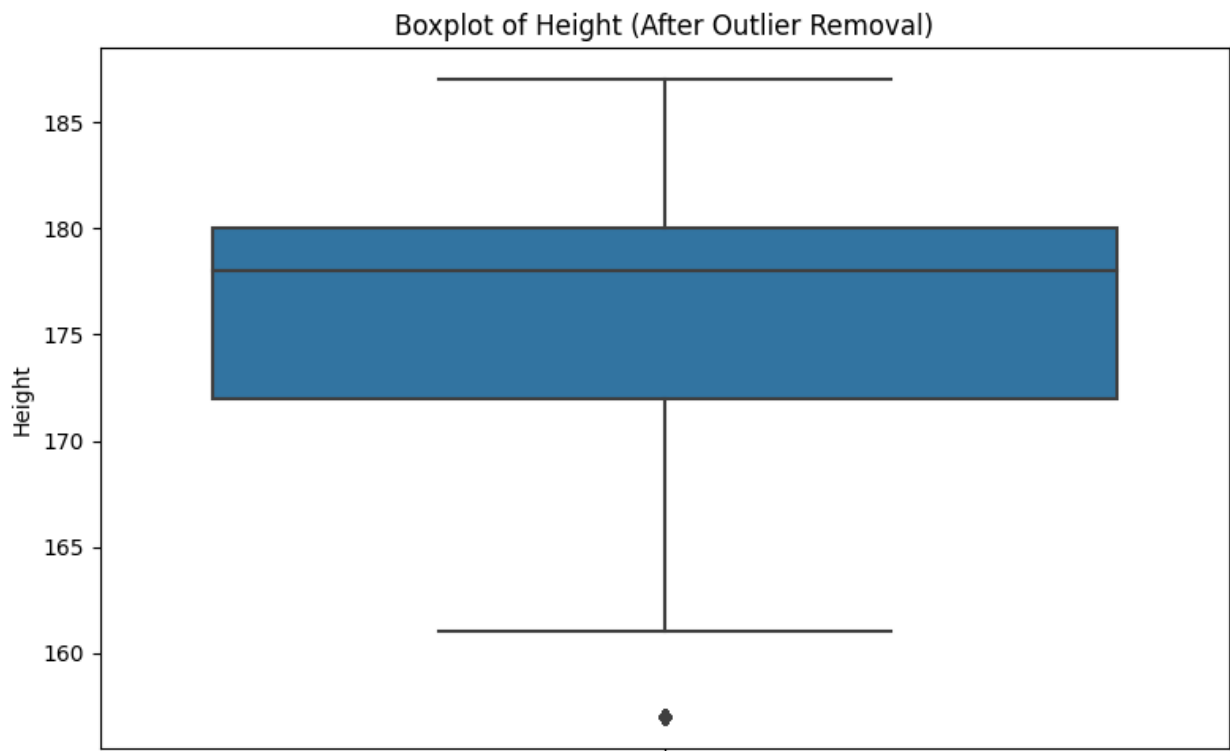


PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak		
Diastolic_Peak \					
704505 510	20	79.0	521.0		
506.0					
704506 510	20	79.0	521.0		
506.0					
704507 510	20	79.0	521.0		
506.0					
704508 510	20	79.0	521.0		
506.0					
704509 510	20	79.0	521.0		
506.0					
...	...	...	...		
...					
731766 507	20	65.0	521.0		
507.0					
731767 507	20	65.0	521.0		
507.0					
731768 507	20	65.0	521.0		
507.0					
731769 507	20	65.0	521.0		
507.0					
731770 507	20	65.0	521.0		
507.0					
Pulse_Area	index	Gender	Glucose_level	Height	Weight
pl \					
704505 388.0	34	0	120	154	42
1252852					
704506 388.0	35	0	124	154	42
1252853					
704507 388.0	36	0	136	154	42
1252854					
704508 388.0	34	0	120	154	42
1252855					
704509 388.0	35	0	124	154	42
1252856					
...	...	...	...	...	...
...					
731766 468.0	34	0	120	154	42
1313893					
731767 468.0	35	0	124	154	42
1313894					
731768 468.0	36	0	136	154	42
1313895					
731769 468.0	34	0	120	154	42
1313896					
731770 468.0	35	0	124	154	42
1313897					

	Age Range
704505	1
704506	1
704507	1
704508	1
704509	1
...	...
731766	1
731767	1
731768	1
731769	1
731770	1

[24985 rows x 13 columns]

Dataset size after removing outliers: (771576, 13)



df	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0
505.0				

2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				
844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0
510.0				
844945	513	23	83.0	516.0
510.0				

	Pulse_Area	index	Gender	Glucose_level	Height	Weight
pl \						
0	393.0	0	1	99	180	53
1						
1	393.0	1	1	102	180	53
2						
2	393.0	2	1	103	180	53
3						
3	393.0	3	1	128	180	53
4						
4	393.0	4	1	130	180	53
5						
...	...	...	...	...	...	...
...						
844941	366.0	43	1	108	173	57
1463368						
844942	366.0	42	1	100	173	57
1463369						
844943	366.0	43	1	108	173	57
1463370						
844944	366.0	42	1	100	173	57
1463371						
844945	366.0	43	1	108	173	57
1463372						

	Age Range
0	2
1	2
2	2
3	2

```

4          2
...      ...
844941    1
844942    1
844943    1
844944    1
844945    1

[771576 rows x 13 columns]

df.columns
Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender',
      'Glucose_level',
      'Height', 'Weight', 'pl', 'Age Range'],
      dtype='object')

def plot_boxplots_alternative(df):
    num_columns = df.select_dtypes(include='number').columns
    num_features = len(num_columns)
    rows = (num_features // 3) + 1
    cols = min(num_features, 3)
    fig, axes = plt.subplots(rows, cols, figsize=(20, rows * 6))
    axes = axes.flatten() # Flatten in case of more subplots

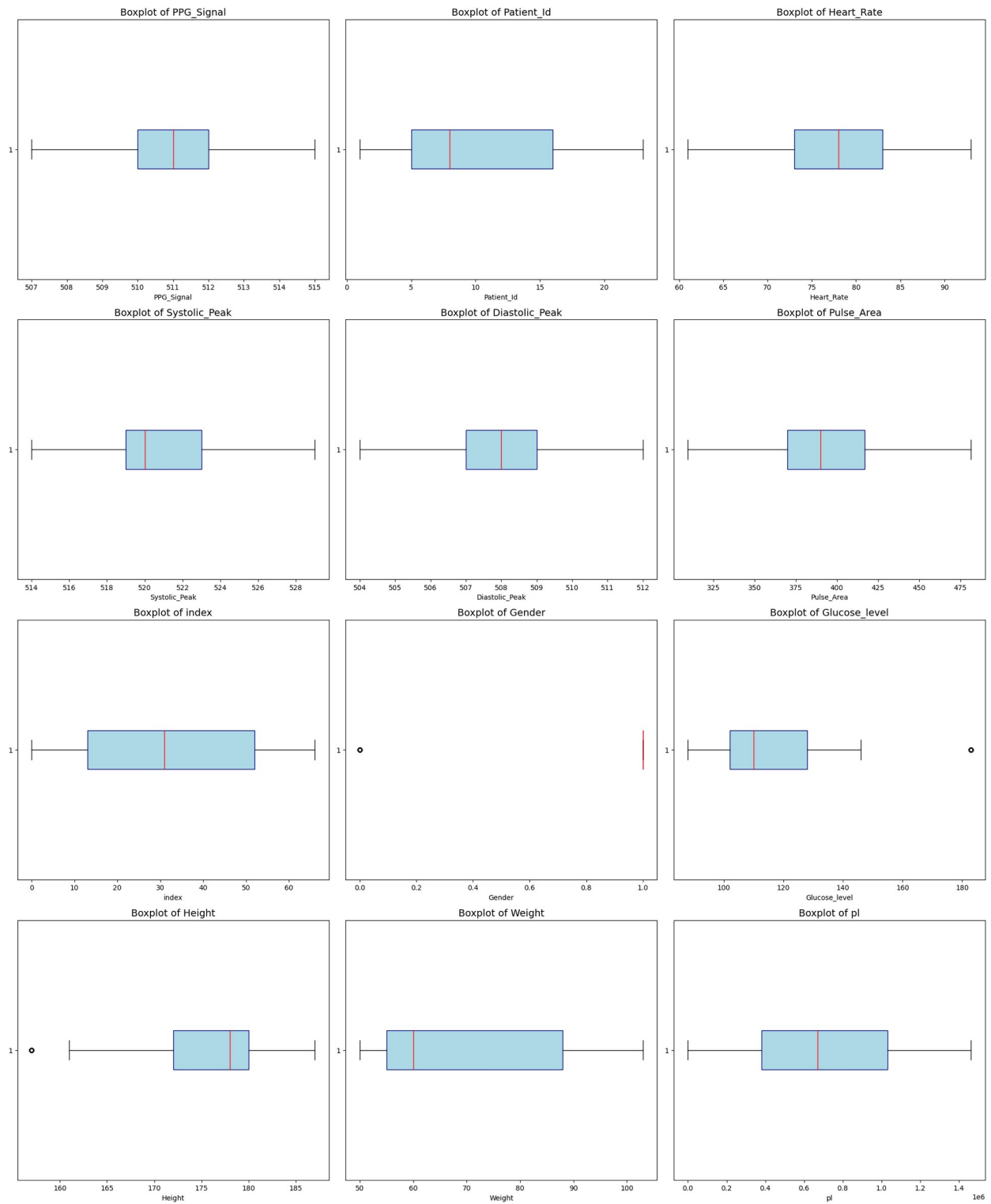
    for i, col in enumerate(num_columns):
        axes[i].boxplot(df[col], vert=False, patch_artist=True,
                        boxprops=dict(facecolor='lightblue',
color='navy'),
                        medianprops=dict(color='red'))
        axes[i].set_title(f'Boxplot of {col}', fontsize=14)
        axes[i].set_xlabel(col)

    for j in range(i + 1, len(axes)):
        fig.delaxes(axes[j])

    plt.tight_layout()
    plt.show()

plot_boxplots_alternative(df)

