Data Pre-processing

In [169…]
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [170…]
```
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 [171…]
```
from sklearn import tree
from sklearn.svm import SVC
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
from xgboost import XGBClassifier
```

In [172…]
```
pcos_dt = pd.read_csv('PCOS_data.csv')
pcos_dt.head()
```

Out[172]:

	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.Exer
0	1	1	0	28	44.6	152.0	19.3	15	78	22	...	1.0	
1	2	2	0	36	65.0	161.5	24.9	15	74	20	...	0.0	
2	3	3	1	33	68.8	165.0	25.3	11	72	18	...	1.0	
3	4	4	0	37	65.0	148.0	29.7	13	72	20	...	0.0	
4	5	5	0	25	52.0	161.0	20.1	11	72	18	...	0.0	

5 rows × 45 columns

In [173…]
```
pcos_dt.shape
```

Out[173]:
```
(541, 45)
```

In [174…]
```
pcos_dt.columns
```

Out[174]:
```
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 abortions',
       '  I   beta-HCG(mIU/mL)', 'II    beta-HCG(mIU/mL)', '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: 44'],
      dtype='object')
```

In [175…
```
#To remove whitespaces at both ends from a column name

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

In [176…
```
pcos_dt.columns
```

Out[176]:
```
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 abortions',
       'I   beta-HCG(mIU/mL)', 'II    beta-HCG(mIU/mL)', '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: 44'],
      dtype='object')
```

Removing unwanted columns

In [177…
```
pcos_dt.drop(['Sl. No', 'Patient File No.','Unnamed: 44'],axis='columns',inplace=True)
```

Imputing Missing values

Rows with unmatching values are removed and some values are replaced

In [178…
```
pcos_dt = pcos_dt.replace(pcos_dt['II    beta-HCG(mIU/mL)'][123],'1.99')
pcos_dt.drop(labels=305,axis=0,inplace=True)
```

Searching for columns with missing values

In [179…
```
pcos_dt.isnull().sum()
```

Out[179]:
```
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 abortions          0
I   beta-HCG(mIU/mL)       0
II    beta-HCG(mIU/mL)    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
dtype: int64
```

In [180…
```
# Replacing the missing values in a feature column with the median of the feature

pcos_dt['Marraige Status (Yrs)'].fillna(pcos_dt['Marraige Status (Yrs)'].median(), inplace =
pcos_dt['Fast food (Y/N)'].fillna(pcos_dt['Fast food (Y/N)'].median(), inplace = True)
```

In [181…
```
pcos_dt.isnull().sum()
```

Out[181]:
```
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)     0
Pregnant(Y/N)             0
No. of abortions          0
I   beta-HCG(mIU/mL)       0
II    beta-HCG(mIU/mL)    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)           0
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
dtype: int64
```

Standardization

In [182…
```
scaler = ps.StandardScaler()
pcos_sc = scaler.fit_transform(pcos_dt)
pcos_standardized_dt = pd.DataFrame(pcos_sc,columns = pcos_dt.columns)
```

In [183…
```
pcos_standardized_dt.head()
```

Out[183]:

	PCOS (Y/N)	Age (yrs)	Weight (Kg)	Height(Cm)	BMI	Blood Group	Pulse rate(bpm)	RR (breaths/min)	Hb(g/dl)	Cycl
0	-0.698286	-0.632736	-1.364256	-0.745075	-1.234925	0.649989	1.07303	1.633230	-0.783571	-0.6
1	-0.698286	0.847188	0.485719	0.830263	0.146043	0.649989	0.17013	0.448617	0.624242	-0.6
2	1.432078	0.292216	0.830323	1.410651	0.244683	-1.523349	-0.28132	-0.735996	0.739636	-0.6
3	-0.698286	1.032178	0.485719	-1.408376	1.329730	-0.436680	-0.28132	0.448617	0.970425	-0.6
4	-0.698286	-1.187707	-0.693187	0.747350	-1.037644	-1.523349	-0.28132	-0.735996	-1.337465	-0.6

5 rows × 42 columns

Normalization

In [184…

```
scaler = ps.MinMaxScaler()
pcos_sc = scaler.fit_transform(pcos_dt)
pcos_normalized_dt = pd.DataFrame(pcos_sc,columns = pcos_dt.columns)
```

In [185…

```
pcos_normalized_dt.head()
```

Out[185]:

	PCOS (Y/N)	Age (yrs)	Weight (Kg)	Height(Cm)	BMI	Blood Group	Pulse rate(bpm)	RR (breaths/min)	Hb(g/dl)	Cycle(R/I)
0	0.0	0.285714	0.176623	0.348837	0.260377	0.571429	0.942029	0.500000	0.314286	0.0
1	0.0	0.571429	0.441558	0.569767	0.471698	0.571429	0.884058	0.333333	0.507937	0.0
2	1.0	0.464286	0.490909	0.651163	0.486792	0.000000	0.855072	0.166667	0.523810	0.0
3	0.0	0.607143	0.441558	0.255814	0.652830	0.285714	0.855072	0.333333	0.555556	0.0
4	0.0	0.178571	0.272727	0.558140	0.290566	0.000000	0.855072	0.166667	0.238095	0.0

5 rows × 42 columns

Data Summarization

In [186…

```
pcos_dt.shape
```

Out[186]:

```
(540, 42)
```

In [187…

```
pcos_dt.dtypes
```

Out[187]:

```
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 abortions           int64
I   beta-HCG(mIU/mL)     float64
II    beta-HCG(mIU/mL)    object
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
dtype: object
```

In [188…

```
pcos_dt.describe()
```

Out[188]:

	PCOS (Y/N)	Age (yrs)	Weight (Kg)	Height(Cm)	BMI	Blood Group	Pulse rate(bpm)	RR (breaths/min)	H
count	540.000000	540.000000	540.000000	540.000000	540.000000	540.000000	540.000000	540.000000	540
mean	0.327778	31.420370	59.643889	156.493141	24.307778	13.803704	73.246296	19.242593	11
std	0.469839	5.410698	11.037399	6.036043	4.058886	1.842194	4.434274	1.689881	0
min	0.000000	20.000000	31.000000	137.000000	12.400000	11.000000	13.000000	16.000000	8
25%	0.000000	27.750000	52.000000	152.000000	21.600000	13.000000	72.000000	18.000000	10
50%	0.000000	31.000000	59.300000	156.000000	24.200000	14.000000	72.000000	18.000000	11
75%	1.000000	35.000000	65.000000	160.000000	26.625000	15.000000	74.000000	20.000000	11
max	1.000000	48.000000	108.000000	180.000000	38.900000	18.000000	82.000000	28.000000	14

8 rows × 40 columns

In [189…]
```
pcos_dt.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 540 entries, 0 to 540
Data columns (total 42 columns):
 #   Column                  Non-Null Count  Dtype  
---  ------                  --------------  -----  
 0   PCOS (Y/N)              540 non-null    int64  
 1   Age (yrs)               540 non-null    int64  
 2   Weight (Kg)             540 non-null    float64
 3   Height(Cm)              540 non-null    float64
 4   BMI                     540 non-null    float64
 5   Blood Group             540 non-null    int64  
 6   Pulse rate(bpm)         540 non-null    int64  
 7   RR (breaths/min)        540 non-null    int64  
 8   Hb(g/dl)                540 non-null    float64
 9   Cycle(R/I)              540 non-null    int64  
 10  Cycle length(days)      540 non-null    int64  
 11  Marraige Status (Yrs)   540 non-null    float64
 12  Pregnant(Y/N)           540 non-null    int64  
 13  No. of abortions        540 non-null    int64  
 14  I   beta-HCG(mIU/mL)    540 non-null    float64
 15  II    beta-HCG(mIU/mL)  540 non-null    object 
 16  FSH(mIU/mL)             540 non-null    float64
 17  LH(mIU/mL)              540 non-null    float64
 18  FSH/LH                  540 non-null    float64
 19  Hip(inch)               540 non-null    int64  
 20  Waist(inch)             540 non-null    int64  
 21  Waist:Hip Ratio         540 non-null    float64
 22  TSH (mIU/L)             540 non-null    float64
 23  AMH(ng/mL)              540 non-null    object 
 24  PRL(ng/mL)              540 non-null    float64
 25  Vit D3 (ng/mL)          540 non-null    float64
 26  PRG(ng/mL)              540 non-null    float64
 27  RBS(mg/dl)              540 non-null    float64
 28  Weight gain(Y/N)        540 non-null    int64  
 29  hair growth(Y/N)        540 non-null    int64  
 30  Skin darkening (Y/N)    540 non-null    int64  
 31  Hair loss(Y/N)          540 non-null    int64  
 32  Pimples(Y/N)            540 non-null    int64  
 33  Fast food (Y/N)         540 non-null    float64
 34  Reg.Exercise(Y/N)       540 non-null    int64  
 35  BP _Systolic (mmHg)     540 non-null    int64  
 36  BP _Diastolic (mmHg)    540 non-null    int64  
 37  Follicle No. (L)        540 non-null    int64  
 38  Follicle No. (R)        540 non-null    int64  
 39  Avg. F size (L) (mm)    540 non-null    float64
 40  Avg. F size (R) (mm)    540 non-null    float64
 41  Endometrium (mm)        540 non-null    float64
dtypes: float64(19), int64(21), object(2)
memory usage: 181.4+ KB
```

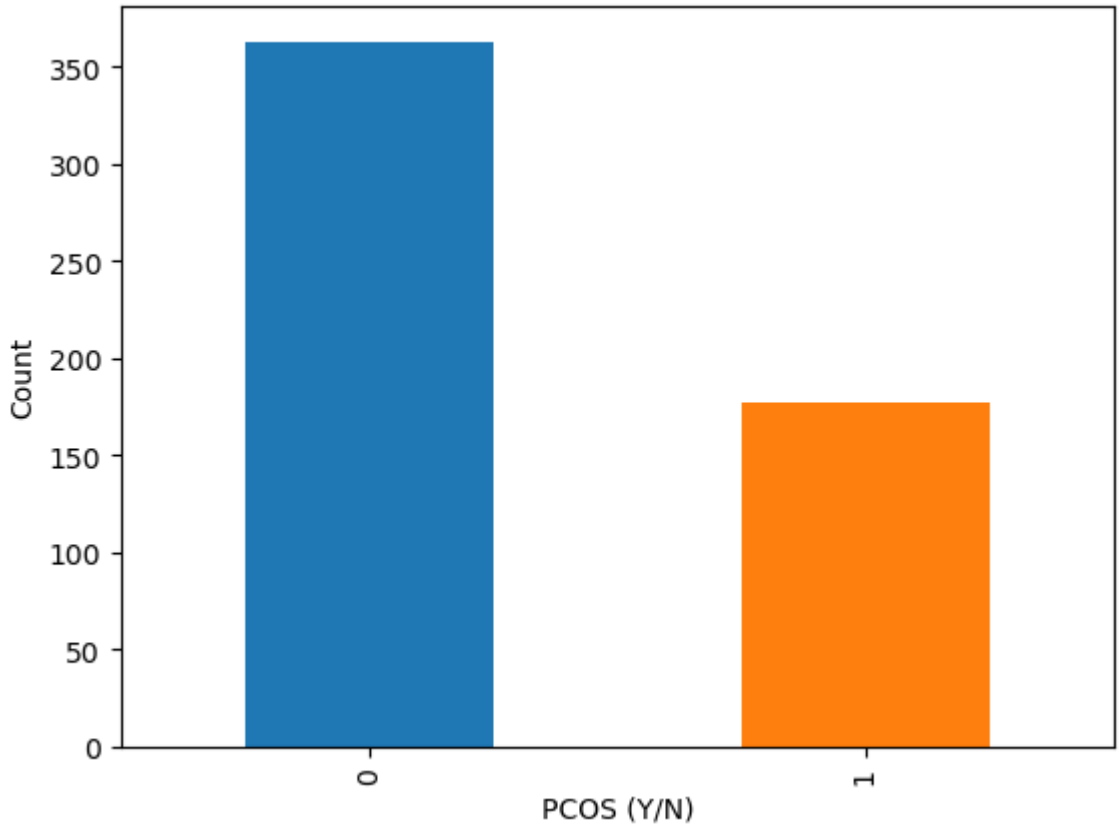
In [190…]
```
pcos_dt.to_csv("pcos_datatset_cleaned.csv")
```

