Data Pre-processing

In [132…

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

In [133…

```
from sklearn import preprocessing as ps
from sklearn import metrics
from sklearn.model_selection import RepeatedKFold , StratifiedKFold
from sklearn.preprocessing import StandardScaler as sc
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, ConfusionMatrixDisplay
```

In [134…

```
from sklearn import tree
from sklearn.svm import SVC
from sklearn.naive_bayes import GaussianNB
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
```

In [135…

```
from google.colab import drive

# Mount Google Drive
drive.mount('/content/drive')

# Access the file in MyDrive/Colab Notebooks/
file_path = '/content/drive/MyDrive/Colab Notebooks/POC.csv'
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/c
ontent/drive", force_remount=True).
```

In [136…

```
file_path = '/content/drive/MyDrive/Colab Notebooks/POC.csv'
```

In [137…

```
import pandas as pd
from google.colab import drive

# Mount Google Drive
drive.mount('/content/drive')

# Specify the full path to the CSV file
file_path = '/content/drive/MyDrive/Colab Notebooks/POC.csv'

# Read the CSV file
pcos_dt = pd.read_csv(file_path)
pcos_dt.head()
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/c
ontent/drive", force_remount=True).
```

Out[137]:

	Sl. No	Patient File No.	PCOS (Y/N)	Age (yrs)	Weight (Kg)	Height(Cm)	BMI	Blood Group	Pulse rate(bpm)	RR (breaths/min)	...	Fast food (Y/N)	Reg
0	1	10001	0	28	44.6	152.0	19.300000	15	78	22	...	1.0	
1	2	10002	0	36	65.0	161.5	24.921163	15	74	20	...	0.0	
2	3	10003	1	33	68.8	165.0	25.270891	11	72	18	...	1.0	
3	4	10004	0	37	65.0	148.0	29.674945	13	72	20	...	0.0	
4	5	10005	0	25	52.0	161.0	20.060954	11	72	18	...	0.0	

5 rows × 43 columns

In [138…

```
pcos_dt.shape
```

Out[138]:

```
(541, 43)
```

In [139…

```
pcos_dt.columns
```

Out[139]:

```
Index(['Sl. No', 'Patient File No.', 'PCOS (Y/N)', ' Age (yrs)', 'Weight (Kg)',
       'Height(Cm) ', 'BMI', 'Blood Group', 'Pulse rate(bpm) ',
       'RR (breaths/min)', 'Hb(g/dl)', 'Cycle(R/I)', 'Cycle length(days)',
       'Marraige Status (Yrs)', 'Pregnant(Y/N)', 'No. of aborptions',
       'FSH(mIU/mL)', 'LH(mIU/mL)', 'FSH/LH', 'Hip(inch)', 'Waist(inch)',
       'Waist:Hip Ratio', 'TSH (mIU/L)', 'AMH(ng/mL)', 'PRL(ng/mL)',
       'Vit D3 (ng/mL)', 'PRG(ng/mL)', 'RBS(mg/dl)', 'Weight gain(Y/N)',
       'hair growth(Y/N)', 'Skin darkening (Y/N)', 'Hair loss(Y/N)',
       'Pimples(Y/N)', 'Fast food (Y/N)', 'Reg.Exercise(Y/N)',
       'BP _Systolic (mmHg)', 'BP _Diastolic (mmHg)', 'Follicle No. (L)',
       'Follicle No. (R)', 'Avg. F size (L) (mm)', 'Avg. F size (R) (mm)',
       'Endometrium (mm)', 'Unnamed: 42'],
      dtype='object')
```

In [140…

```
#To remove whitespaces at both ends from a column name

pcos_dt.columns = pcos_dt.columns.str.strip()
```

In [141…

```
pcos_dt.columns
```

Out[141]:

```
Index(['Sl. No', 'Patient File No.', 'PCOS (Y/N)', 'Age (yrs)', 'Weight (Kg)',
       'Height(Cm)', 'BMI', 'Blood Group', 'Pulse rate(bpm)',
       'RR (breaths/min)', 'Hb(g/dl)', 'Cycle(R/I)', 'Cycle length(days)',
       'Marraige Status (Yrs)', 'Pregnant(Y/N)', 'No. of aborptions',
       'FSH(mIU/mL)', 'LH(mIU/mL)', 'FSH/LH', 'Hip(inch)', 'Waist(inch)',
       'Waist:Hip Ratio', 'TSH (mIU/L)', 'AMH(ng/mL)', 'PRL(ng/mL)',
       'Vit D3 (ng/mL)', 'PRG(ng/mL)', 'RBS(mg/dl)', 'Weight gain(Y/N)',
       'hair growth(Y/N)', 'Skin darkening (Y/N)', 'Hair loss(Y/N)',
       'Pimples(Y/N)', 'Fast food (Y/N)', 'Reg.Exercise(Y/N)',
       'BP _Systolic (mmHg)', 'BP _Diastolic (mmHg)', 'Follicle No. (L)',
       'Follicle No. (R)', 'Avg. F size (L) (mm)', 'Avg. F size (R) (mm)',
       'Endometrium (mm)', 'Unnamed: 42'],
      dtype='object')
```

Removing unwanted columns

In [142…

```
pcos_dt.drop(['Sl. No', 'Patient File No.','Fast food (Y/N)'],axis='columns',inplace=True)
```

Imputing Missing values

Rows with unmatching values are removed and some values are replaced

In [146…

```python
import pandas as pd
from google.colab import drive

# Mount Google Drive
drive.mount('/content/drive')

# Specify the full path to the CSV file
file_path = '/content/drive/MyDrive/Colab Notebooks/POC.csv'

# Read the CSV file
pcos_dt = pd.read_csv(file_path)

# Display the columns in the DataFrame
print(pcos_dt.columns)

# Replace missing values in a specific column with the median of that column
# Example: Replace missing values in ')' with the median of the column
median_value = pcos_dt['Blood Group'].median()
pcos_dt['Blood Group'].fillna(median_value, inplace=True)

# Verify the changes
pcos_dt.head()
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/c
ontent/drive", force_remount=True).
Index(['Sl. No', 'Patient File No.', 'PCOS (Y/N)', ' Age (yrs)', 'Weight (Kg)',
       'Height(Cm) ', 'BMI', 'Blood Group', 'Pulse rate(bpm) ',
       'RR (breaths/min)', 'Hb(g/dl)', 'Cycle(R/I)', 'Cycle length(days)',
       'Marraige Status (Yrs)', 'Pregnant(Y/N)', 'No. of aborptions',
       'FSH(mIU/mL)', 'LH(mIU/mL)', 'FSH/LH', 'Hip(inch)', 'Waist(inch)',
       'Waist:Hip Ratio', 'TSH (mIU/L)', 'AMH(ng/mL)', 'PRL(ng/mL)',
       'Vit D3 (ng/mL)', 'PRG(ng/mL)', 'RBS(mg/dl)', 'Weight gain(Y/N)',
       'hair growth(Y/N)', 'Skin darkening (Y/N)', 'Hair loss(Y/N)',
       'Pimples(Y/N)', 'Fast food (Y/N)', 'Reg.Exercise(Y/N)',
       'BP _Systolic (mmHg)', 'BP _Diastolic (mmHg)', 'Follicle No. (L)',
       'Follicle No. (R)', 'Avg. F size (L) (mm)', 'Avg. F size (R) (mm)',
       'Endometrium (mm)', 'Unnamed: 42'],
      dtype='object')
```

Out[146]:

	Sl. No	Patient File No.	PCOS (Y/N)	Age (yrs)	Weight (Kg)	Height(Cm)	BMI	Blood Group	Pulse rate(bpm)	RR (breaths/min)	...	Fast food (Y/N)	Reg
0	1	10001	0	28	44.6	152.0	19.300000	15	78	22	...	1.0	
1	2	10002	0	36	65.0	161.5	24.921163	15	74	20	...	0.0	
2	3	10003	1	33	68.8	165.0	25.270891	11	72	18	...	1.0	
3	4	10004	0	37	65.0	148.0	29.674945	13	72	20	...	0.0	
4	5	10005	0	25	52.0	161.0	20.060954	11	72	18	...	0.0	

5 rows × 43 columns

Searching for columns with missing values

In [147…

```python
pcos_dt.isnull().sum()
```

Out[147]:

```
Sl. No                        0
Patient File No.              0
PCOS (Y/N)                    0
 Age (yrs)                    0
Weight (Kg)                   0
Height(Cm)                    0
BMI                           0
Blood Group                   0
Pulse rate(bpm)               0
RR (breaths/min)              0
Hb(g/dl)                      0
Cycle(R/I)                    0
Cycle length(days)            0
Marraige Status (Yrs)         1
Pregnant(Y/N)                 0
No. of aborptions             0
FSH(mIU/mL)                   0
LH(mIU/mL)                    0
FSH/LH                        0
Hip(inch)                     0
Waist(inch)                   0
Waist:Hip Ratio               0
TSH (mIU/L)                   0
AMH(ng/mL)                    0
PRL(ng/mL)                    0
Vit D3 (ng/mL)                0
PRG(ng/mL)                    0
RBS(mg/dl)                    0
Weight gain(Y/N)              0
hair growth(Y/N)              0
Skin darkening (Y/N)          0
Hair loss(Y/N)                0
Pimples(Y/N)                  0
Fast food (Y/N)               1
Reg.Exercise(Y/N)             0
BP _Systolic (mmHg)           0
BP _Diastolic (mmHg)          0
Follicle No. (L)              0
Follicle No. (R)              0
Avg. F size (L) (mm)          0
Avg. F size (R) (mm)          0
Endometrium (mm)              0
Unnamed: 42                 539
dtype: int64
```

In [148…

```python
# Replacing the missing values in a feature column with the median of the feature

pcos_dt['Pimples(Y/N)'].fillna(pcos_dt['Pimples(Y/N)'].median(), inplace = True)
pcos_dt['Endometrium (mm)'].fillna(pcos_dt['Endometrium (mm)'].median(), inplace = True)
```

In [149…

```python
pcos_dt.isnull().sum()
```

Out[149]:

```
Sl. No                     0
Patient File No.           0
PCOS (Y/N)                 0
 Age (yrs)                 0
Weight (Kg)                0
Height(Cm)                 0
BMI                        0
Blood Group                0
Pulse rate(bpm)            0
RR (breaths/min)           0
Hb(g/dl)                   0
Cycle(R/I)                 0
Cycle length(days)         0
Marraige Status (Yrs)      1
Pregnant(Y/N)              0
No. of aborptions          0
FSH(mIU/mL)                0
LH(mIU/mL)                 0
FSH/LH                     0
Hip(inch)                  0
Waist(inch)                0
Waist:Hip Ratio            0
TSH (mIU/L)                0
AMH(ng/mL)                 0
PRL(ng/mL)                 0
Vit D3 (ng/mL)             0
PRG(ng/mL)                 0
RBS(mg/dl)                 0
Weight gain(Y/N)           0
hair growth(Y/N)           0
Skin darkening (Y/N)       0
Hair loss(Y/N)             0
Pimples(Y/N)               0
Fast food (Y/N)            1
Reg.Exercise(Y/N)          0
BP _Systolic (mmHg)        0
BP _Diastolic (mmHg)       0
Follicle No. (L)           0
Follicle No. (R)           0
Avg. F size (L) (mm)       0
Avg. F size (R) (mm)       0
Endometrium (mm)           0
Unnamed: 42              539
dtype: int64
```

Standardization

In [151…

```python
from sklearn.preprocessing import StandardScaler
import pandas as pd
from google.colab import drive

# Mount Google Drive
drive.mount('/content/drive')

# Specify the full path to the CSV file
file_path = '/content/drive/MyDrive/Colab Notebooks/POC.csv'

# Read the CSV file
pcos_dt = pd.read_csv(file_path)

# Identify non-numeric columns
non_numeric_columns = pcos_dt.select_dtypes(exclude=['float64', 'int64']).columns

# Exclude non-numeric columns from the scaling process
numeric_columns = pcos_dt.columns.difference(non_numeric_columns)
pcos_numeric = pcos_dt[numeric_columns]

# Standardize the numeric columns
```

```
scaler = StandardScaler()
pcos_standardized = scaler.fit_transform(pcos_numeric)

# Create a DataFrame with the standardized values
pcos_standardized_dt = pd.DataFrame(pcos_standardized, columns=numeric_columns)

# Concatenate the non-numeric columns with the standardized numeric columns
pcos_standardized_dt[non_numeric_columns] = pcos_dt[non_numeric_columns]

# Verify the changes
pcos_standardized_dt.head()
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/c
ontent/drive", force_remount=True).
```

Out[151]:

	Age (yrs)	Avg. F size (L) (mm)	Avg. F size (R) (mm)	BMI	BP _Diastolic (mmHg)	BP _Systolic (mmHg)	Blood Group	Cycle length(days)	Cycle(R/I)	Endome
0	-0.634606	0.836776	0.768537	-1.236546	0.551645	-0.631866	0.651284	0.039681	-0.621534	0.0
1	0.845230	-0.005083	-0.437816	0.150489	-1.244023	0.723565	0.651284	0.039681	-0.621534	-2.2
2	0.290291	0.836776	1.371714	0.236785	0.551645	0.723565	-1.523682	0.039681	-0.621534	0.7
3	1.030210	-0.005083	-0.437816	1.323495	-1.244023	0.723565	-0.436199	0.039681	-0.621534	-0.4
4	-1.189545	0.275536	-0.437816	-1.048778	0.551645	0.723565	-1.523682	0.039681	-0.621534	-0.6

5 rows × 43 columns

In [152…

```
pcos_standardized_dt.head()
```

Out[152]:

	Age (yrs)	Avg. F size (L) (mm)	Avg. F size (R) (mm)	BMI	BP _Diastolic (mmHg)	BP _Systolic (mmHg)	Blood Group	Cycle length(days)	Cycle(R/I)	Endome
0	-0.634606	0.836776	0.768537	-1.236546	0.551645	-0.631866	0.651284	0.039681	-0.621534	0.0
1	0.845230	-0.005083	-0.437816	0.150489	-1.244023	0.723565	0.651284	0.039681	-0.621534	-2.2
2	0.290291	0.836776	1.371714	0.236785	0.551645	0.723565	-1.523682	0.039681	-0.621534	0.7
3	1.030210	-0.005083	-0.437816	1.323495	-1.244023	0.723565	-0.436199	0.039681	-0.621534	-0.4
4	-1.189545	0.275536	-0.437816	-1.048778	0.551645	0.723565	-1.523682	0.039681	-0.621534	-0.6

5 rows × 43 columns

Normalization

In [154…

```
from sklearn.preprocessing import MinMaxScaler
import pandas as pd
from google.colab import drive

# Mount Google Drive
drive.mount('/content/drive')

# Specify the full path to the CSV file
file_path = '/content/drive/MyDrive/Colab Notebooks/POC.csv'

# Read the CSV file
pcos_dt = pd.read_csv(file_path)

# Identify non-numeric columns
```

```
non_numeric_columns = pcos_dt.select_dtypes(exclude=['float64', 'int64']).columns

# Exclude non-numeric columns from the normalization process
numeric_columns = pcos_dt.columns.difference(non_numeric_columns)
pcos_numeric = pcos_dt[numeric_columns]

# Normalize the numeric columns
scaler = MinMaxScaler()
pcos_normalized = scaler.fit_transform(pcos_numeric)

# Create a DataFrame with the normalized values
pcos_normalized_dt = pd.DataFrame(pcos_normalized, columns=numeric_columns)

# Concatenate the non-numeric columns with the normalized numeric columns
pcos_normalized_dt[non_numeric_columns] = pcos_dt[non_numeric_columns]

# Verify the changes
pcos_normalized_dt.head()
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/c
ontent/drive", force_remount=True).
```

Out[154]:

	Age (yrs)	Avg. F size (L) (mm)	Avg. F size (R) (mm)	BMI	BP _Diastolic (mmHg)	BP _Systolic (mmHg)	Blood Group	Cycle length(days)	Cycle(R/I)	Endometriun (mm
0	0.285714	0.750000	0.750000	0.259878	0.782609	0.765625	0.571429	0.416667	0.0	0.47222
1	0.571429	0.625000	0.583333	0.472141	0.673913	0.843750	0.571429	0.416667	0.0	0.20555
2	0.464286	0.750000	0.833333	0.485347	0.782609	0.843750	0.000000	0.416667	0.0	0.55555
3	0.607143	0.625000	0.583333	0.651650	0.673913	0.843750	0.285714	0.416667	0.0	0.41666
4	0.178571	0.666667	0.583333	0.288613	0.782609	0.843750	0.000000	0.416667	0.0	0.38888

5 rows × 43 columns

In [155…

```
pcos_normalized_dt.head()
```

Out[155]:

	Age (yrs)	Avg. F size (L) (mm)	Avg. F size (R) (mm)	BMI	BP _Diastolic (mmHg)	BP _Systolic (mmHg)	Blood Group	Cycle length(days)	Cycle(R/I)	Endometriun (mm
0	0.285714	0.750000	0.750000	0.259878	0.782609	0.765625	0.571429	0.416667	0.0	0.47222
1	0.571429	0.625000	0.583333	0.472141	0.673913	0.843750	0.571429	0.416667	0.0	0.20555
2	0.464286	0.750000	0.833333	0.485347	0.782609	0.843750	0.000000	0.416667	0.0	0.55555
3	0.607143	0.625000	0.583333	0.651650	0.673913	0.843750	0.285714	0.416667	0.0	0.41666
4	0.178571	0.666667	0.583333	0.288613	0.782609	0.843750	0.000000	0.416667	0.0	0.38888

5 rows × 43 columns

Data Summarization

In [156…

```
pcos_dt.shape
```

Out[156]:

```
(541, 43)
```

In [157…

```
pcos_dt.dtypes
```

Out[157]:

```
Sl. No                     int64
Patient File No.           int64
PCOS (Y/N)                 int64
 Age (yrs)                 int64
Weight (Kg)              float64
Height(Cm)               float64
BMI                      float64
Blood Group                int64
Pulse rate(bpm)            int64
RR (breaths/min)           int64
Hb(g/dl)                 float64
Cycle(R/I)                 int64
Cycle length(days)         int64
Marraige Status (Yrs)    float64
Pregnant(Y/N)              int64
No. of aborptions          int64
FSH(mIU/mL)              float64
LH(mIU/mL)               float64
FSH/LH                   float64
Hip(inch)                  int64
Waist(inch)                int64
Waist:Hip Ratio          float64
TSH (mIU/L)              float64
AMH(ng/mL)                object
PRL(ng/mL)               float64
Vit D3 (ng/mL)           float64
PRG(ng/mL)               float64
RBS(mg/dl)               float64
Weight gain(Y/N)           int64
hair growth(Y/N)           int64
Skin darkening (Y/N)       int64
Hair loss(Y/N)             int64
Pimples(Y/N)               int64
Fast food (Y/N)          float64
Reg.Exercise(Y/N)          int64
BP _Systolic (mmHg)        int64
BP _Diastolic (mmHg)       int64
Follicle No. (L)           int64
Follicle No. (R)           int64
Avg. F size (L) (mm)     float64
Avg. F size (R) (mm)     float64
Endometrium (mm)         float64
Unnamed: 42               object
dtype: object
```

In [158…

```
pcos_dt.describe()
```

Out[158]:

	Sl. No	Patient File No.	PCOS (Y/N)	Age (yrs)	Weight (Kg)	Height(Cm)	BMI	Blood Group	rat
count	541.000000	541.000000	541.000000	541.000000	541.000000	541.000000	541.000000	541.000000	541.
mean	271.000000	10271.000000	0.327172	31.430684	59.637153	156.484835	24.311285	13.802218	73.
std	156.317519	156.317519	0.469615	5.411006	11.028287	6.033545	4.056399	1.840812	4.
min	1.000000	10001.000000	0.000000	20.000000	31.000000	137.000000	12.417882	11.000000	13.
25%	136.000000	10136.000000	0.000000	28.000000	52.000000	152.000000	21.641274	13.000000	72.
50%	271.000000	10271.000000	0.000000	31.000000	59.000000	156.000000	24.238227	14.000000	72.
75%	406.000000	10406.000000	1.000000	35.000000	65.000000	160.000000	26.634958	15.000000	74.
max	541.000000	10541.000000	1.000000	48.000000	108.000000	180.000000	38.900000	18.000000	82.

8 rows × 41 columns

In [159…

```
pcos_dt.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 541 entries, 0 to 540
Data columns (total 43 columns):
 #   Column                  Non-Null Count  Dtype  
---  ------                  --------------  -----  
 0   Sl. No                  541 non-null    int64  
 1   Patient File No.        541 non-null    int64  
 2   PCOS (Y/N)              541 non-null    int64  
 3    Age (yrs)              541 non-null    int64  
 4   Weight (Kg)             541 non-null    float64
 5   Height(Cm)              541 non-null    float64
 6   BMI                     541 non-null    float64
 7   Blood Group             541 non-null    int64  
 8   Pulse rate(bpm)         541 non-null    int64  
 9   RR (breaths/min)        541 non-null    int64  
 10  Hb(g/dl)                541 non-null    float64
 11  Cycle(R/I)              541 non-null    int64  
 12  Cycle length(days)      541 non-null    int64  
 13  Marraige Status (Yrs)   540 non-null    float64
 14  Pregnant(Y/N)           541 non-null    int64  
 15  No. of aborptions       541 non-null    int64  
 16  FSH(mIU/mL)             541 non-null    float64
 17  LH(mIU/mL)              541 non-null    float64
 18  FSH/LH                  541 non-null    float64
 19  Hip(inch)               541 non-null    int64  
 20  Waist(inch)             541 non-null    int64  
 21  Waist:Hip Ratio         541 non-null    float64
 22  TSH (mIU/L)             541 non-null    float64
 23  AMH(ng/mL)              541 non-null    object 
 24  PRL(ng/mL)              541 non-null    float64
 25  Vit D3 (ng/mL)          541 non-null    float64
 26  PRG(ng/mL)              541 non-null    float64
 27  RBS(mg/dl)              541 non-null    float64
 28  Weight gain(Y/N)        541 non-null    int64  
 29  hair growth(Y/N)        541 non-null    int64  
 30  Skin darkening (Y/N)    541 non-null    int64  
 31  Hair loss(Y/N)          541 non-null    int64  
 32  Pimples(Y/N)            541 non-null    int64  
 33  Fast food (Y/N)         540 non-null    float64
 34  Reg.Exercise(Y/N)       541 non-null    int64  
 35  BP _Systolic (mmHg)     541 non-null    int64  
 36  BP _Diastolic (mmHg)    541 non-null    int64  
 37  Follicle No. (L)        541 non-null    int64  
 38  Follicle No. (R)        541 non-null    int64  
 39  Avg. F size (L) (mm)    541 non-null    float64
 40  Avg. F size (R) (mm)    541 non-null    float64
 41  Endometrium (mm)        541 non-null    float64
 42  Unnamed: 42             2 non-null      object 
dtypes: float64(18), int64(23), object(2)
memory usage: 181.9+ KB
```

In [160…

```
pcos_dt.to_csv("pcos_datatset_cleaned.csv")
```

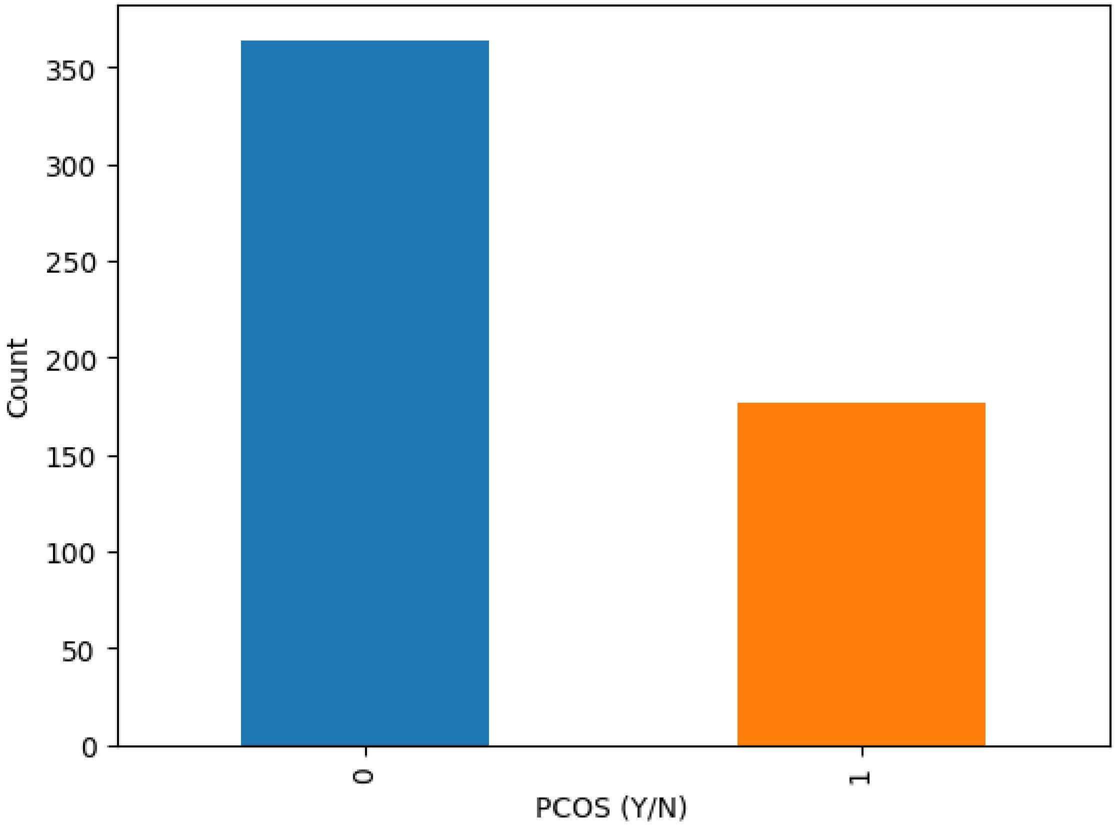
Data Visualization

In [161…

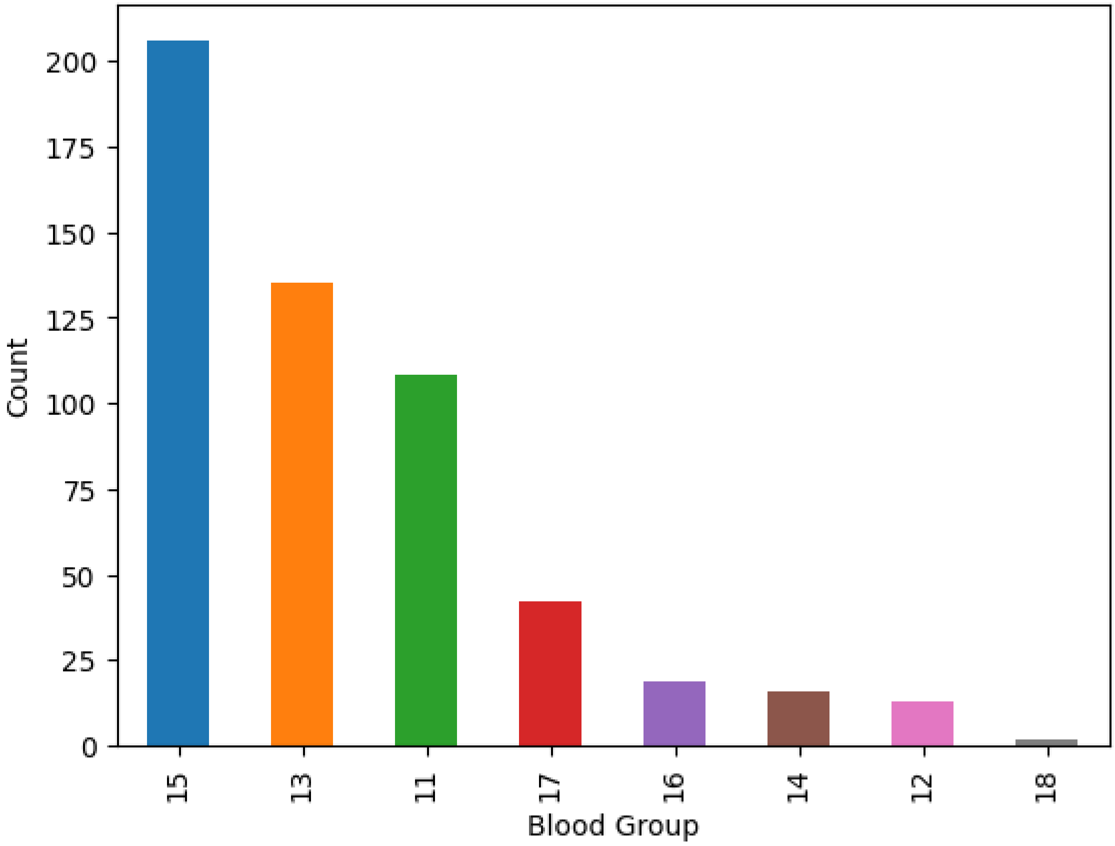
```
# Plotting all the categorical variables using bar plot
cv = ['PCOS (Y/N)','Blood Group','Pregnant(Y/N)','Weight gain(Y/N)','hair growth(Y/N)','Skin
      'Fast food (Y/N)', 'Reg.Exercise(Y/N)']

for i in cv:
  plt.xlabel(i)
  plt.ylabel('Count')
  c=pcos_dt[i].value_counts()
  print(i)
  print(c)
  colors = [('C'+str(j)) for j in range(len(c))]
```

```
    pcos_dt[i].value_counts().plot(kind='bar',color=colors)
    plt.show()
```

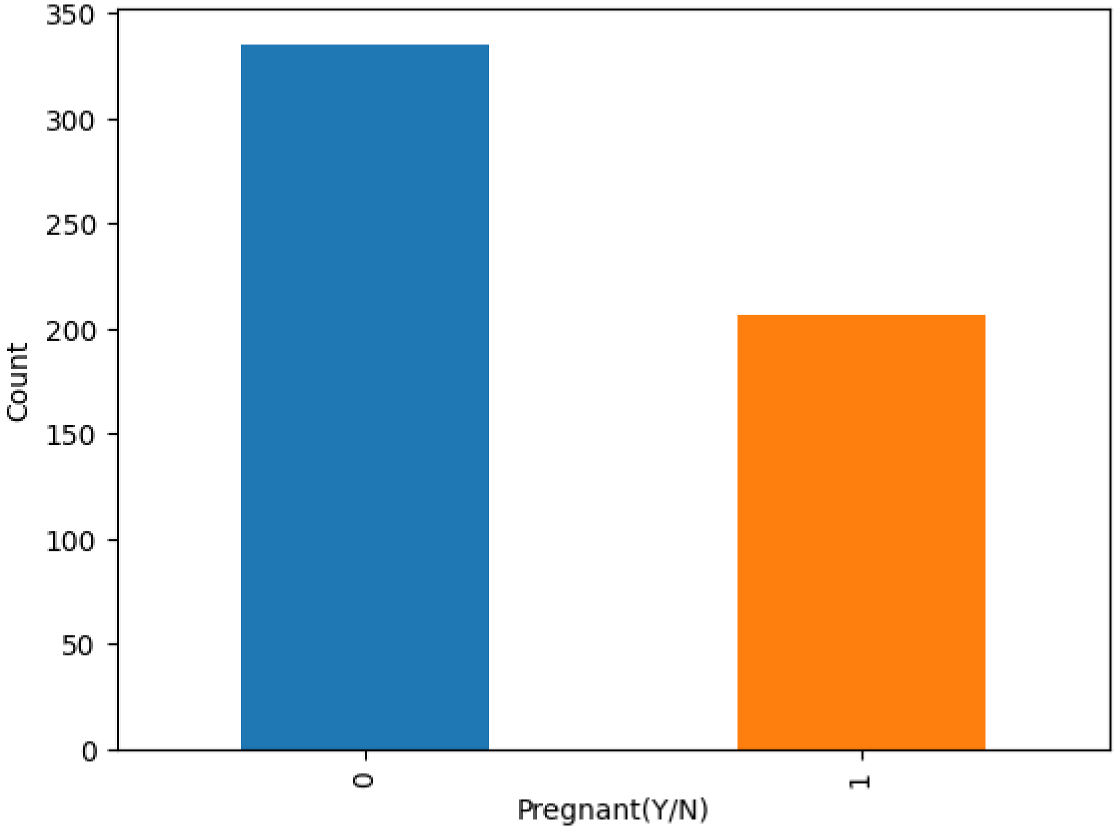
```
PCOS (Y/N)
0    364
1    177
Name: PCOS (Y/N), dtype: int64
```