```



```
df.columns
```

```
Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',  
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender',
```

```

'Glucose_level',
    'Height', 'Weight', 'pl', 'Age Range'],
    dtype='object')

import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np

# Create a synthetic dataset (replace with your actual dataset)
np.random.seed(42)

# Print available columns to verify if 'Signal' is present
#print("Columns in the dataset:", df.columns)

# List of columns to handle outliers (in this case, just the 'Signal'
column)
columns_with_outliers = ['Glucose_level']

# Create a boxplot for the 'Signal' column before handling outliers
plt.figure(figsize=(8, 5))
sns.boxplot(y=df['Glucose_level'])
plt.title('Boxplot of Glucose_level (Before Outlier Removal)')
plt.tight_layout()
plt.show()

# Define a function to handle outliers using the IQR method
def find_outliers(df, column, iqr_multiplier=1.5):
    Q1 = df[column].quantile(0.25)
    Q3 = df[column].quantile(0.75)
    IQR = Q3 - Q1
    lower_bound = Q1 - iqr_multiplier * IQR
    upper_bound = Q3 + iqr_multiplier * IQR

    # Identify the indices of rows that are outliers
    outlier_indices = df[(df[column] < lower_bound) | (df[column] >
upper_bound)].index
    return outlier_indices

# Find the outliers in the 'Signal' column
outlier_indices = find_outliers(df, 'Glucose_level')

# Show the dataset rows that contain outliers
print("Outliers Found at Indices:")
print(outlier_indices)

# Show dataset rows containing the outliers
print("\nRows containing outliers:")
print(df.loc[outlier_indices])

```

```

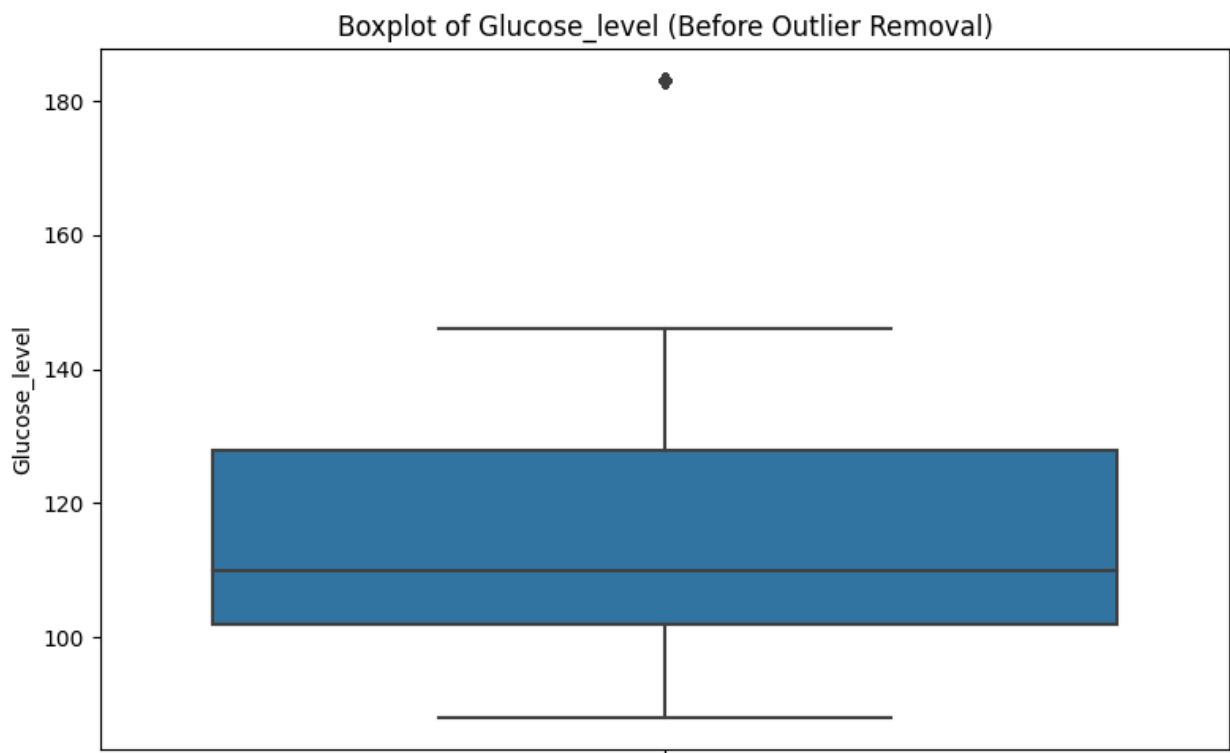
# Remove outliers from the dataset
df = df.drop(outlier_indices)

# Print the size of the dataset after removing outliers
print("\nDataset size after removing outliers:", df.shape)

# Create a boxplot for the 'Signal' column after handling outliers
plt.figure(figsize=(8, 5))
sns.boxplot(y=df['Height'])
plt.title('Boxplot of Glucose_level (After Outlier Removal)')
plt.tight_layout()
plt.show()

# Optional: Save the cleaned data to a new CSV
# df_no_outliers.to_csv('/mnt/data/cleaned_data.csv', index=False)

```



```

Outliers Found at Indices:
Index([522867, 522869, 522871, 522873, 522875, 522877, 522879, 522881,
522883,
      522885,
      ...,
      693060, 693063, 693066, 693069, 693072, 693075, 693078, 693081,
693084,
      693087],
      dtype='int64', length=26602)

```

Rows containing outliers:

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
522867	512	13	76.0	514.0
511.0				
522869	512	13	76.0	514.0
511.0				
522871	512	13	76.0	514.0
511.0				
522873	512	13	76.0	514.0
511.0				
522875	512	13	76.0	514.0
511.0				
...	...	...	...	...
...				
693075	511	18	93.0	522.0
510.0				
693078	511	18	93.0	522.0
510.0				
693081	511	18	93.0	522.0
510.0				
693084	511	18	93.0	522.0
510.0				
693087	511	18	93.0	522.0
510.0				