Data Visualization

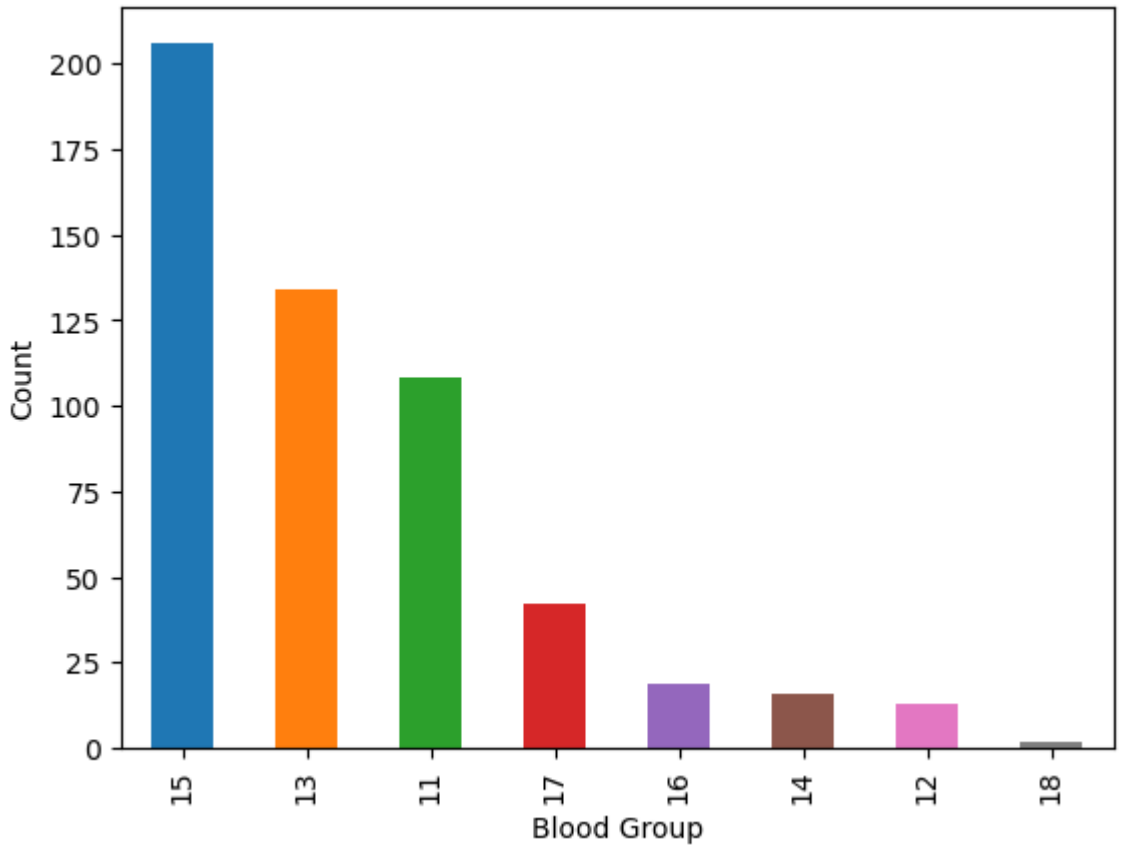
In [191…]
```
# Plotting all the categorical variables using bar plot
cv = ['PCOS (Y/N)','Blood Group','Pregnant(Y/N)','Weight gain(Y/N)','hair growth(Y/N)','Skin
       'Fast food (Y/N)', 'Reg.Exercise(Y/N)']

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()
```

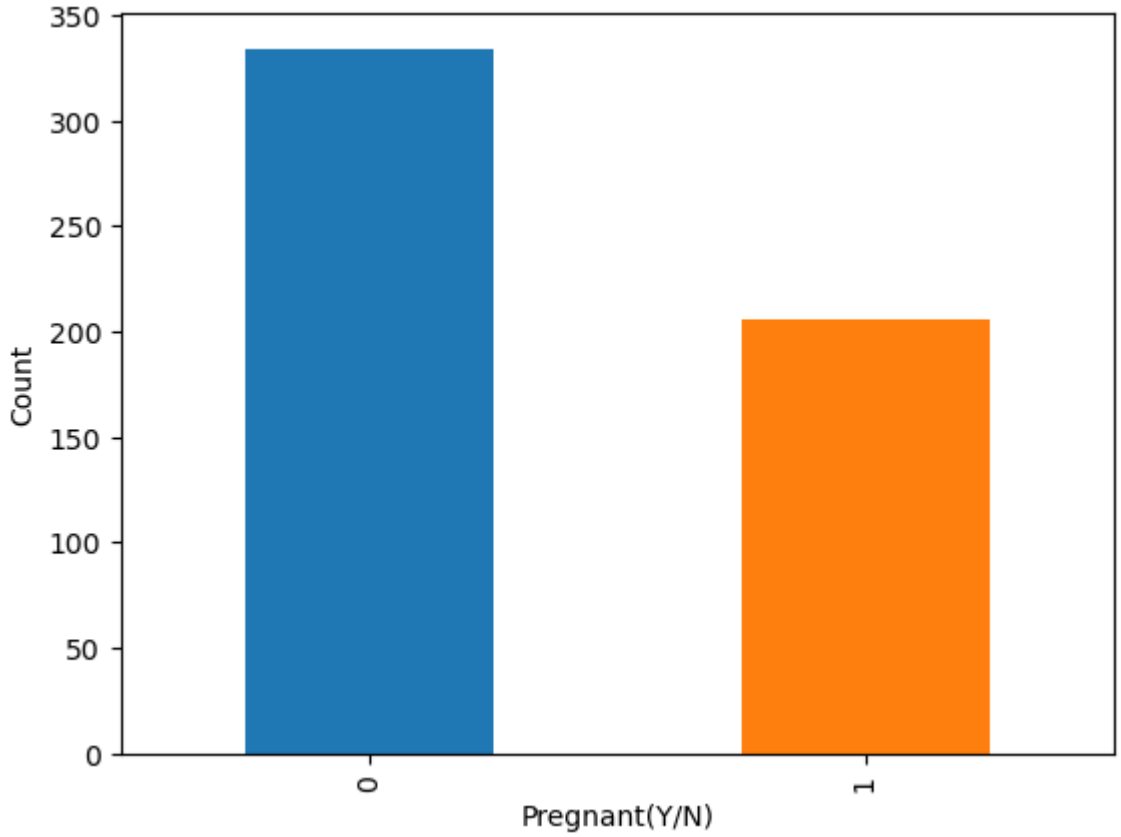
```
PCOS (Y/N)
PCOS (Y/N)
0    363
1    177
Name: count, dtype: int64
```



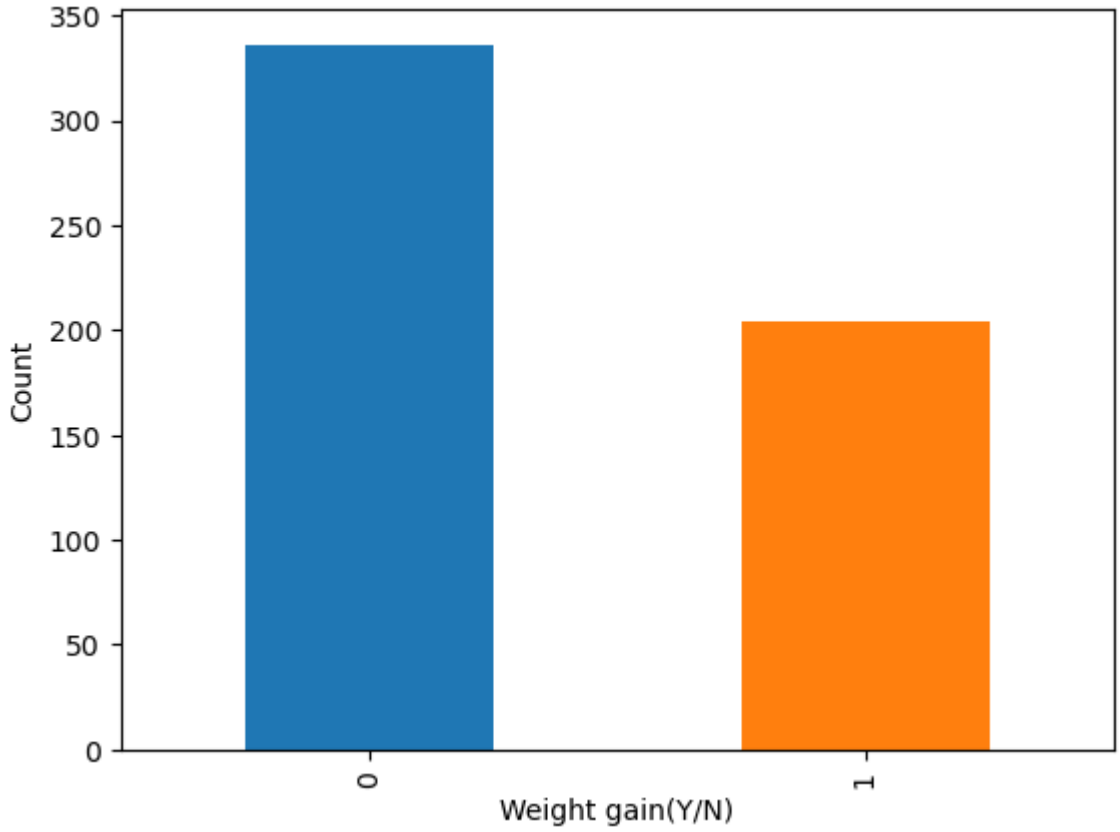

```
Blood Group
Blood Group
15    206
13    134
11    108
17     42
16     19
14     16
12     13
18      2
Name: count, dtype: int64
```



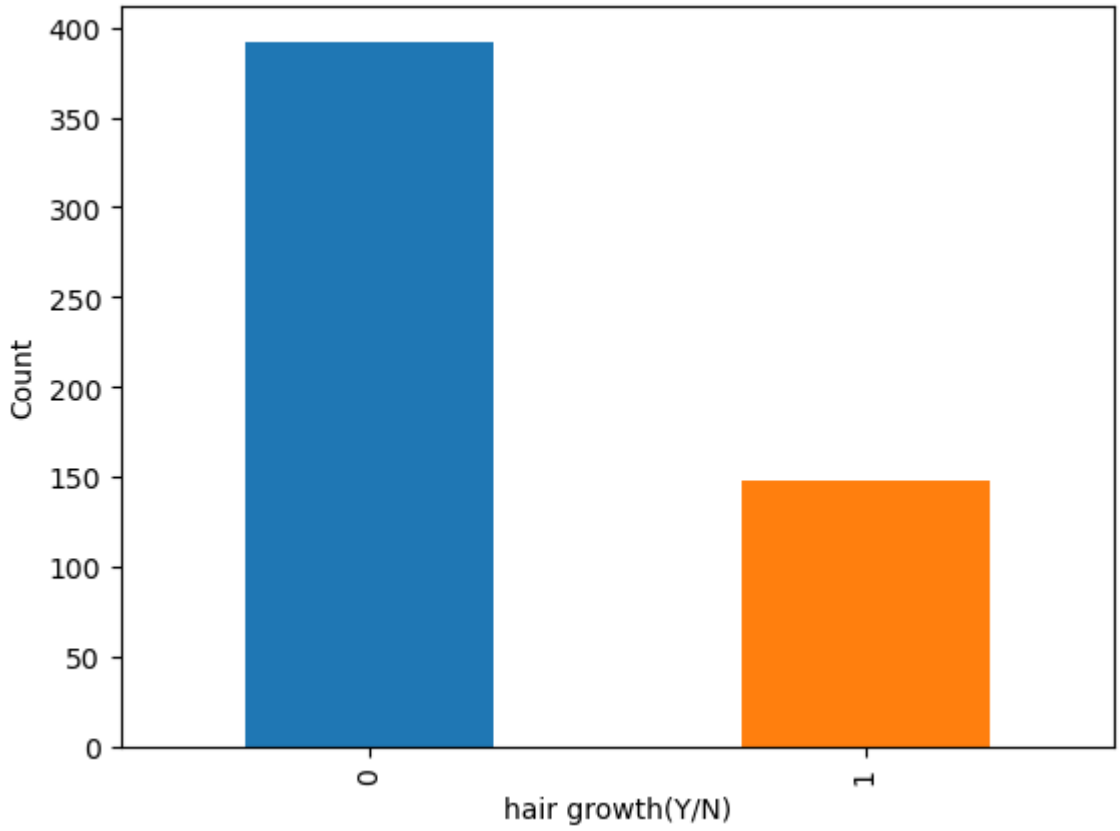

```
Pregnant(Y/N)
Pregnant(Y/N)
0    334
1    206
Name: count, dtype: int64
```