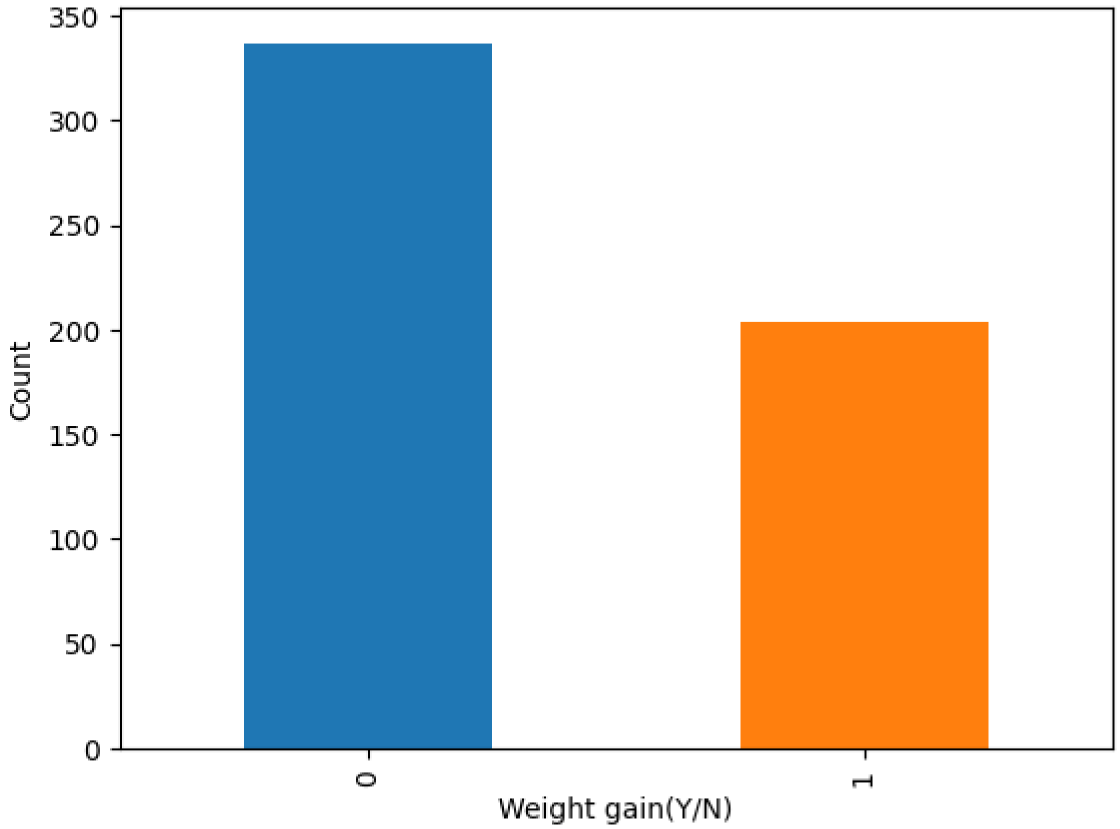
```
Blood Group
15    206
13    135
11    108
17     42
16     19
14     16
12     13
18      2
Name: Blood Group, dtype: int64
```



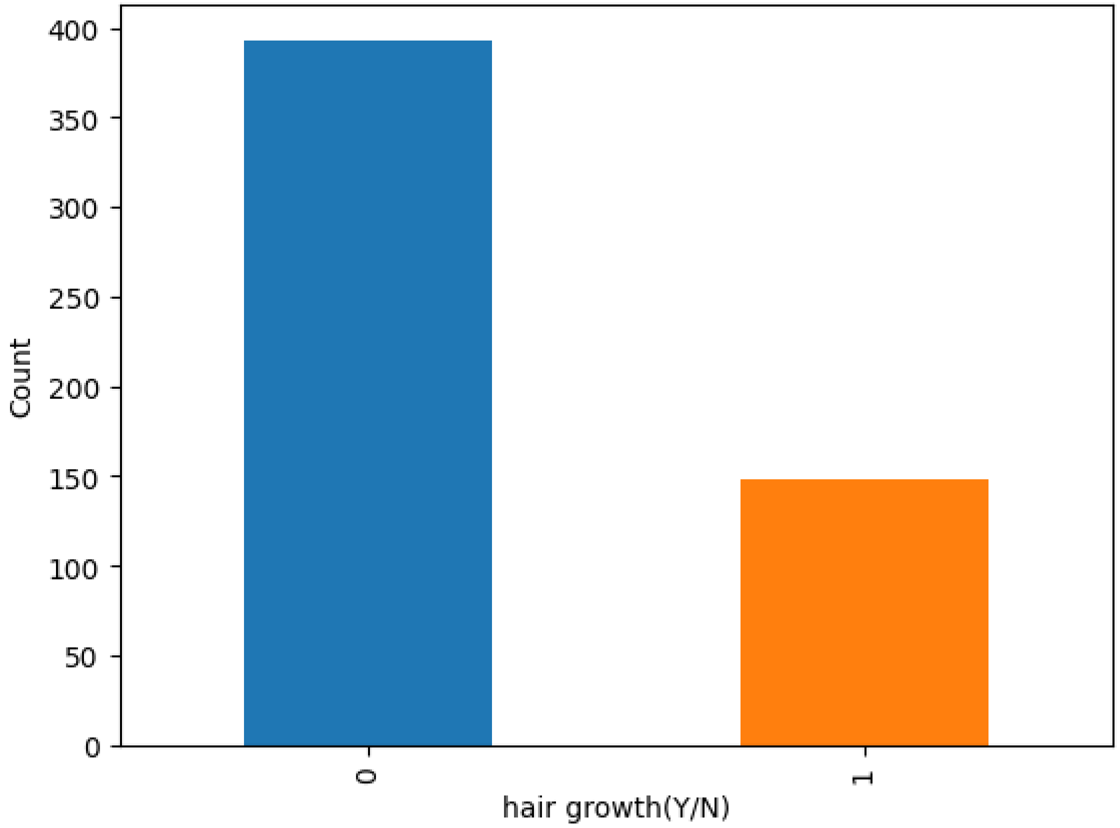
```
Pregnant(Y/N)
0    335
1    206
Name: Pregnant(Y/N), dtype: int64
```



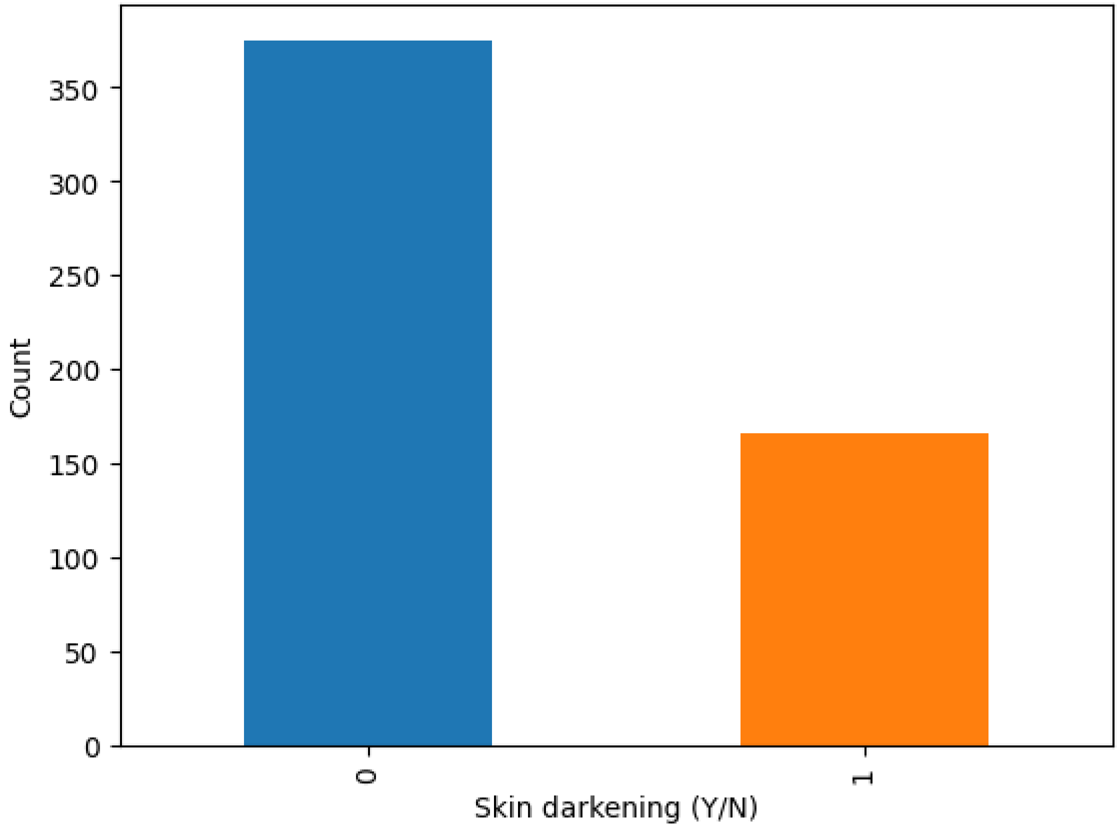
```
Weight gain(Y/N)
0    337
1    204
Name: Weight gain(Y/N), dtype: int64
```



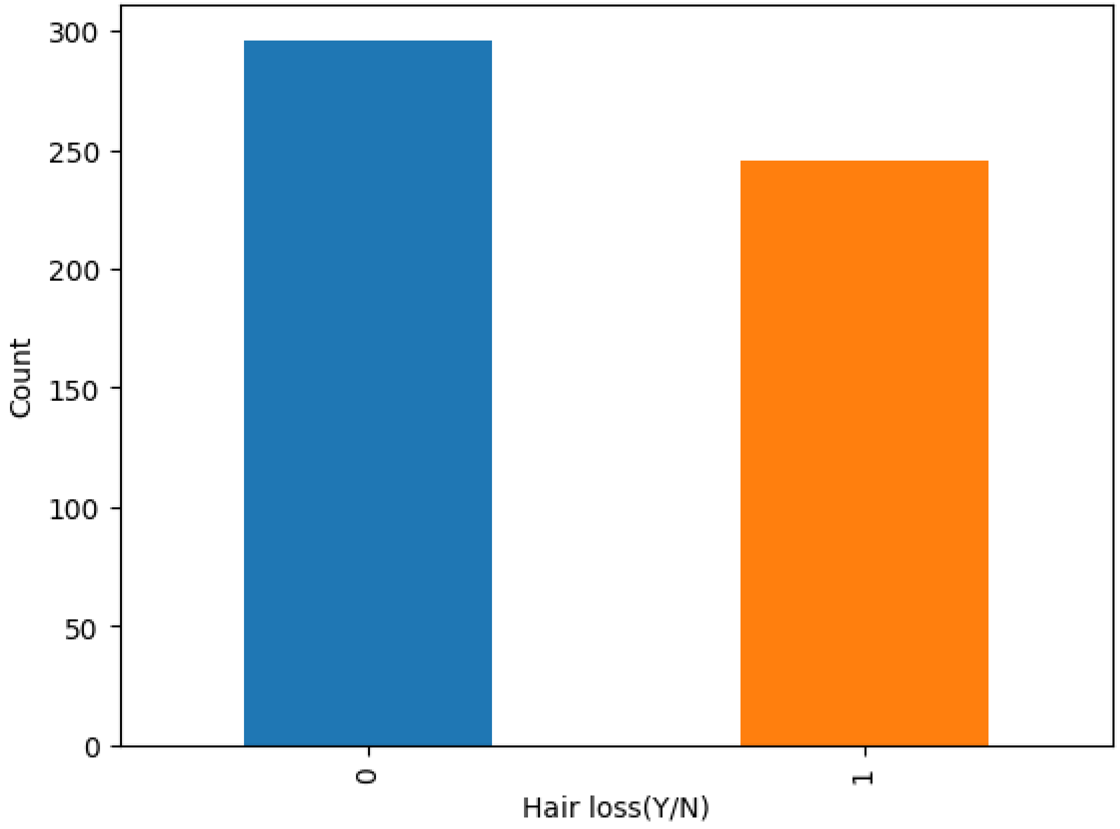
```
hair growth(Y/N)
0    393
1    148
Name: hair growth(Y/N), dtype: int64
```



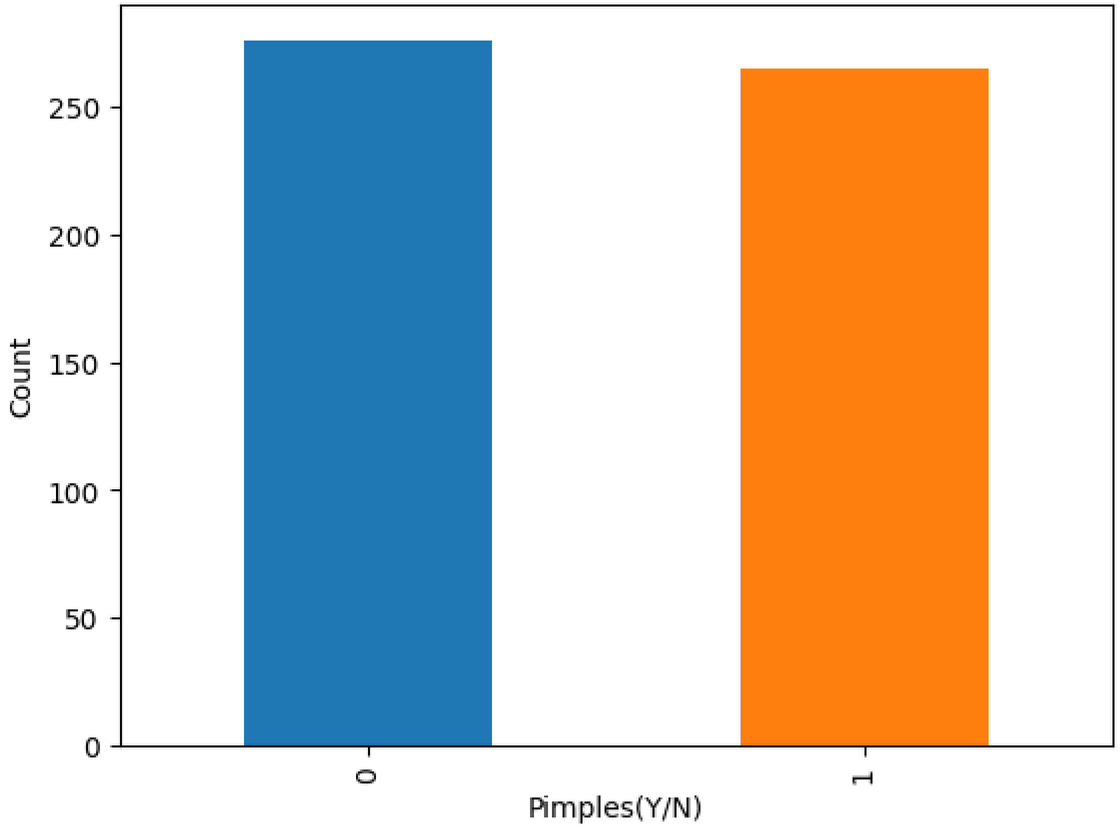
```
Skin darkening (Y/N)
0    375
1    166
Name: Skin darkening (Y/N), dtype: int64
```



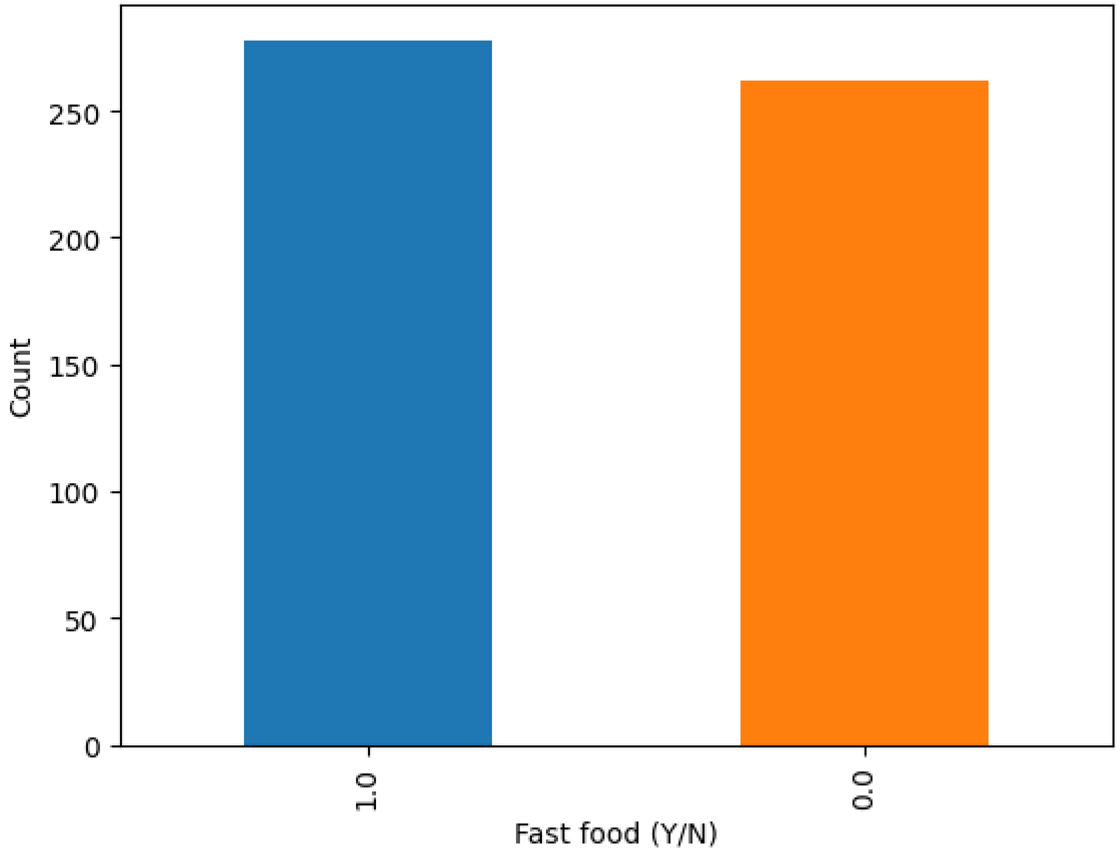
```
Hair loss(Y/N)
0    296
1    245
Name: Hair loss(Y/N), dtype: int64
```



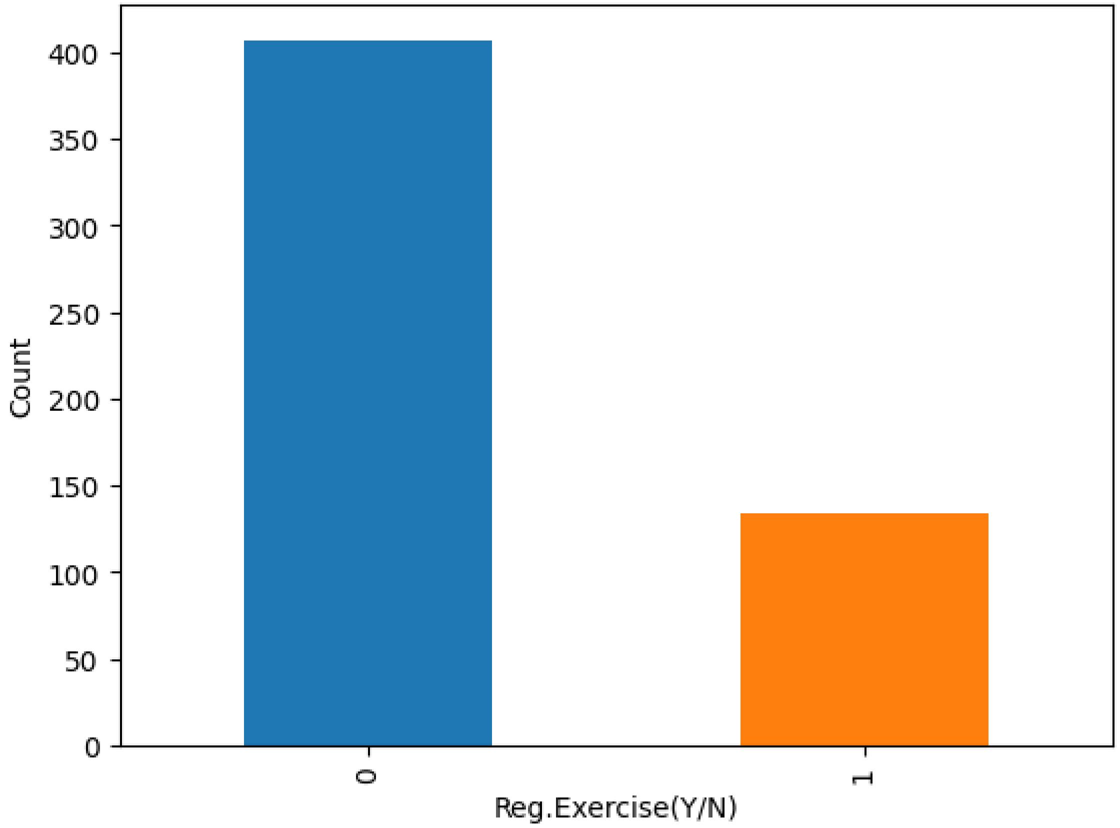
```
Pimples(Y/N)
0    276
1    265
Name: Pimples(Y/N), dtype: int64
```



```
Fast food (Y/N)
1.0    278
0.0    262
Name: Fast food (Y/N), dtype: int64
```



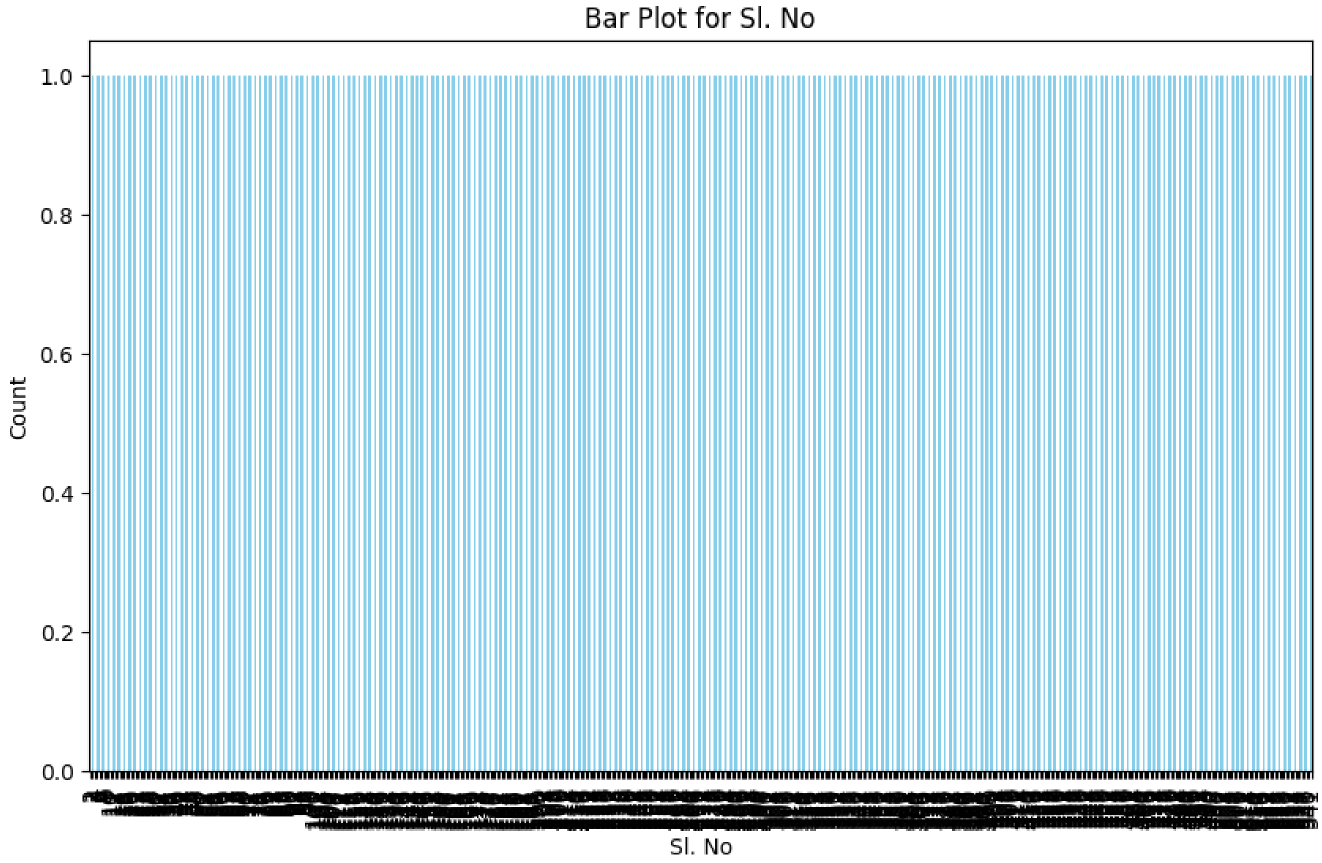
```
Reg.Exercise(Y/N)
0    407
1    134
Name: Reg.Exercise(Y/N), dtype: int64
```

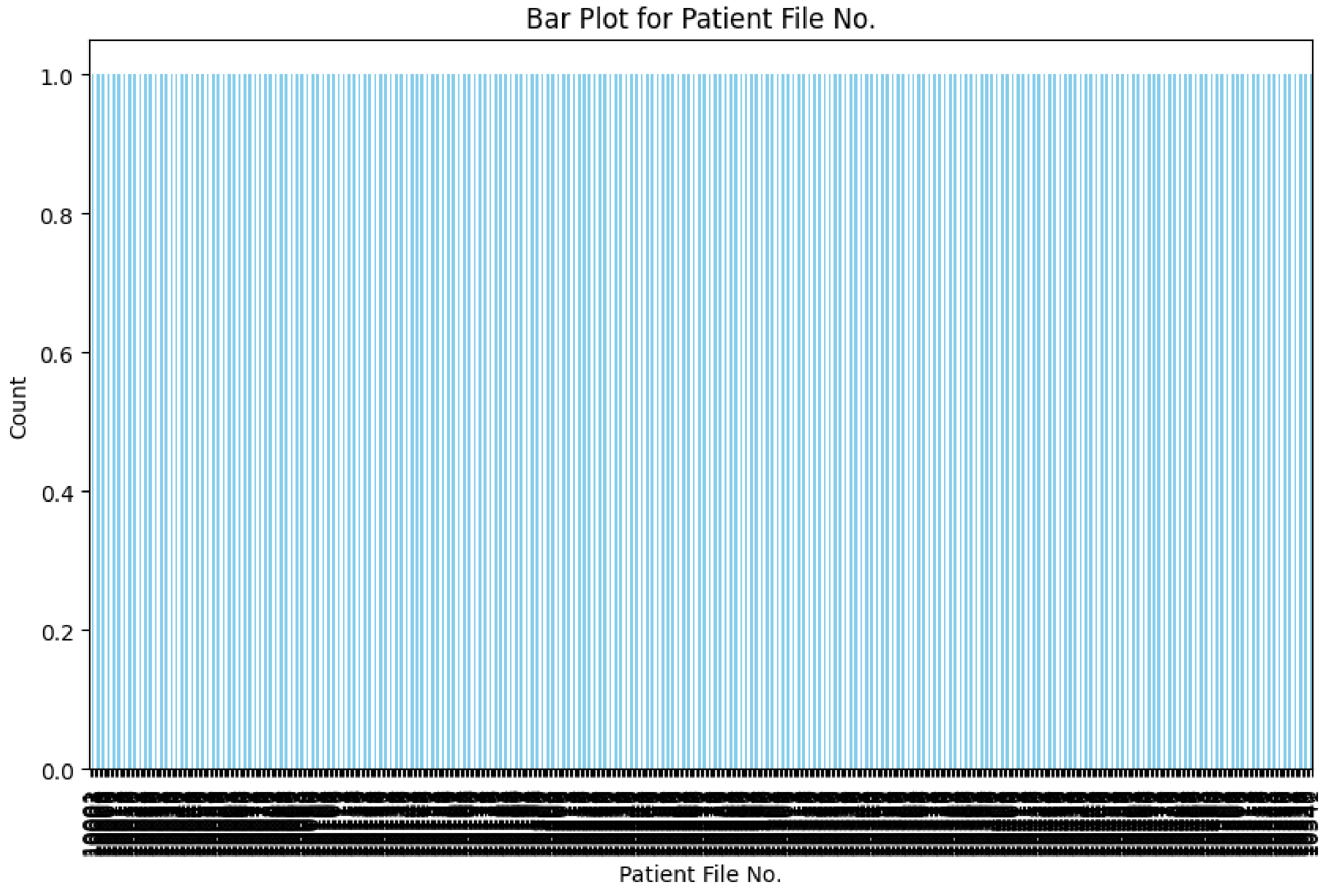


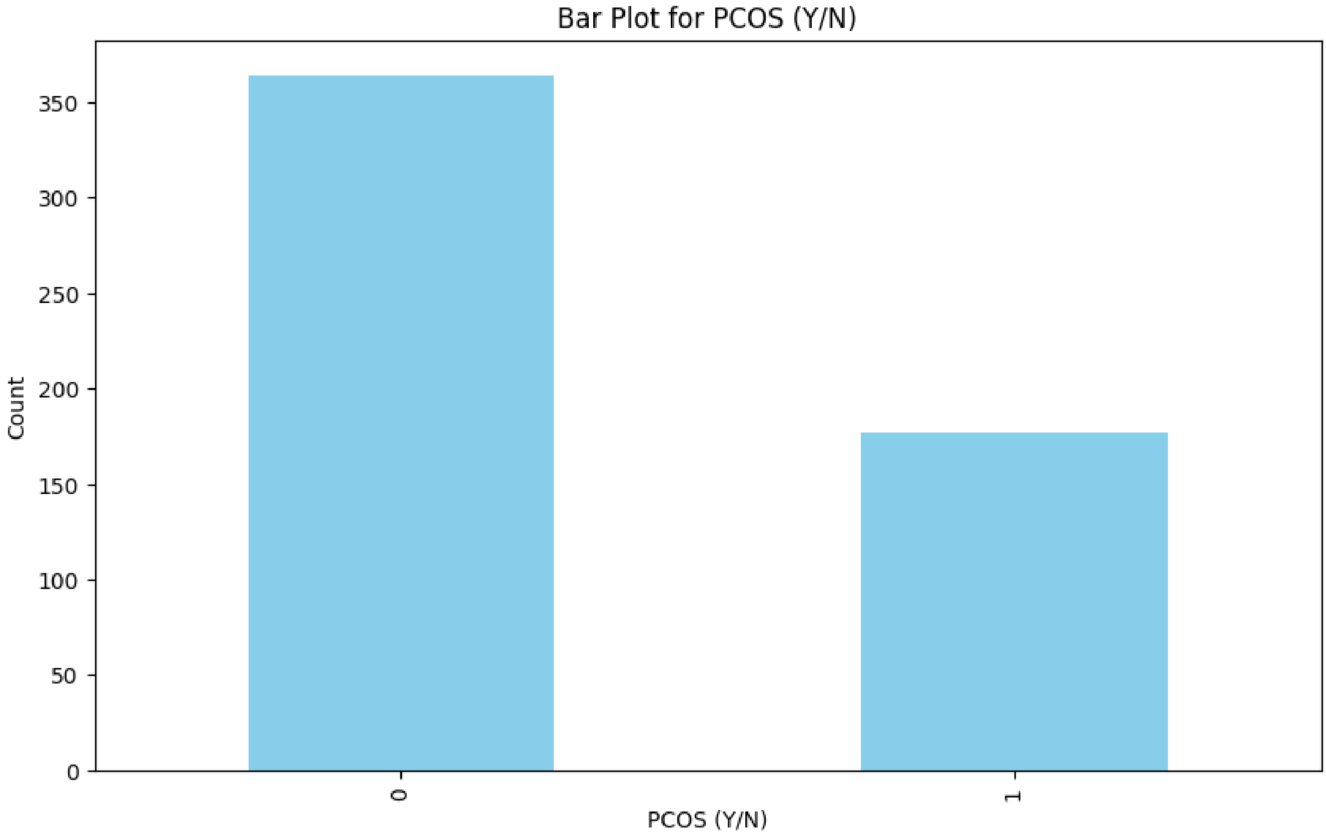
In [166…

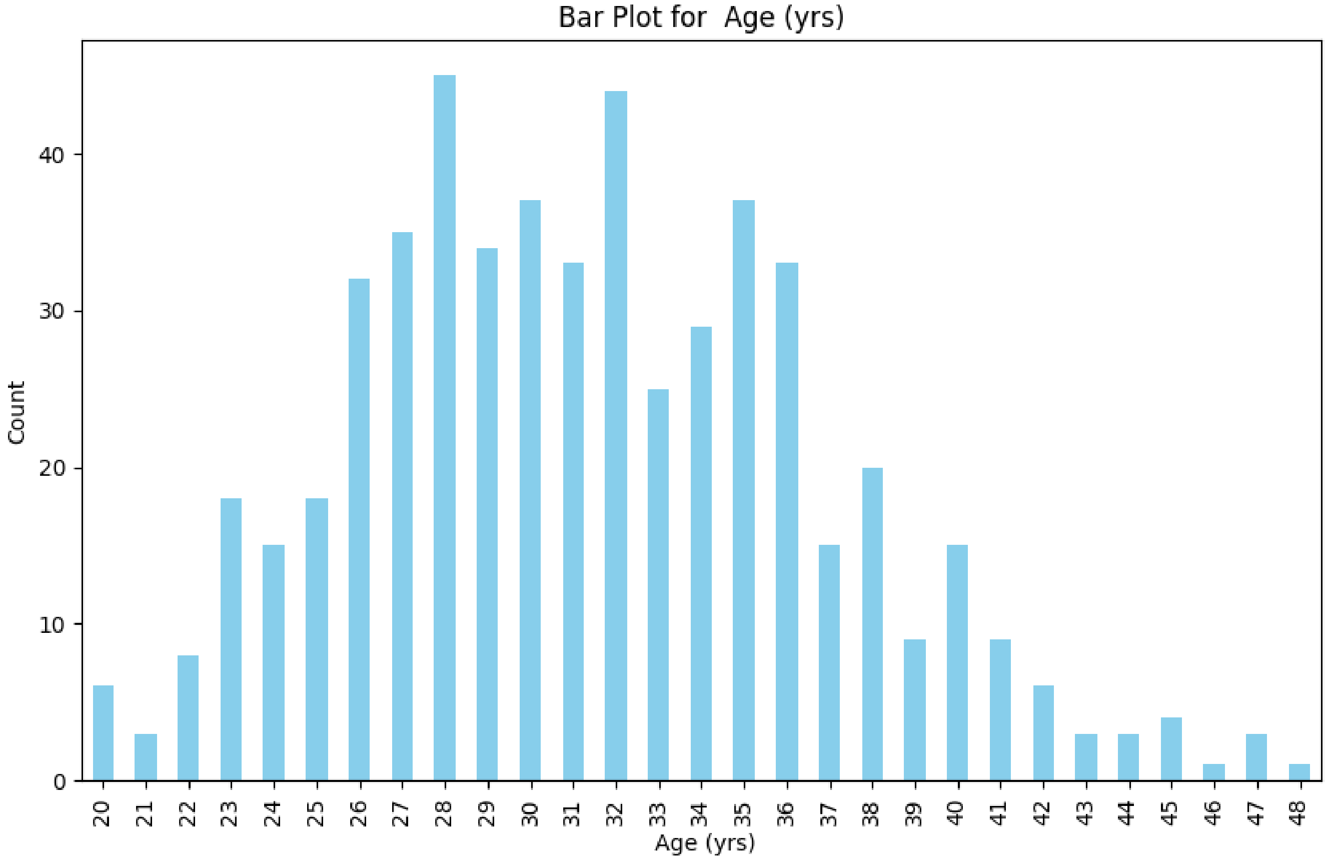
```python
import matplotlib.pyplot as plt
import pandas as pd
from google.colab import drive

# Mount Google Drive
drive.mount('/content/drive')

# Specify the full path to the CSV file
file_path = '/content/drive/MyDrive/Colab Notebooks/POC.csv'

# Read the CSV file
pcos_dt = pd.read_csv(file_path)

# Identify numerical columns
numeric_columns = pcos_dt.select_dtypes(include=['float64', 'int64']).columns

# Plot bar charts for each numerical column
for column in numeric_columns:
    plt.figure(figsize=(10, 6))
    pcos_dt[column].value_counts().sort_index().plot(kind='bar', color='skyblue')
    plt.title(f'Bar Plot for {column}')
    plt.xlabel(column)
    plt.ylabel('Count')
    plt.show()
```