	Pulse_Area	index	Gender	Glucose_level	Height	Weight
pl \						
522867	401.0	15	1	183	175	96
884030						
522869	401.0	15	1	183	175	96
884032						
522871	401.0	15	1	183	175	96
884034						
522873	401.0	15	1	183	175	96
884036						
522875	401.0	15	1	183	175	96
884038						
...	...	...	...	...	...	...
...						
693075	323.0	28	1	183	180	90
1202688						
693078	323.0	28	1	183	180	90
1202691						
693081	323.0	28	1	183	180	90
1202694						
693084	323.0	28	1	183	180	90
1202697						
693087	323.0	28	1	183	180	90

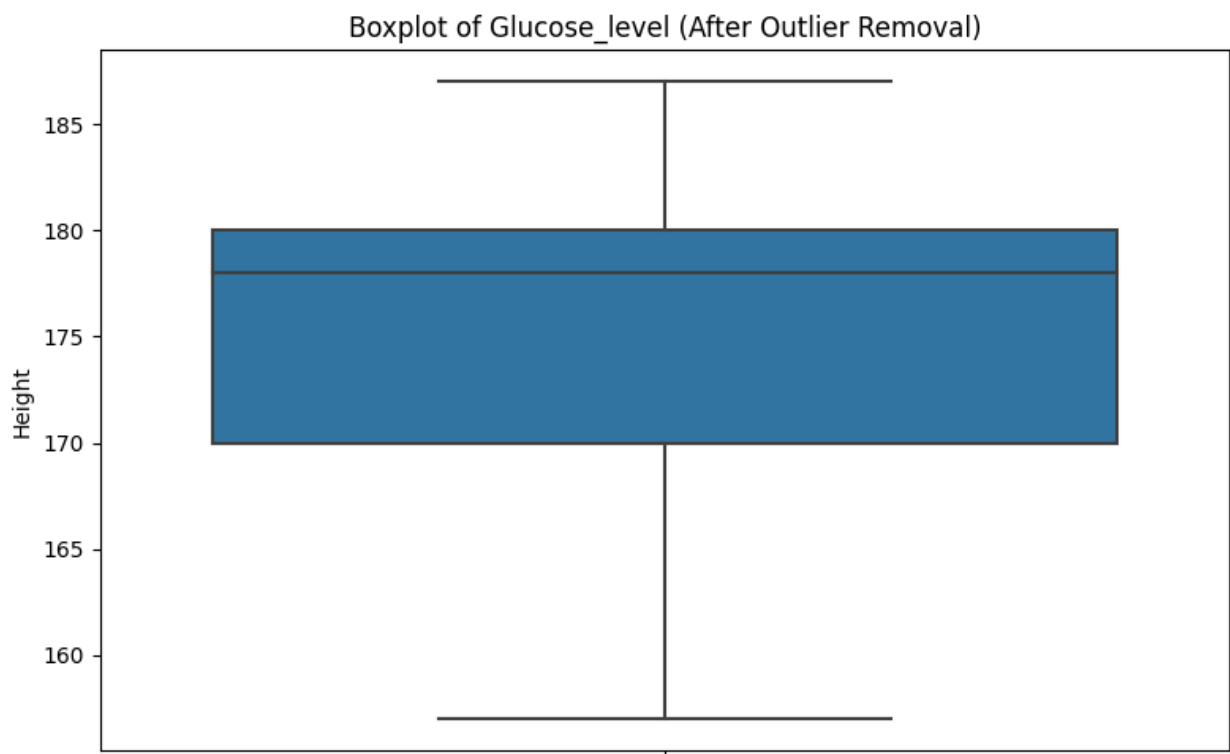


1202700

	Age	Range
522867	4	
522869	4	
522871	4	
522873	4	
522875	4	
...	...	
693075	1	
693078	1	
693081	1	
693084	1	
693087	1	

[26602 rows x 13 columns]

Dataset size after removing outliers: (744974, 13)



df

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0

505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				
844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0
510.0				
844945	513	23	83.0	516.0
510.0				

	Pulse_Area	index	Gender	Glucose_level	Height	Weight
pl \						
0	393.0	0	1	99	180	53
1						
1	393.0	1	1	102	180	53
2						
2	393.0	2	1	103	180	53
3						
3	393.0	3	1	128	180	53
4						
4	393.0	4	1	130	180	53
5						
...	...	...	...	...	...	...
...						
844941	366.0	43	1	108	173	57
1463368						
844942	366.0	42	1	100	173	57
1463369						
844943	366.0	43	1	108	173	57
1463370						
844944	366.0	42	1	100	173	57
1463371						
844945	366.0	43	1	108	173	57
1463372						

	Age Range
0	2
1	2
2	2

```

3          2
4          2
...      ...
844941     1
844942     1
844943     1
844944     1
844945     1

```

```
[744974 rows x 13 columns]
```

```

# Calculate skewness for each numeric column in the DataFrame and
print the result
numeric_columns = df.select_dtypes(include=['number']) # Select only
numeric columns

```

```

for column in numeric_columns.columns:
    skew_value = df[column].skew()
    print(f"Skewness of '{column}': {skew_value:.4f}")

```

```

Skewness of 'PPG_Signal': 0.2806
Skewness of 'Patient_Id': 0.4458
Skewness of 'Heart_Rate': -0.2021
Skewness of 'Systolic_Peak': -0.0570
Skewness of 'Diastolic_Peak': 0.0812
Skewness of 'Pulse_Area': 0.3989
Skewness of 'index': 0.0101
Skewness of 'Gender': -1.3466
Skewness of 'Glucose_level': 0.5332
Skewness of 'Height': -0.2644
Skewness of 'Weight': 0.7997
Skewness of 'pl': 0.1683

```

```
df
```

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0
505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				

844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0
510.0				
844945	513	23	83.0	516.0
510.0				

	Pulse_Area	index	Gender	Glucose_level	Height	Weight
pl \						
0	393.0	0	1	99	180	53
1						
1	393.0	1	1	102	180	53
2						
2	393.0	2	1	103	180	53
3						
3	393.0	3	1	128	180	53
4						
4	393.0	4	1	130	180	53
5						
...	...	...	...	...	...	...
...						
844941	366.0	43	1	108	173	57
1463368						
844942	366.0	42	1	100	173	57
1463369						
844943	366.0	43	1	108	173	57
1463370						
844944	366.0	42	1	100	173	57
1463371						
844945	366.0	43	1	108	173	57
1463372						

	Age Range
0	2
1	2
2	2
3	2
4	2
...	...
844941	1
844942	1
844943	1
844944	1
844945	1

[744974 rows x 13 columns]