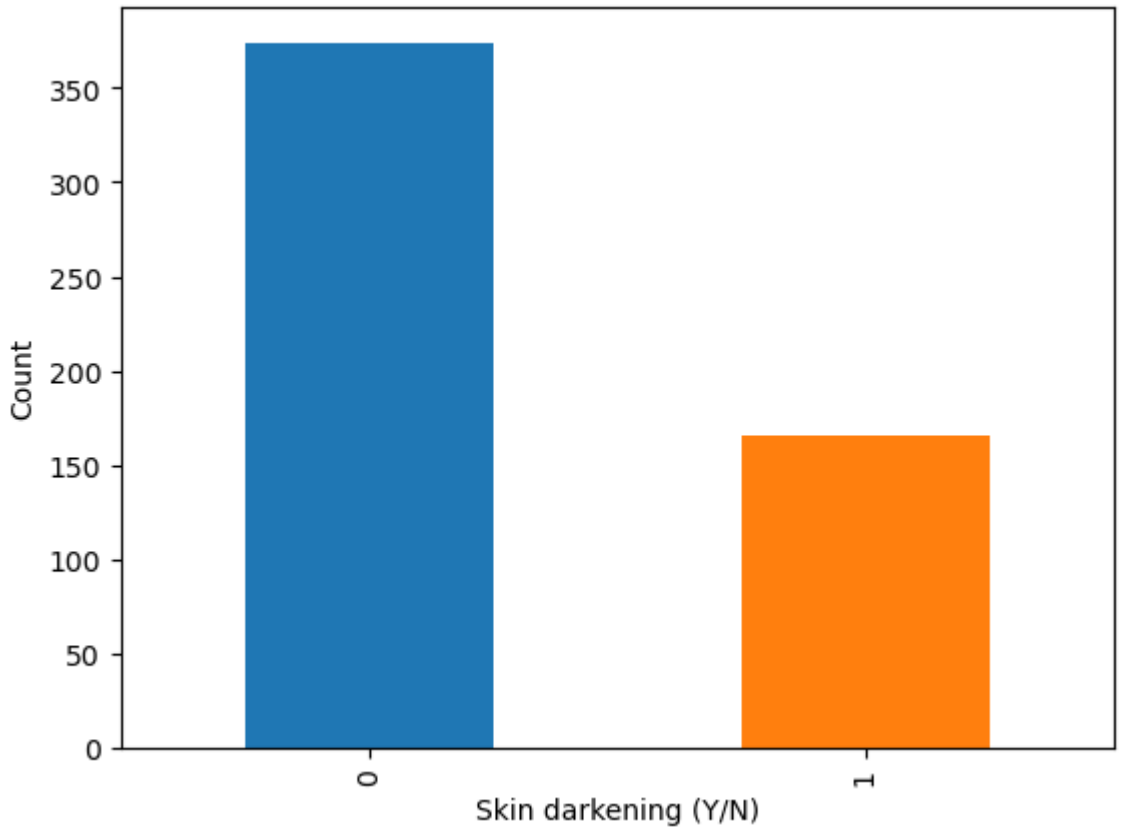

```
Weight gain(Y/N)
Weight gain(Y/N)
0    336
1    204
Name: count, dtype: int64
```



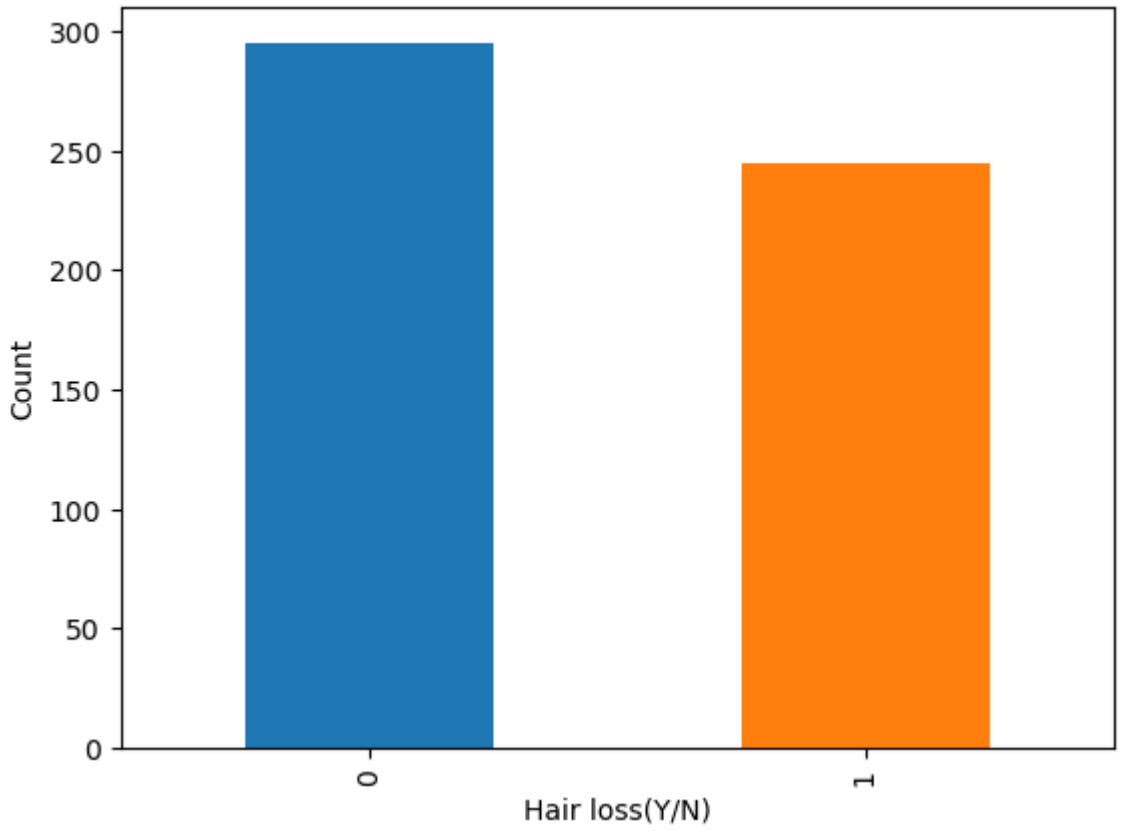

```
hair growth(Y/N)
hair growth(Y/N)
0    392
1    148
Name: count, dtype: int64
```



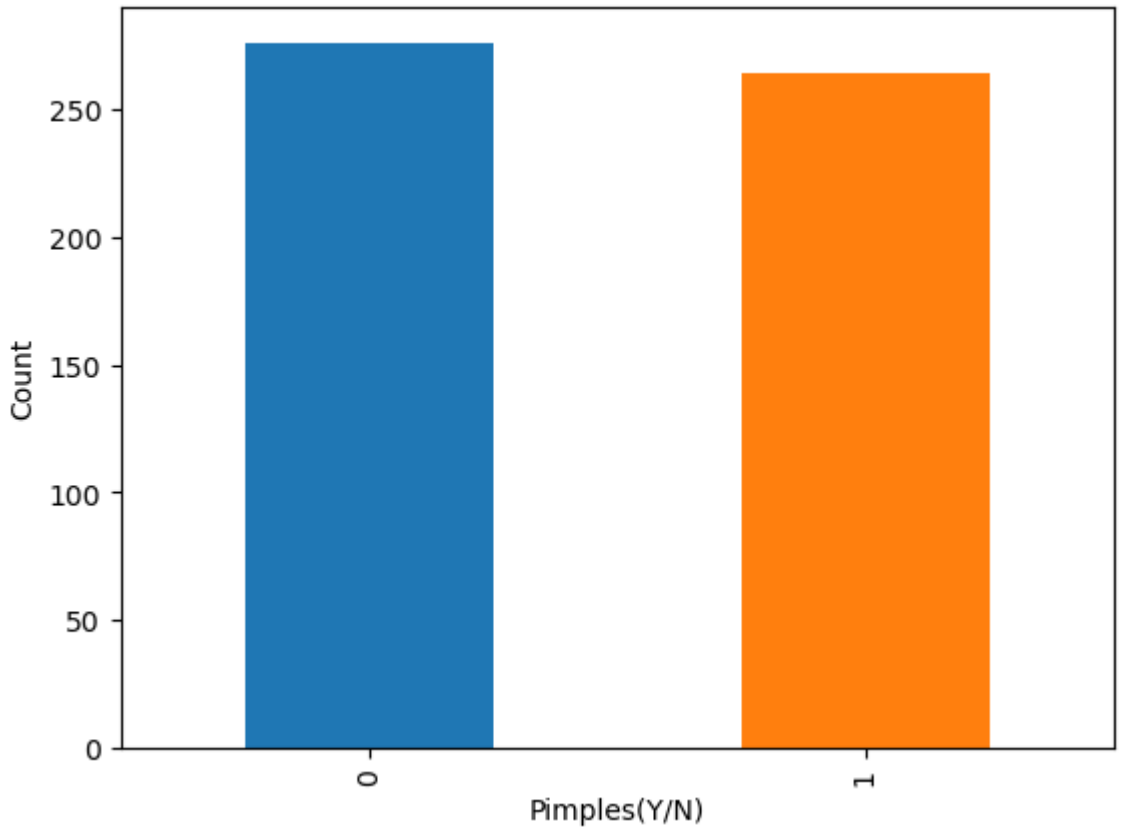

```
Skin darkening (Y/N)
Skin darkening (Y/N)
0    374
1    166
Name: count, dtype: int64
```