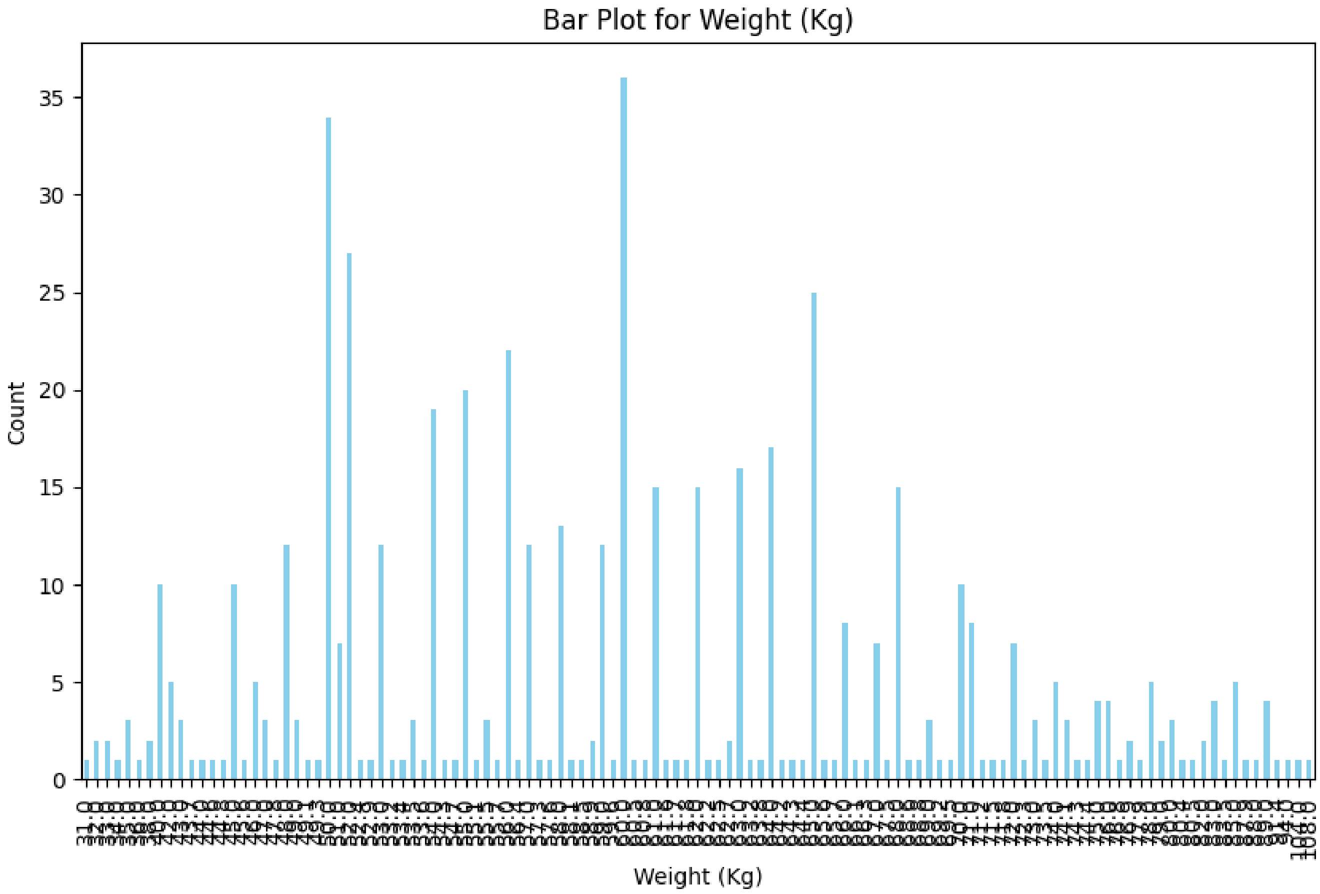
```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/c
ontent/drive", force_remount=True).
```

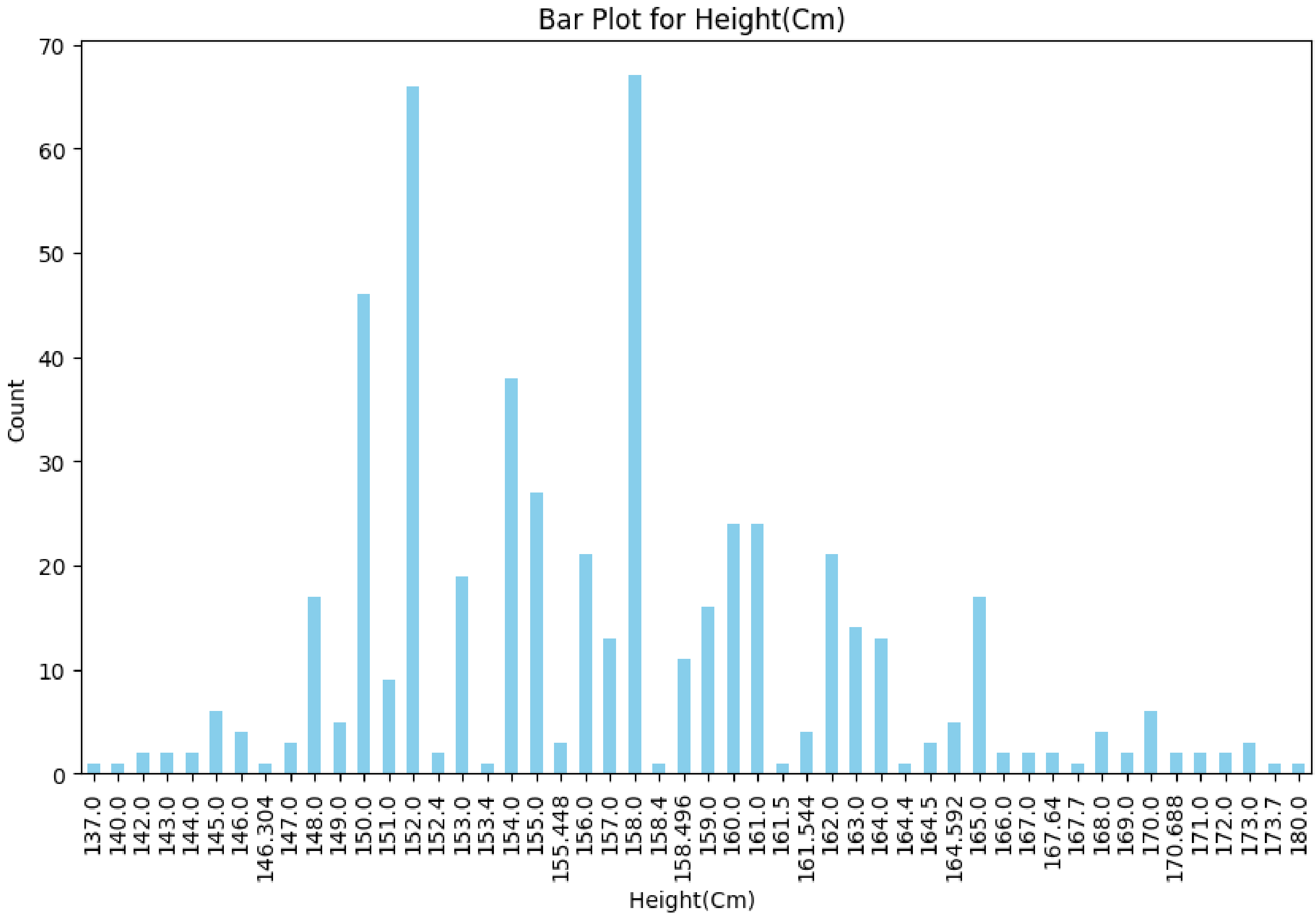

Bar Plot for Sl. No
Count
1.0
0.8
0.6
0.4
0.2
0.0
Sl. No

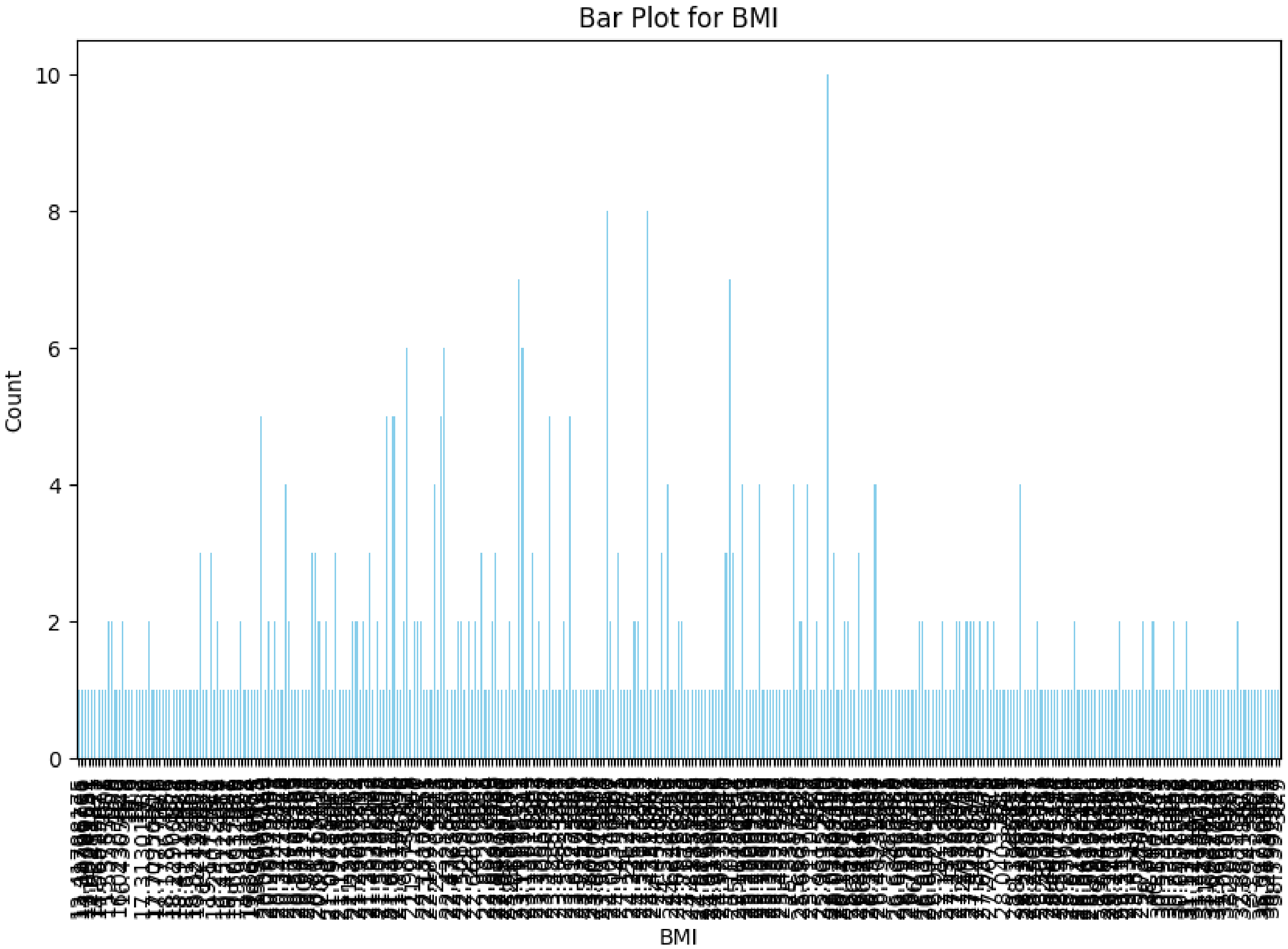

Bar Plot for Patient File No.
Count
1.0
0.8
0.6
0.4
0.2
0.0
Patient File No.

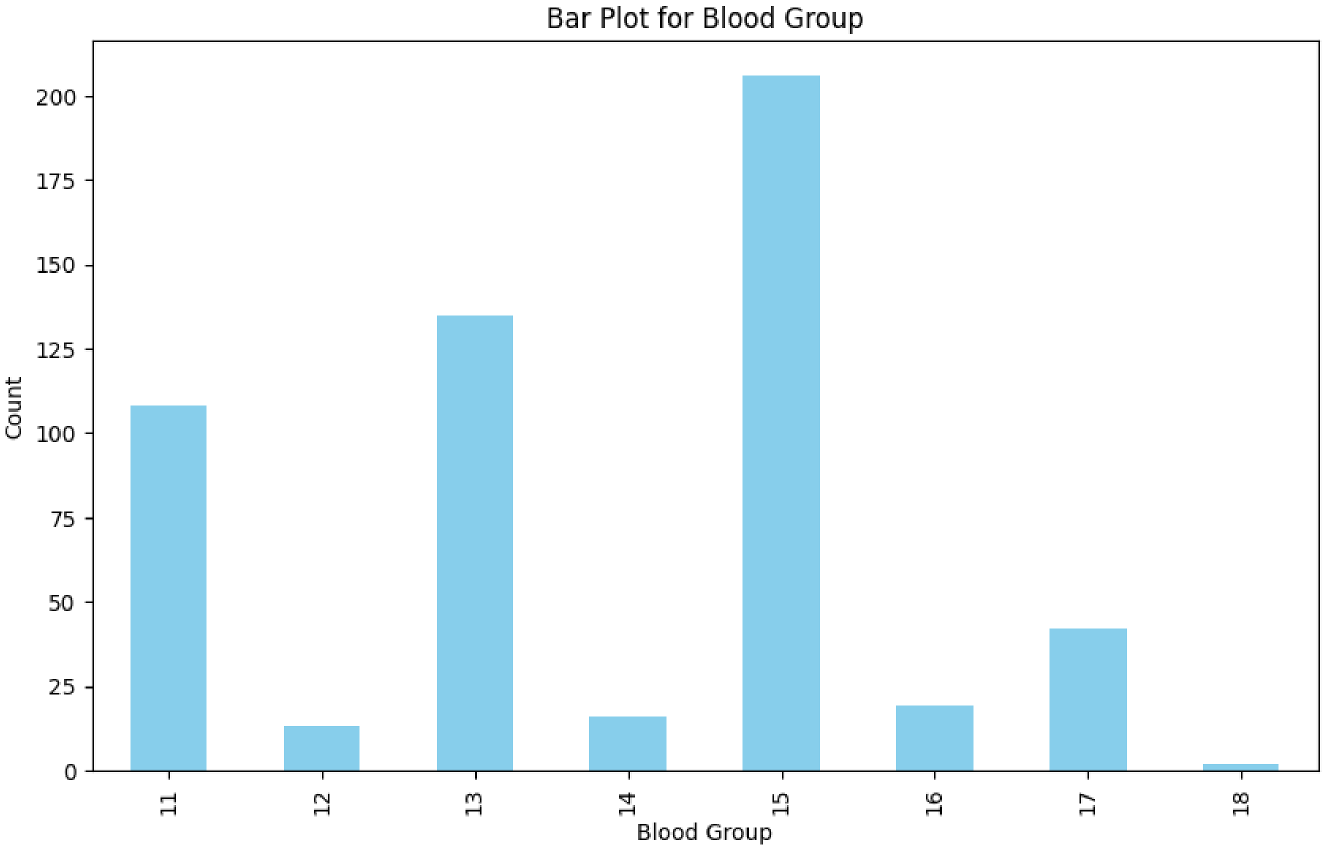

Bar Plot for PCOS (Y/N)
Count
0
50
100
150
200
250
300
350
0
1
PCOS (Y/N)

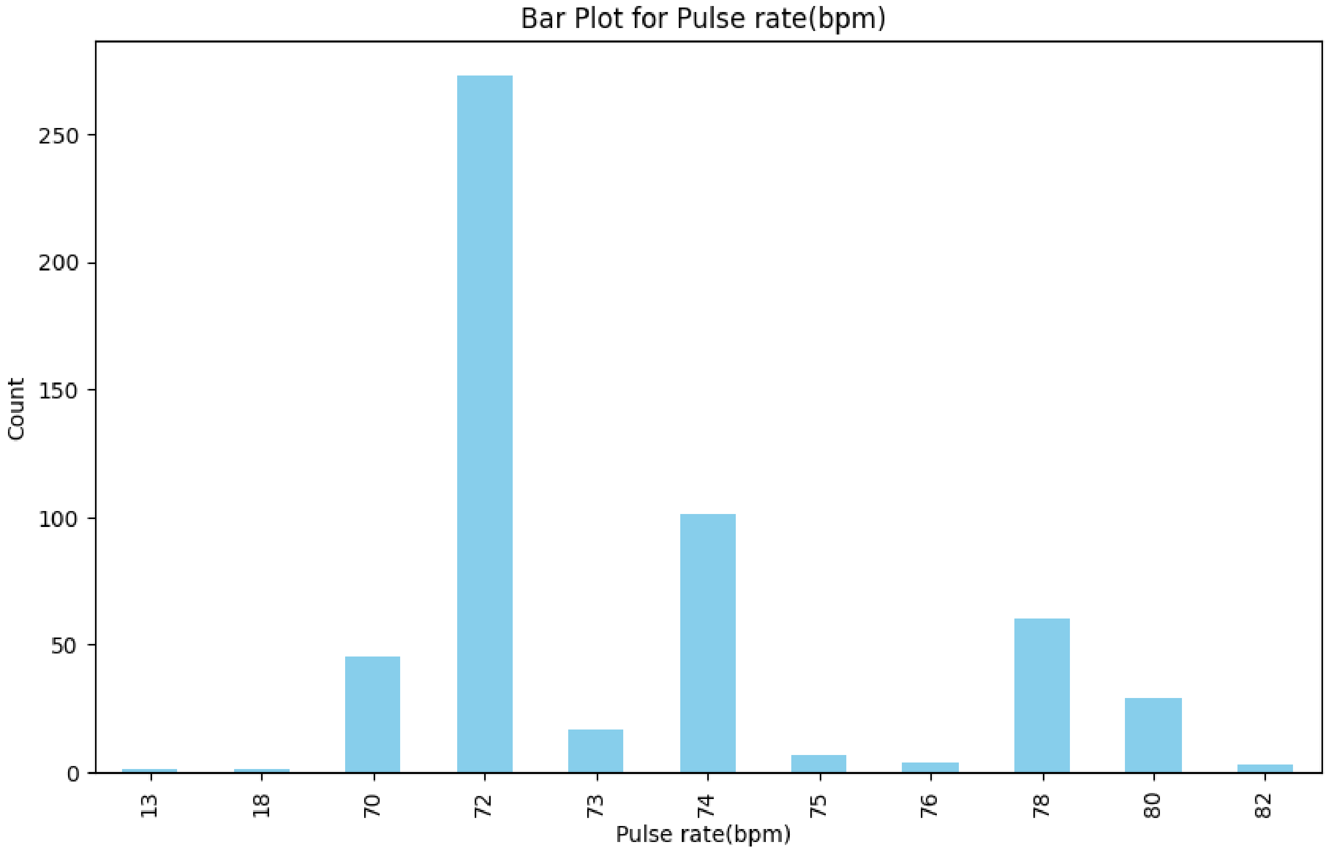

Bar Plot for Age (yrs)
Count
0
10
20
30
40
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
Age (yrs)

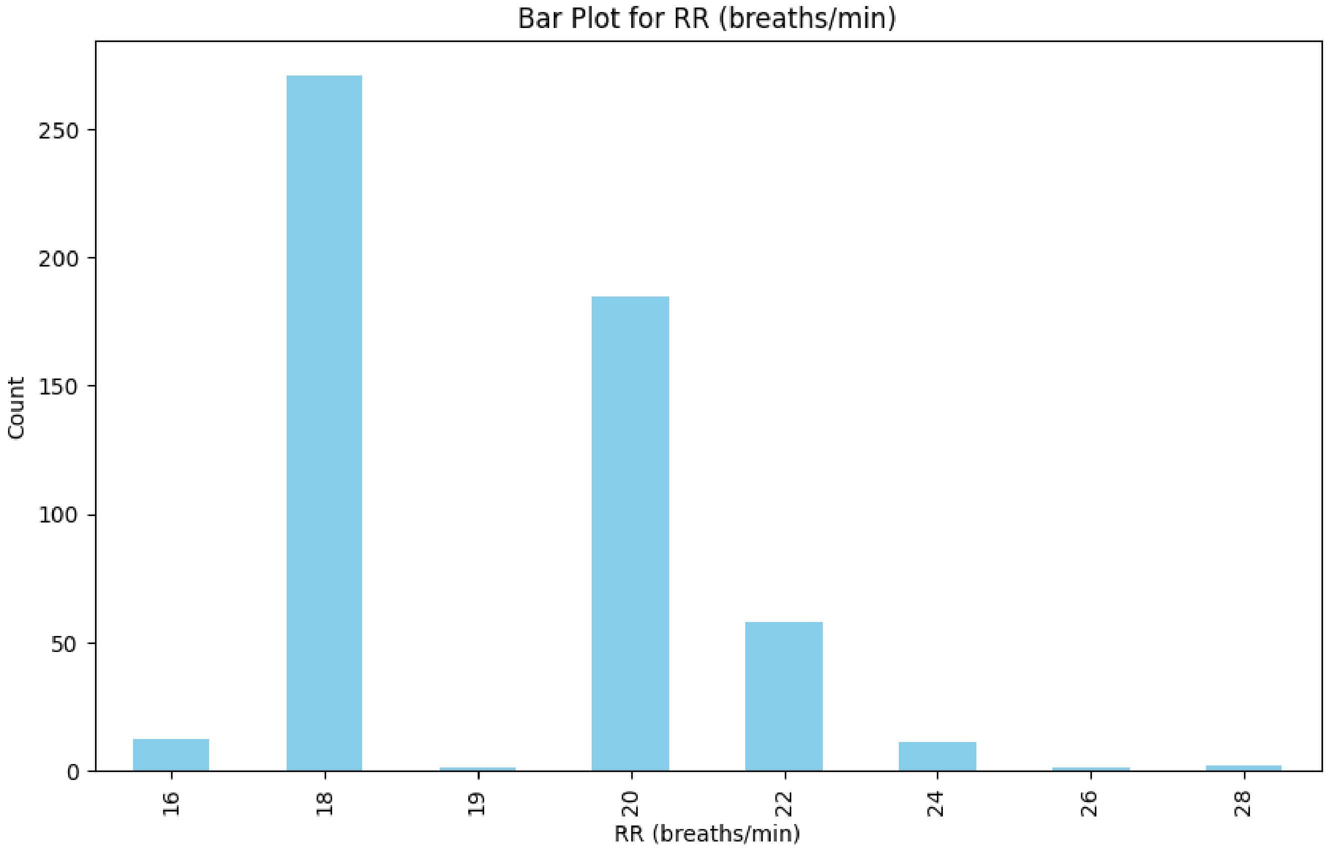

Bar Plot for Weight (Kg)
Count
0
5
10
15
20
25
30
35
31.0
108.0
Weight (Kg)

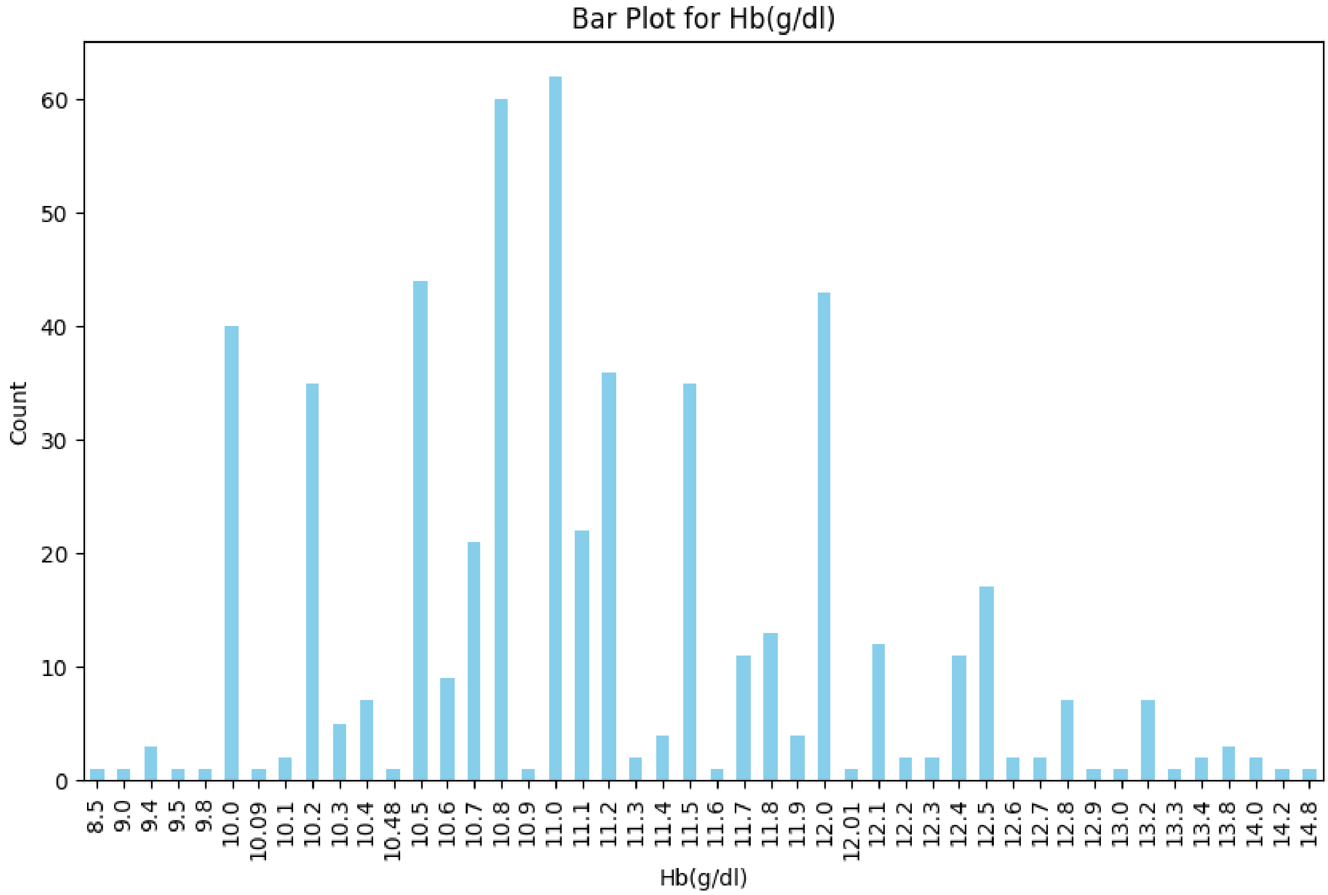

Bar Plot for Height(Cm)
Count
0
10
20
30
40
50
60
70
137.0
140.0
142.0
143.0
144.0
145.0
146.0
146.304
147.0
148.0
149.0
150.0
151.0
152.0
152.4
153.0
153.4
154.0
155.0
155.448
156.0
157.0
158.0
158.4
158.496
159.0
160.0
161.0
161.5
161.544
162.0
163.0
164.0
164.4
164.5
164.592
165.0
166.0
167.0
167.64
167.7
168.0
169.0
170.0
170.688
171.0
172.0
173.0
173.7
180.0
Height(Cm)