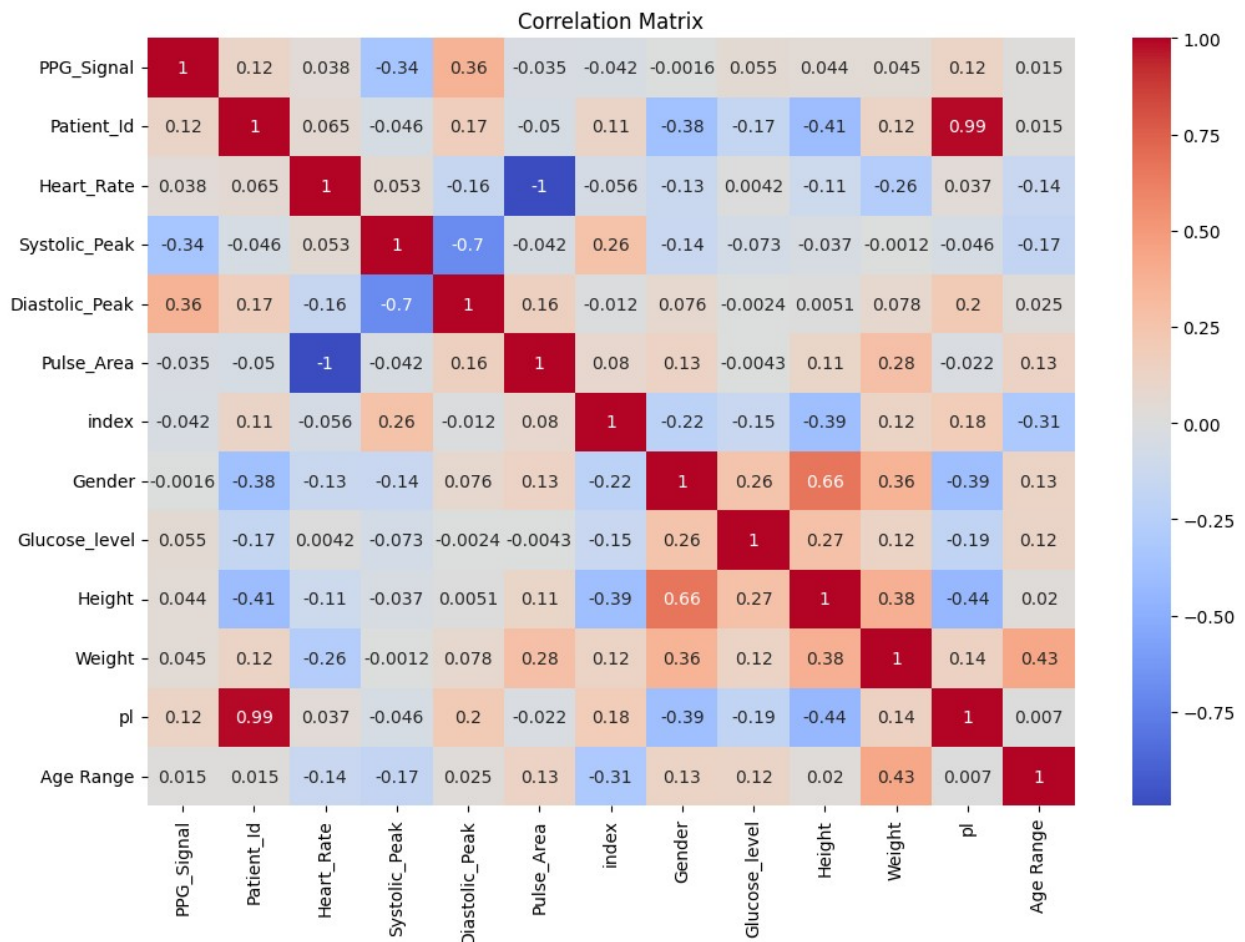
```

import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestRegressor
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import r2_score
import seaborn as sns
import matplotlib.pyplot as plt

import seaborn as sns
import matplotlib.pyplot as plt

plt.figure(figsize=(12, 8))
sns.heatmap(df.corr(), annot=True, cmap="coolwarm")
plt.title('Correlation Matrix')
plt.show()

```



```
df.columns
```

```

Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender',

```

```
'Glucose_level',
    'Height', 'Weight', 'pl', 'Age Range'],
    dtype='object')
```

```
# Drop columns without modifying the original DataFrame
#merged_df1 = merged_df1.drop(columns=['pl'])
# Drop columns without modifying the original DataFrame
df = df.drop(columns=['pl',])
```

```
# Check the result
#df.head()
```

```
df
```

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0
505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				
844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0
510.0				
844945	513	23	83.0	516.0
510.0				

	Pulse_Area	index	Gender	Glucose_level	Height	Weight	Age
Range							
0	393.0	0	1	99	180	53	
2							
1	393.0	1	1	102	180	53	
2							
2	393.0	2	1	103	180	53	
2							
3	393.0	3	1	128	180	53	
2							
4	393.0	4	1	130	180	53	

```

2
...      ...      ...      ...      ...      ...      ...
...
844941      366.0      43      1      108      173      57
1
844942      366.0      42      1      100      173      57
1
844943      366.0      43      1      108      173      57
1
844944      366.0      42      1      100      173      57
1
844945      366.0      43      1      108      173      57
1

```

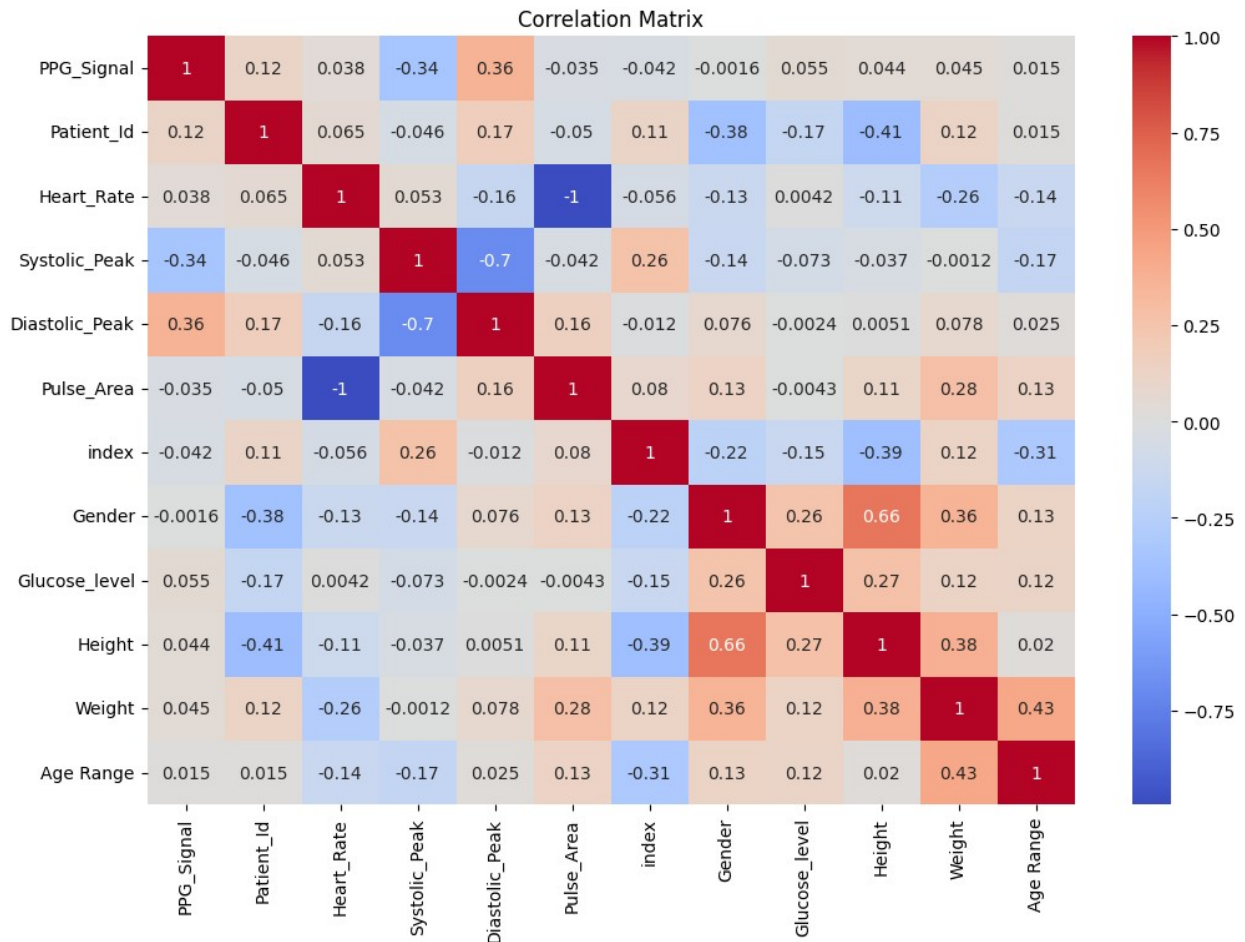
```
[744974 rows x 12 columns]
```

```

import seaborn as sns
import matplotlib.pyplot as plt

plt.figure(figsize=(12, 8))
sns.heatmap(df.corr(), annot=True, cmap="coolwarm")
plt.title('Correlation Matrix')
plt.show()

```



```
df.columns
```

```
Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender',
      'Glucose_level',
      'Height', 'Weight', 'Age Range'],
      dtype='object')
```

```
# Drop columns without modifying the original DataFrame
#df = df.drop(columns=['Systolic_Peak'])
```

```
# Check the result
#df.head()
```

```
# Apply one-hot encoding to the 'Gender' column
#df = pd.get_dummies(df, columns=['Gender', 'Age Range'], dtype=int)
```

```
# Display the result
df
```