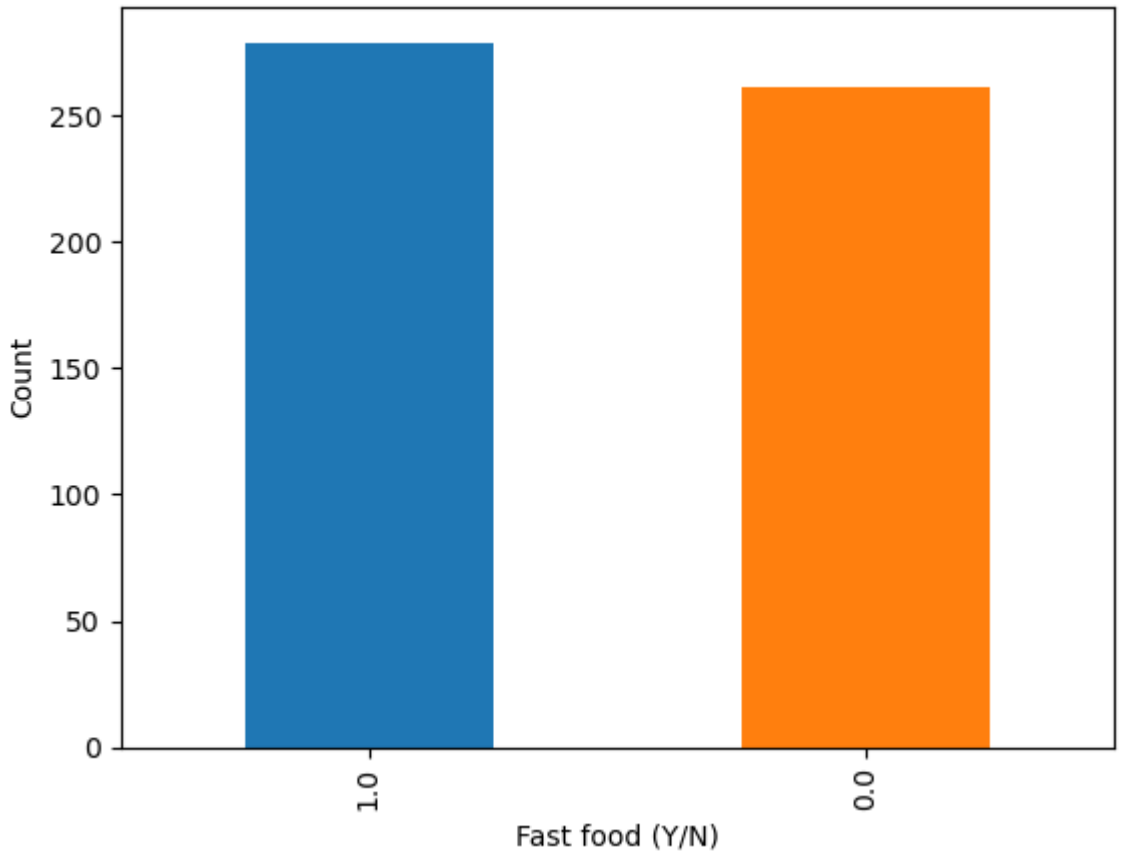

```
Hair loss(Y/N)
Hair loss(Y/N)
0    295
1    245
Name: count, dtype: int64
```



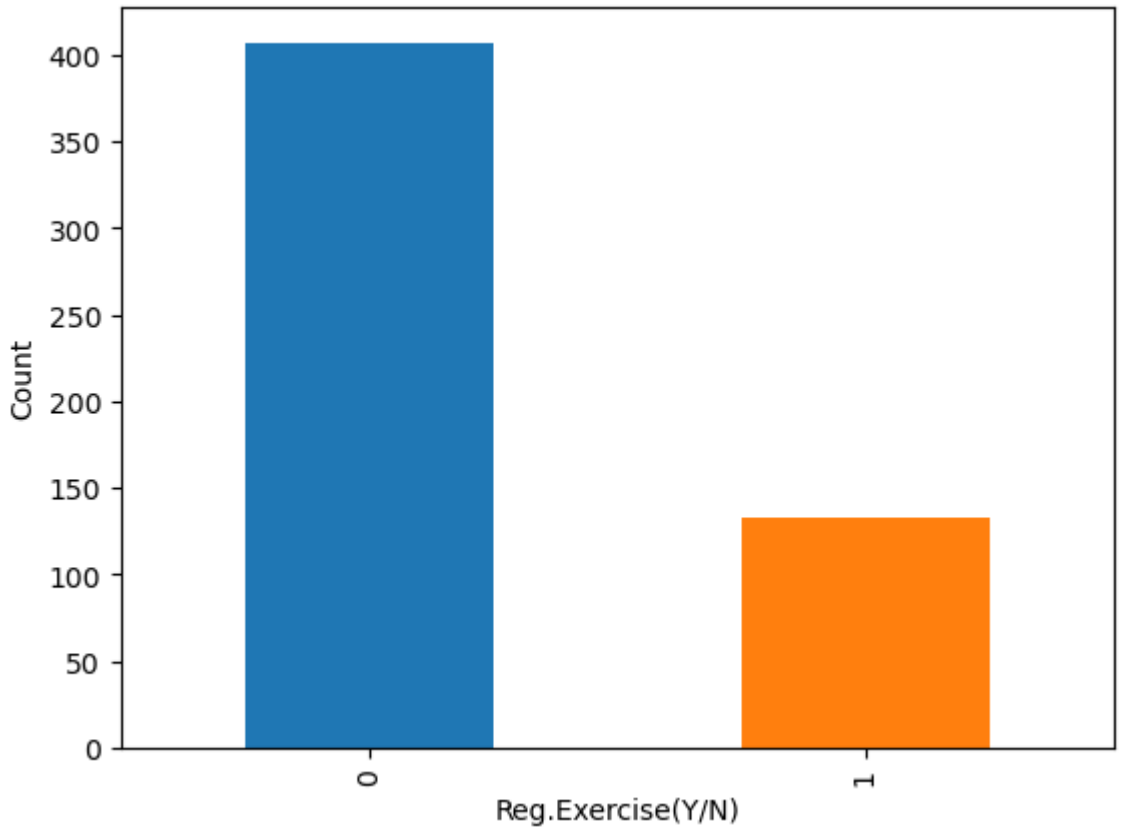

```
Pimples(Y/N)
Pimples(Y/N)
0    276
1    264
Name: count, dtype: int64
```




```
Fast food (Y/N)
Fast food (Y/N)
1.0    279
0.0    261
Name: count, dtype: int64
```

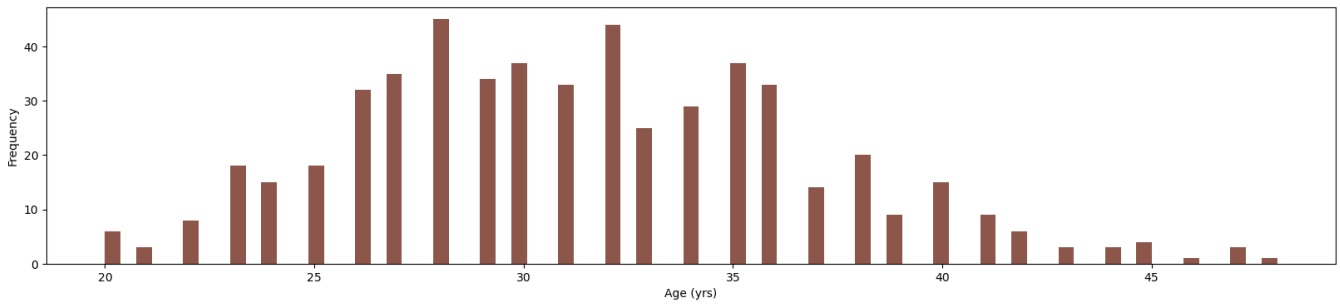


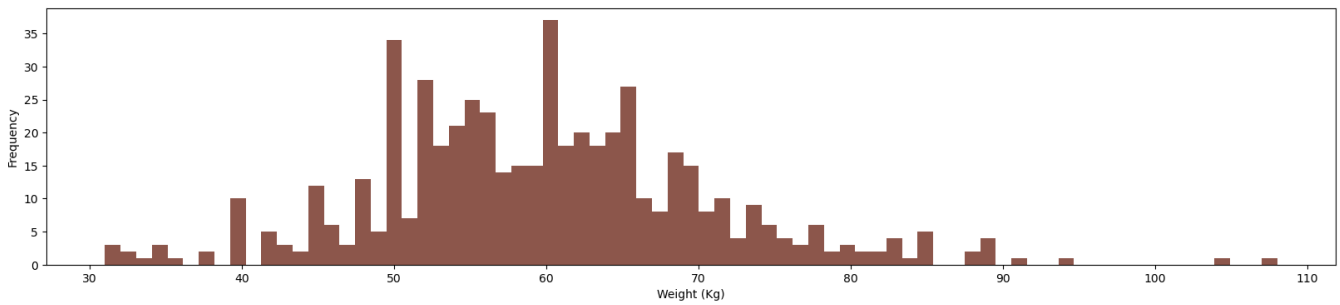

```
Reg.Exercise(Y/N)
Reg.Exercise(Y/N)
0    407
1    133
Name: count, dtype: int64
```

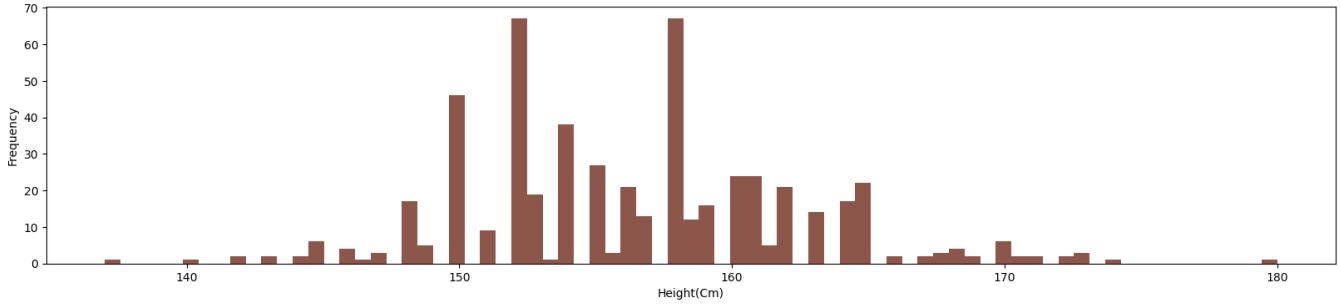


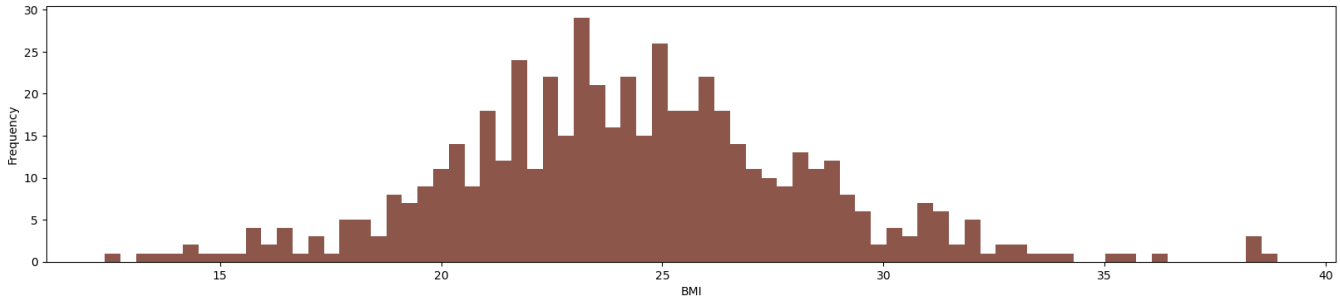
In [192…

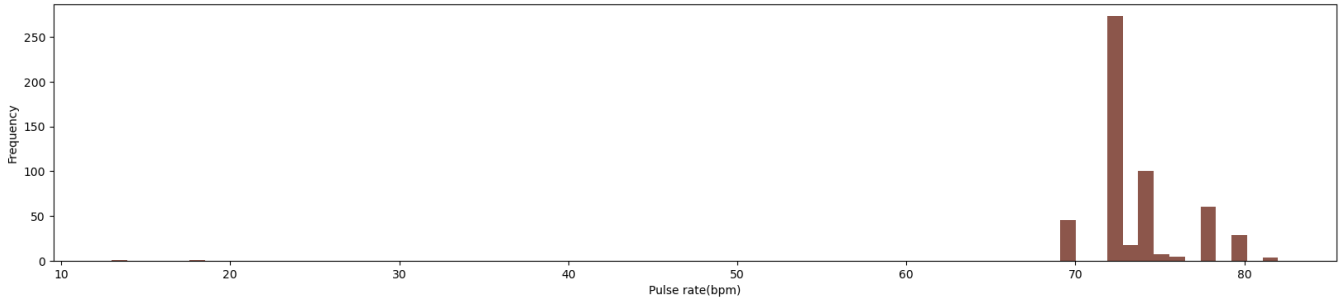
```
# Plotting all the numerical variables using bar plot
nv = ['Age (yrs)', 'Weight (Kg)','Height(Cm)', 'BMI','Pulse rate(bpm)',
       'RR (breaths/min)', 'Hb(g/dl)', 'Cycle(R/I)', 'Cycle length(days)',
       'Marraige Status (Yrs)','I   beta-HCG(mIU/mL)', 'FSH(mIU/mL)',
       'LH(mIU/mL)', 'FSH/LH', 'Hip(inch)', 'Waist(inch)', 'Waist:Hip Ratio',
       'TSH (mIU/L)', 'PRL(ng/mL)', 'Vit D3 (ng/mL)',
       'PRG(ng/mL)', 'RBS(mg/dl)','BP _Systolic (mmHg)',
       'BP _Diastolic (mmHg)', 'Follicle No. (L)', 'Follicle No. (R)',
       'Avg. F size (L) (mm)', 'Avg. F size (R) (mm)', 'Endometrium (mm)']
for i in nv:
  plt.figure(figsize=(20,4))
  plt.hist(pcos_dt[i], bins = 75,color='C5')
  plt.xlabel(i)
  plt.ylabel('Frequency')
  plt.show()
```