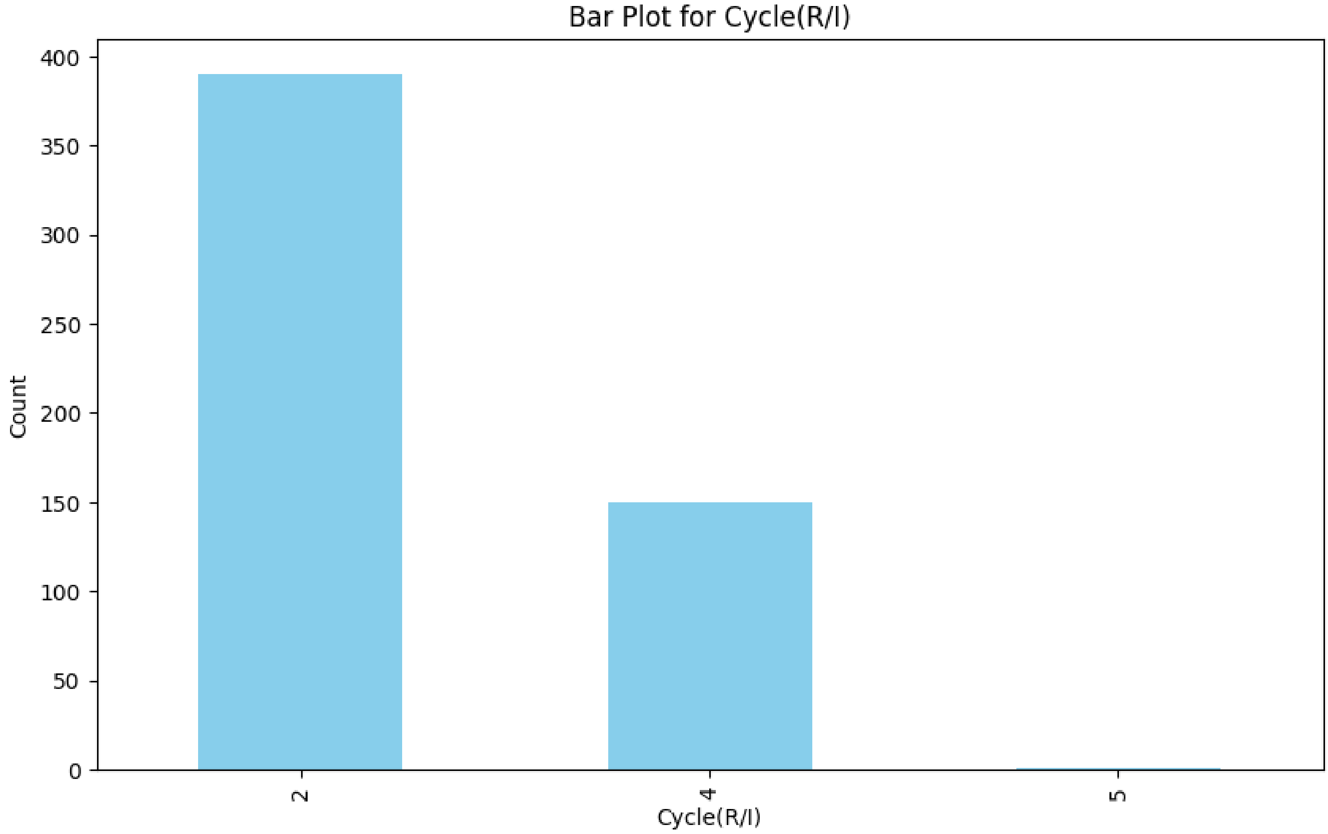

Bar Plot for BMI
Count
0
2
4
6
8
10
BMI

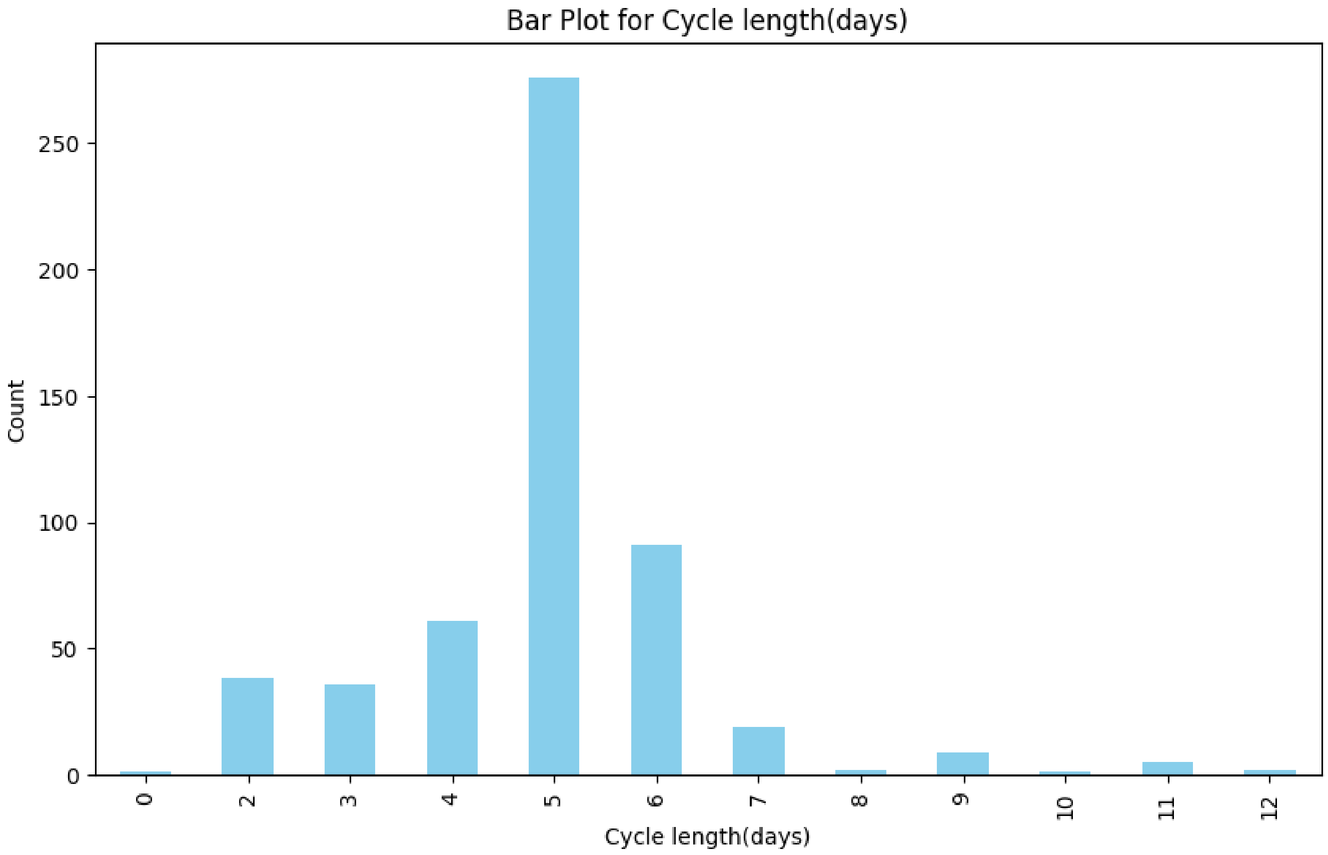

Bar Plot for Blood Group
Count
0
25
50
75
100
125
150
175
200
11
12
13
14
15
16
17
18
Blood Group

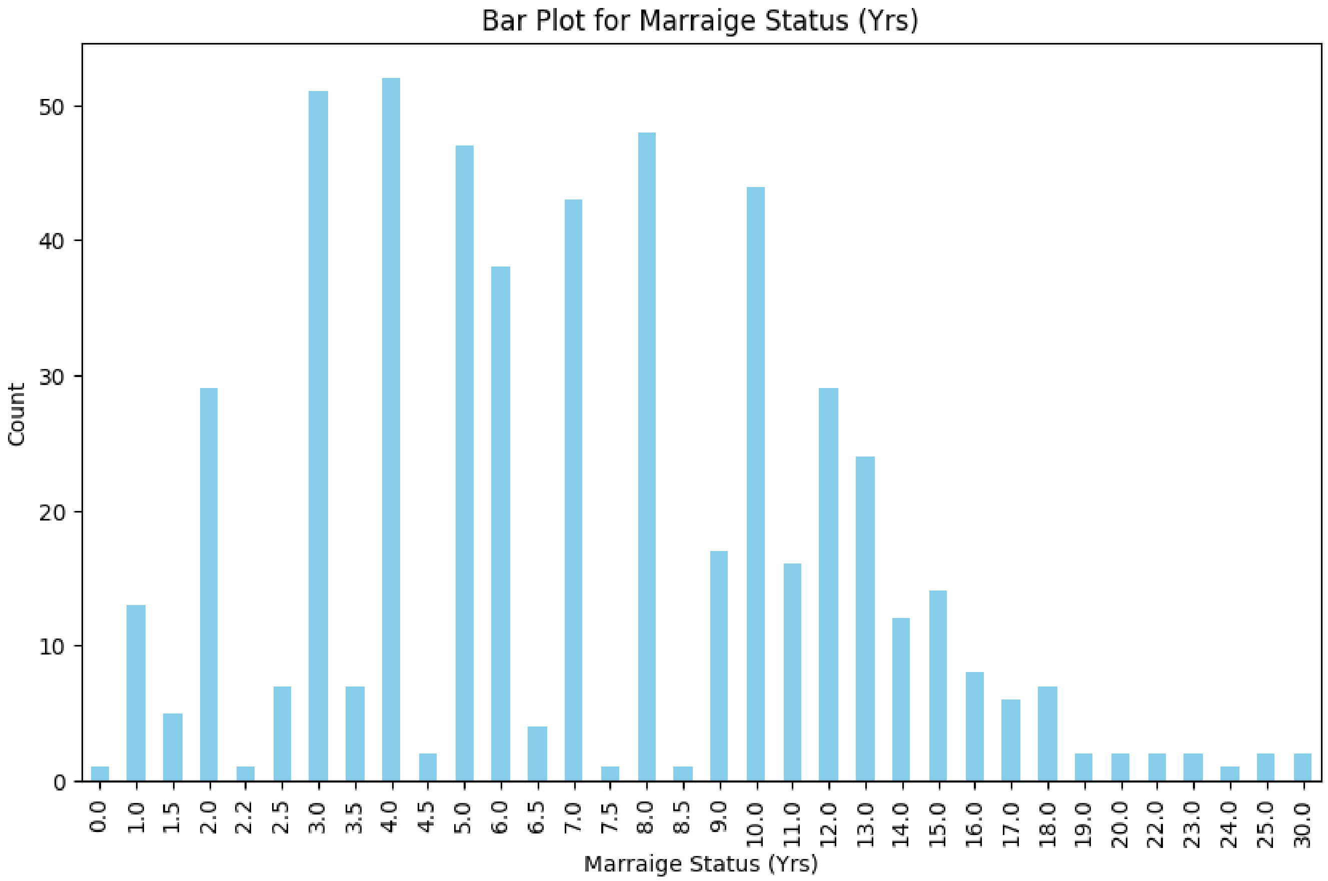

Bar Plot for Pulse rate(bpm)
Count
0
50
100
150
200
250
13
18
70
72
73
74
75
76
78
80
82
Pulse rate(bpm)

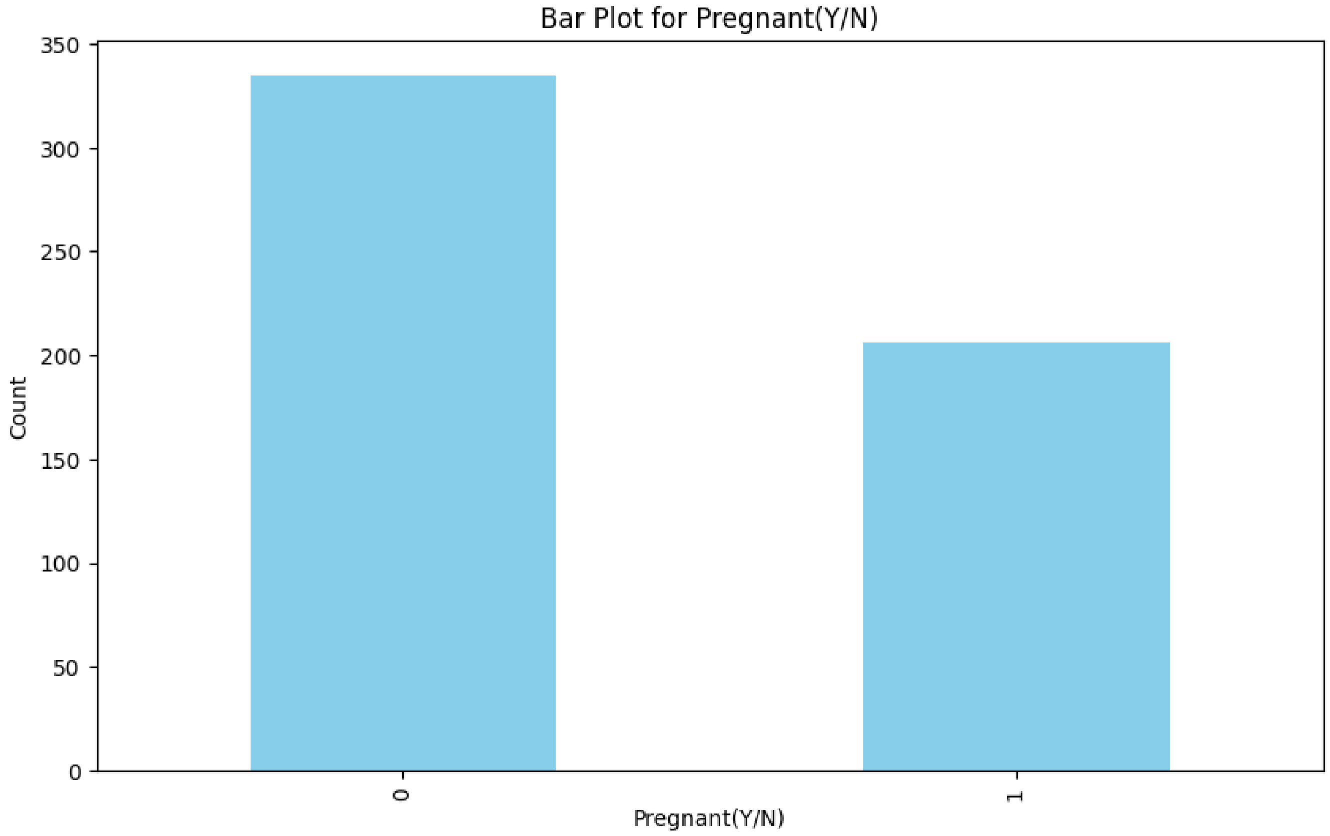

Bar Plot for RR (breaths/min)
Count
0
50
100
150
200
250
16
18
19
20
22
24
26
28
RR (breaths/min)

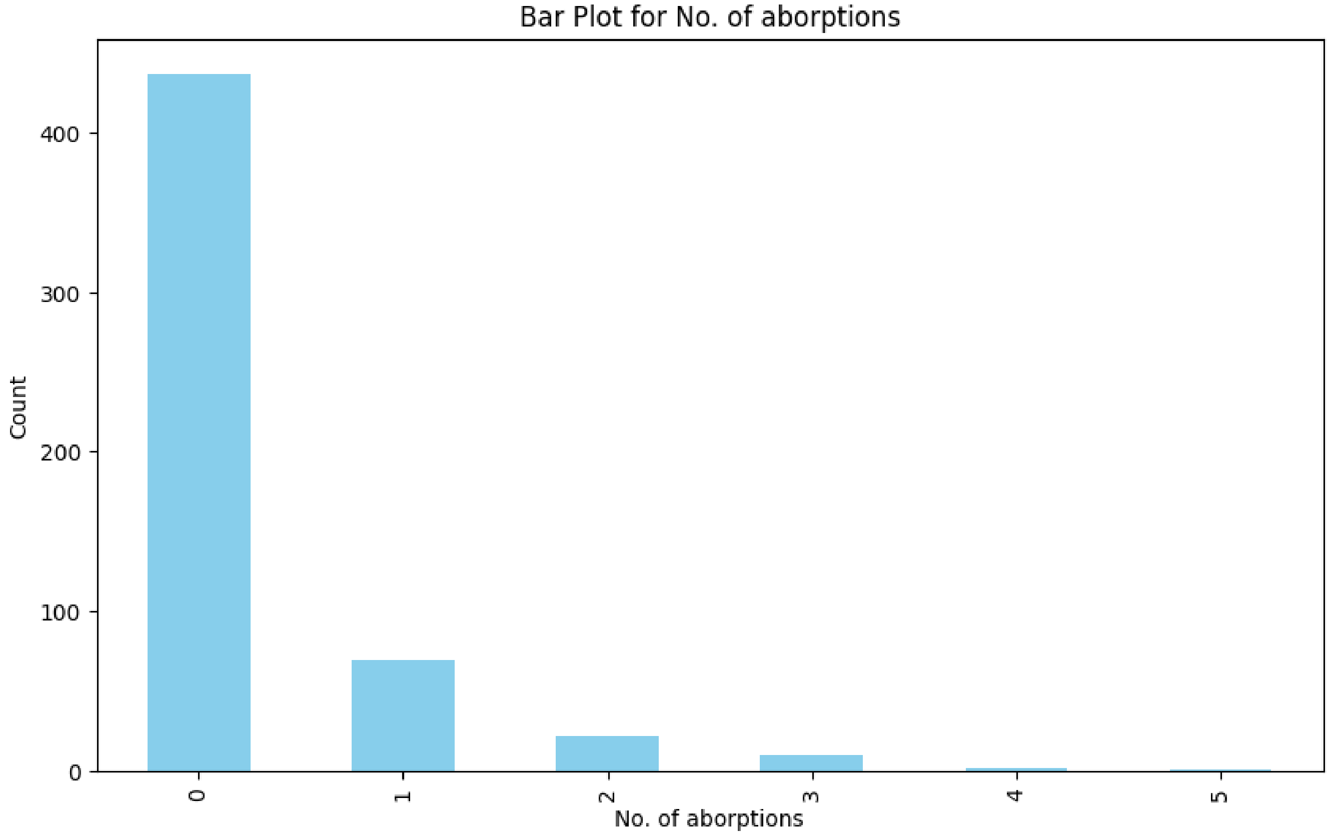

Bar Plot for Hb(g/dl)
Count
0
10
20
30
40
50
60
8.5
9.0
9.4
9.5
9.8
10.0
10.09
10.1
10.2
10.3
10.4
10.48
10.5
10.6
10.7
10.8
10.9
11.0
11.1
11.2
11.3
11.4
11.5
11.6
11.7
11.8
11.9
12.0
12.01
12.1
12.2
12.3
12.4
12.5
12.6
12.7
12.8
12.9
13.0
13.2
13.3
13.4
13.8
14.0
14.2
14.8
Hb(g/dl)

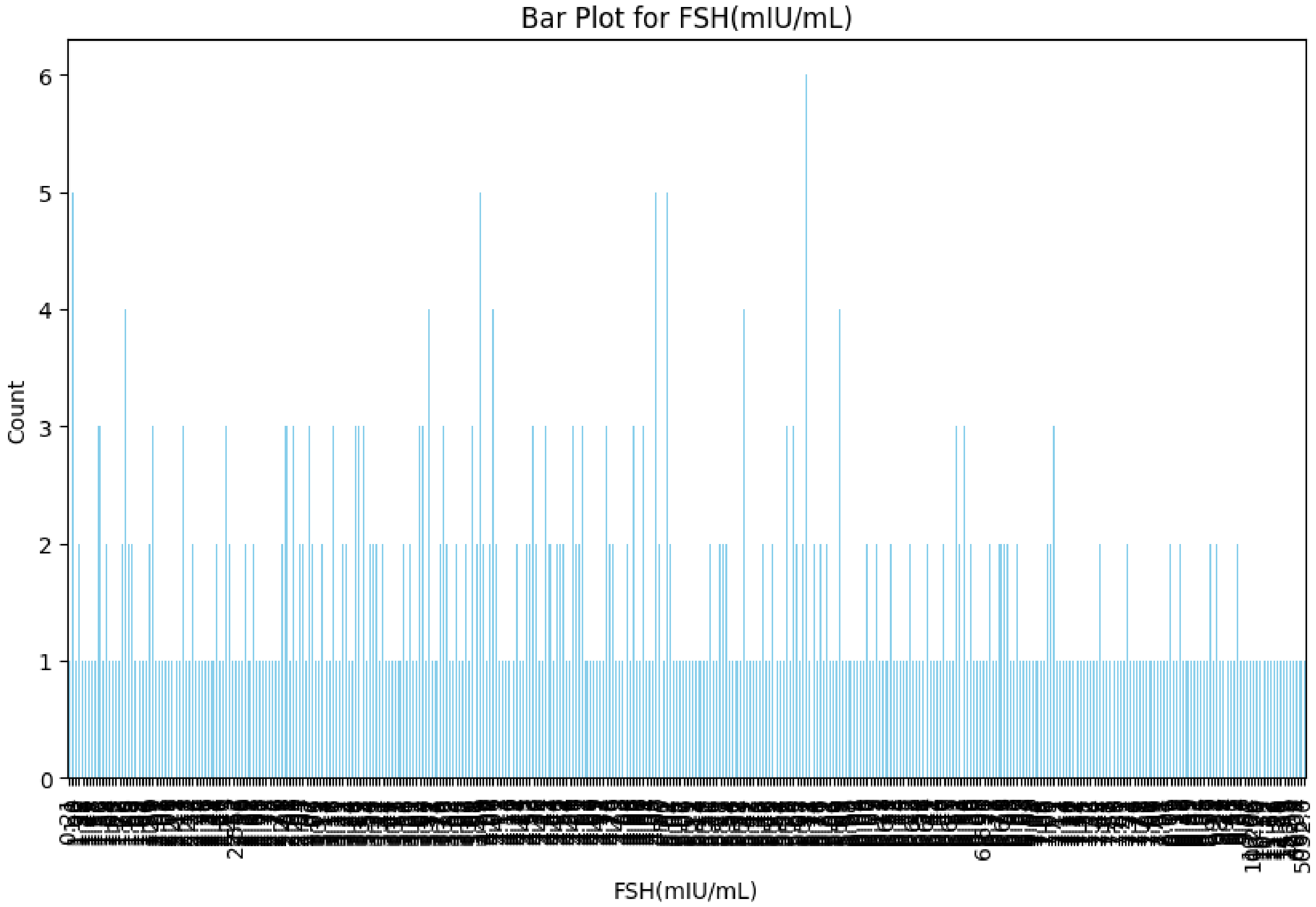

Bar Plot for Cycle(R/I)
Count
0
50
100
150
200
250
300
350
400
2
4
5
Cycle(R/I)

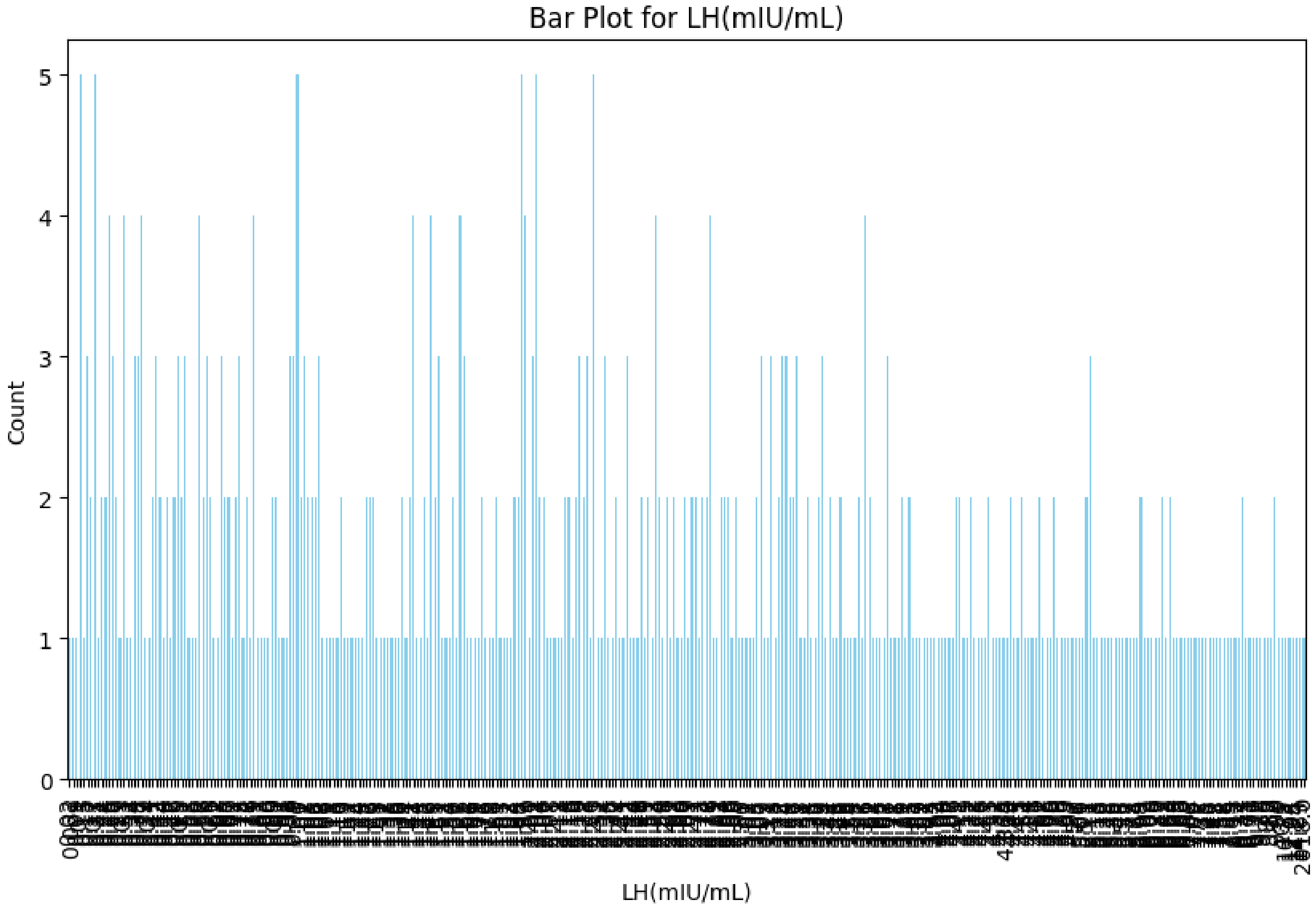

Bar Plot for Cycle length(days)
Count
0
50
100
150
200
250
0
2
3
4
5
6
7
8
9
10
11
12
Cycle length(days)

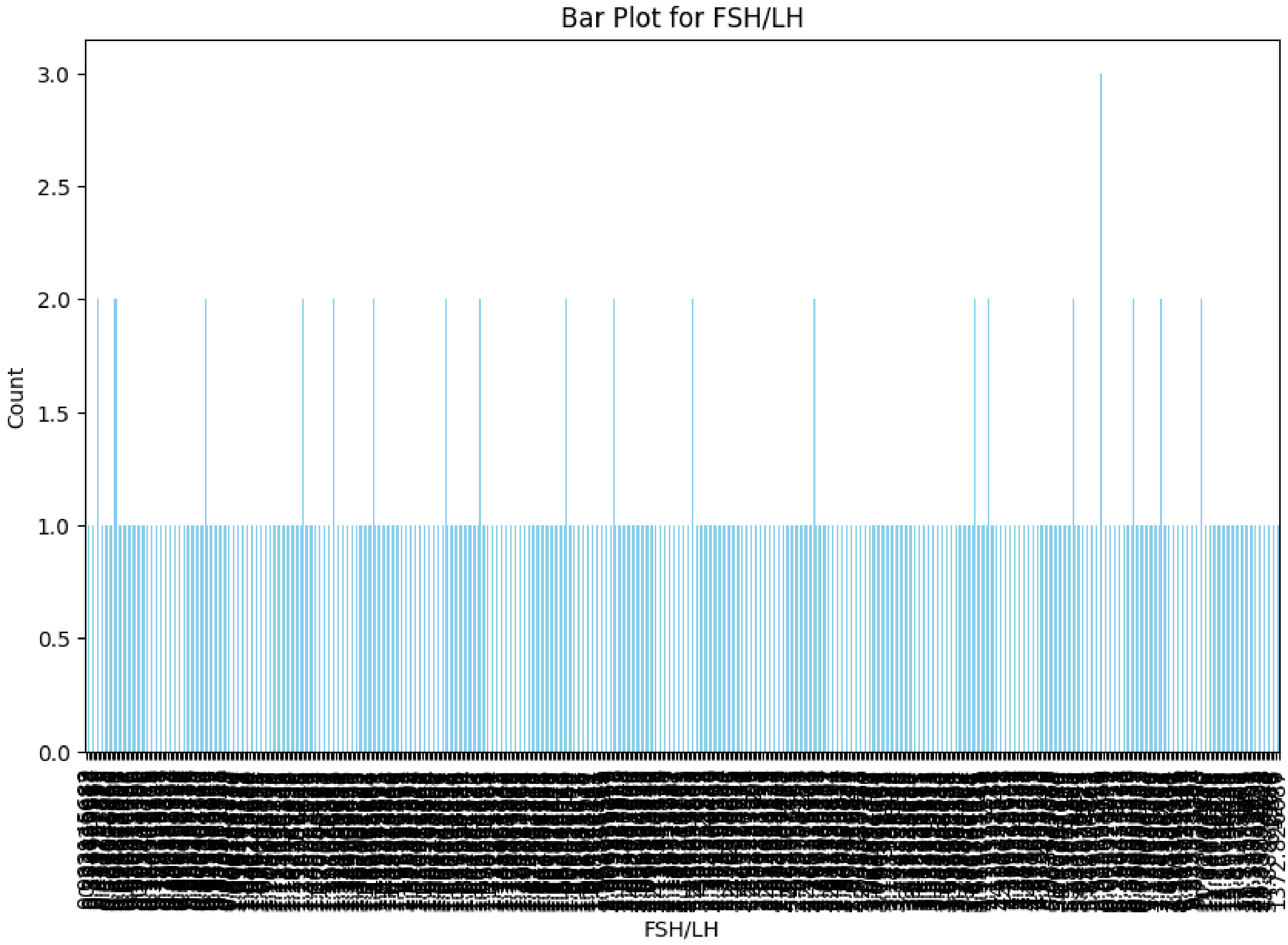

Bar Plot for Marraige Status (Yrs)
Count
0
10
20
30
40
50
0.0
1.0
1.5
2.0
2.2
2.5
3.0
3.5
4.0
4.5
5.0
6.0
6.5
7.0
7.5
8.0
8.5
9.0
10.0
11.0
12.0
13.0
14.0
15.0
16.0
17.0
18.0
19.0
20.0
22.0
23.0
24.0
25.0
30.0
Marraige Status (Yrs)

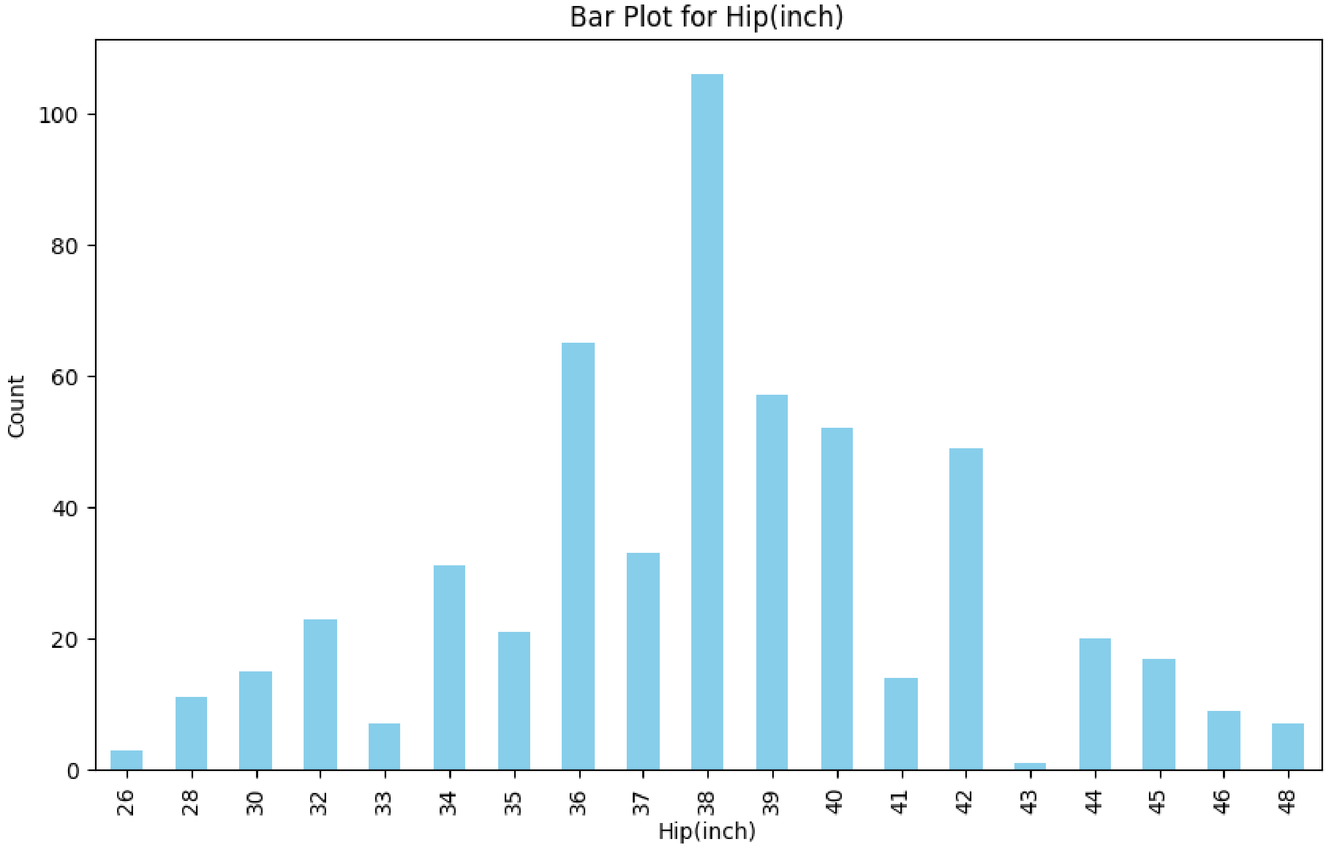

Bar Plot for Pregnant(Y/N)
Count
350
300
250
200
150
100
50
0
0
1
Pregnant(Y/N)