	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak			
Diastolic_Peak \							
0	511	1	77.0	522.0			
505.0							
1	511	1	77.0	522.0			
505.0							
2	511	1	77.0	522.0			
505.0							
3	511	1	77.0	522.0			
505.0							
4	511	1	77.0	522.0			
505.0							
...	...	...	...	...			
...							
844941	513	23	83.0	516.0			
510.0							
844942	513	23	83.0	516.0			
510.0							
844943	513	23	83.0	516.0			
510.0							
844944	513	23	83.0	516.0			
510.0							
844945	513	23	83.0	516.0			
510.0							
	Pulse_Area	index	Gender	Glucose_level	Height	Weight	Age
Range							
0	393.0	0	1	99	180	53	
2							
1	393.0	1	1	102	180	53	
2							
2	393.0	2	1	103	180	53	
2							
3	393.0	3	1	128	180	53	
2							
4	393.0	4	1	130	180	53	
2							
...	...	...	...	...	...	...	
...							
844941	366.0	43	1	108	173	57	
1							
844942	366.0	42	1	100	173	57	
1							
844943	366.0	43	1	108	173	57	
1							
844944	366.0	42	1	100	173	57	
1							
844945	366.0	43	1	108	173	57	
1							

```
[744974 rows x 12 columns]

# Check for missing values in each column
missing_values = df.isnull().sum()

# Print the count of missing values for each column
print("Missing Values in Each Column:")
print(missing_values)
```

Missing Values in Each Column:

```
PPG_Signal      0
Patient_Id      0
Heart_Rate      0
Systolic_Peak   0
Diastolic_Peak  0
Pulse_Area      0
index          0
Gender          0
Glucose_level   0
Height          0
Weight          0
Age_Range       0
dtype: int64
```

df

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0
505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				
844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0
510.0				
844945	513	23	83.0	516.0

510.0

	Pulse_Area	index	Gender	Glucose_level	Height	Weight	Age
Range							
0	393.0	0	1	99	180	53	
2							
1	393.0	1	1	102	180	53	
2							
2	393.0	2	1	103	180	53	
2							
3	393.0	3	1	128	180	53	
2							
4	393.0	4	1	130	180	53	
2							
...	...	...	...	...	...	...	...
...							
844941	366.0	43	1	108	173	57	
1							
844942	366.0	42	1	100	173	57	
1							
844943	366.0	43	1	108	173	57	
1							
844944	366.0	42	1	100	173	57	
1							
844945	366.0	43	1	108	173	57	
1							

[744974 rows x 12 columns]

*# Step 5: Apply inverse transformation to convert the scaled data back to its original values*

```
#df_original = scaler.inverse_transform(df)
```

*# Step 6: Convert back to a DataFrame with original column names*

```
#df_original = pd.DataFrame(df_original, columns=df.columns)
```

```
#print("\nOriginal Dataset after Inverse Transformation:\n",  
df_original)
```

```
#df_original
```

```
X = df.drop(['Glucose_level'], axis=1)
```

```
Y = df[['Glucose_level']]
```

X

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
0	511	1	77.0	522.0
505.0				
1	511	1	77.0	522.0

505.0				
2	511	1	77.0	522.0
505.0				
3	511	1	77.0	522.0
505.0				
4	511	1	77.0	522.0
505.0				
...	...	...	...	...
...				
844941	513	23	83.0	516.0
510.0				
844942	513	23	83.0	516.0
510.0				
844943	513	23	83.0	516.0
510.0				
844944	513	23	83.0	516.0
510.0				
844945	513	23	83.0	516.0
510.0				

	Pulse_Area	index	Gender	Height	Weight	Age	Range
0	393.0	0	1	180	53		2
1	393.0	1	1	180	53		2
2	393.0	2	1	180	53		2
3	393.0	3	1	180	53		2
4	393.0	4	1	180	53		2
...	...	...	...	...	...		...
844941	366.0	43	1	173	57		1
844942	366.0	42	1	173	57		1
844943	366.0	43	1	173	57		1
844944	366.0	42	1	173	57		1
844945	366.0	43	1	173	57		1

[744974 rows x 11 columns]

X.columns

```
Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender', 'Height',
      'Weight',
      'Age Range'],
      dtype='object')
```

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, Y, test_size =
0.20, random_state = 0)
```

## Min Max Scaler

```
import pandas as pd
from sklearn.preprocessing import MinMaxScaler

# Initialize the MinMaxScaler
scaler_features = MinMaxScaler()
scaler_target = MinMaxScaler()
```

### Fit the Scaler Only on the Training Set:

```
X_train_scaled = scaler_features.fit_transform(X_train)
X_train_scaled
array([[0.5      , 0.      , 0.5      , ..., 0.76666667,
0.05660377,
       0.25     ],
       [0.625    , 1.      , 0.28125  , ..., 0.53333333,
0.13207547,
       0.      ],
       [0.5      , 0.18181818, 0.625    , ..., 0.6      ,
0.11320755,
       0.      ],
       ...,
       [0.5      , 0.      , 0.46875  , ..., 0.76666667,
0.05660377,
       0.25     ],
       [0.375    , 0.45454545, 0.6875   , ..., 0.83333333,
0.22641509,
       0.      ],
       [0.125    , 0.22727273, 0.59375  , ..., 0.26666667,
0.18867925,
       0.25     ]])
```

### Transform the Test Set Using the Same Scaler:

```
X_test_scaled = scaler_features.transform(X_test)
X_test_scaled
array([[0.25     , 0.18181818, 0.5625    , ..., 0.6      ,
0.11320755,
       0.      ],
       [0.5      , 0.95454545, 1.      , ..., 0.43333333, 0.
,
       0.      ],
       [0.625    , 0.36363636, 0.5625    , ..., 0.5      ,
0.18867925,
       0.      ],
       ...,
       ...])
```

```

        [0.625      , 0.04545455, 0.75      , ..., 1.      ,
0.47169811,
        0.      ],
        [0.375      , 0.45454545, 0.71875   , ..., 0.83333333,
0.22641509,
        0.      ],
        [0.5        , 0.18181818, 0.5625    , ..., 0.6      ,
0.11320755,
        0.      ]])

```

scale for the y\_train and y\_test

```

# Scale the target (Glucose_level) for y_train and y_test
y_train_scaled = scaler_target.fit_transform(y_train)
y_test_scaled = scaler_target.transform(y_test)

y_train_scaled
array([[0.82758621],
       [0.34482759],
       [0.37931034],
       ...,
       [0.25862069],
       [0.43103448],
       [0.13793103]])

y_test_scaled
array([[0.82758621],
       [0.62068966],
       [0.62068966],
       ...,
       [0.39655172],
       [0.20689655],
       [0.13793103]])

```

## Apply Algorithms on dataset

### Linear Regression Model

```

#write code here
from sklearn.linear_model import LinearRegression

#write code here
lr = LinearRegression()
lr.fit(X_train_scaled,y_train_scaled)

LinearRegression()

```

```

#write code here
lr_predict = lr.predict(X_test_scaled)

lr_predict

array([[0.41185275],
       [0.3215901 ],
       [0.33928684],
       ...,
       [0.50345417],
       [0.4803961 ],
       [0.42643983]])

```

Inverse transform  $X_{\text{test}}$ ,  $y_{\text{test}}$ , and the predictions back to their original values

```

# Step 8: Inverse transform X_test, y_test, and the predictions back
to their original values
X_test_original = scaler_features.inverse_transform(X_test_scaled)
y_test_original = scaler_target.inverse_transform(y_test_scaled)
y_pred_original = scaler_target.inverse_transform(lr_predict)

X_test_original

array([[509.,  5.,  79., ..., 175.,  56.,  1.],
       [511., 22.,  93., ..., 170.,  50.,  1.],
       [512.,  9.,  79., ..., 172.,  60.,  1.],
       ...,
       [512.,  2.,  85., ..., 187.,  75.,  1.],
       [510., 11.,  84., ..., 182.,  62.,  1.],
       [511.,  5.,  79., ..., 175.,  56.,  1.]])