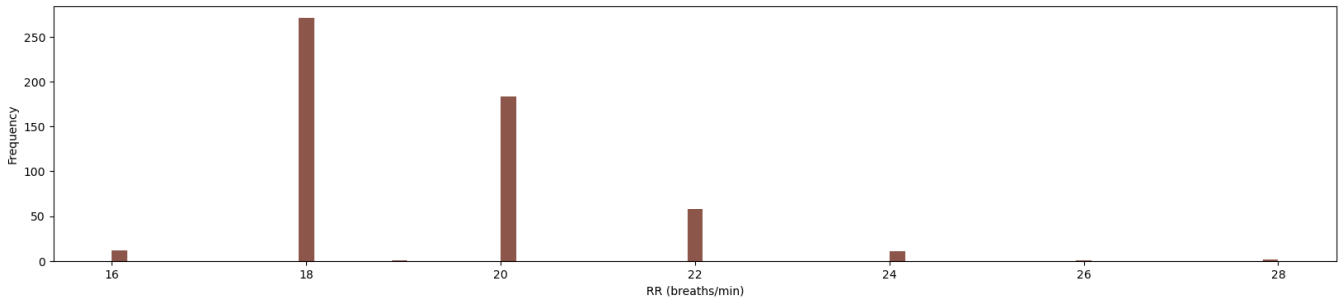


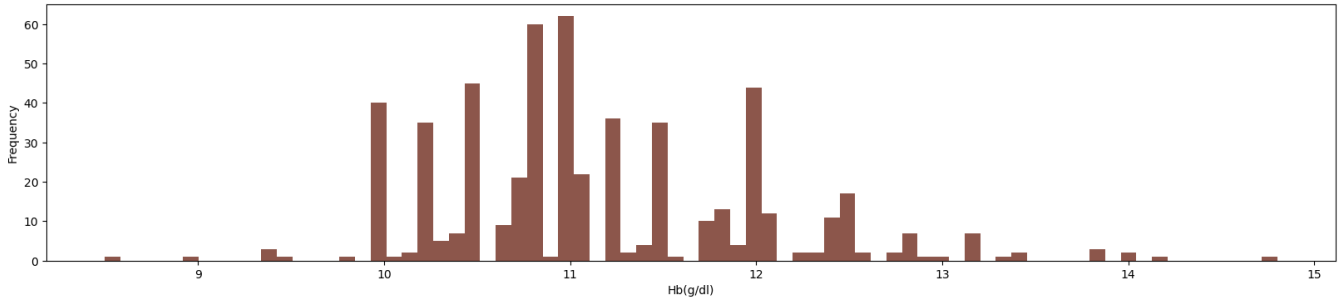


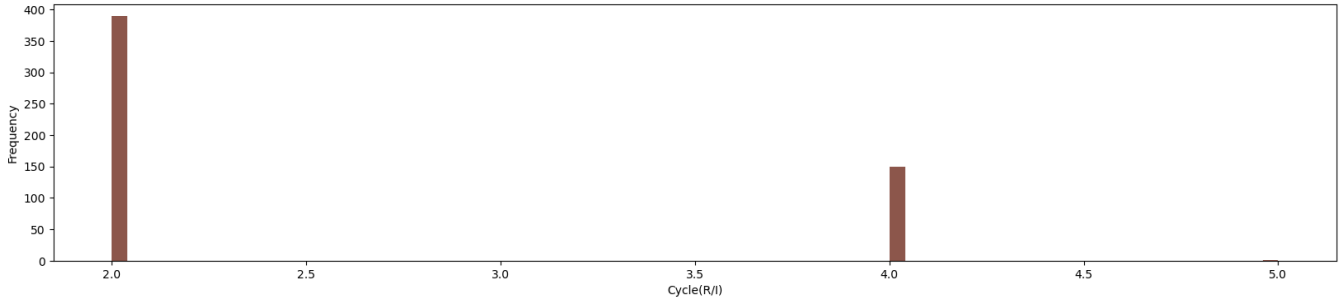

Frequency
Height(Cm)

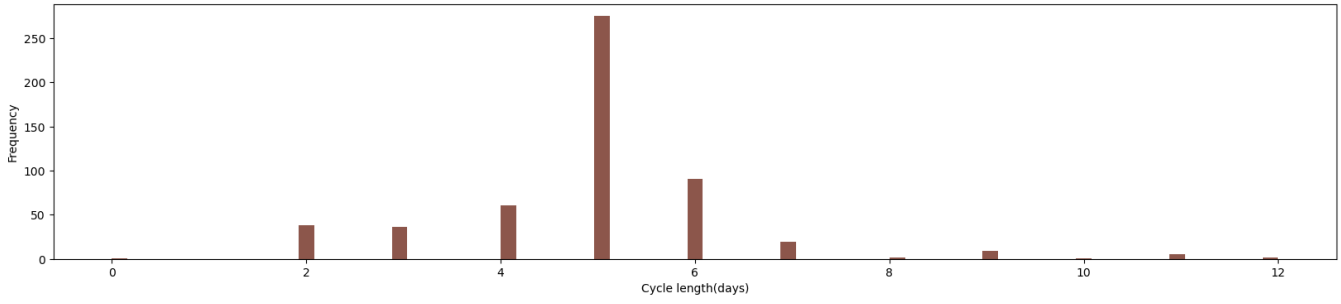

Frequency
BMI

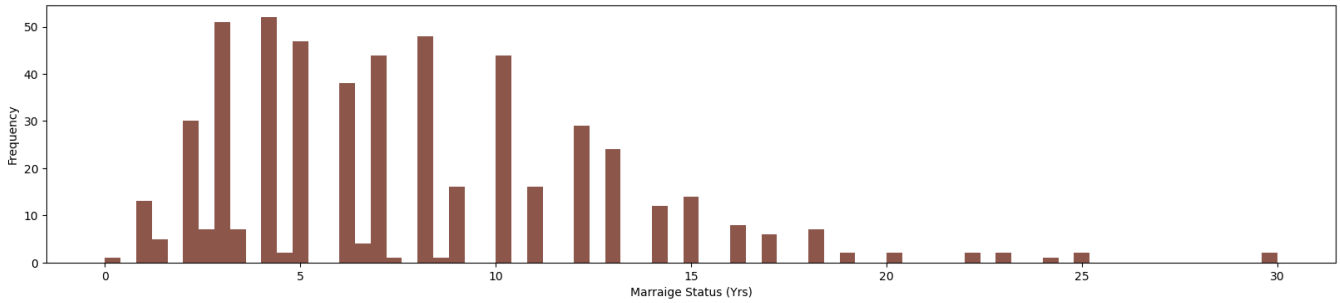

Frequency
Pulse rate(bpm)

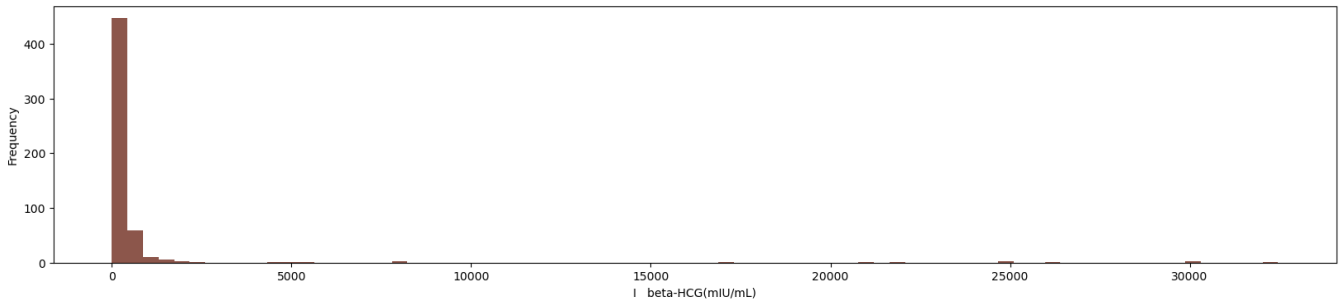

Frequency
RR (breaths/min)

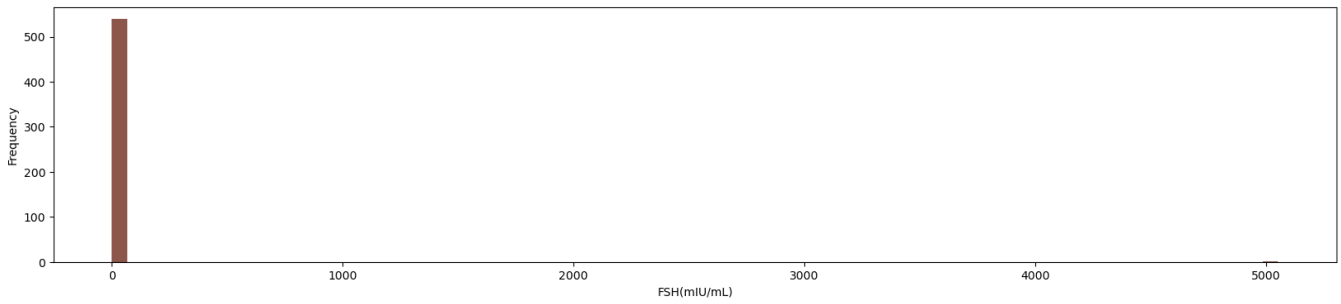

Frequency
Hb(g/dl)

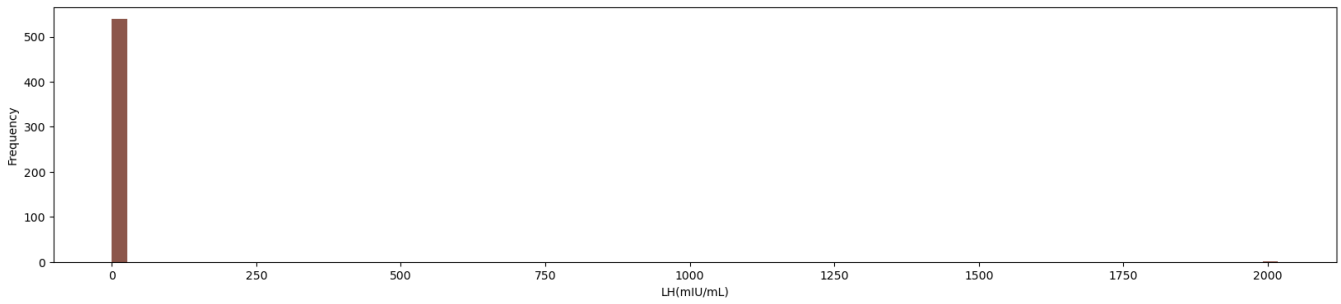

Frequency
Cycle(R/I)