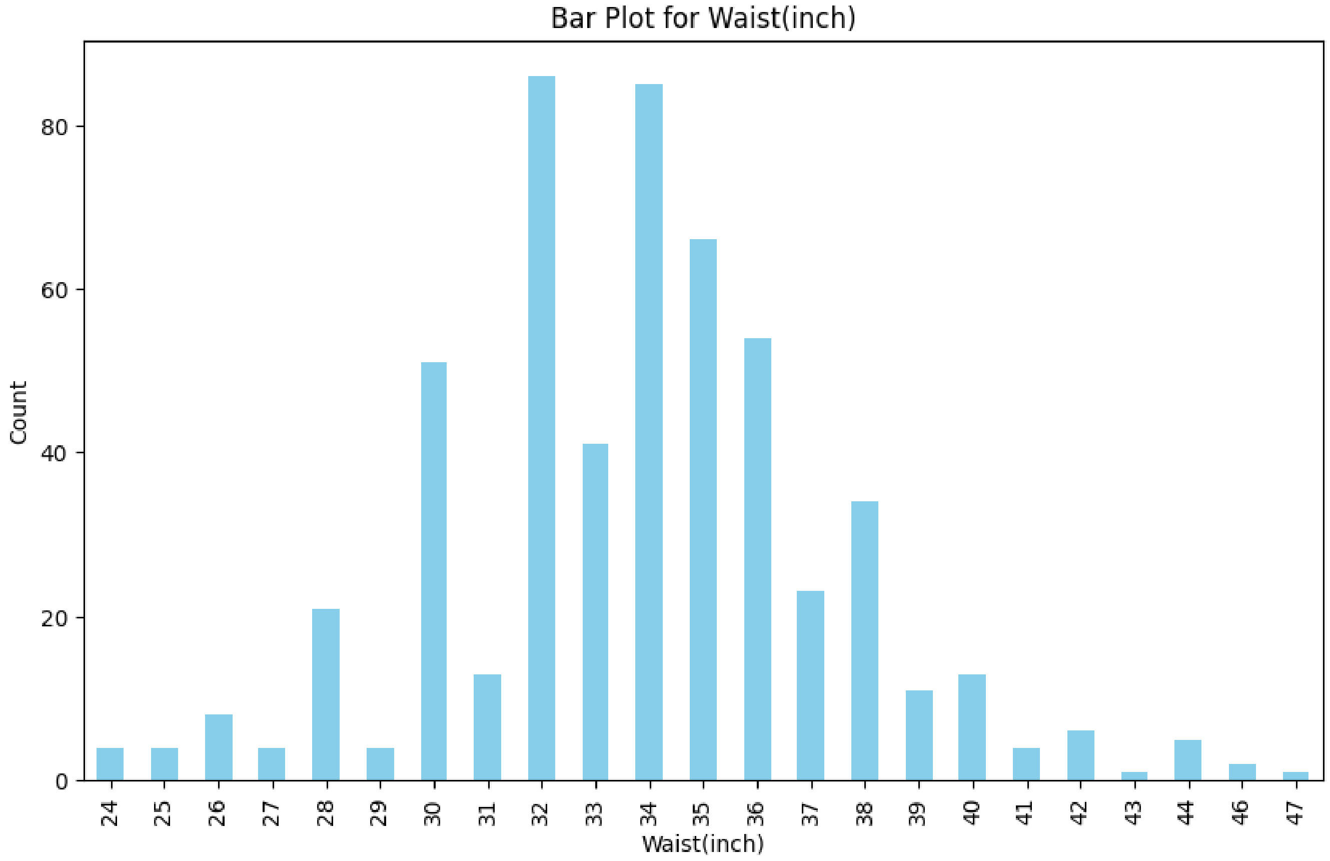

Bar Plot for No. of aborptions
Count
400
300
200
100
0
0
1
2
3
4
5
No. of aborptions

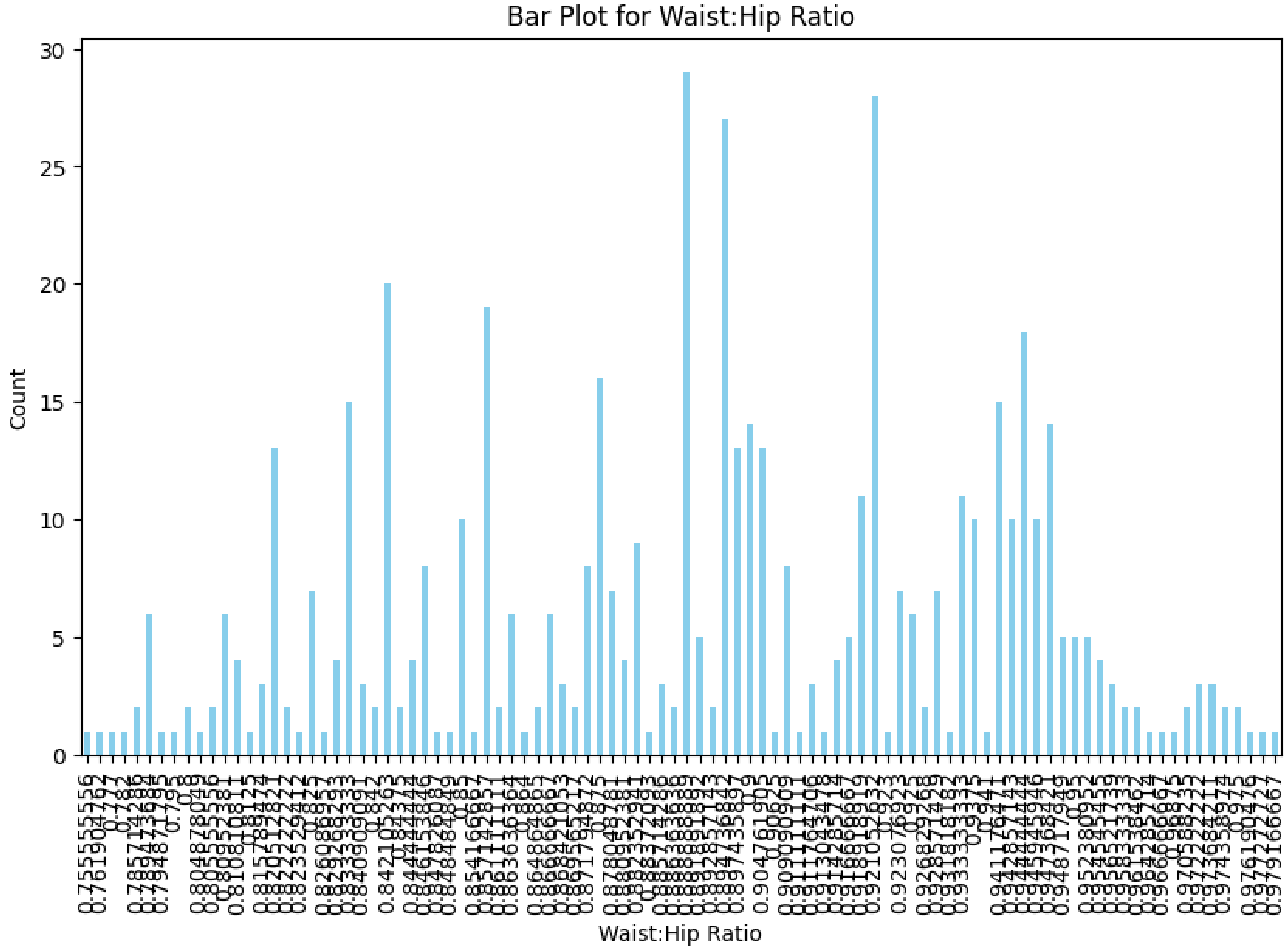

Bar Plot for FSH(mIU/mL)
Count
0
1
2
3
4
5
6
FSH(mIU/mL)
2
6

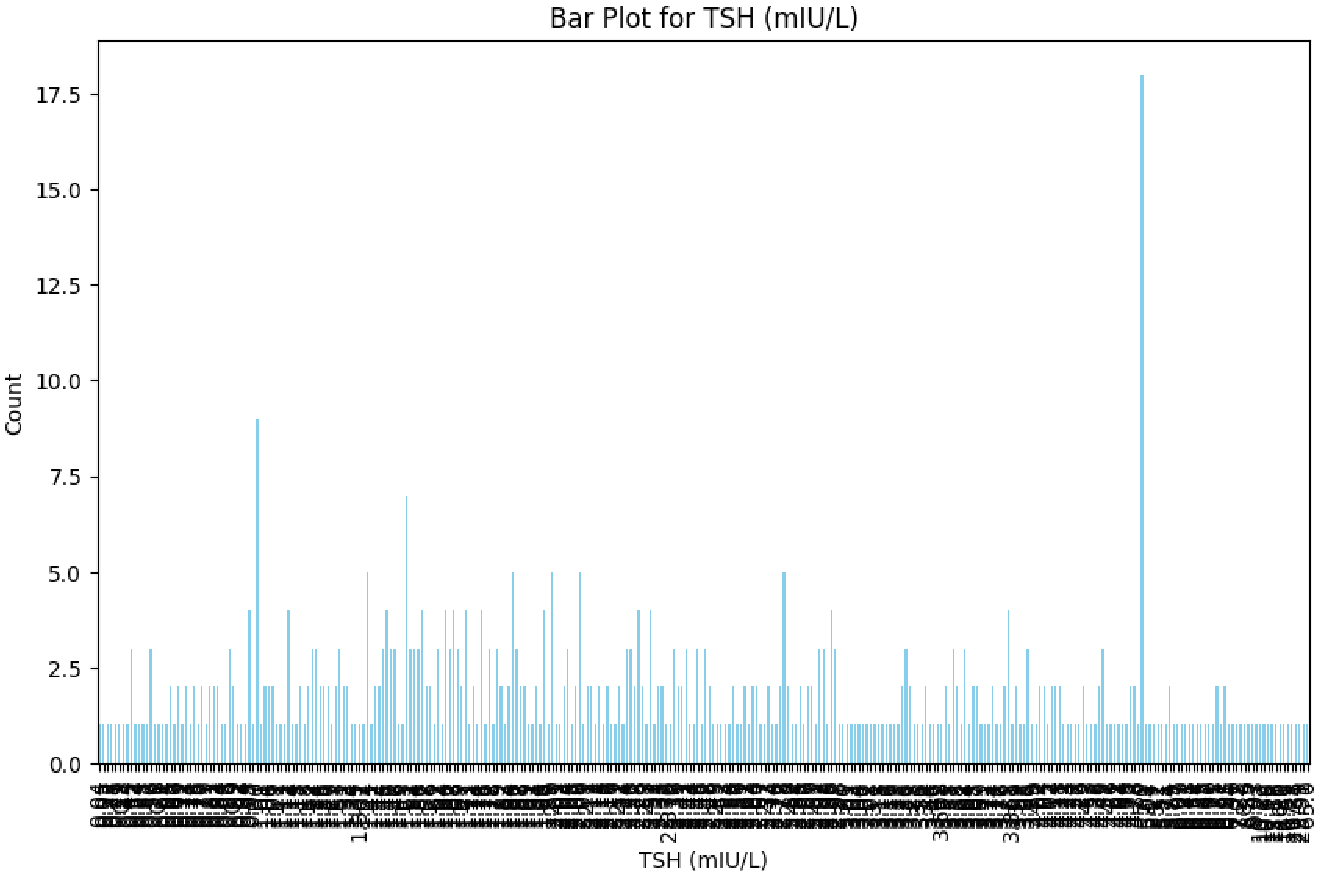

Bar Plot for LH(mIU/mL)
Count
0
1
2
3
4
5
LH(mIU/mL)
4

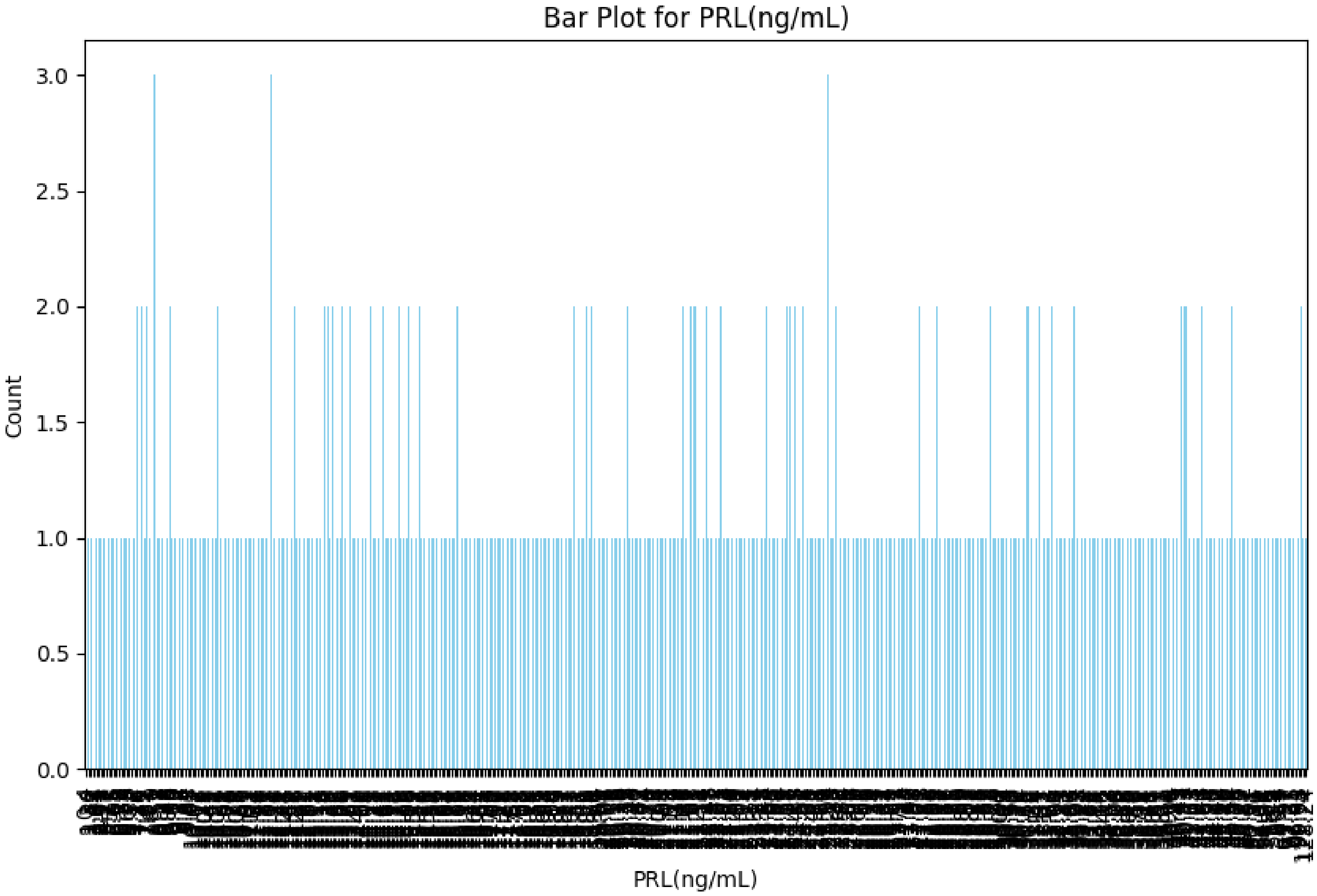

Bar Plot for FSH/LH
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Count
1372.826087
FSH/LH

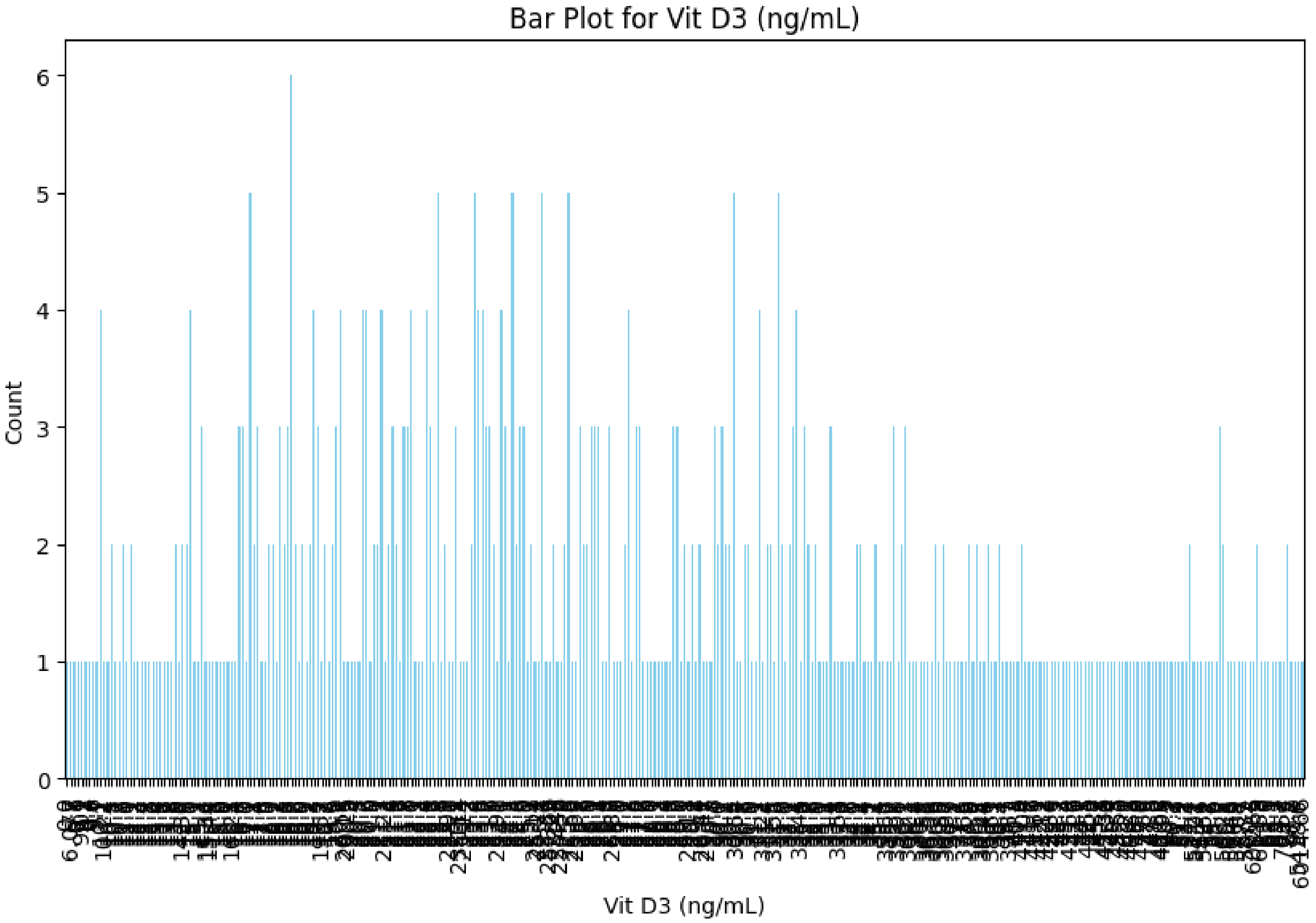

Bar Plot for Hip(inch)
100
80
60
40
20
0
Count
26
28
30
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
48
Hip(inch)

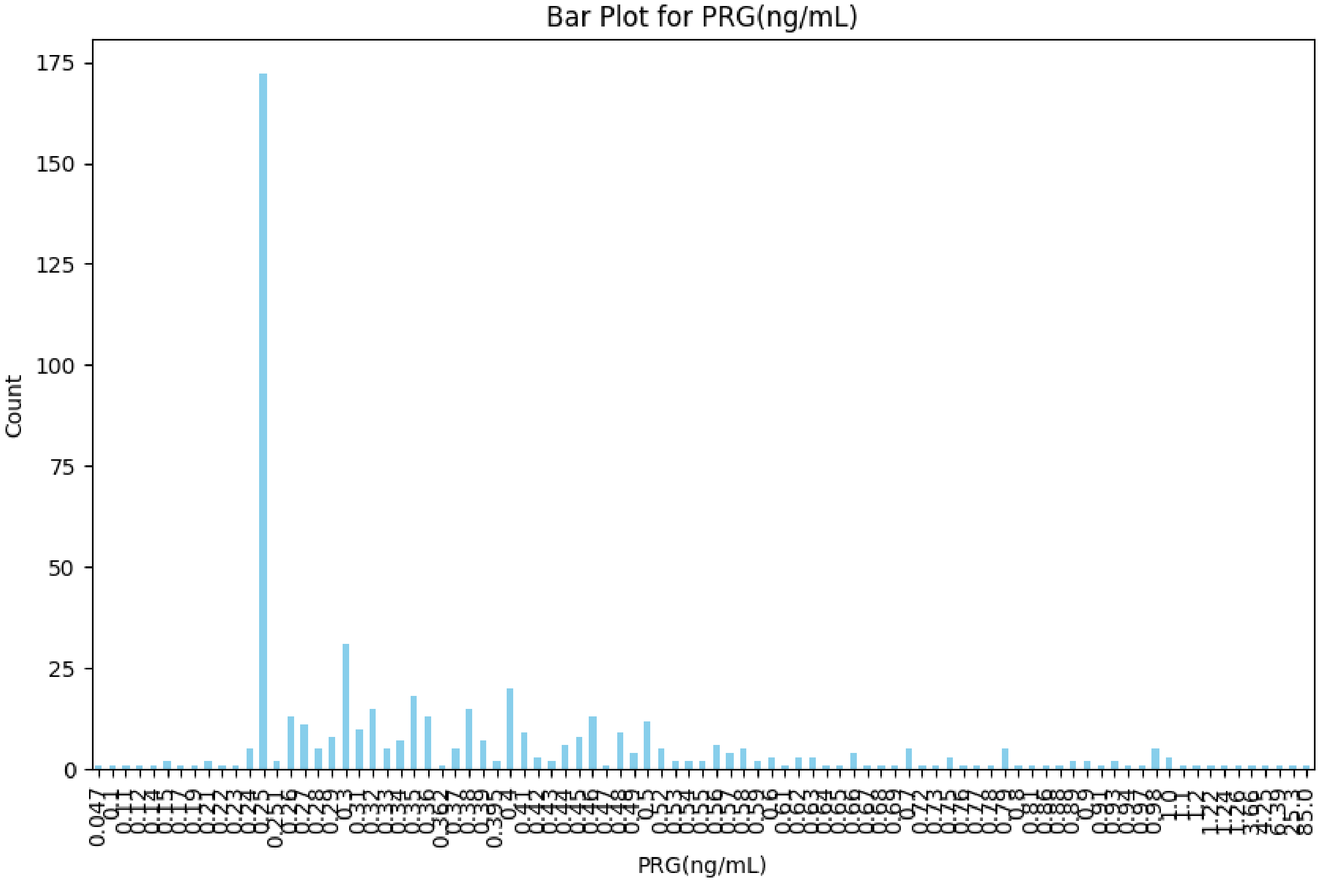

Bar Plot for Waist(inch)
Count
0
20
40
60
80
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
46
47
Waist(inch)

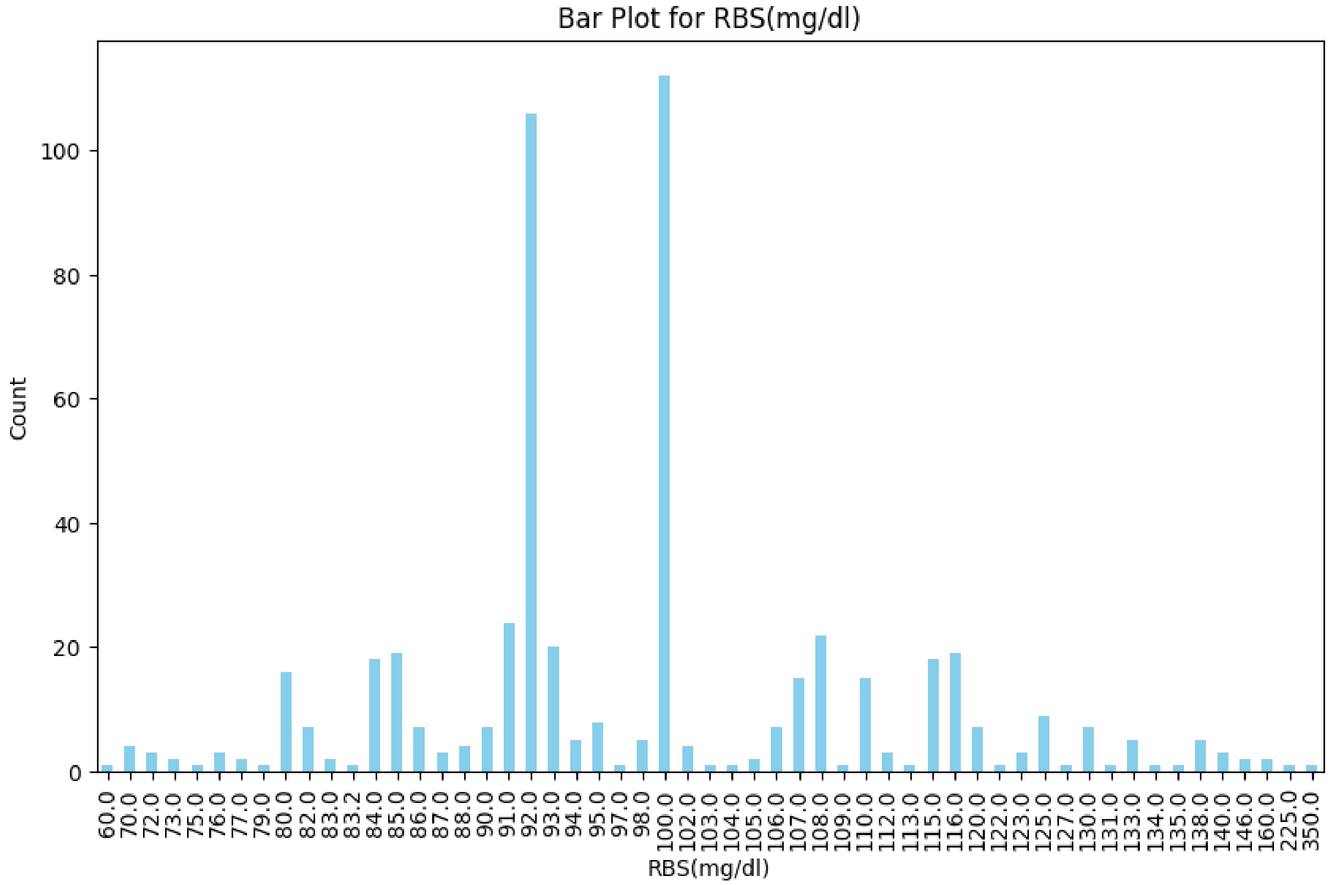

Bar Plot for Waist:Hip Ratio
Count
0
5
10
15
20
25
30
Waist:Hip Ratio

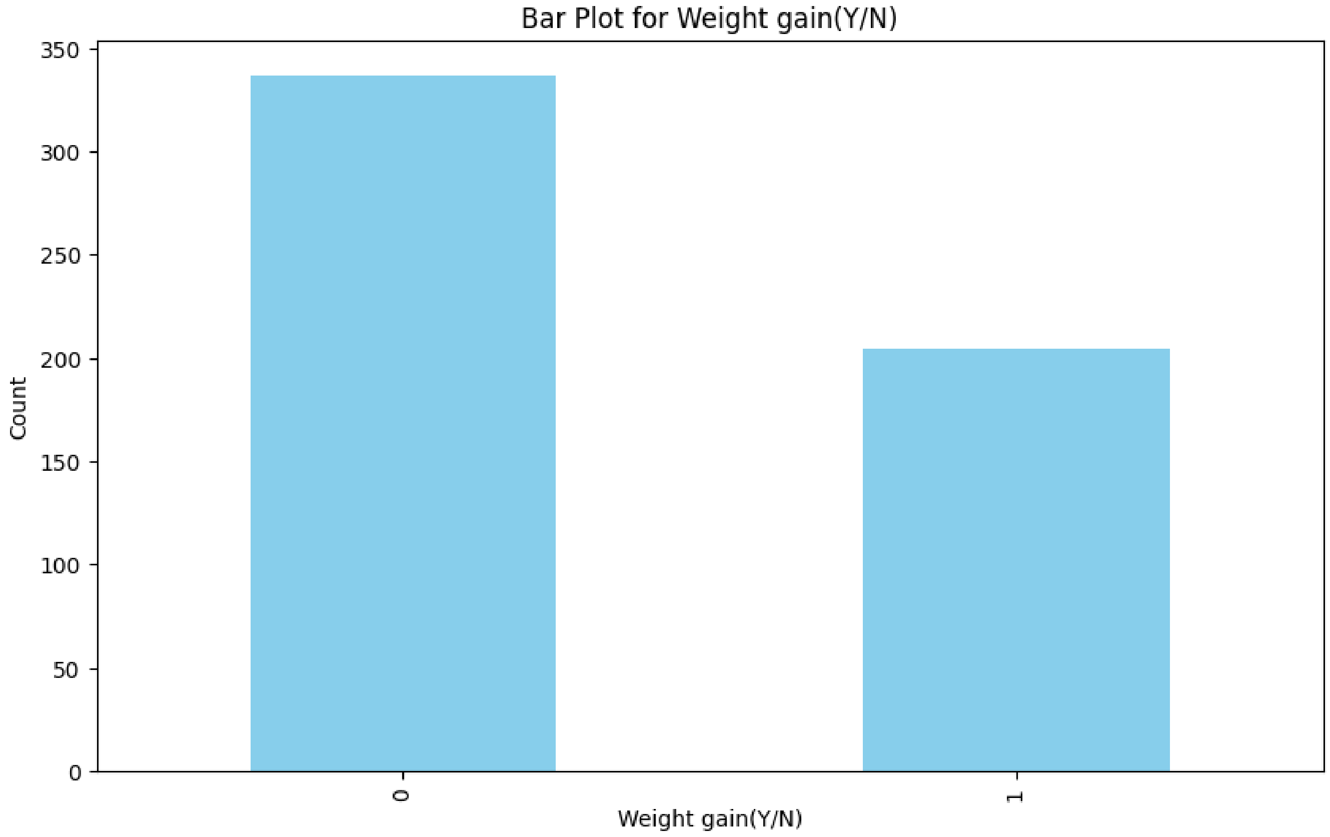

Bar Plot for TSH (mIU/L)
Count
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
TSH (mIU/L)