y_test_original

array([[136.],
       [124.],
       [124.],
       ...,
       [111.],
       [100.],
       [ 96.]])

y_pred_original

array([[111.88745976],
       [106.65222568],
       [107.6786369 ],
       ...,
       [117.20034192],
       [115.86297381],
       [112.73351039]])

```

combine dataset and show

```
df.columns
```

```
Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',  
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender',  
      'Glucose_level',  
      'Height', 'Weight', 'Age_Range'],  
      dtype='object')
```

```
# Step 9: Create a DataFrame for comparison of actual and predicted  
values in the original scale
```

```
# Make sure that the number of columns in np.column_stack matches the  
number of columns in the column names
```

```
#comparison_df = pd.DataFrame(  
    #np.column_stack((X_test_original, y_test_original.flatten(),  
y_pred_original.flatten()))),  
    #columns=[  
        #'PPG_Signal', 'Systolic_Peak', 'Diastolic_Peak',  
'Pulse_Area', 'index',  
        #'Height', 'Weight', 'pl', 'Gender_0', 'Gender_1',  
        #'Age_Range_1', 'Age_Range_2', 'Age_Range_3', 'Age_Range_4',  
        #'Age_Range_5', 'Patient_Id_1', 'Patient_Id_2',  
'Patient_Id_3',  
        #'Patient_Id_5', 'Patient_Id_6', 'Patient_Id_7',  
'Patient_Id_8',  
        #'Patient_Id_9', 'Patient_Id_10', 'Patient_Id_11',  
'Patient_Id_12',  
        #'Patient_Id_13', 'Patient_Id_14', 'Patient_Id_15',  
'Patient_Id_16',  
        #'Patient_Id_17', 'Patient_Id_18', 'Patient_Id_19',  
'Patient_Id_21',  
        #'Patient_Id_22', 'Patient_Id_23', 'Actual Glucose Level',  
'Predicted Glucose Level'  
    #]  
#)
```

```
# Step 10: Display the comparison of actual and predicted values in  
the original scale
```

```
#print("\nComparison of Actual and Predicted Glucose Levels (Original  
Scale):\n", comparison_df)
```

```
#comparison_df
```



## Evaluate Using Performance Metrics

### Mean Absolute Error

Mean Absolute Error (MAE) in the context of a linear regression model is a performance metric that measures the average magnitude of the errors between the predicted values and the actual values. It is used to quantify how close the predictions of your model are to the actual outcomes.

- Lower MAE is better:

The smaller the MAE, the closer your predicted values are to the actual values. A perfect model would have an MAE of 0.

```
from sklearn.metrics import mean_absolute_error

mae = mean_absolute_error(y_test_scaled,lr_predict)
print(f"Mean Absolute Error of the testing data : {mae}")

Mean Absolute Error of the testing data : 0.19709807189448006
```

### Mean Squared Error

Mean Squared Error (MSE) in the context of a linear regression model is a commonly used performance metric that measures the average of the squared differences between the predicted values and the actual values. It provides a way to quantify how well your regression model predicts the dependent variable.

A very low MSE on training data but high MSE on testing data often indicates overfitting — the model has learned the training data too well, including noise, and cannot generalize well to new data. In contrast, if MSE is high on both training and testing datasets, it may indicate underfitting, meaning the model is too simple to capture the underlying pattern.

The closer the MSE is to zero, the more accurate the model is, implying that the predicted values are very close to the actual values.

```
from sklearn.metrics import mean_squared_error

mse = mean_squared_error(y_test_scaled,lr_predict)
print(f"Mean Squared Error of testing data : {mse}")

Mean Squared Error of testing data : 0.05703854735623502
```

### Root Mean Squared Error (RMSE)

Root Mean Squared Error (RMSE) is a popular metric for evaluating the performance of a linear regression model. It measures the average error between the predicted and actual values in the same units as the target variable (in this case, glucose levels). RMSE is essentially the square root of the Mean Squared Error (MSE), and it is widely used because it is more interpretable than MSE, as it provides the error in the same scale as the predicted values.

RMSE can be used to compare different models. When comparing models on the same dataset, the model with the lower RMSE is generally better at making accurate predictions.

```
# Calculate Mean Squared Error
#mse = mean_squared_error(y_test,lr_predict)
import numpy as np
# Calculate Root Mean Squared Error
rmse = np.sqrt(mse)
print(f"Root Mean Squared Error of testing data : {rmse}")
```

Root Mean Squared Error of testing data : 0.23882744263638345

## R-squared ( $R^2$ )

R-squared ( $R^2$ ), also known as the coefficient of determination, is a statistical measure used to evaluate how well a linear regression model explains the variance in the dependent variable (in your case, glucose levels). It provides insight into how well the independent variables in the model are predicting the target variable.

Interpretation

$R^2 = 0$

The model explains none of the variability of the target variable. In other words, the model's predictions are no better than simply predicting the mean of the target variable for all observations.

$R^2 = 1$

The model explains all the variability of the target variable, meaning it perfectly predicts the outcome.

$R^2$  between 0 and 1:

The model explains part of the variability of the outcome. The closer is to 1, the better the model fits the data.

For example, if

$R^2 = 0.85$

this means that 85% of the variance in the target variable (glucose levels) is explained by the model, while the remaining 15% is unexplained (due to factors not captured by the model).

## R2\_score

```
#write code here
#mean square error
from sklearn.metrics import r2_score
lr_r2_test= r2_score(y_test_scaled,lr_predict)
```

```
#print('R2 score for Linear Regression Testing Data is: ',  
lr_r2_train)  
print('R2 score for Linear Regression Testing Data is: ', lr_r2_test)  
R2 score for Linear Regression Testing Data is: 0.10819721957201589
```

## Random Forest

```
# Importing the model from sklearn  
from sklearn.ensemble import RandomForestRegressor  
  
# Making instance and training the model  
rf_reg = RandomForestRegressor(n_estimators=100, max_depth=5,  
random_state=42)  
  
rf_reg.fit(X_train_scaled, y_train_scaled)  
  
/tmp/ipykernel_93/3160336221.py:1: DataConversionWarning: A column-  
vector y was passed when a 1d array was expected. Please change the  
shape of y to (n_samples,), for example using ravel().  
    rf_reg.fit(X_train_scaled, y_train_scaled)  
  
RandomForestRegressor(max_depth=5, random_state=42)  
  
y_pred = rf_reg.predict(X_test_scaled)  
  
# Evaluate the model's performance  
mse3 = mean_squared_error(y_test_scaled, y_pred)  
rmse3 = mean_squared_error(y_test_scaled, y_pred, squared=False)  
mae3 = mean_absolute_error(y_test_scaled, y_pred)  
r2 = r2_score(y_test_scaled, y_pred)  
  
# Print evaluation metrics  
print(f"Mean Squared Error (MSE): {mse3:.2f}")  
print(f"Root Mean Squared Error (RMSE): {rmse3:.2f}")  
print(f"Mean Absolute Error (MAE): {mae3:.2f}")  
print(f"R-squared (R2): {r2:.2f}")  
  
Mean Squared Error (MSE): 0.03  
Root Mean Squared Error (RMSE): 0.17  
Mean Absolute Error (MAE): 0.11  
R-squared (R2): 0.54
```

## Decision Tree Classifier

```
from sklearn.tree import DecisionTreeRegressor  
  
# Initialize the DecisionTreeRegressor (similar to  
DecisionTreeClassifier style)  
lf_dt = DecisionTreeRegressor(max_depth=3, criterion='squared_error',  
random_state=100)
```

```

# Train the model on the training data
lf_dt.fit(X_train_scaled,y_train_scaled)

DecisionTreeRegressor(max_depth=3, random_state=100)

# Predict the target values for the test set
y_pred = lf_dt.predict(X_test_scaled)

# Evaluate the model's performance
mse4 = mean_squared_error(y_test_scaled, y_pred)
rmse4 = mean_squared_error(y_test_scaled, y_pred, squared=False)
mae4 = mean_absolute_error(y_test_scaled, y_pred)
r2 = r2_score(y_test_scaled, y_pred)

# Print evaluation metrics
print(f"Mean Squared Error (MSE): {mse4:.2f}")
print(f"Root Mean Squared Error (RMSE): {rmse4:.2f}")
print(f"Mean Absolute Error (MAE): {mae4:.2f}")
print(f"R-squared (R2): {r2:.2f}")

Mean Squared Error (MSE): 0.04
Root Mean Squared Error (RMSE): 0.21
Mean Absolute Error (MAE): 0.15
R-squared (R2): 0.33

```

lag.

## Polynomial Features

This helps models capture non-linear relationships between the input features and the target variable, making simple linear models more expressive and able to approximate more complex patterns

```

#write code here
from sklearn.preprocessing import PolynomialFeatures

#write code here
poly_reg = PolynomialFeatures(degree=2)

```

## Polynomial Feature Transformation

### 1- fit\_transform()

- Purpose:

Combines the operations of fit() and transform() into one step.

- Usage:

Used when you need to compute the parameters (like mean, variance, etc.) of the transformation based on the training data, and then apply the transformation.

- Process:

Fit: Calculates the parameters required for the transformation (e.g., scaling factors). Transform: Applies the transformation using these parameters to the given data.