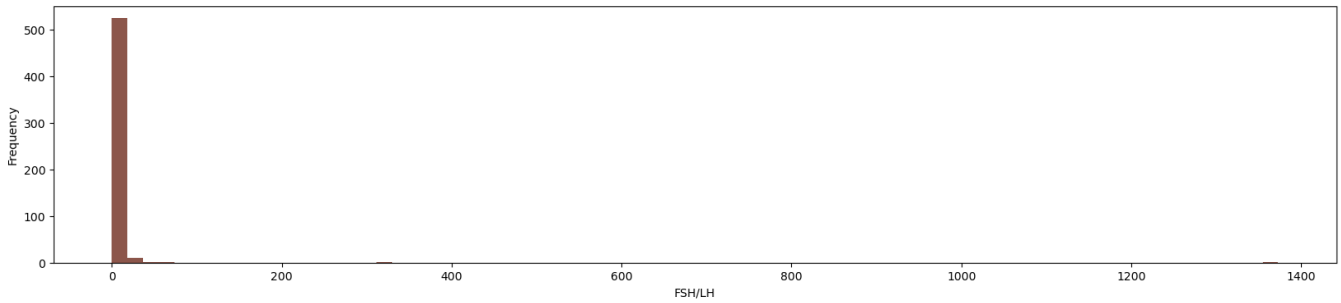

Frequency
Cycle length(days)

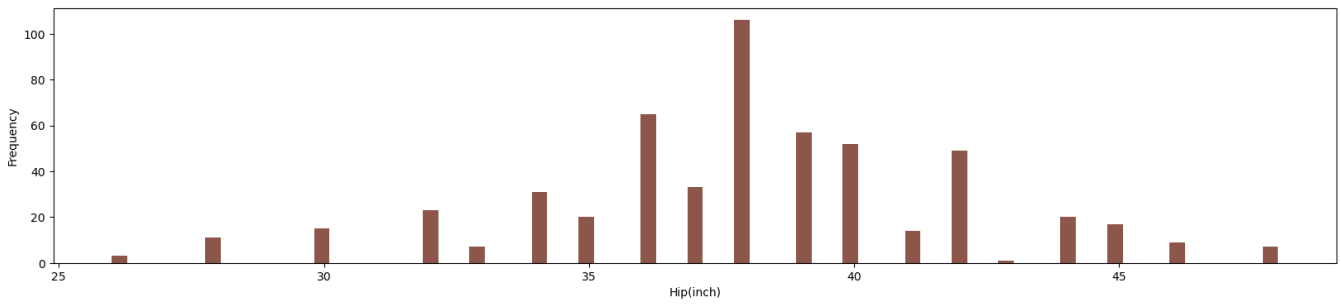

Frequency
Marraige Status (Yrs)

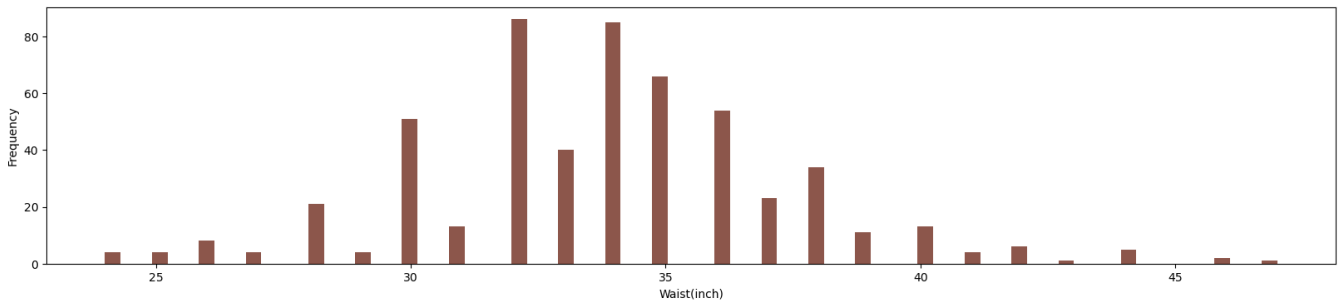

Frequency
I beta-HCG(mIU/mL)

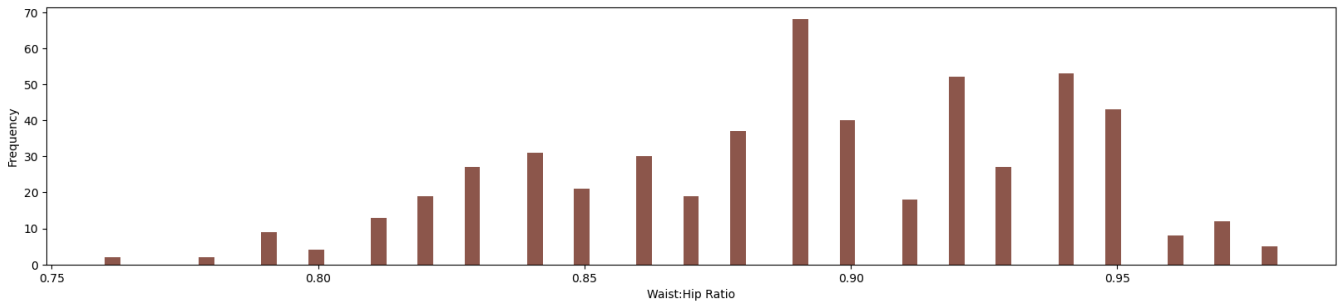

Frequency
FSH(mIU/mL)

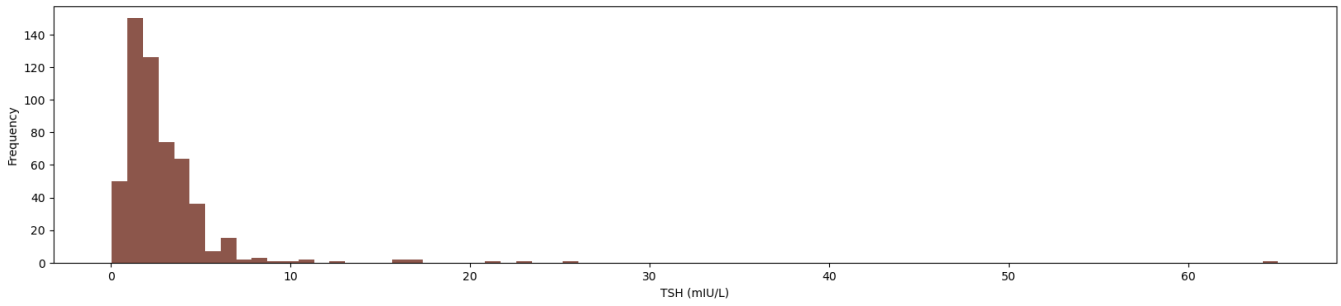

Frequency
LH(mIU/mL)

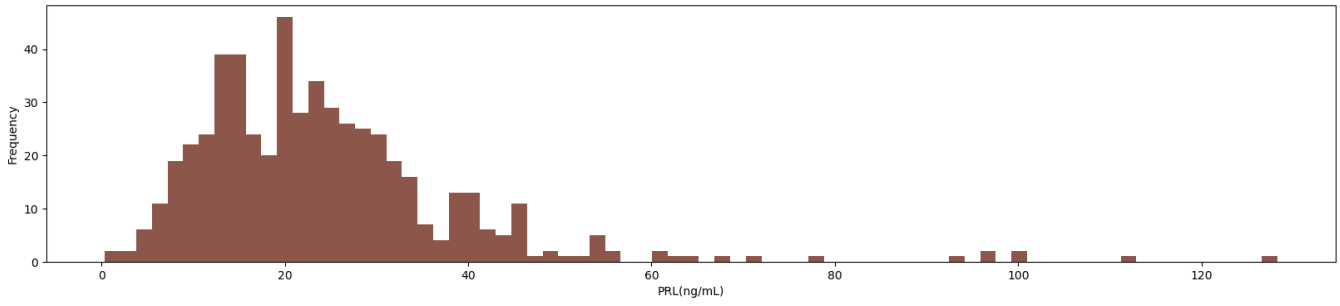

Frequency
FSH/LH

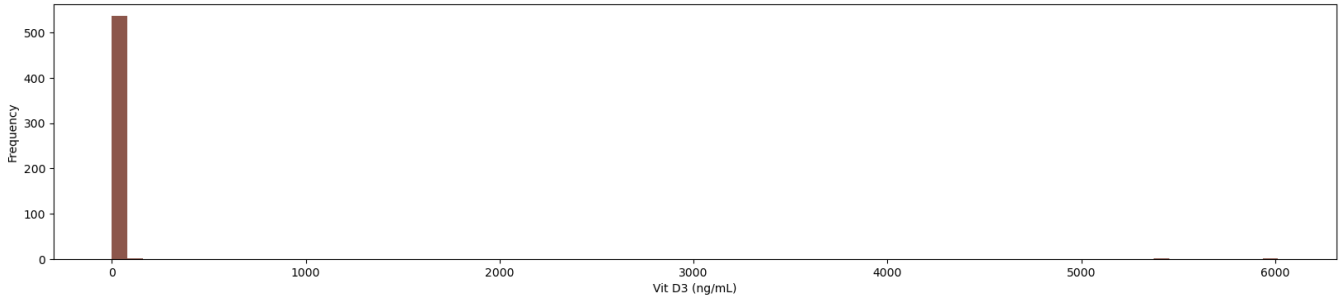

Frequency
Hip(inch)

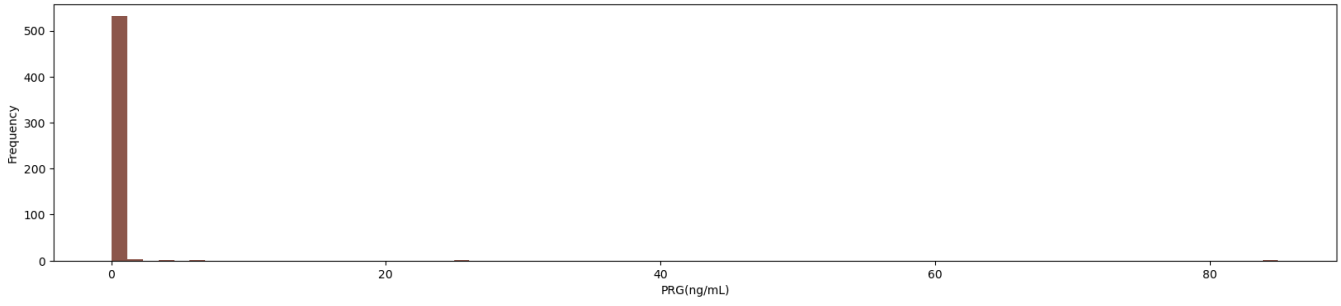

Frequency
Waist(inch)

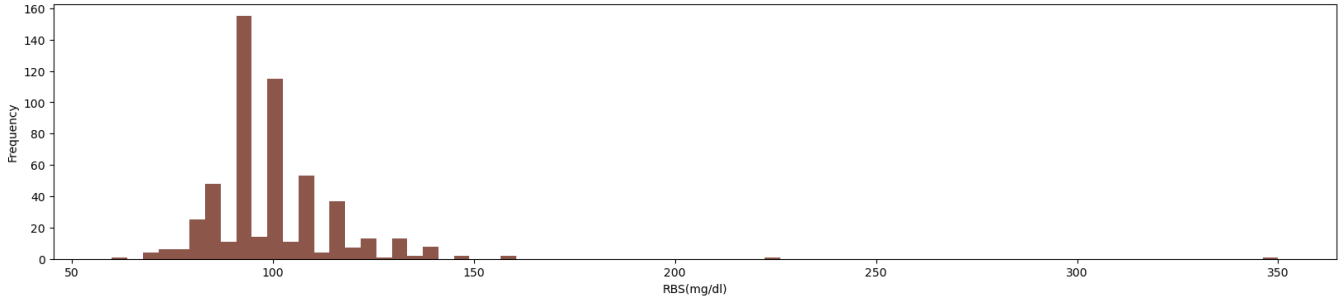

Frequency
Waist:Hip Ratio

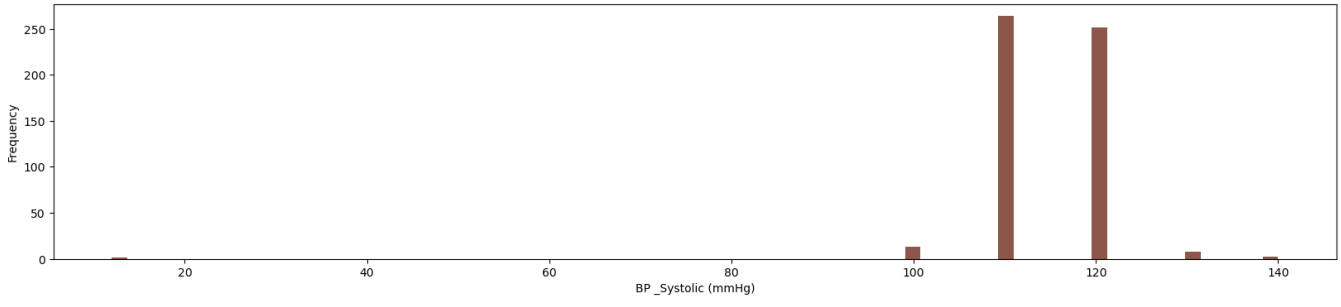

Frequency
TSH (mIU/L)