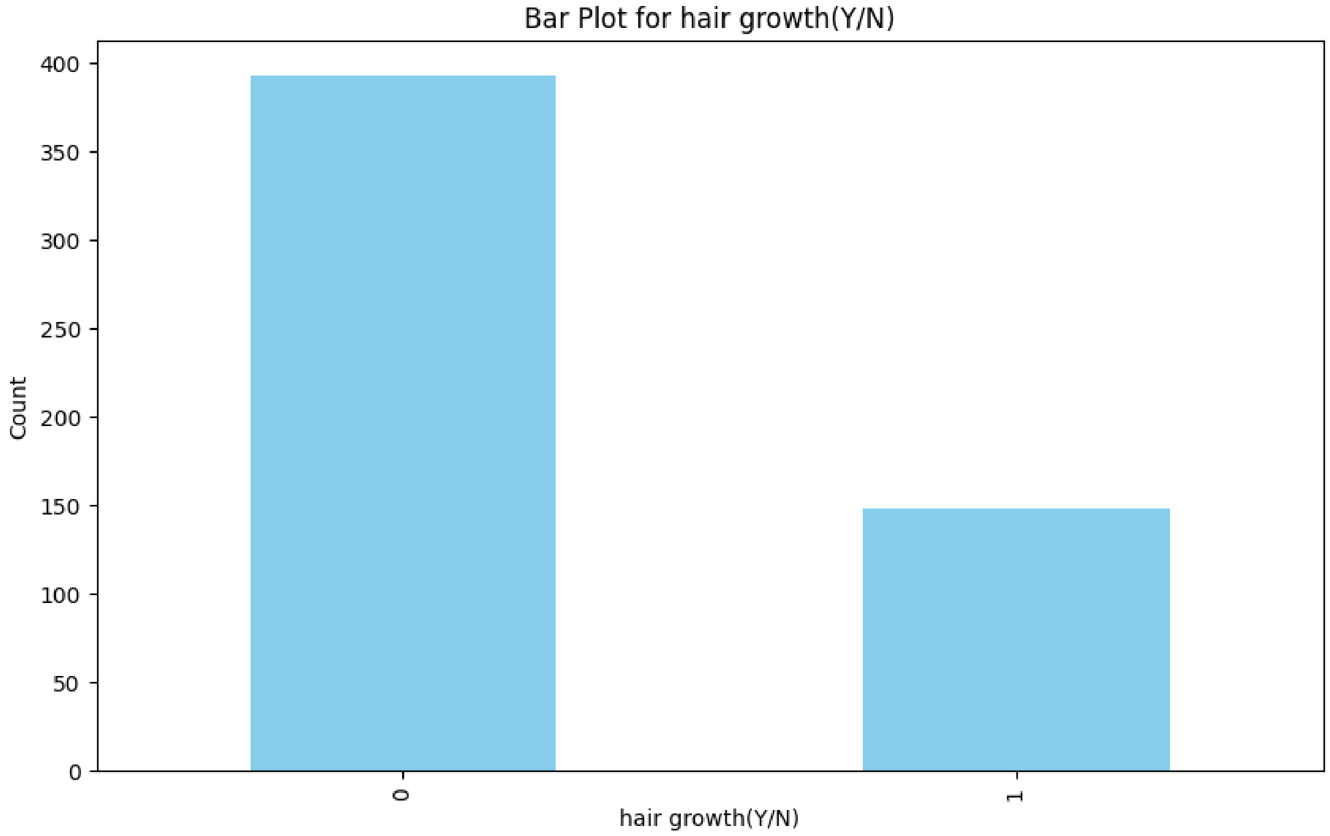

Bar Plot for PRL(ng/mL)
Count
3.0
2.5
2.0
1.5
1.0
0.5
0.0
PRL(ng/mL)


Bar Plot for Vit D3 (ng/mL)
Count
0
1
2
3
4
5
6
Vit D3 (ng/mL)

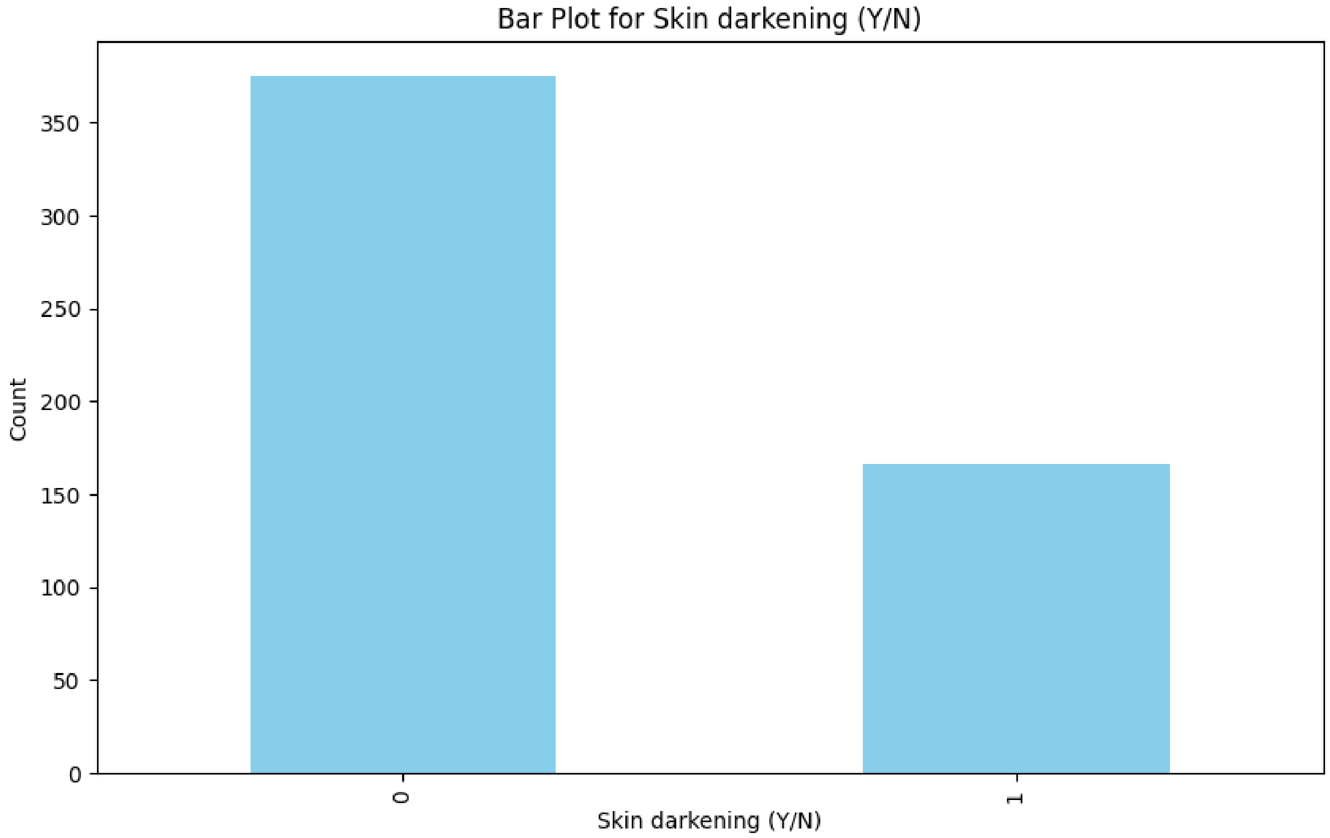

Bar Plot for PRG(ng/mL)
Count
0
25
50
75
100
125
150
175
0.047
0.1
0.11
0.12
0.14
0.15
0.17
0.19
0.21
0.22
0.23
0.24
0.25
0.251
0.26
0.27
0.28
0.29
0.3
0.31
0.32
0.33
0.34
0.35
0.36
0.362
0.37
0.38
0.39
0.395
0.4
0.41
0.42
0.43
0.44
0.45
0.46
0.47
0.48
0.49
0.5
0.52
0.53
0.54
0.55
0.56
0.57
0.58
0.59
0.6
0.61
0.62
0.63
0.64
0.65
0.66
0.67
0.68
0.69
0.7
0.72
0.73
0.75
0.76
0.77
0.78
0.79
0.8
0.81
0.86
0.88
0.89
0.9
0.91
0.93
0.94
0.97
0.98
1.0
1.1
1.2
1.22
1.24
1.26
3.26
4.25
6.39
7.3
85.0
PRG(ng/mL)


Bar Plot for RBS(mg/dl)
Count
0
20
40
60
80
100
60.0
70.0
72.0
73.0
75.0
76.0
77.0
79.0
80.0
82.0
83.0
83.2
84.0
85.0
86.0
87.0
88.0
90.0
91.0
92.0
93.0
94.0
95.0
97.0
98.0
100.0
102.0
103.0
104.0
105.0
106.0
107.0
108.0
109.0
110.0
112.0
113.0
115.0
116.0
120.0
122.0
123.0
125.0
127.0
130.0
131.0
133.0
134.0
135.0
138.0
140.0
146.0
160.0
225.0
350.0
RBS(mg/dl)

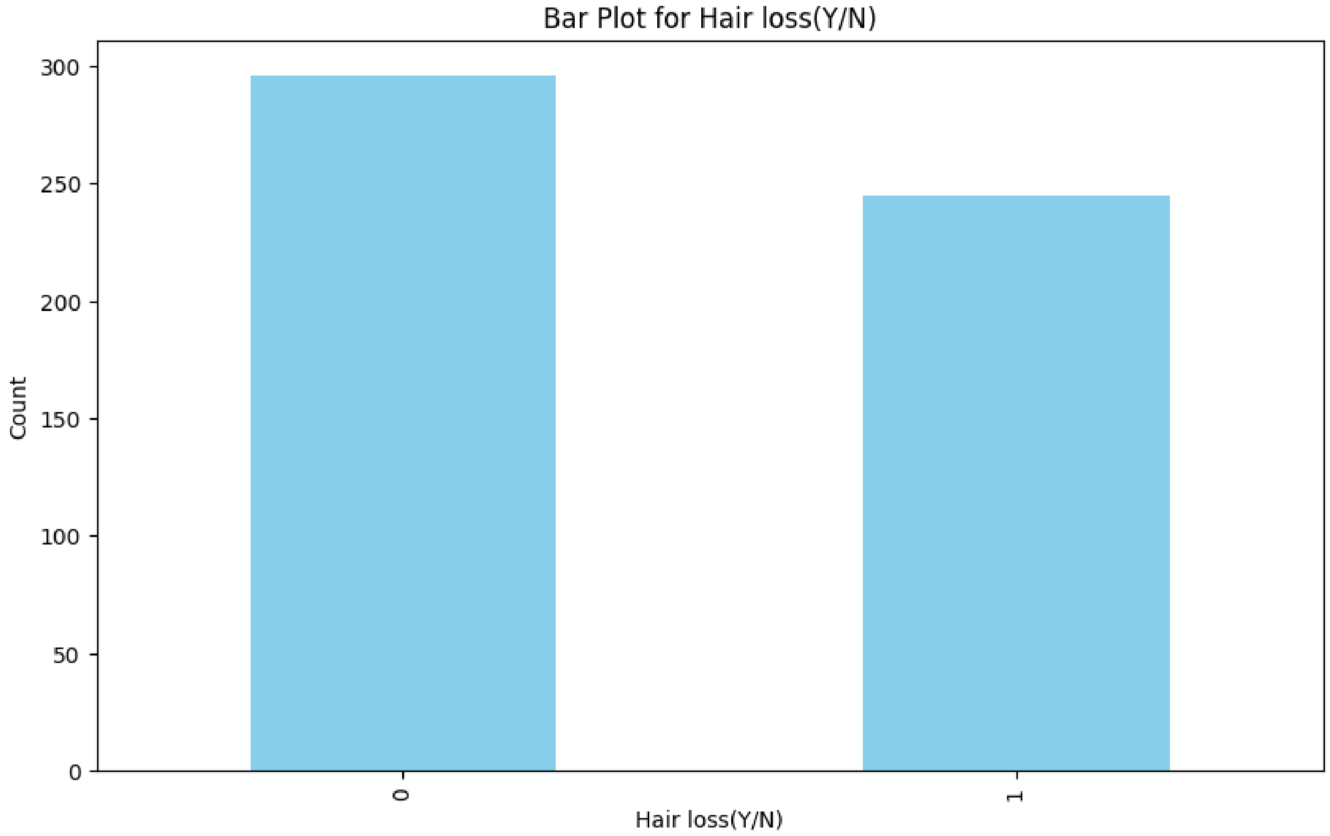

Bar Plot for Weight gain(Y/N)
Count
0
50
100
150
200
250
300
350
0
1
Weight gain(Y/N)

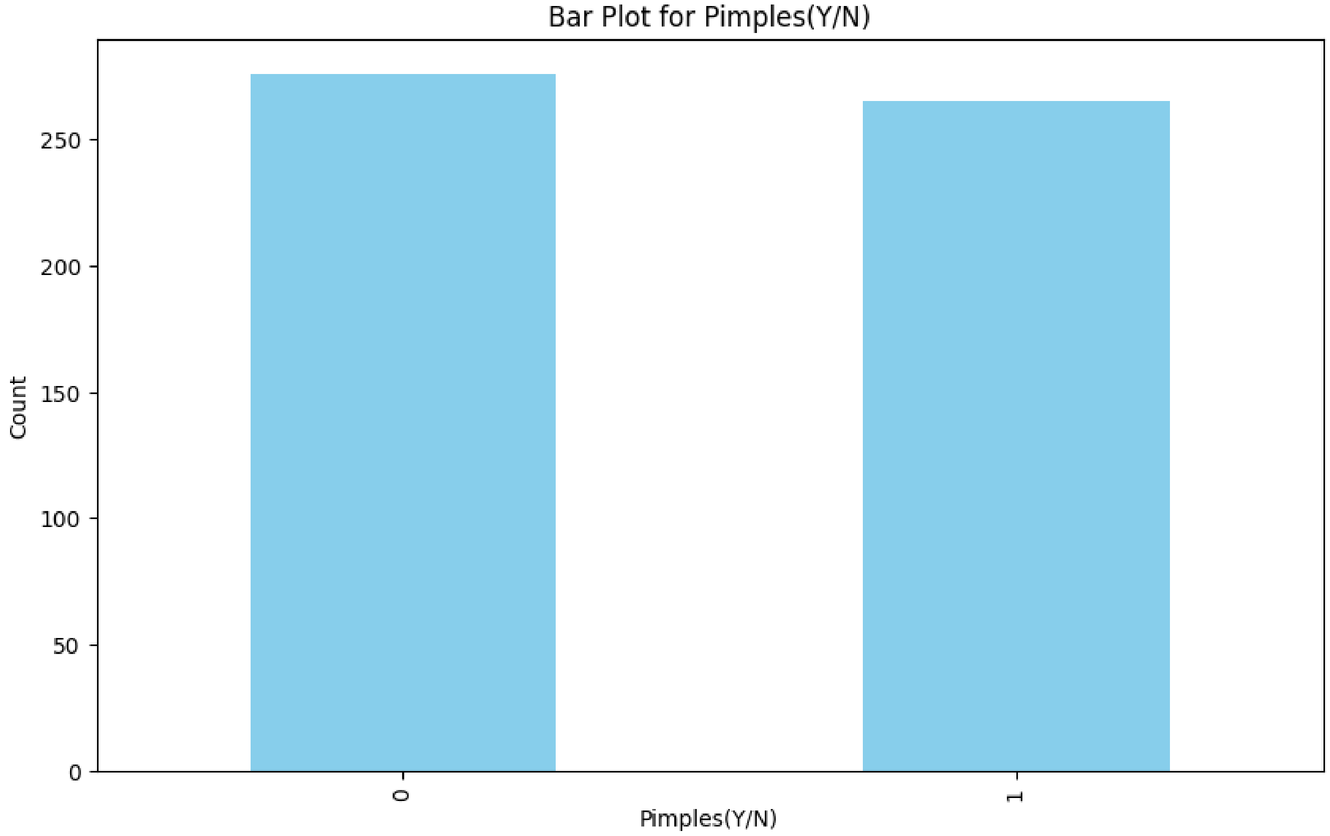


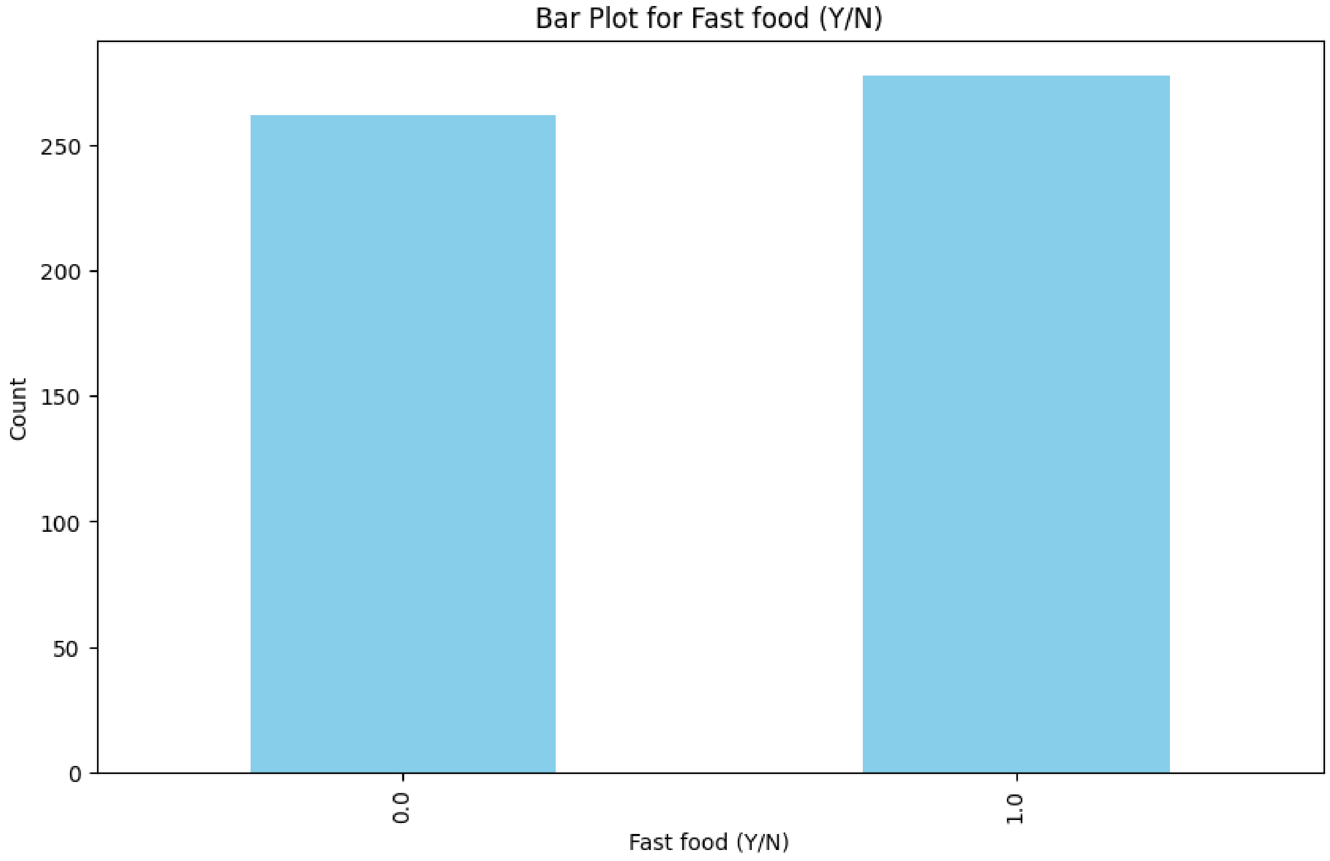
Bar Plot for hair growth(Y/N)

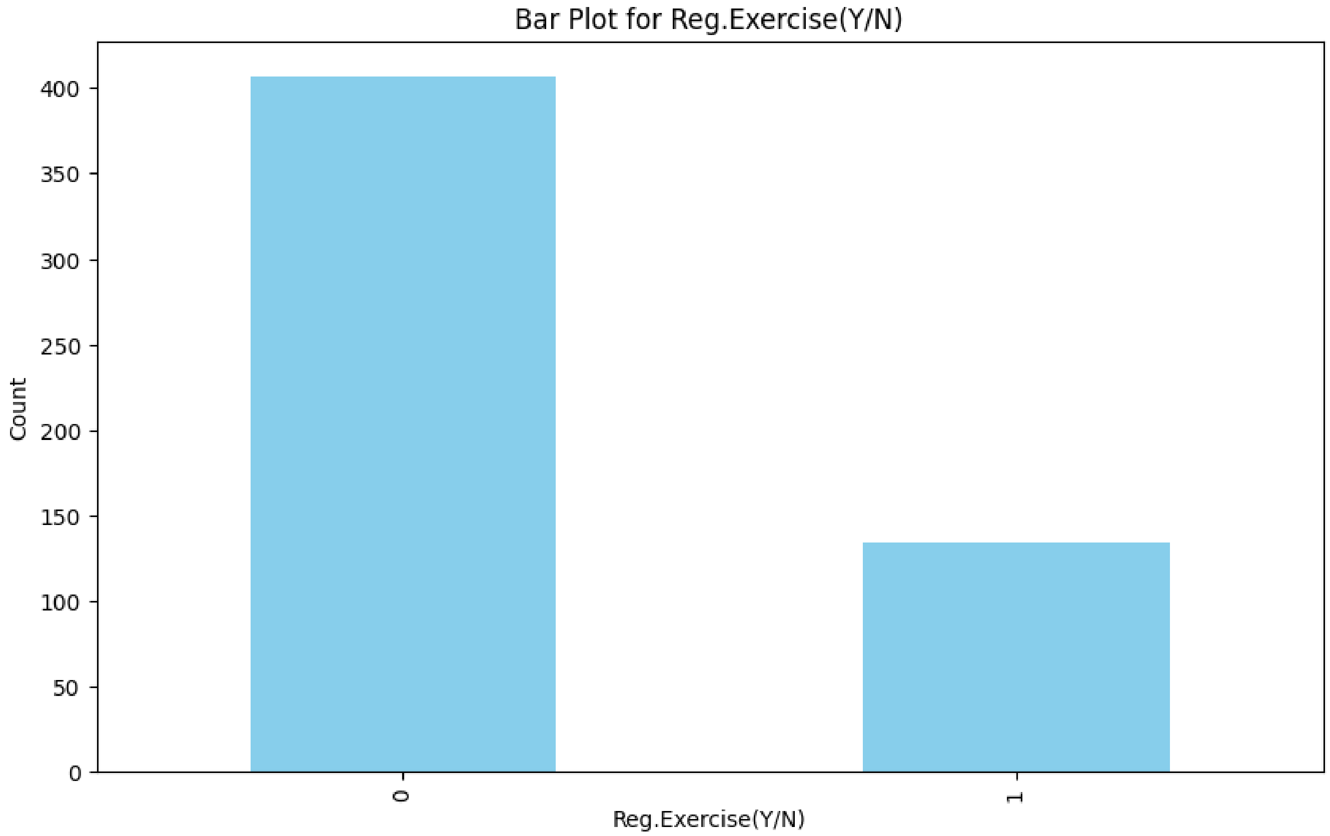


Bar Plot for Skin darkening (Y/N)

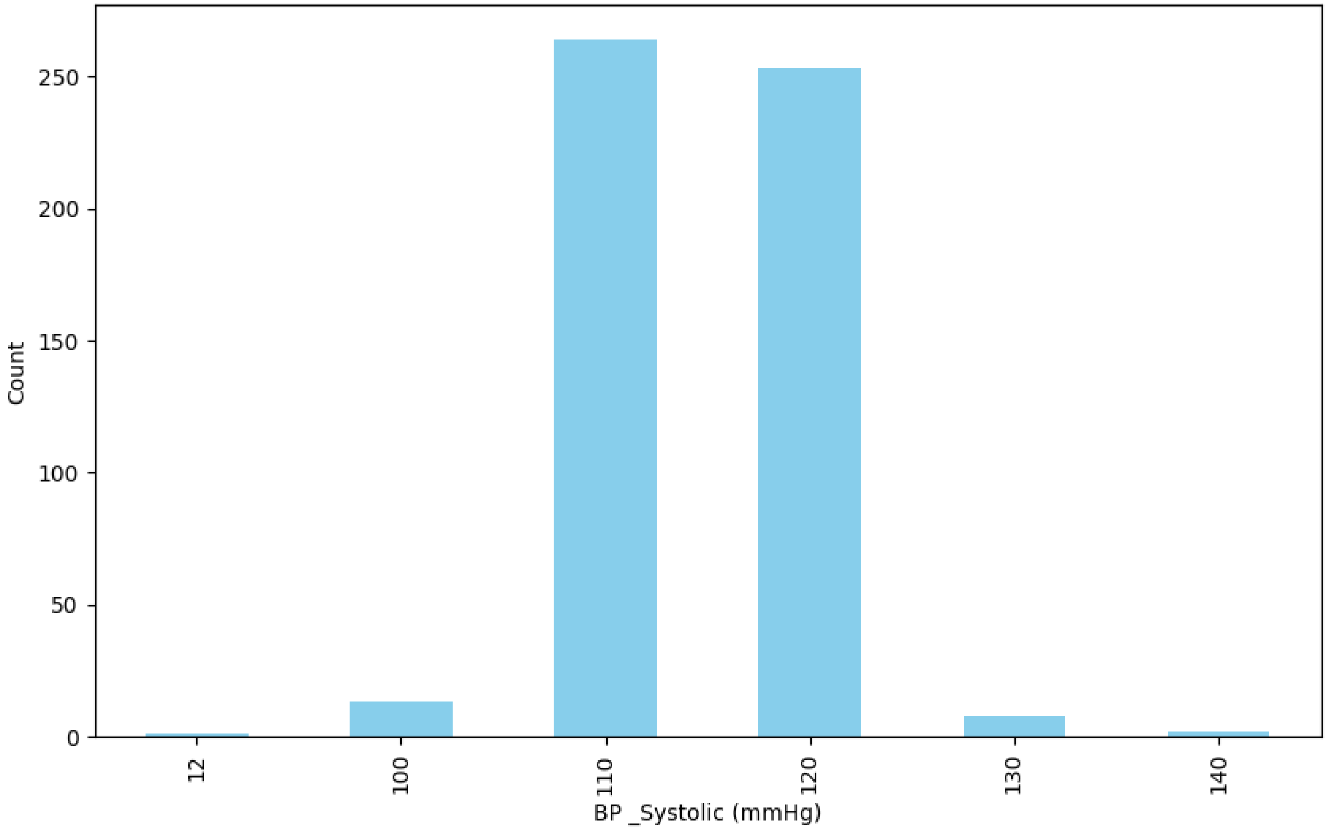

Bar Plot for Hair loss(Y/N)
Count
300
250
200
150
100
50
0
0
1
Hair loss(Y/N)


Bar Plot for Pimples(Y/N)
Count
250
200
150
100
50
0
0
1
Pimples(Y/N)

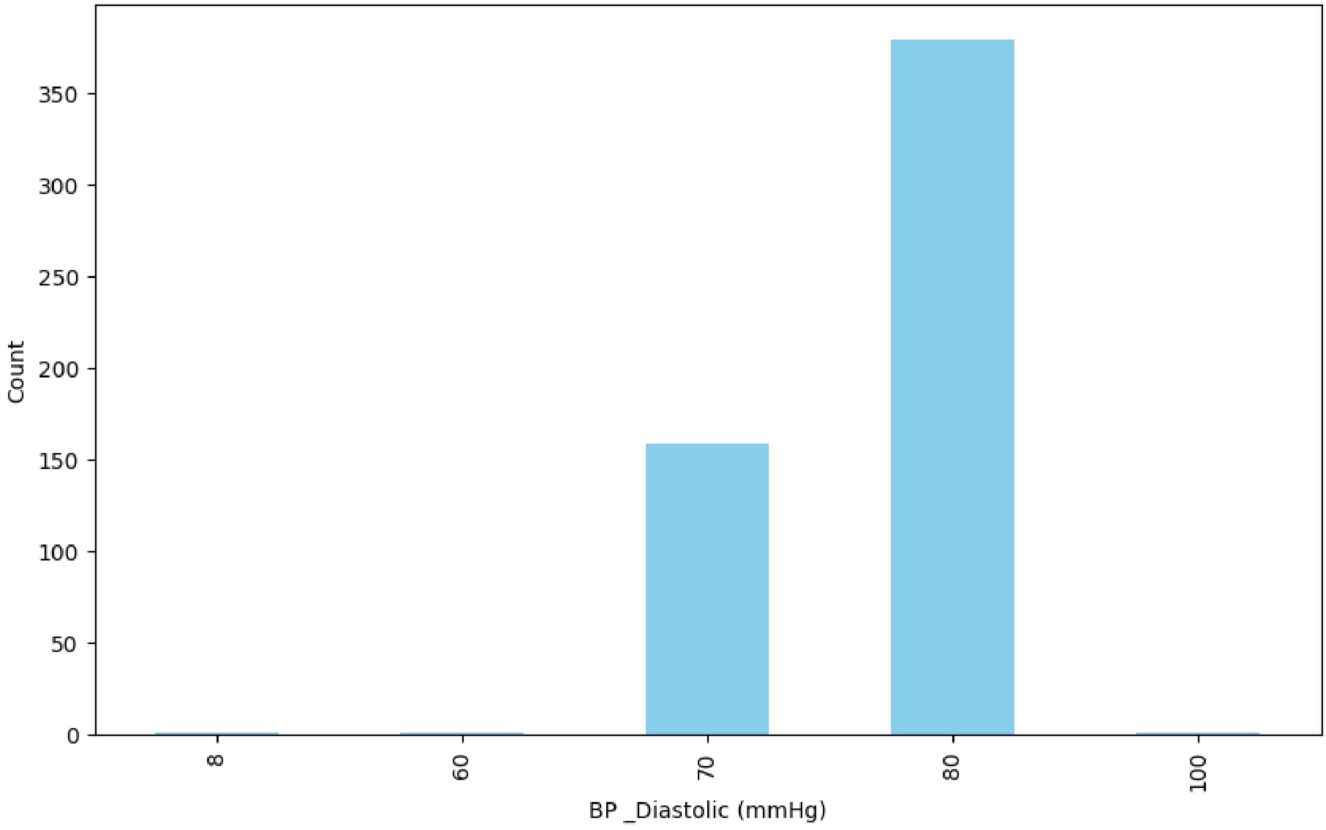

Bar Plot for Fast food (Y/N)
Count
0
50
100
150
200
250
0.0
1.0
Fast food (Y/N)

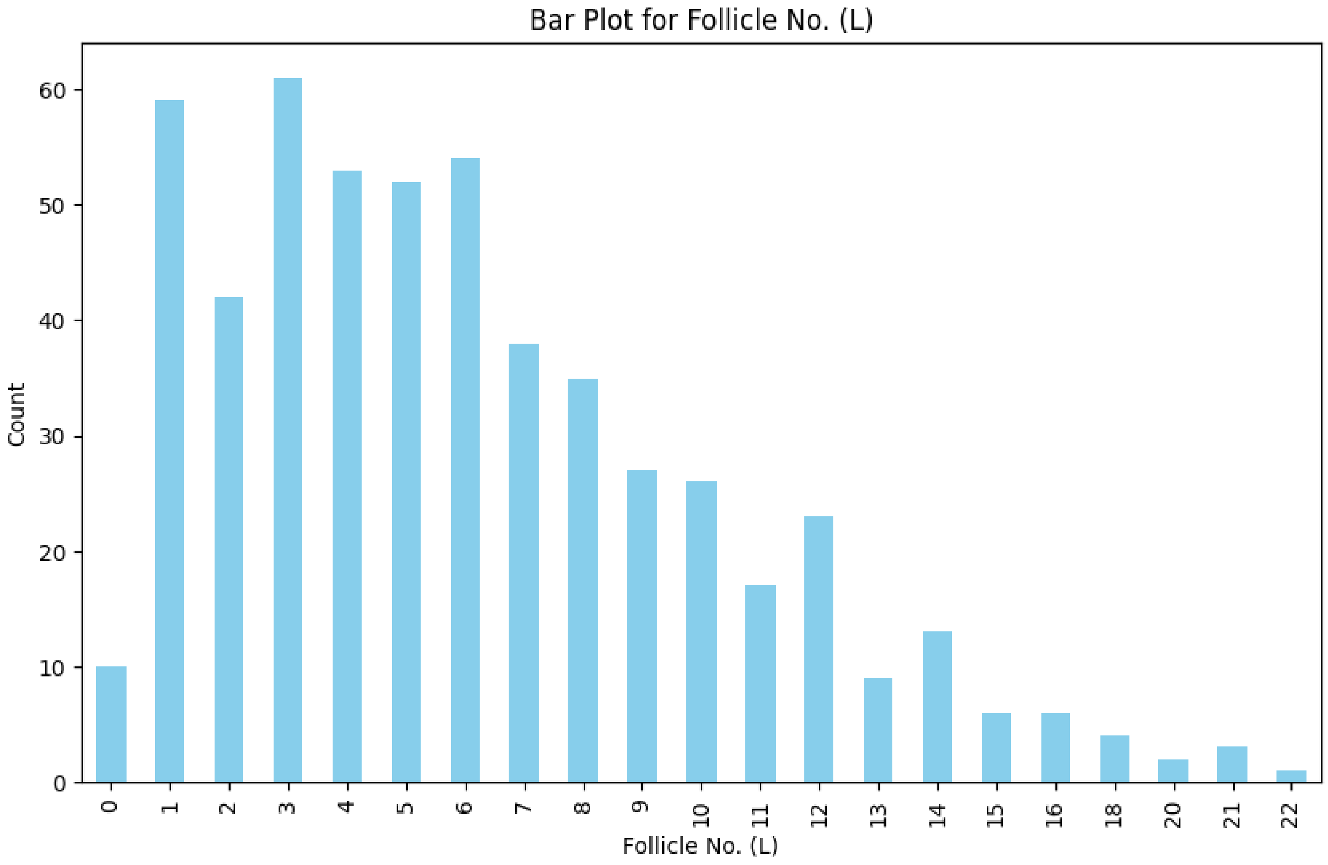

Bar Plot for Reg.Exercise(Y/N)
Count
0
50
100
150
200
250
300
350
400
0
1
Reg.Exercise(Y/N)