```
X_train_poly = poly_reg.fit_transform(X_train_scaled)
```

## 2- transform()

- Purpose: Applies a transformation to data using parameters that were computed from fit().
- Usage: Used when you already have the parameters from fit() (typically on training data) and you want to apply the same transformation to new data, like test data or unseen data.

```
X_test_poly = poly_reg.transform(X_test_scaled)
```

fit\_transform() is used on the training dataset to learn the parameters and apply the transformation.

transform() is used on the test or unseen dataset to apply the learned transformation, ensuring consistency.

Using fit\_transform() on the training data and transform() on the test data helps prevent data leakage, where information from the test set influences the model during training.

## model training

```
#write code here
```

```
poly_model = LinearRegression()  
poly_model.fit(X_train_poly, y_train_scaled)
```

```
LinearRegression()
```

```
#y_train_predicted = poly_model.predict(X_train_poly)
```

## Model Prediction

```
y_test_predict = poly_model.predict(X_test_poly)
```

```
#write code here
```

```
#y_train_predicted, y_test_predict =  
poly_model.predict(X_train_poly), poly_model.predict(X_test_poly)
```

## polynomial Regression matrix performance

```
#from sklearn.metrics import mean_absolute_error

mae = mean_absolute_error(y_test_scaled,y_test_predict)
print(f"Mean Absolute Error of the testing data : {mae}")

Mean Absolute Error of the testing data : 0.06893090280093409

#from sklearn.metrics import mean_squared_error

mse1 = mean_squared_error(y_test_scaled,y_test_predict)
print(f"Mean Absolute Error of testing data : {mse}")

Mean Absolute Error of testing data : 0.05703854735623502

#import numpy as np
# Calculate Root Mean Squared Error
rmse = np.sqrt(mse1)
print(f"Root Mean Squared Error of testing data : {rmse}")

Root Mean Squared Error of testing data : 0.09313701562682071

r2_test = r2_score(y_test_scaled, y_test_predict)

#print('R2 score for Linear Regression Testing Data is: ',
lr_r2_train)

print('R2 score for Poly Regression Testing Data is: ', r2_test)

R2 score for Poly Regression Testing Data is: 0.8643733604885401

y_test_scaled
array([[0.82758621],
       [0.62068966],
       [0.62068966],
       ...,
       [0.39655172],
       [0.20689655],
       [0.13793103]])

y_test_predict
array([[0.78390151],
       [0.65652239],
       [0.55547893],
       ...,
       [0.41847203],
       [0.23054237],
       [0.18168164]])
```

```
# Inverse transform the scaled values
y_test_actual = scaler_target.inverse_transform(y_test_scaled)
y_test_predict_actual =
scaler_target.inverse_transform(y_test_predict)

# Show the model predictions vs actual values
y_test_actual = pd.Series(y_test_actual.flatten(), name='Actual
Glucose Level')
y_test_predict_actual = pd.Series(y_test_predict_actual.flatten(),
name='Predicted Glucose Level')
predictions = pd.DataFrame({'Actual': y_test_actual, 'Predicted':
y_test_predict_actual})
predictions
```

	Actual	Predicted
0	136.0	133.466288
1	124.0	126.078298
2	124.0	120.217778
3	136.0	123.102675
4	96.0	91.423398
...	...	...
148990	108.0	111.327062
148991	108.0	111.327062
148992	111.0	112.271378
148993	100.0	101.371457
148994	96.0	98.537535

[148995 rows x 2 columns]

after polynomial feature technique then make 2d data format

*#only calculating feature*

```
feature_names = poly_reg.get_feature_names_out()
#print("Feature names:", feature_names)

X_train_poly_2d = pd.DataFrame(X_train_poly, columns=feature_names)
X_train_poly_2d
```

	1	x0	x1	x2	x3	x4	x5
x6 \							
0	1.0	0.500	0.000000	0.50000	0.400000	0.500	0.491279
0.090909							
1	1.0	0.625	1.000000	0.28125	0.066667	0.875	0.747093
0.651515							
2	1.0	0.500	0.181818	0.62500	0.400000	0.375	0.386628
0.818182							
3	1.0	0.625	0.409091	1.00000	0.200000	0.625	0.000000
0.121212							

4	1.0	0.500	0.000000	0.56250	0.400000	0.375	0.438953
0.075758							
...	...	...	...	...	...	...	...
...							
595974	1.0	0.375	0.272727	0.000000	0.666667	0.625	1.000000
0.939394							
595975	1.0	0.500	0.045455	0.28125	0.333333	0.375	0.747093
0.484848							
595976	1.0	0.500	0.000000	0.46875	0.533333	0.375	0.520349
0.030303							
595977	1.0	0.375	0.454545	0.68750	0.600000	0.625	0.328488
0.181818							
595978	1.0	0.125	0.227273	0.59375	0.666667	0.000	0.404070
0.863636							

	x7	x8	...	x7^2	x7 x8	x7 x9	x7 x10	x8^2
\								
0	1.0	0.766667	...	1.0	0.766667	0.056604	0.25	0.587778
1	1.0	0.533333	...	1.0	0.533333	0.132075	0.00	0.284444
2	1.0	0.600000	...	1.0	0.600000	0.113208	0.00	0.360000
3	1.0	0.733333	...	1.0	0.733333	0.754717	0.25	0.537778
4	1.0	0.766667	...	1.0	0.766667	0.056604	0.25	0.587778
...	...	...	...	...	...	...	...	...
595974	1.0	0.733333	...	1.0	0.733333	0.811321	0.25	0.537778
595975	1.0	1.000000	...	1.0	1.000000	0.471698	0.00	1.000000
595976	1.0	0.766667	...	1.0	0.766667	0.056604	0.25	0.587778
595977	1.0	0.833333	...	1.0	0.833333	0.226415	0.00	0.694444
595978	0.0	0.266667	...	0.0	0.000000	0.000000	0.00	0.071111

	x8 x9	x8 x10	x9^2	x9 x10	x10^2
0	0.043396	0.191667	0.003204	0.014151	0.0625
1	0.070440	0.000000	0.017444	0.000000	0.0000
2	0.067925	0.000000	0.012816	0.000000	0.0000
3	0.553459	0.183333	0.569598	0.188679	0.0625
4	0.043396	0.191667	0.003204	0.014151	0.0625
...	...	...	...	...	...
595974	0.594969	0.183333	0.658241	0.202830	0.0625
595975	0.471698	0.000000	0.222499	0.000000	0.0000
595976	0.043396	0.191667	0.003204	0.014151	0.0625



```
595977 0.188679 0.000000 0.051264 0.000000 0.0000
595978 0.050314 0.066667 0.035600 0.047170 0.0625
```