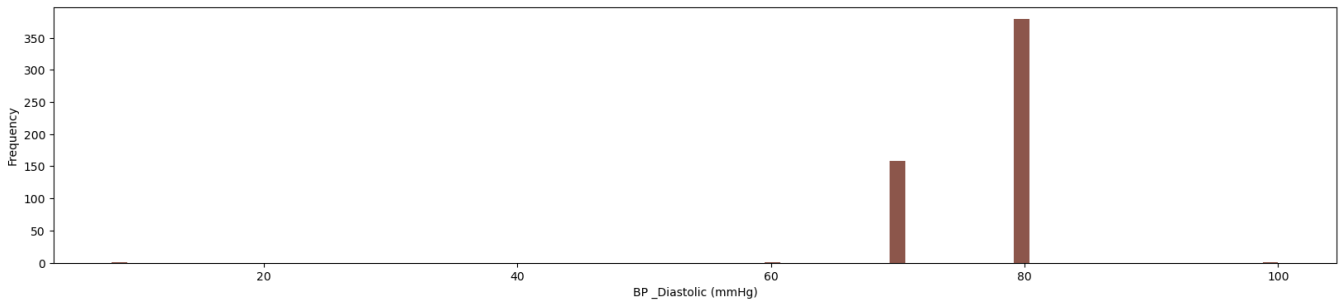

Frequency
PRL(ng/mL)

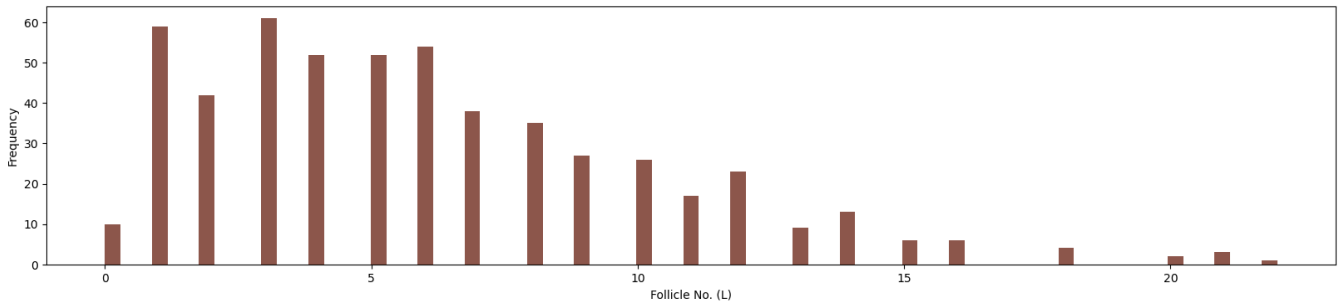

Frequency
Vit D3 (ng/mL)

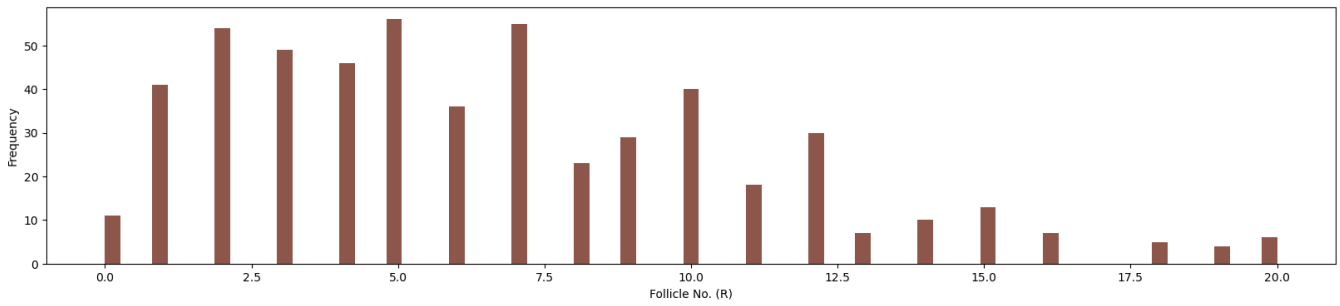

Frequency
PRG(ng/mL)

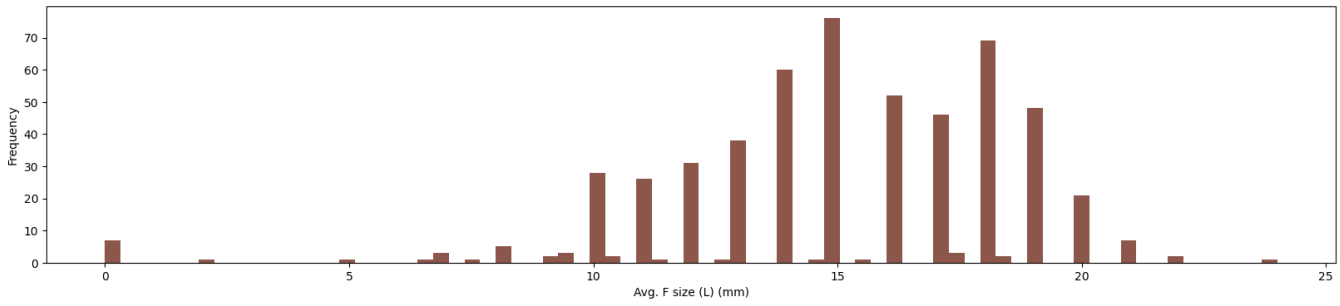

Frequency
RBS(mg/dl)

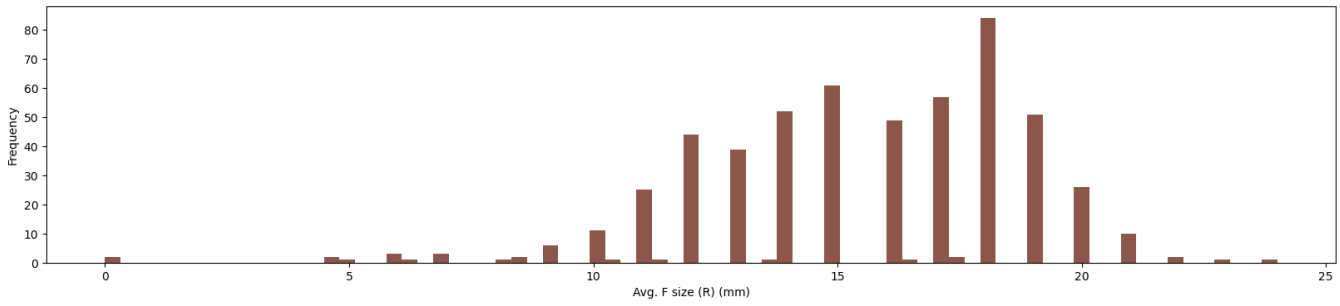

Frequency
BP _Systolic (mmHg)

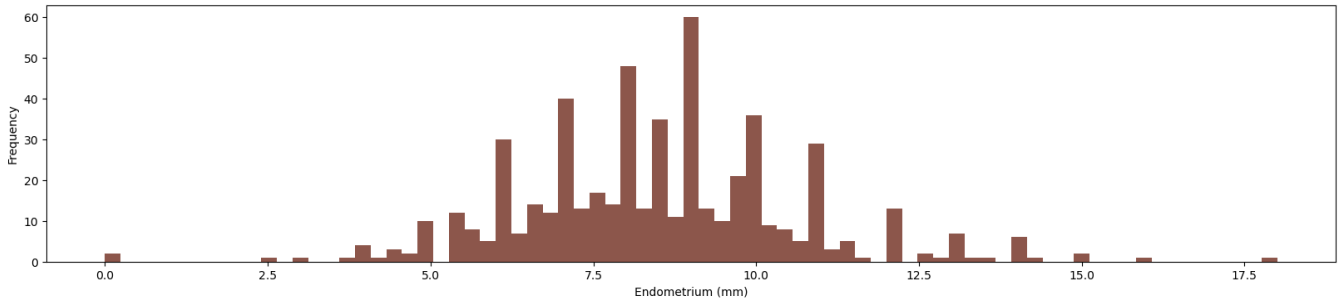












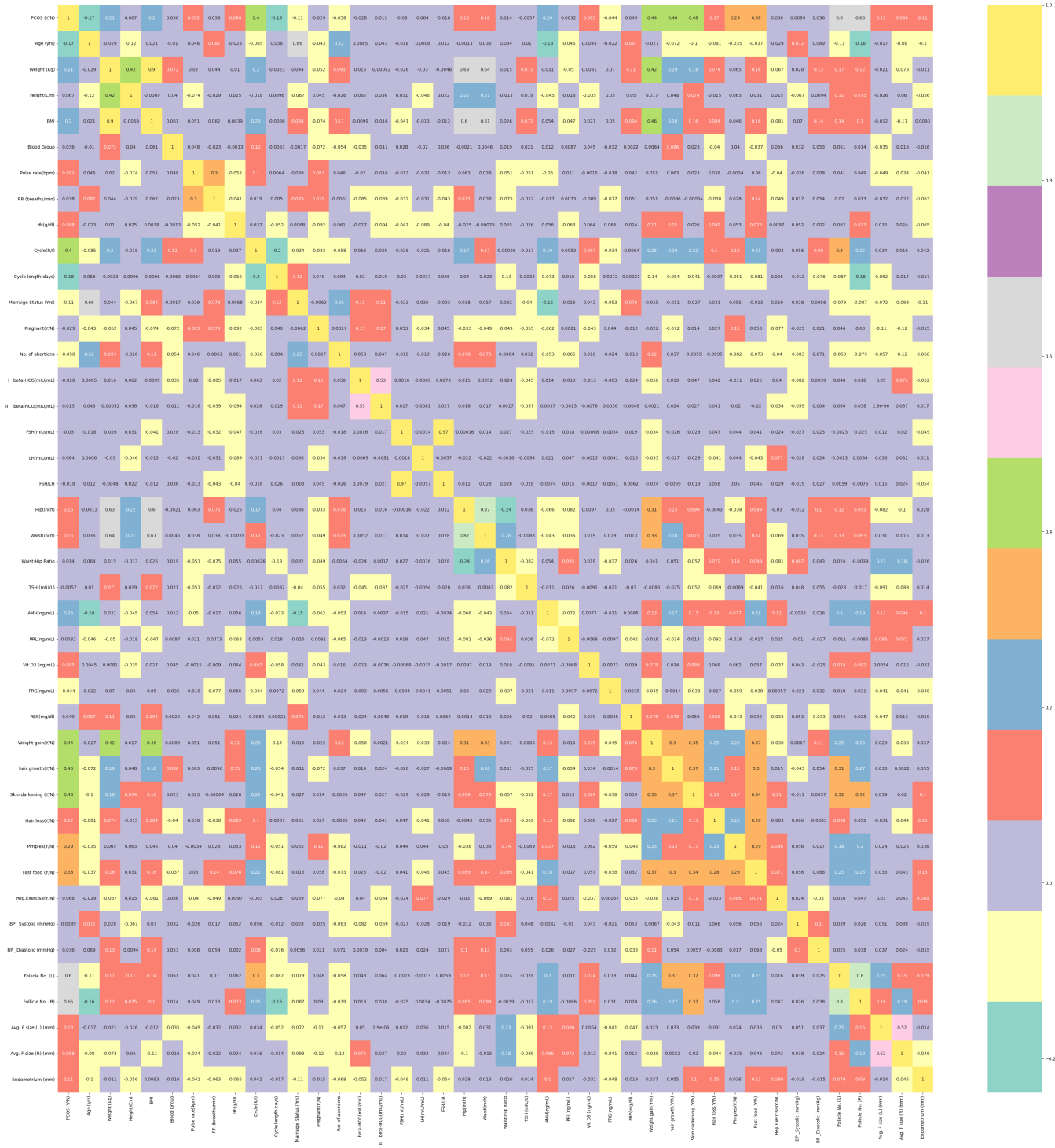
Feature Selection

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 [193…

```
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")
```