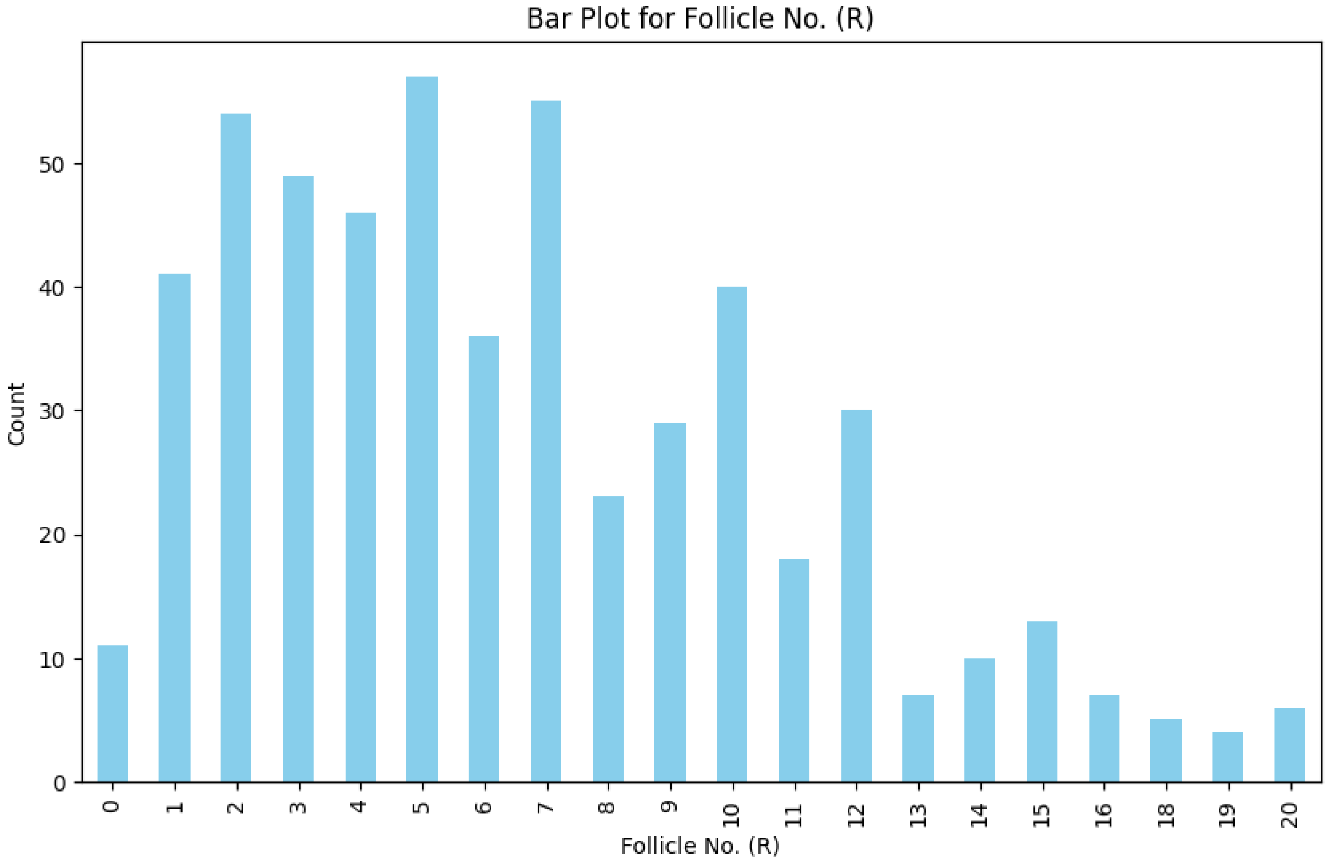
Bar Plot for BP _Systolic (mmHg)

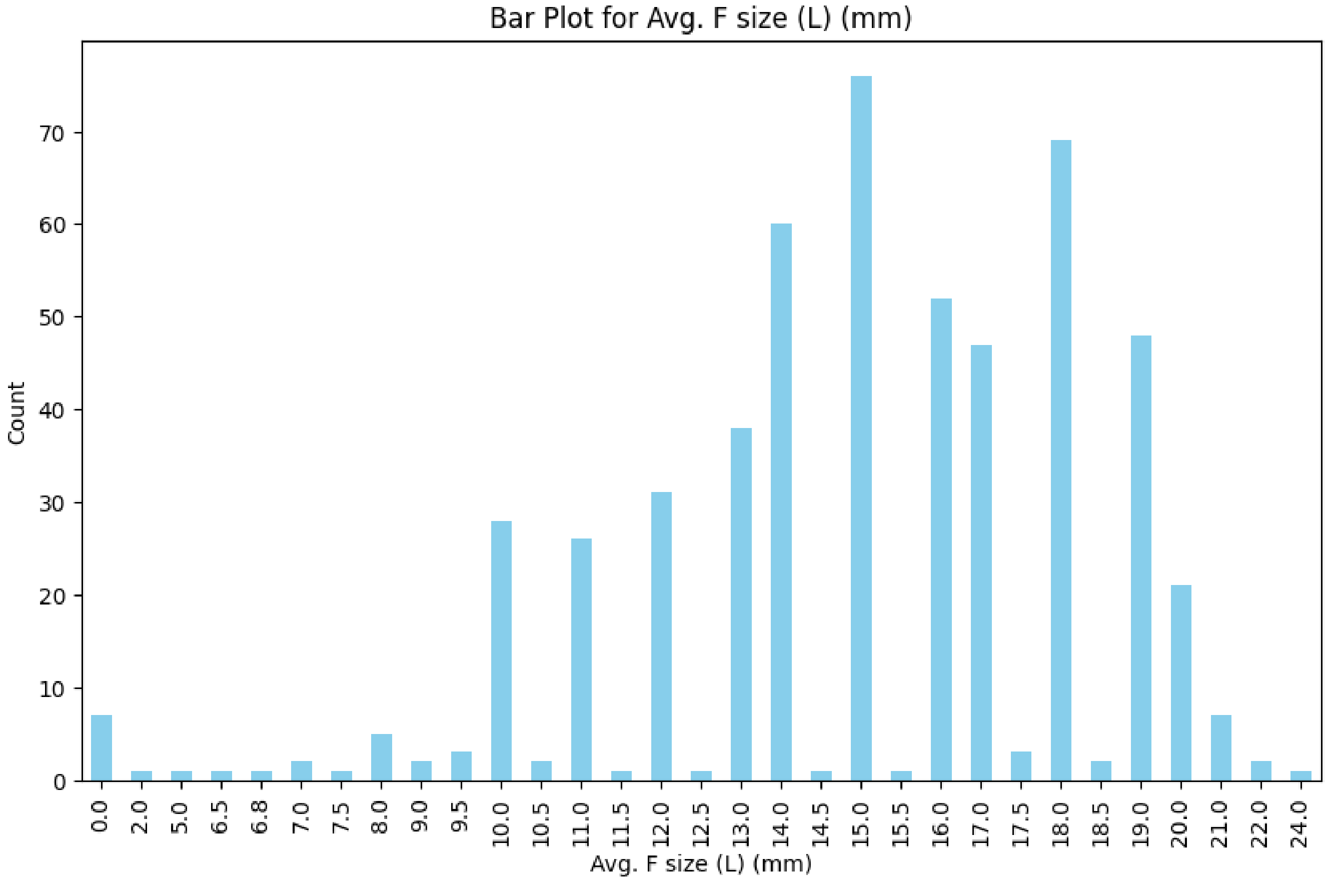


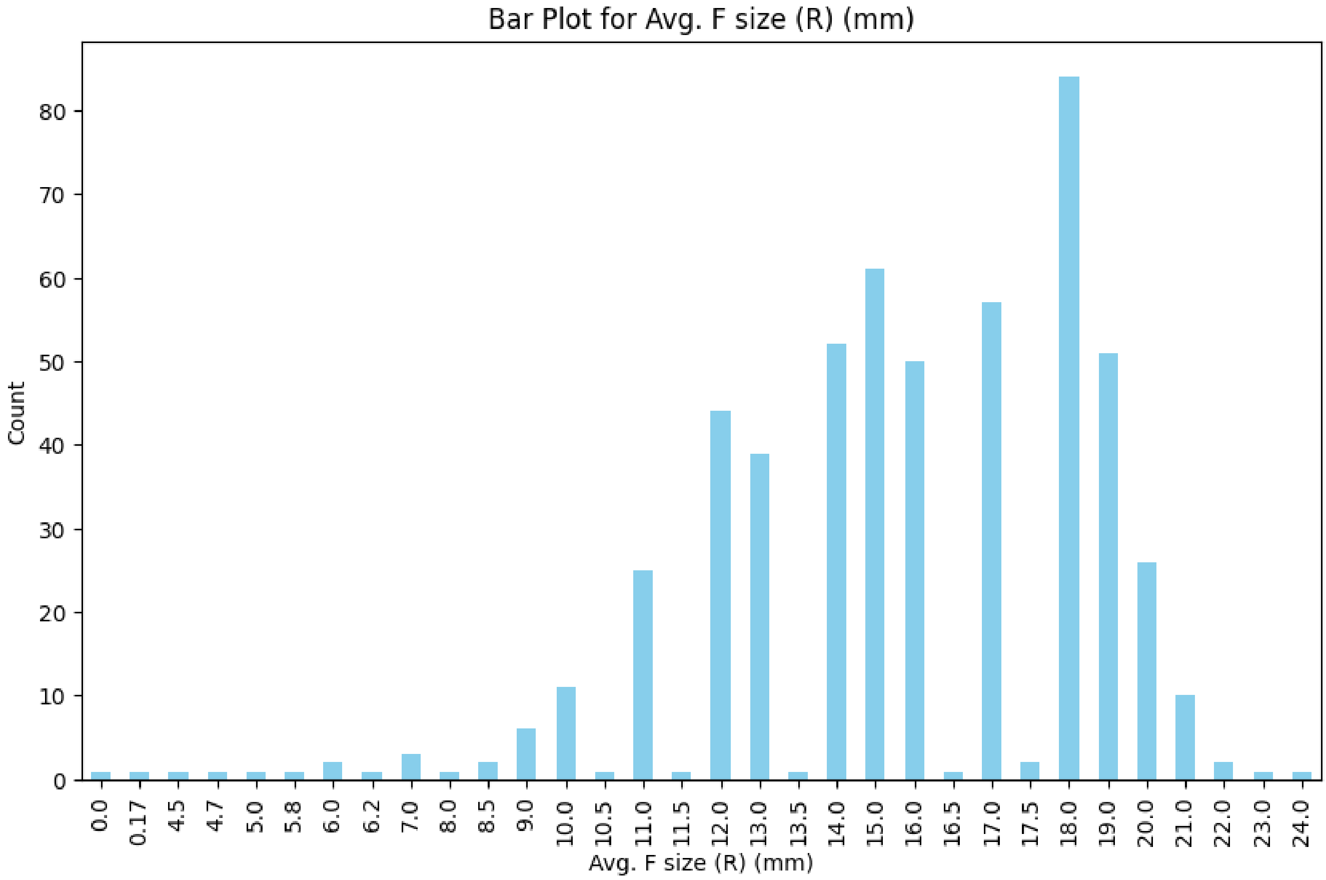
Bar Plot for BP _Diastolic (mmHg)

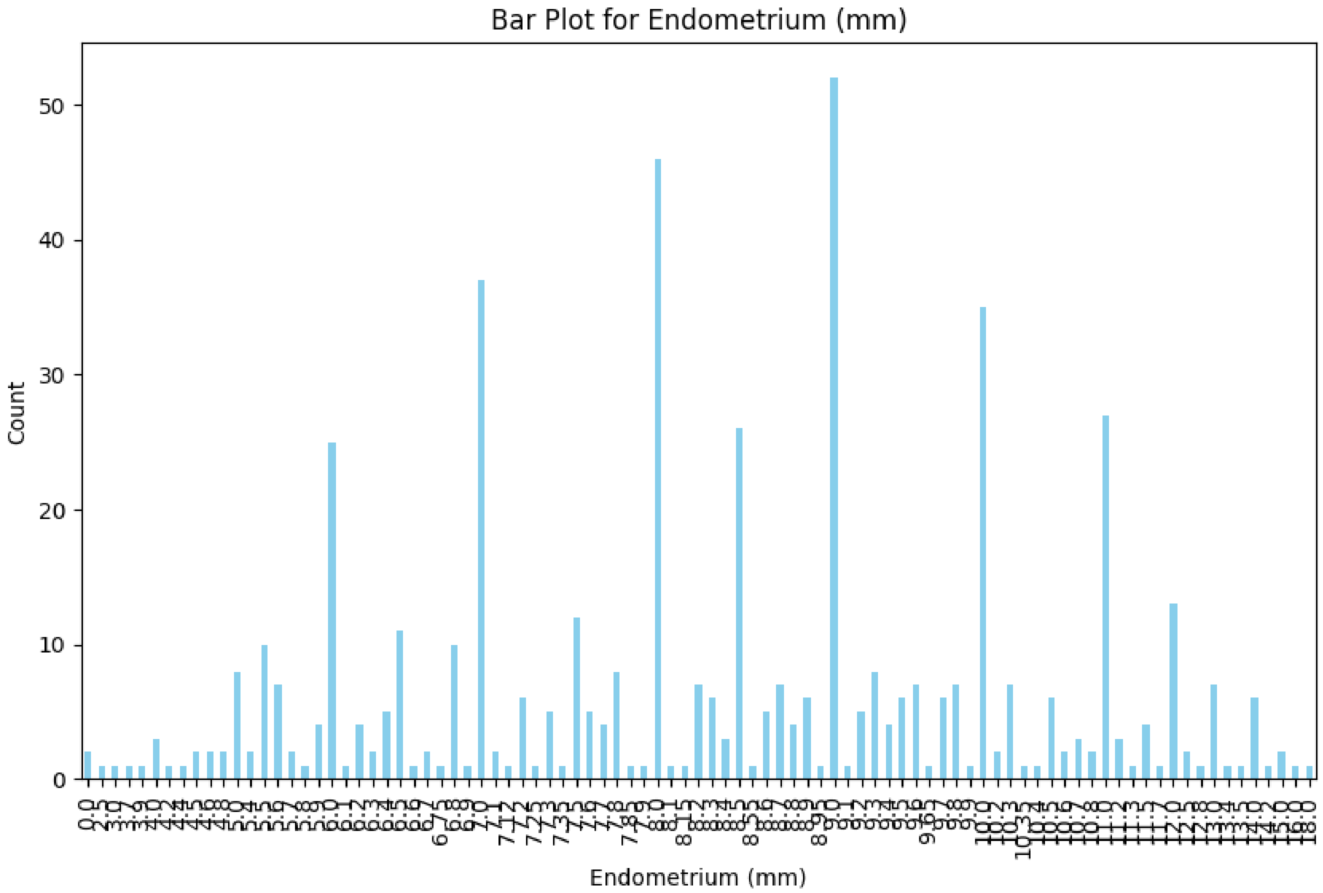



Bar Plot for Follicle No. (L)
Count
0
10
20
30
40
50
60
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
18
20
21
22
Follicle No. (L)


Bar Plot for Follicle No. (R)
Count
0
10
20
30
40
50
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
18
19
20
Follicle No. (R)


Bar Plot for Avg. F size (L) (mm)
Count
0
10
20
30
40
50
60
70
0.0
2.0
5.0
6.5
6.8
7.0
7.5
8.0
9.0
9.5
10.0
10.5
11.0
11.5
12.0
12.5
13.0
14.0
14.5
15.0
15.5
16.0
17.0
17.5
18.0
18.5
19.0
20.0
21.0
22.0
24.0
Avg. F size (L) (mm)


Bar Plot for Avg. F size (R) (mm)
Count
0
10
20
30
40
50
60
70
80
0.0
0.17
4.5
4.7
5.0
5.8
6.0
6.2
7.0
8.0
8.5
9.0
10.0
10.5
11.0
11.5
12.0
13.0
13.5
14.0
15.0
16.0
16.5
17.0
17.5
18.0
19.0
20.0
21.0
22.0
23.0
24.0
Avg. F size (R) (mm)



Feature Selection

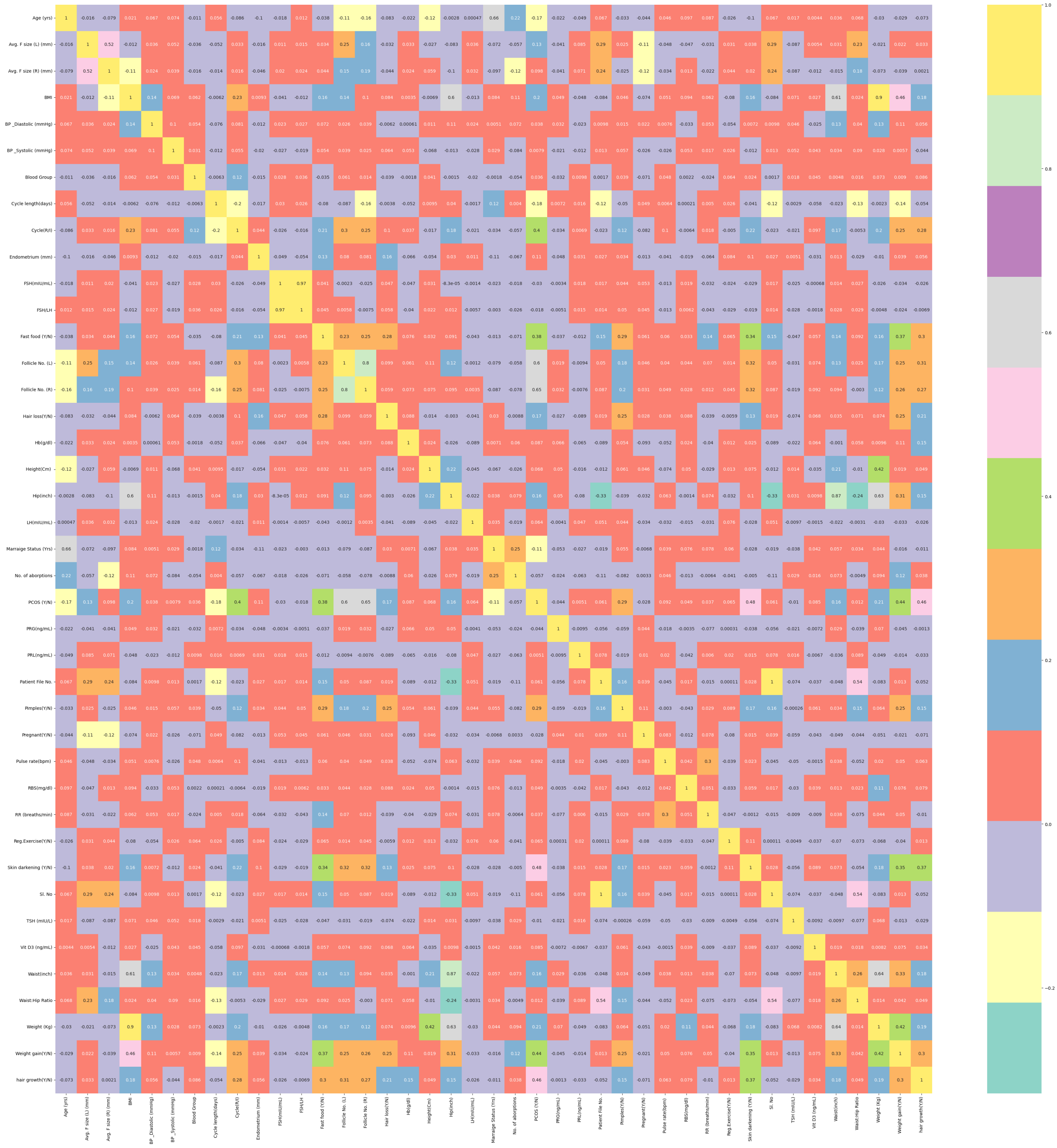
Correlation can be positive (increase in one value of feature increases the value of the target variable) or negative (increase in one value of feature decreases the value of the target variable)

Using correlation with heatmap to identify the important features

In [167…

```
correlation_mat = pcos_normalized_dt.corr()

#get correlations of each features in dataset
feature_index = correlation_mat.index
plt.figure(figsize = (45,45))

#plot heat map
plot_heatmap = sns.heatmap(pcos_normalized_dt[feature_index].corr(),annot=True,cmap="Set3")
```

```
<ipython-input-167-75617772b3fa>:1: FutureWarning: The default value of numeric_only in DataF
rame.corr is deprecated. In a future version, it will default to False. Select only valid col
umns or specify the value of numeric_only to silence this warning.
  correlation_mat = pcos_normalized_dt.corr()
```



In [168…

```
correlation_mat['PCOS (Y/N)'].sort_values(ascending=False)
```

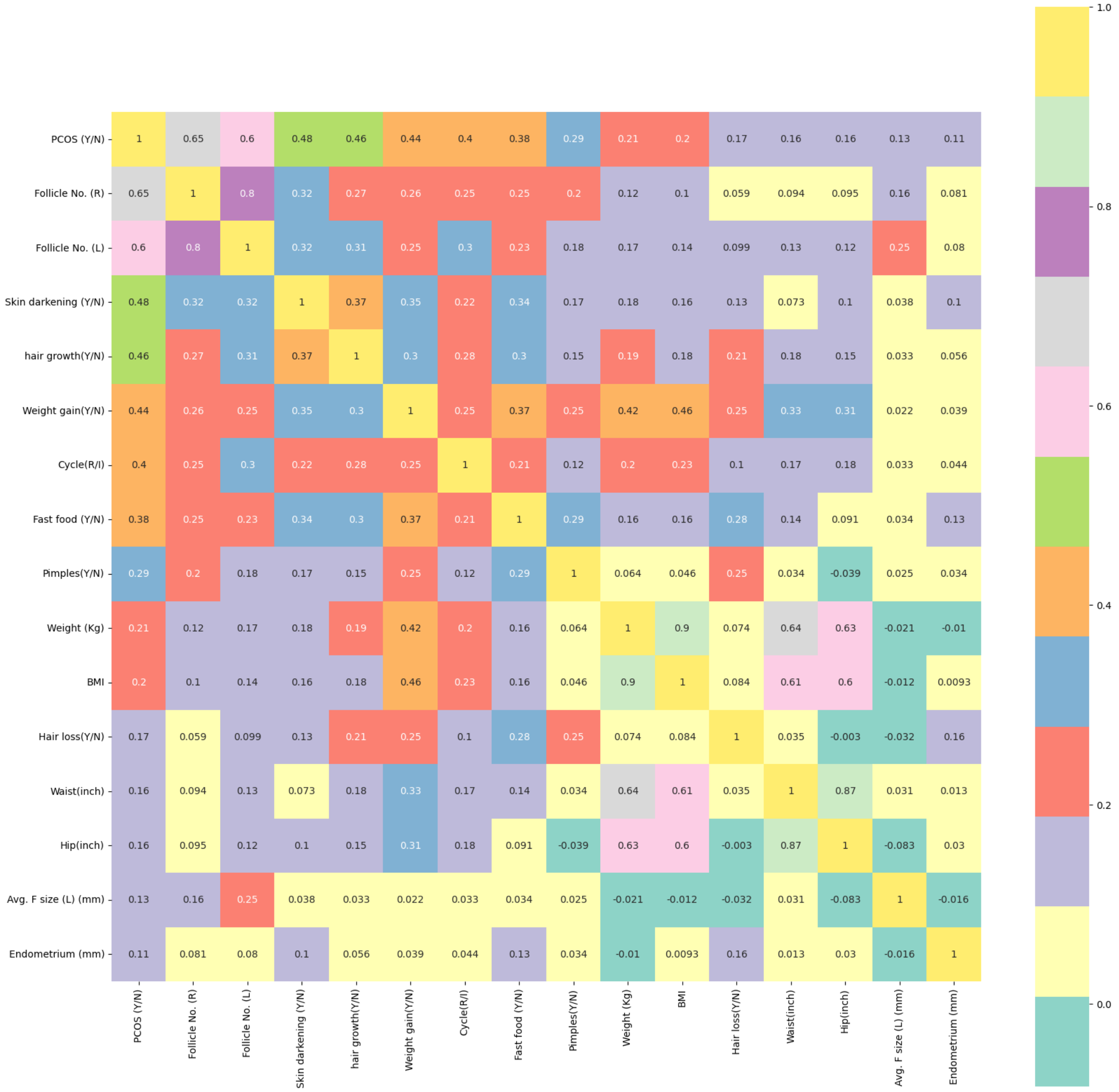
Out[168]:

```
PCOS (Y/N)                1.000000
Follicle No. (R)          0.648327
Follicle No. (L)          0.603346
Skin darkening (Y/N)      0.475733
hair growth(Y/N)          0.464667
Weight gain(Y/N)          0.441047
Cycle(R/I)                0.401644
Fast food (Y/N)           0.377933
Pimples(Y/N)              0.286077
Weight (Kg)               0.211938
BMI                       0.199534
Hair loss(Y/N)            0.172879
Waist(inch)               0.164598
Hip(inch)                 0.162297
Avg. F size (L) (mm)      0.132992
Endometrium (mm)          0.106648
Avg. F size (R) (mm)      0.097690
Pulse rate(bpm)           0.091821
Hb(g/dl)                  0.087170
Vit D3 (ng/mL)            0.085494
Height(Cm)                0.068254
Reg.Exercise(Y/N)         0.065337
LH(mIU/mL)                0.063879
Patient File No.          0.060998
Sl. No                    0.060998
RBS(mg/dl)                0.048922
BP _Diastolic (mmHg)      0.038032
RR (breaths/min)          0.036928
Blood Group               0.036433
Waist:Hip Ratio           0.012386
BP _Systolic (mmHg)       0.007942
PRL(ng/mL)                0.005143
TSH (mIU/L)              -0.010140
FSH/LH                   -0.018336
Pregnant(Y/N)            -0.027565
FSH(mIU/mL)              -0.030319
PRG(ng/mL)               -0.043834
No. of aborptions        -0.057158
Marraige Status (Yrs)    -0.112897
 Age (yrs)               -0.168513
Cycle length(days)       -0.178480
Name: PCOS (Y/N), dtype: float64
```

Selecting the top 15 features with highest p-value

In [169…

```
imp_features = correlation_mat.nlargest(16,'PCOS (Y/N)')['PCOS (Y/N)'].index
plt.figure(figsize = (20,20))
plot_heat_map_after = sns.heatmap(pcos_normalized_dt[imp_features].corr(),annot=True,square=T
                                  cmap="Set3",annot_kws={'size':10})
```



In [170…

```
correlation_mat.nlargest(16,'PCOS (Y/N)')['PCOS (Y/N)']
```

Out[170]:

```
PCOS (Y/N)              1.000000
Follicle No. (R)        0.648327
Follicle No. (L)        0.603346
Skin darkening (Y/N)    0.475733
hair growth(Y/N)        0.464667
Weight gain(Y/N)        0.441047
Cycle(R/I)              0.401644
Fast food (Y/N)         0.377933
Pimples(Y/N)            0.286077
Weight (Kg)             0.211938
BMI                     0.199534
Hair loss(Y/N)          0.172879
Waist(inch)             0.164598
Hip(inch)               0.162297
Avg. F size (L) (mm)    0.132992
Endometrium (mm)        0.106648
Name: PCOS (Y/N), dtype: float64
```

In [171…

```
imp_features
```

Out[171]:

```
Index(['PCOS (Y/N)', 'Follicle No. (R)', 'Follicle No. (L)',
       'Skin darkening (Y/N)', 'hair growth(Y/N)', 'Weight gain(Y/N)',
       'Cycle(R/I)', 'Fast food (Y/N)', 'Pimples(Y/N)', 'Weight (Kg)', 'BMI',
       'Hair loss(Y/N)', 'Waist(inch)', 'Hip(inch)', 'Avg. F size (L) (mm)',
       'Endometrium (mm)'],
      dtype='object')
```

In [172…

```
pcos_df = pcos_normalized_dt[imp_features]
```

In [173…

```
pcos_df.head()
# pcos_df.shape
```

Out[173]:

	PCOS (Y/N)	Follicle No. (R)	Follicle No. (L)	Skin darkening (Y/N)	hair growth(Y/N)	Weight gain(Y/N)	Cycle(R/I)	Fast food (Y/N)	Pimples(Y/N)	Weight (Kg)	
0	0.0	0.15	0.136364	0.0	0.0	0.0	0.0	1.0	0.0	0.176623	0.2
1	0.0	0.25	0.136364	0.0	0.0	0.0	0.0	0.0	0.0	0.441558	0.4
2	1.0	0.75	0.590909	0.0	0.0	0.0	0.0	1.0	1.0	0.490909	0.4
3	0.0	0.10	0.090909	0.0	0.0	0.0	0.0	0.0	0.0	0.441558	0.6
4	0.0	0.20	0.136364	0.0	0.0	0.0	0.0	0.0	0.0	0.272727	0.2

Model

Dataset splitting

Splitting dataset into training, validation, and test sets.