```
[595979 rows x 78 columns]
```

```
X_test_poly_2d = pd.DataFrame(X_test_poly, columns=feature_names)
X_test_poly_2d
```

	1	x0	x1	x2	x3	x4	x5
x6 \							
0	1.0	0.250	0.181818	0.56250	0.466667	0.375	0.456395
0.848485							
1	1.0	0.500	0.954545	1.00000	0.800000	0.125	0.084302
0.621212							
2	1.0	0.625	0.363636	0.56250	0.133333	0.750	0.462209
1.000000							
3	1.0	0.875	0.772727	1.00000	0.600000	0.750	0.000000
0.409091							
4	1.0	0.125	0.227273	0.43750	0.666667	0.000	0.555233
0.863636							
...	...	...	...	...	...	...	...
...							
148990	1.0	0.375	0.727273	0.68750	0.333333	0.375	0.322674
0.378788							
148991	1.0	0.375	0.727273	0.68750	0.333333	0.375	0.322674
0.378788							
148992	1.0	0.625	0.045455	0.75000	0.466667	0.625	0.264535
0.484848							
148993	1.0	0.375	0.454545	0.71875	0.333333	0.250	0.311047
0.151515							
148994	1.0	0.500	0.181818	0.56250	0.466667	0.375	0.456395
0.787879							

	x7	x8	...	x7^2	x7 x8	x7 x9	x7 x10	x8^2
\								
0	1.0	0.600000	...	1.0	0.600000	0.113208	0.0	0.360000
1	0.0	0.433333	...	0.0	0.000000	0.000000	0.0	0.187778
2	0.0	0.500000	...	0.0	0.000000	0.000000	0.0	0.250000
3	1.0	0.766667	...	1.0	0.766667	0.754717	0.0	0.587778
4	0.0	0.266667	...	0.0	0.000000	0.000000	0.0	0.071111
...	...	...	...	...	...	...	...	...
148990	0.0	0.400000	...	0.0	0.000000	0.000000	0.0	0.160000
148991	0.0	0.400000	...	0.0	0.000000	0.000000	0.0	0.160000

148992	1.0	1.000000	...	1.0	1.000000	0.471698	0.0	1.000000
148993	1.0	0.833333	...	1.0	0.833333	0.226415	0.0	0.694444
148994	1.0	0.600000	...	1.0	0.600000	0.113208	0.0	0.360000

	x8 x9	x8 x10	x9^2	x9 x10	x10^2
0	0.067925	0.000000	0.012816	0.000000	0.0000
1	0.000000	0.000000	0.000000	0.000000	0.0000
2	0.094340	0.000000	0.035600	0.000000	0.0000
3	0.578616	0.000000	0.569598	0.000000	0.0000
4	0.050314	0.066667	0.035600	0.04717	0.0625
...	...	...	...	...	...
148990	0.037736	0.000000	0.008900	0.000000	0.0000
148991	0.037736	0.000000	0.008900	0.000000	0.0000
148992	0.471698	0.000000	0.222499	0.000000	0.0000
148993	0.188679	0.000000	0.051264	0.000000	0.0000
148994	0.067925	0.000000	0.012816	0.000000	0.0000

[148995 rows x 78 columns]

y\_train\_scaled

```
array([[0.82758621],
       [0.34482759],
       [0.37931034],
       ...,
       [0.25862069],
       [0.43103448],
       [0.13793103]])
```

y\_test\_scaled

```
array([[0.82758621],
       [0.62068966],
       [0.62068966],
       ...,
       [0.39655172],
       [0.20689655],
       [0.13793103]])
```

y\_test\_predict

```
array([[0.78390151],
       [0.65652239],
       [0.55547893],
       ...,
       [0.41847203],
       [0.23054237],
       [0.18168164]])
```

## Model input then output

X.columns

```
Index(['PPG_Signal', 'Patient_Id', 'Heart_Rate', 'Systolic_Peak',  
      'Diastolic_Peak', 'Pulse_Area', 'index', 'Gender', 'Height',  
      'Weight',  
      'Age_Range'],  
      dtype='object')
```

X

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak	Diastolic_Peak \	
0	511	1	77.0	522.0	505.0	
1	511	1	77.0	522.0	505.0	
2	511	1	77.0	522.0	505.0	
3	511	1	77.0	522.0	505.0	
4	511	1	77.0	522.0	505.0	
...	...	...	...	...	...	
844941	513	23	83.0	516.0	510.0	
844942	513	23	83.0	516.0	510.0	
844943	513	23	83.0	516.0	510.0	
844944	513	23	83.0	516.0	510.0	
844945	513	23	83.0	516.0	510.0	
	Pulse_Area	index	Gender	Height	Weight	Age_Range
0	393.0	0	1	180	53	2
1	393.0	1	1	180	53	2
2	393.0	2	1	180	53	2
3	393.0	3	1	180	53	2
4	393.0	4	1	180	53	2
...	...	...	...	...	...	...
844941	366.0	43	1	173	57	1
844942	366.0	42	1	173	57	1
844943	366.0	43	1	173	57	1
844944	366.0	42	1	173	57	1
844945	366.0	43	1	173	57	1

[744974 rows x 11 columns]

Y

	Glucose_level
0	99
1	102
2	103
3	128
4	130
...	...
844941	108
844942	100
844943	108
844944	100
844945	108

[744974 rows x 1 columns]

511 177.0 522.0 505.0 393.0 0 1180 53 2

'PPG\_Signal', 'Patient\_Id', 'Heart\_Rate', 'Systolic\_Peak', 'Diastolic\_Peak', 'Pulse\_Area', 'index',  
'Gender', 'Height', 'Weight', 'Age Range'

X\_test

	PPG_Signal	Patient_Id	Heart_Rate	Systolic_Peak
Diastolic_Peak \				
305947	509	5	79.0	521.0
507.0				
765658	511	22	93.0	526.0
505.0				
413976	512	9	79.0	516.0
510.0				
649421	514	18	93.0	523.0
510.0				
335190	508	6	75.0	524.0
504.0				
...	...	...	...	...
...				
632822	510	17	83.0	519.0
507.0				
633890	510	17	83.0	519.0
507.0				
173720	512	2	85.0	521.0
509.0				
455922	510	11	84.0	519.0
506.0				
308325	511	5	79.0	521.0
507.0				

Pulse_Area	index	Gender	Height	Weight	Age	Range
------------	-------	--------	--------	--------	-----	-------

305947	388.0	56	1	175	56	1
765658	324.0	41	0	170	50	1
413976	389.0	66	0	172	60	1
649421	309.5	27	1	180	90	1
335190	405.0	57	0	165	60	2
...	...	...	...	...	...	...
632822	365.0	25	0	169	55	1
633890	365.0	25	0	169	55	1
173720	355.0	32	1	187	75	1
455922	363.0	10	1	182	62	1
308325	388.0	52	1	175	56	1

[148995 rows x 11 columns]

y\_test

	Glucose_level
305947	136
765658	124
413976	124
649421	136
335190	96
...	...
632822	108
633890	108
173720	111
455922	100
308325	96

[148995 rows x 1 columns]

*## # Define the column names*

```
column_names = [
    'PPG_Signal(mV)', 'Patient_Id(ID number)', 'Heart_Rate(bpm)',
    'Systolic_Peak(mmHg)', 'Diastolic_Peak(mmHg)',
    'Pulse_Area', 'index(integer)', 'Gender(1 for Male, 0 for Female)',
    'Height(cm)', 'Weight(kg)', 'Age_Range[1,2,3,4,5]'
]
```

*# Get input from user (11 values) in a user-friendly way*

```
input_values = []
for column_name in column_names:
    value = float(input(f"Enter value for {column_name}: "))
    input_values.append(value)
```

*# Transform the input and make prediction*

```
input_df = pd.DataFrame([input_values], columns=X.columns) # Create a
```

```
DataFrame to maintain feature names
input_scaled = scaler_features.transform(input_df)
input_poly = poly_reg.transform(input_scaled)
output_scaled = poly_model.predict(input_poly)

# Convert the prediction back to the original glucose level scale
output = scaler_target.inverse_transform(output_scaled)

# Show the predicted glucose level in original value
print(f"Predicted Glucose Level: {output[0][0]}")


# Show the predicted glucose level in original value
#print(f"Predicted Glucose Level: {output_scaled[0][0]}")

X
df
min(X_test['Weight'])
min(X_test['index'])
min(X_test['PPG_Signal'])
max(X_test['PPG_Signal'])
max(X_test['Patient_Id'])
```