In [174…

```
X = pcos_df.iloc[:,1:].values
y = pcos_df.iloc[:,0].values
```

In [175…

```
print(X.shape)
print(y.shape)
```

```
(541, 15)
(541,)
```

In [176…

```
X_train,X_test,y_train,y_test = train_test_split(X, y,test_size=0.3,random_state=189)
X_val,X_test,y_val,y_test = train_test_split(X_test, y_test,test_size=0.3,random_state=189)
```

1. Decision Tree

In [177…

```
depths = [5,10,15,20,25,30,35,40,45,50,55,60,65,70,75,80,85,90,95,100,110,120,130,140,150,160
ac=[]
```

In [190…

```
print(np.isnan(X_train).any(), np.isnan(X_val).any())
```

```
False False
```

In [181…

```
from sklearn.impute import SimpleImputer

# Create an imputer instance
imputer = SimpleImputer(strategy='mean')  # You can choose other strategies like 'median' or

# Fit the imputer on X_train and transform X_train
X_train_imputed = imputer.fit_transform(X_train)
```

```
# Apply the same imputer to X_val
X_val_imputed = imputer.transform(X_val)
```

In [184…

```
# Find indices of rows without NaN in X_train
valid_indices_train = ~np.isnan(X_train).any(axis=1)

# Apply boolean indexing to X_train and y_train
X_train = X_train[valid_indices_train]
y_train = y_train[valid_indices_train]

# Find indices of rows without NaN in X_val
valid_indices_val = ~np.isnan(X_val).any(axis=1)

# Apply boolean indexing to X_val and y_val
X_val = X_val[valid_indices_val]
y_val = y_val[valid_indices_val]
```

In [185…

```
# Drop rows with missing values in both X_train and X_val
X_train = X_train.dropna()
y_train = y_train[X_train.index]  # Adjust y_train accordingly
X_val = X_val.dropna()
y_val = y_val[X_val.index]  # Adjust y_val accordingly
```

```
---------------------------------------------------------------------------
AttributeError                            Traceback (most recent call last)
<ipython-input-185-2db13bd6921d> in <cell line: 2>()
      1 # Drop rows with missing values in both X_train and X_val
----> 2 X_train = X_train.dropna()
      3 y_train = y_train[X_train.index]  # Adjust y_train accordingly
      4 X_val = X_val.dropna()
      5 y_val = y_val[X_val.index]  # Adjust y_val accordingly

AttributeError: 'numpy.ndarray' object has no attribute 'dropna'
```

In [191…

```
for i in depths:
  dtree_clf = tree.DecisionTreeClassifier(max_depth=i,min_samples_leaf=4)
  dtree_clf.fit(X_train,y_train)
  y_pred_dtree = dtree_clf.predict(X_val)
  ac.append(accuracy_score(y_val,y_pred_dtree)*100)
```

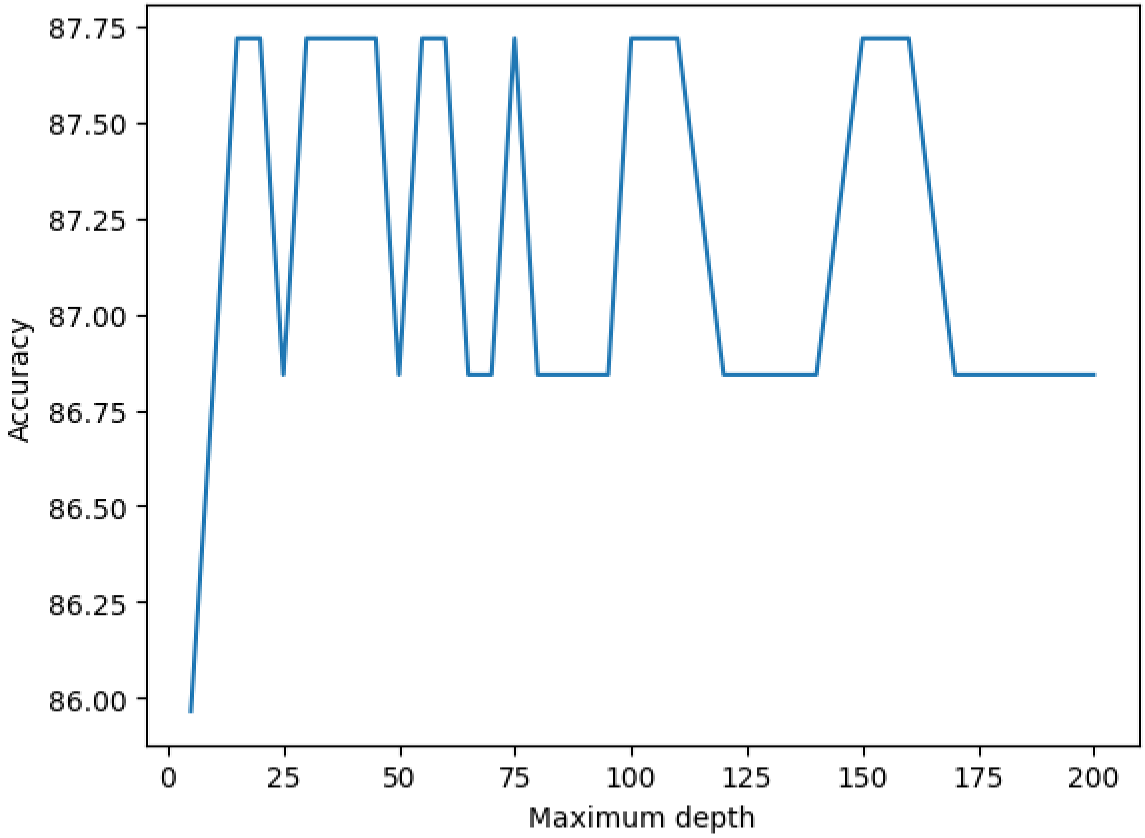
In [188…

```
print(len(depths), len(ac))
```

```
29 0
```

In [192…

```
plt.plot(depths,ac,label='Test_accuracy')
plt.xlabel('Maximum depth')
plt.ylabel('Accuracy')
plt.show()
```



In [193…

```
#Finding the depth for which Accuracy is maximum

max_acc = max(ac)
max_dt = depths[ac.index(max_acc)]
print(max_acc, max_dt)
```

```
87.71929824561403 15
```

In [194…

```
#Using the depth which gave the maximum a15,ccuracy to train the model
dtree_clf = tree.DecisionTreeClassifier(max_depth=max_dt,min_samples_leaf=4)
dtree_clf.fit(X_train,y_train)
```

Out[194]:

```
▾ DecisionTreeClassifier
DecisionTreeClassifier(max_depth=15, min_samples_leaf=4)
```

In [195…

```
y_pred_dtree = dtree_clf.predict(X_val)
```

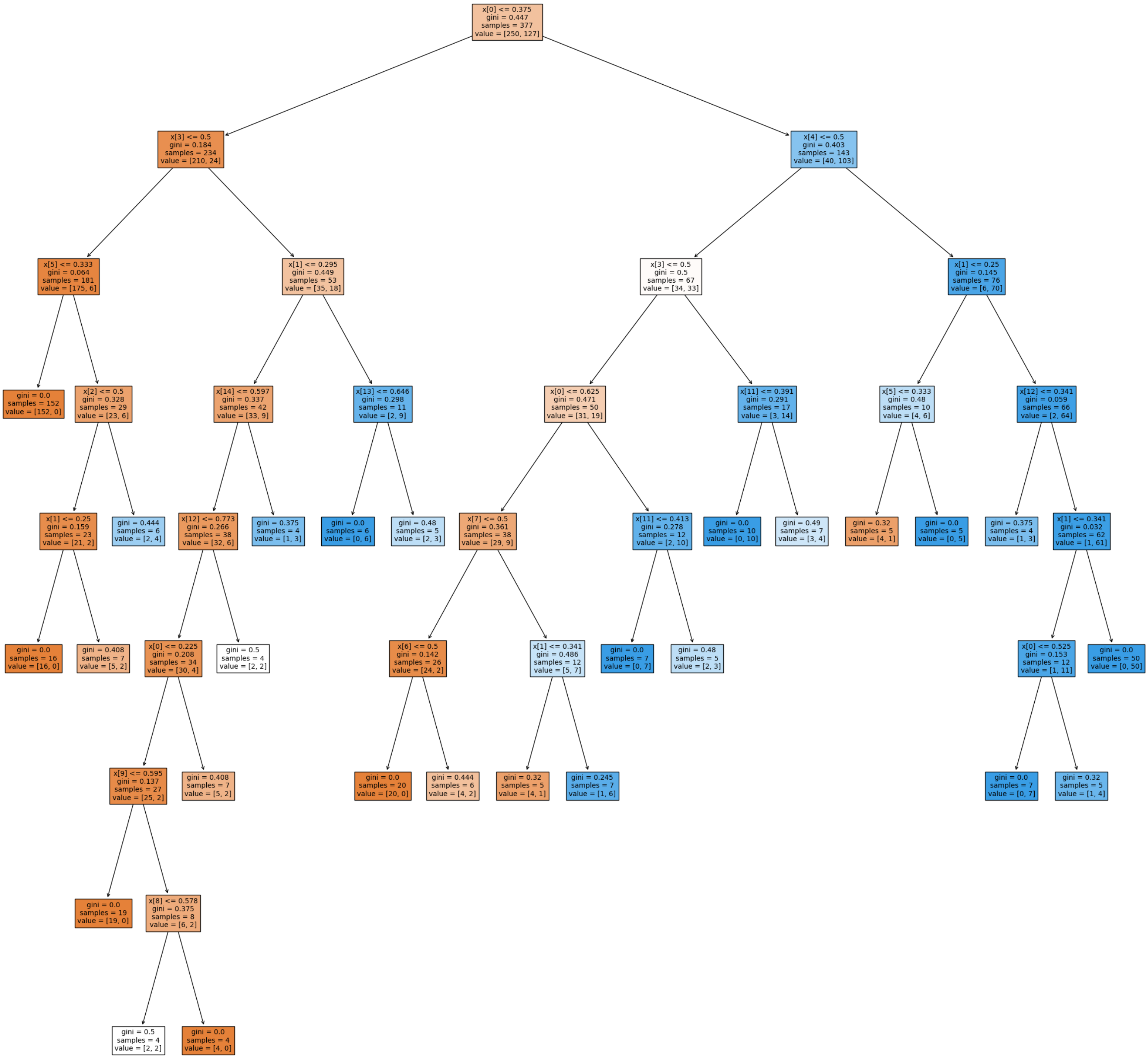
In [196…

```
acc_dtree = accuracy_score(y_val,y_pred_dtree)
print(acc_dtree)
```

```
0.8771929824561403
```

In [197…

```
fig = plt.figure(figsize=(30,30))
dtree_plot = tree.plot_tree(dtree_clf,filled=True)
```


x[0] <= 0.375 gini = 0.447 samples = 377 value = [250, 127]
x[3] <= 0.5 gini = 0.184 samples = 234 value = [210, 24]
x[4] <= 0.5 gini = 0.403 samples = 143 value = [40, 103]
x[5] <= 0.333 gini = 0.064 samples = 181 value = [175, 6]
x[1] <= 0.295 gini = 0.449 samples = 53 value = [35, 18]
x[3] <= 0.5 gini = 0.5 samples = 67 value = [34, 33]
x[1] <= 0.25 gini = 0.145 samples = 76 value = [6, 70]
gini = 0.0 samples = 152 value = [152, 0]
x[2] <= 0.5 gini = 0.328 samples = 29 value = [23, 6]
x[14] <= 0.597 gini = 0.337 samples = 42 value = [33, 9]
x[13] <= 0.646 gini = 0.298 samples = 11 value = [2, 9]
x[0] <= 0.625 gini = 0.471 samples = 50 value = [31, 19]
x[11] <= 0.391 gini = 0.291 samples = 17 value = [3, 14]
x[5] <= 0.333 gini = 0.48 samples = 10 value = [4, 6]
x[12] <= 0.341 gini = 0.059 samples = 66 value = [2, 64]
x[1] <= 0.25 gini = 0.159 samples = 23 value = [21, 2]
gini = 0.444 samples = 6 value = [2, 4]
x[12] <= 0.773 gini = 0.266 samples = 38 value = [32, 6]
gini = 0.375 samples = 4 value = [1, 3]
gini = 0.0 samples = 6 value = [0, 6]
gini = 0.48 samples = 5 value = [2, 3]
x[7] <= 0.5 gini = 0.361 samples = 38 value = [29, 9]
x[11] <= 0.413 gini = 0.278 samples = 12 value = [2, 10]
gini = 0.0 samples = 10 value = [0, 10]
gini = 0.49 samples = 7 value = [3, 4]
gini = 0.32 samples = 5 value = [4, 1]
gini = 0.0 samples = 5 value = [0, 5]
gini = 0.375 samples = 4 value = [1, 3]
x[1] <= 0.341 gini = 0.032 samples = 62 value = [1, 61]
gini = 0.0 samples = 16 value = [16, 0]
gini = 0.408 samples = 7 value = [5, 2]
x[0] <= 0.225 gini = 0.208 samples = 34 value = [30, 4]
gini = 0.5 samples = 4 value = [2, 2]
x[6] <= 0.5 gini = 0.142 samples = 26 value = [24, 2]
x[1] <= 0.341 gini = 0.486 samples = 12 value = [5, 7]
gini = 0.0 samples = 7 value = [0, 7]
gini = 0.48 samples = 5 value = [2, 3]
x[0] <= 0.525 gini = 0.153 samples = 12 value = [1, 11]
gini = 0.0 samples = 50 value = [0, 50]
x[9] <= 0.595 gini = 0.137 samples = 27 value = [25, 2]
gini = 0.408 samples = 7 value = [5, 2]
gini = 0.0 samples = 20 value = [20, 0]
gini = 0.444 samples = 6 value = [4, 2]
gini = 0.32 samples = 5 value = [4, 1]
gini = 0.245 samples = 7 value = [1, 6]
gini = 0.0 samples = 7 value = [0, 7]
gini = 0.32 samples = 5 value = [1, 4]
gini = 0.0 samples = 19 value = [19, 0]
x[8] <= 0.578 gini = 0.375 samples = 8 value = [6, 2]
gini = 0.5 samples = 4 value = [2, 2]
gini = 0.0 samples = 4 value = [4, 0]

Analyzation of the model

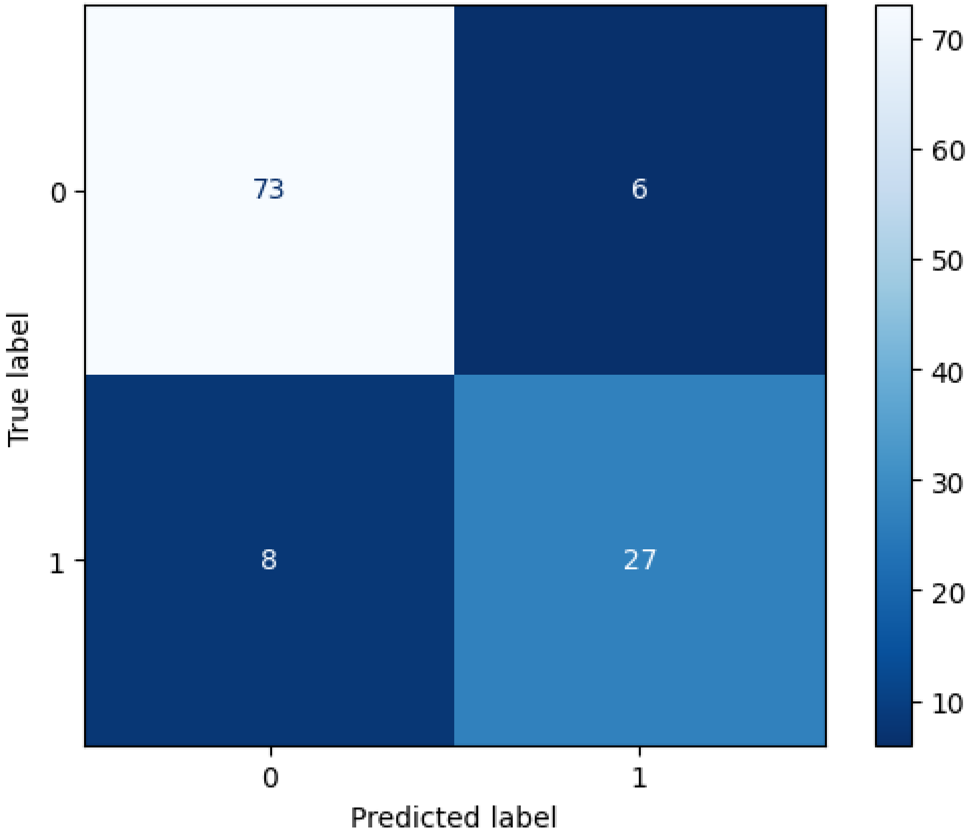
In [198…

```
print(metrics.classification_report(y_val, y_pred_dtree))
```

```
              precision    recall  f1-score   support

         0.0       0.90      0.92      0.91        79
         1.0       0.82      0.77      0.79        35

    accuracy                           0.88       114
   macro avg       0.86      0.85      0.85       114
weighted avg       0.88      0.88      0.88       114
```

In [199…

```
cm_dree = metrics.confusion_matrix(y_val, y_pred_dtree)
disp = ConfusionMatrixDisplay(confusion_matrix = cm_dree, display_labels = ['0','1'])
disp.plot(cmap="Blues_r")
plt.show()
```



2.SVM

In [200…

```
S = SVC(kernel = 'linear')
S.fit(X_train,y_train)
```

Out[200]:

```
▾ SVC
SVC(kernel='linear')
```

In [201…

```
y_pred_svm = S.predict(X_val)
```

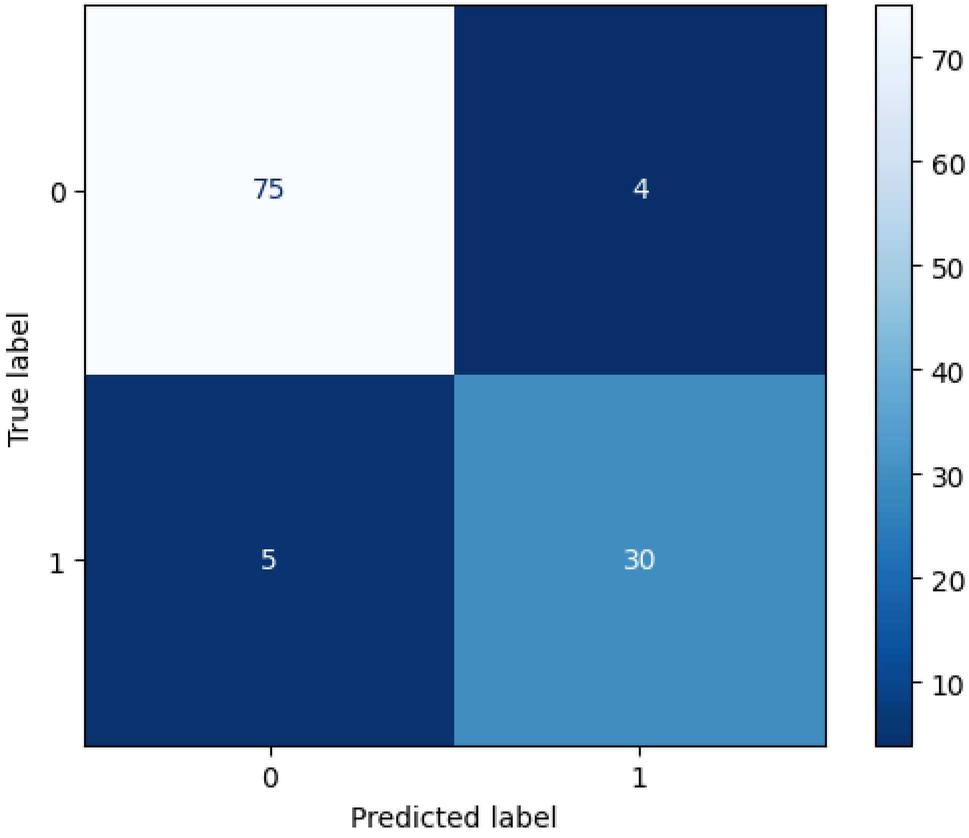
In [202…

```
acc_svm = accuracy_score(y_val,y_pred_svm)
print(acc_svm)
```

```
0.9210526315789473
```

In [203…

```
cm_svm = metrics.confusion_matrix(y_val, y_pred_svm)
disp = ConfusionMatrixDisplay(confusion_matrix = cm_svm, display_labels = ['0','1'])
disp.plot(cmap="Blues_r")
plt.show()
```



3.Naive Bayes classifier

In [204…

```
import numpy as np
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import KFold
from sklearn.metrics import accuracy_score
```

In [206…

```
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import KFold
from sklearn.metrics import accuracy_score
import numpy as np

# Find indices of samples without NaN values
valid_indices = np.where(~np.isnan(X).any(axis=1))[0]

# Use only valid samples for training and testing
X_valid = X[valid_indices]
y_valid = y[valid_indices]

# K-fold cross-validation
kf = KFold(n_splits=5, shuffle=True)
accuracy_scores = []

for train_index, test_index in kf.split(X_valid):
    X_train, X_test = X_valid[train_index], X_valid[test_index]
    y_train, y_test = y_valid[train_index], y_valid[test_index]

    # Gaussian Naive Bayes model
    gnb = GaussianNB()

    # Fit model with Laplace smoothing
    gnb.fit(X_train, y_train)

    # Make predictions
    y_pred = gnb.predict(X_test)

    # Evaluate cross-validation accuracy
    accuracy = accuracy_score(y_test, y_pred)
    accuracy_scores.append(accuracy)
```

```
# Print average accuracy
print("Accuracy:", np.mean(accuracy_scores) * 100, "%")
```

```
Accuracy: 88.14814814814815 %
```

In [210…

```
from sklearn.metrics import accuracy_score

# Assuming you have a Naive Bayes model named nb_model
gnb.fit(X_train, y_train)
y_pred_nb = gnb.predict(X_val)

# Calculate and print accuracy
acc_nb = accuracy_score(y_val, y_pred_nb)
print("Accuracy for Naive Bayes:", acc_nb)
```

```
Accuracy for Naive Bayes: 0.9122807017543859
```

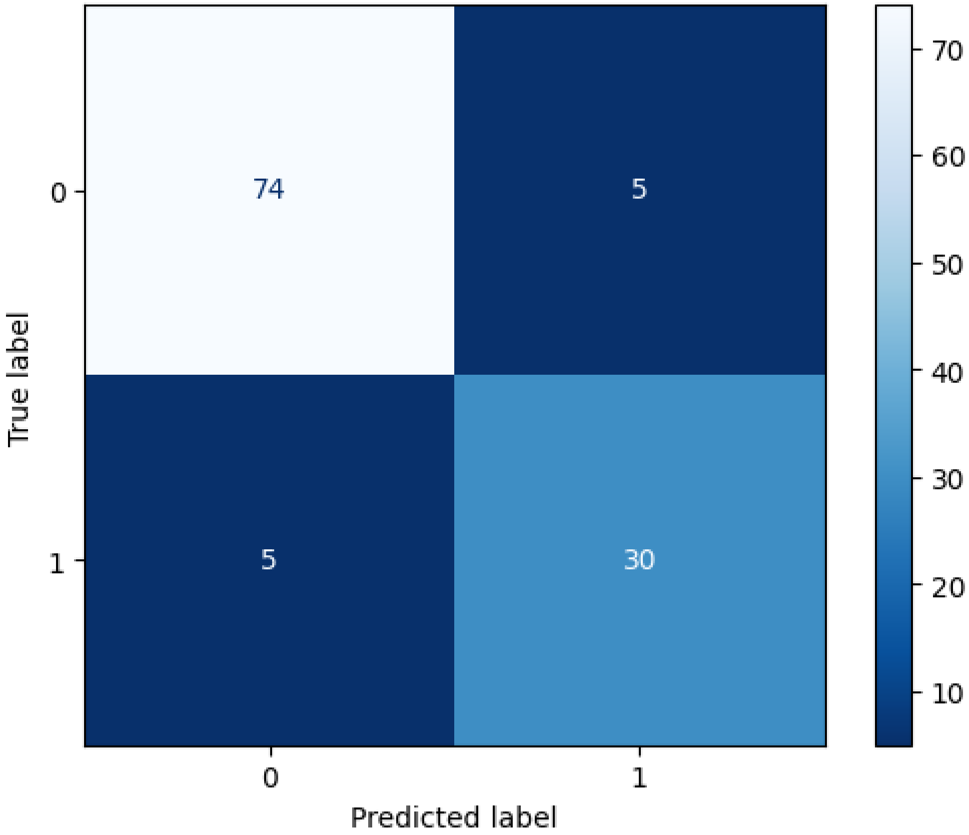
In [211…

```
print(metrics.classification_report(y_val, y_pred_nb))
```

```
              precision    recall  f1-score   support

         0.0       0.94      0.94      0.94        79
         1.0       0.86      0.86      0.86        35

    accuracy                           0.91       114
   macro avg       0.90      0.90      0.90       114
weighted avg       0.91      0.91      0.91       114
```

In [212…

```
cm_nb = metrics.confusion_matrix(y_val, y_pred_nb)
disp = ConfusionMatrixDisplay(confusion_matrix = cm_nb, display_labels = ['0','1'])
disp.plot(cmap="Blues_r")
plt.show()
```



4.XG Boost

In [213…

```
pip install xgboost
```

```
Requirement already satisfied: xgboost in /usr/local/lib/python3.10/dist-packages (2.0.3)
Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages (from xgboos
t) (1.23.5)
Requirement already satisfied: scipy in /usr/local/lib/python3.10/dist-packages (from xgboos
t) (1.11.4)
```

In [214…

```
import pandas as pd
from sklearn import preprocessing
from sklearn.model_selection import train_test_split
from xgboost import XGBClassifier
```

In [215…

```
# Train XGBoost model
model = XGBClassifier()
model.fit(X_train, y_train)

# Make predictions
y_pred = model.predict(X_test)

# Evaluate predictions
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy: %.2f%%" % (accuracy * 100.0))
```

```
Accuracy: 87.96%
```

Comparing Different Models

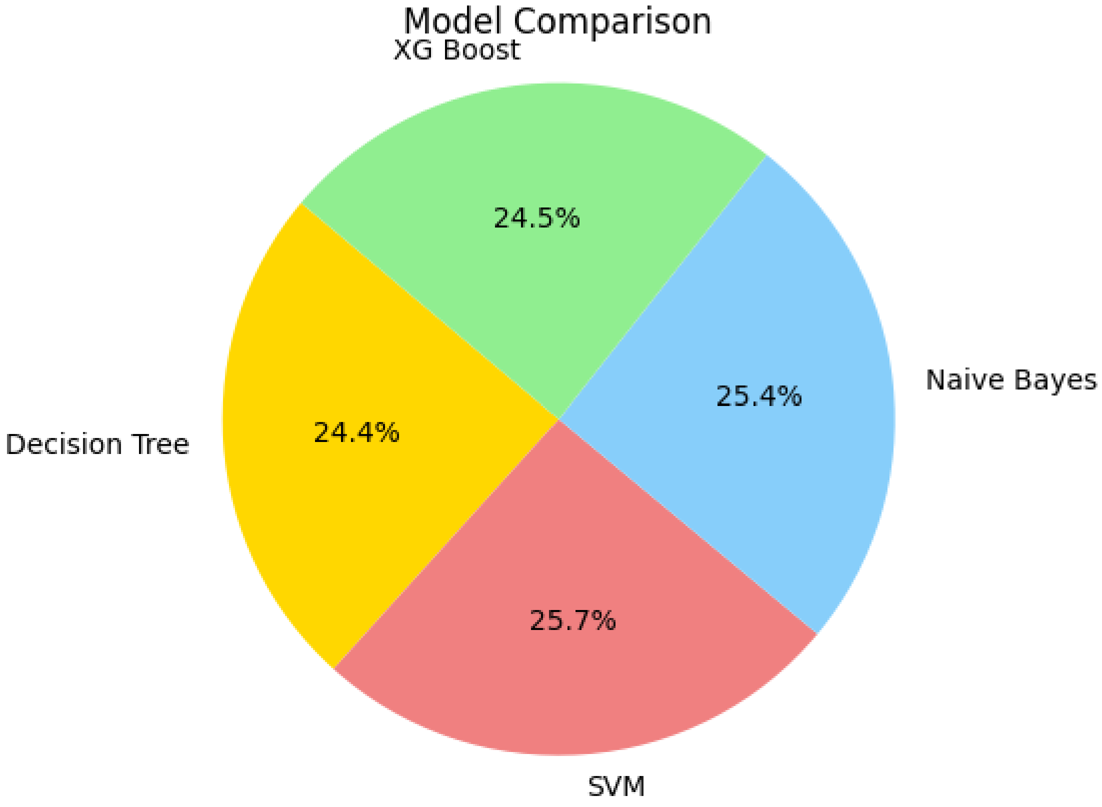
Using a box plot

In [216…

```
# Comparing Different Models - Pie Chart

# Create a dictionary to store the accuracies of different models
model_accuracies = {
    'Decision Tree': acc_dtree,
    'SVM': acc_svm,
    'Naive Bayes': acc_nb,
    'XG Boost': accuracy_score(y_test, y_pred)
}
```

In [217…

```
# Plotting the pie chart
labels = model_accuracies.keys()
sizes = model_accuracies.values()
colors = ['gold', 'lightcoral', 'lightskyblue', 'lightgreen']

plt.pie(sizes, labels=labels, colors=colors, autopct='%1.1f%%', startangle=140)
plt.axis('equal')  # Equal aspect ratio ensures that pie is drawn as a circle.
plt.title('Model Comparison')
plt.show()

plt.show()
```

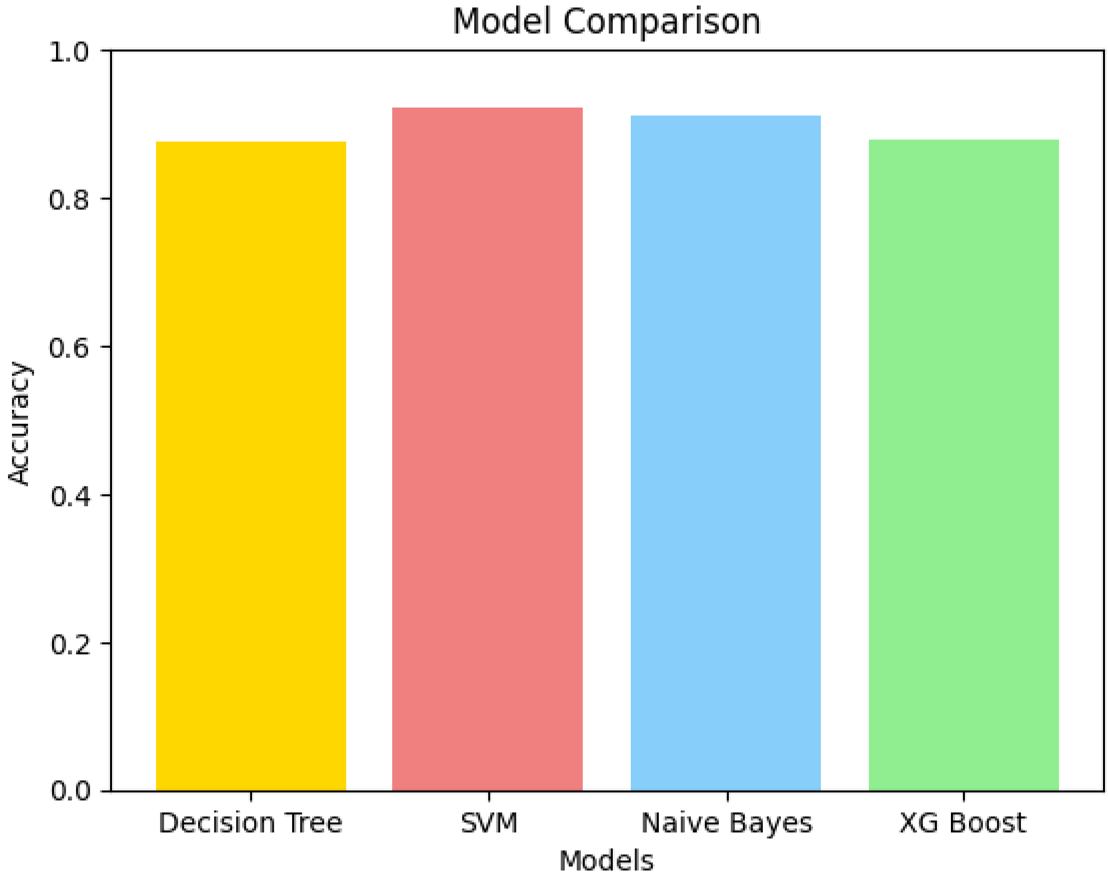


In [218…

```python
# Comparing Different Models - Bar Graph

# Create a dictionary to store the accuracies of different models
model_accuracies = {
    'Decision Tree': acc_dtree,
    'SVM': acc_svm,
    'Naive Bayes': acc_nb,
    'XG Boost': accuracy_score(y_test, y_pred)
}
```

In [219…

```python
# Plotting the bar graph
plt.bar(model_accuracies.keys(), model_accuracies.values(), color=['gold', 'lightcoral', 'lig
plt.xlabel('Models')
plt.ylabel('Accuracy')
plt.title('Model Comparison')
plt.ylim(0, 1)  # Set the y-axis limit between 0 and 1 for accuracy percentage
plt.show()
```



In [220…

```
# Printing the accuracy results of each algorithm
print("Decision Tree Accuracy:", acc_dtree*100)
print("SVM Accuracy:", acc_svm*100)
print("Naive Bayes Accuracy:", acc_nb*100)
print("XG Boost Accuracy:", accuracy_score(y_test, y_pred)*100)
```

```
Decision Tree Accuracy: 87.71929824561403
SVM Accuracy: 92.10526315789474
Naive Bayes Accuracy: 91.22807017543859
XG Boost Accuracy: 87.96296296296296
```