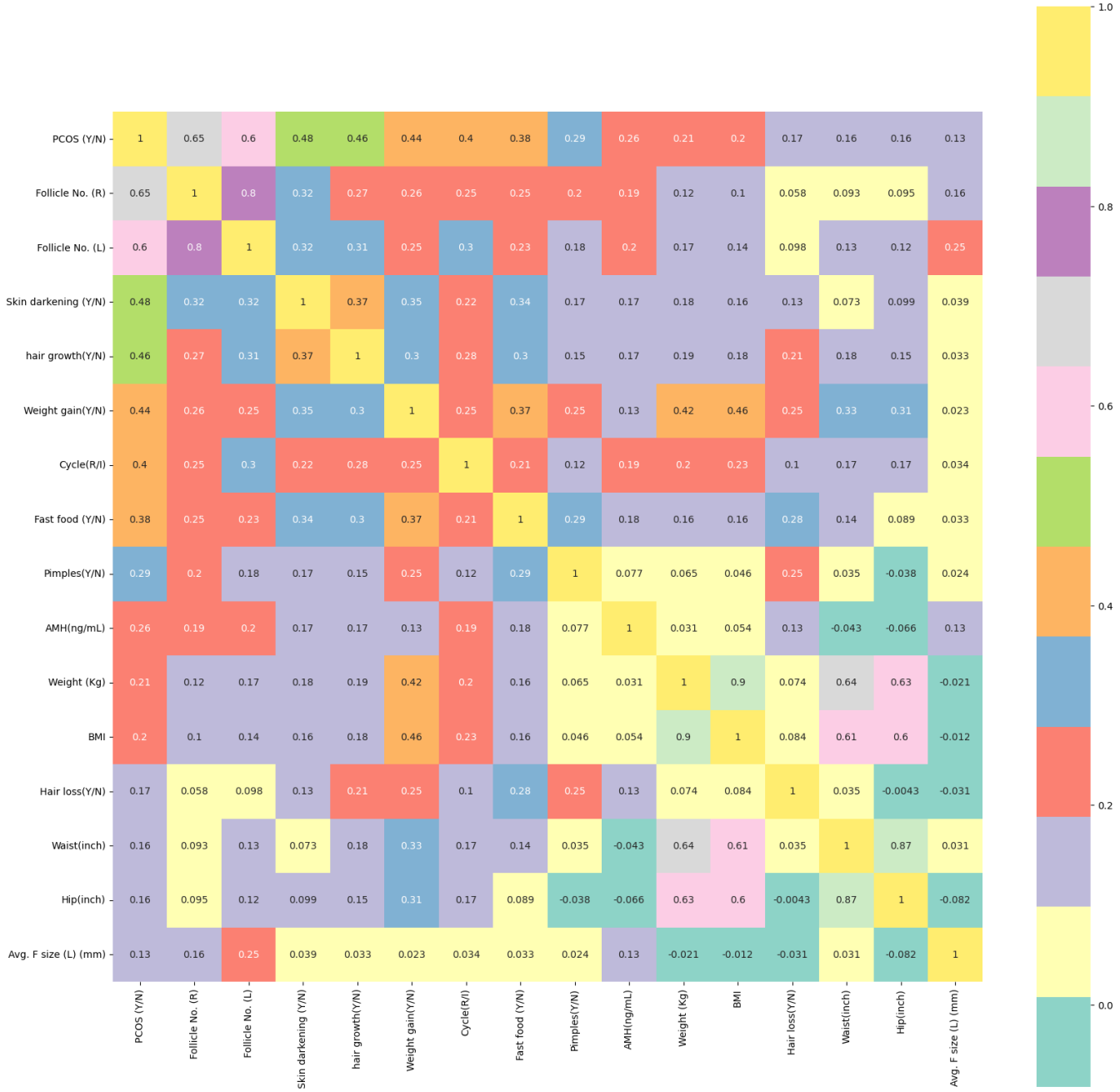
In [194…

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

Out[194]:
```
PCOS (Y/N)                1.000000
Follicle No. (R)          0.648223
Follicle No. (L)          0.603109
Skin darkening (Y/N)      0.475283
hair growth(Y/N)          0.464245
Weight gain(Y/N)          0.440488
Cycle(R/I)                0.401165
Fast food (Y/N)           0.375389
Pimples(Y/N)              0.287802
AMH(ng/mL)                0.263863
Weight (Kg)               0.211628
BMI                       0.199753
Hair loss(Y/N)            0.171913
Waist(inch)               0.164378
Hip(inch)                 0.161480
Avg. F size (L) (mm)      0.133808
Endometrium (mm)          0.105151
Avg. F size (R) (mm)      0.097950
Pulse rate(bpm)           0.092084
Hb(g/dl)                  0.088046
Vit D3 (ng/mL)            0.085491
Reg.Exercise(Y/N)         0.067809
Height(Cm)                0.067358
LH(mIU/mL)                0.063817
RBS(mg/dl)                0.048956
RR (breaths/min)          0.037530
BP _Diastolic (mmHg)      0.036494
Blood Group               0.035892
Waist:Hip Ratio           0.013520
II    beta-HCG(mIU/mL)    0.012576
BP _Systolic (mmHg)       0.008885
PRL(ng/mL)                0.003243
TSH (mIU/L)              -0.005726
FSH/LH                   -0.018312
I   beta-HCG(mIU/mL)     -0.027870
Pregnant(Y/N)            -0.028606
FSH(mIU/mL)              -0.030403
PRG(ng/mL)               -0.043960
No. of abortions         -0.057732
Marraige Status (Yrs)    -0.112759
Age (yrs)                -0.167422
Cycle length(days)       -0.178509
Name: PCOS (Y/N), dtype: float64
```

Selecting the top 15 features with highest p-value

In [195…
```
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 [196…
```
correlation_mat.nlargest(16,'PCOS (Y/N)')['PCOS (Y/N)']
```

Out[196]:
```
PCOS (Y/N)              1.000000
Follicle No. (R)        0.648223
Follicle No. (L)        0.603109
Skin darkening (Y/N)    0.475283
hair growth(Y/N)        0.464245
Weight gain(Y/N)        0.440488
Cycle(R/I)              0.401165
Fast food (Y/N)         0.375389
Pimples(Y/N)            0.287802
AMH(ng/mL)              0.263863
Weight (Kg)             0.211628
BMI                     0.199753
Hair loss(Y/N)          0.171913
Waist(inch)             0.164378
Hip(inch)               0.161480
Avg. F size (L) (mm)    0.133808
Name: PCOS (Y/N), dtype: float64
```

In [197…
```
imp_features
```

Out[197]:
```
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)', 'AMH(ng/mL)',
       'Weight (Kg)', 'BMI', 'Hair loss(Y/N)', 'Waist(inch)', 'Hip(inch)',
       'Avg. F size (L) (mm)'],
      dtype='object')
```

In [198…
```
pcos_df = pcos_normalized_dt[imp_features]
```

In [199…
```
pcos_df.head()
# pcos_df.shape
```

Out[199]:

	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)	AMH(ng/mL)
0	0.0	0.15	0.136364	0.0	0.0	0.0	0.0	1.0	0.0	0.029894
1	0.0	0.25	0.136364	0.0	0.0	0.0	0.0	0.0	0.0	0.021700
2	1.0	0.75	0.590909	0.0	0.0	0.0	0.0	1.0	1.0	0.099090
3	0.0	0.10	0.090909	0.0	0.0	0.0	0.0	0.0	0.0	0.016995
4	0.0	0.20	0.136364	0.0	0.0	0.0	0.0	0.0	0.0	0.032777

Model

Dataset splitting

Splitting dataset into training, validation, and test sets.

In [200…
```
X = pcos_df.iloc[:,1:].values
y = pcos_df.iloc[:,0].values
```

In [201…
```
print(X.shape)
print(y.shape)
```

```
(540, 15)
(540,)
```

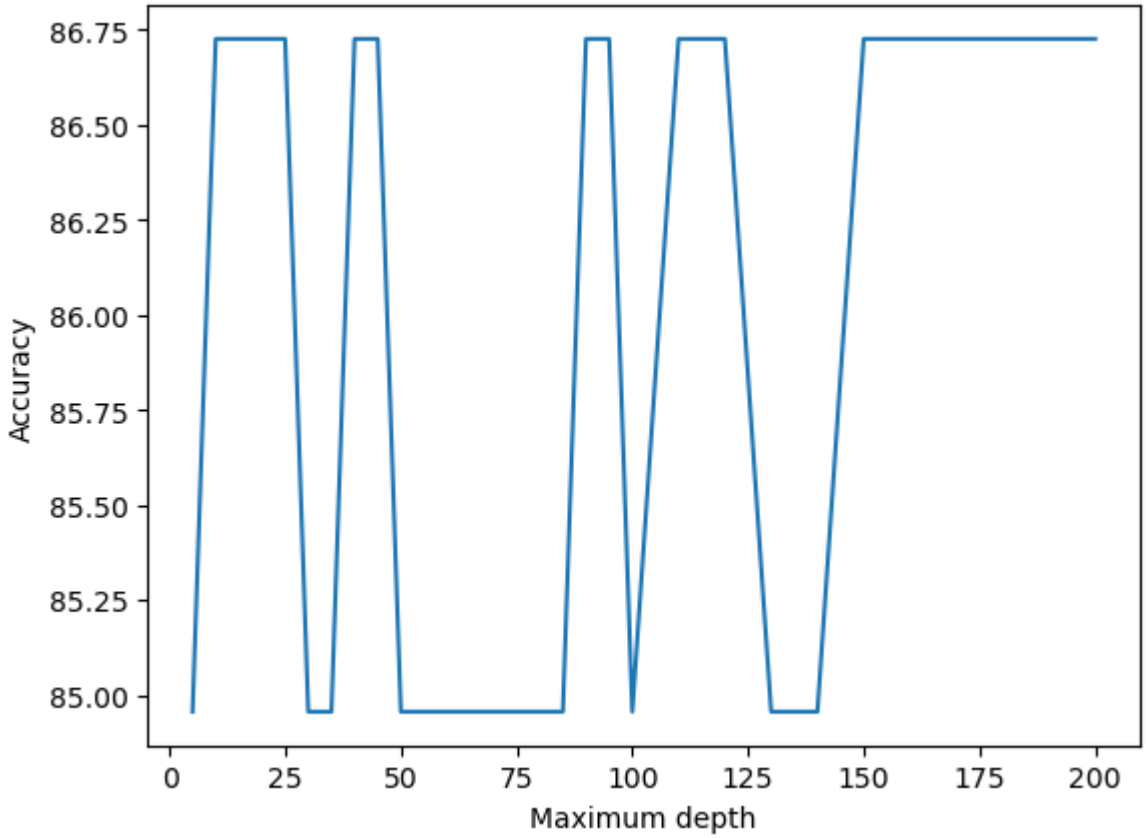
In [202…
```
X_train,X_test,y_train,y_test = train_test_split(X, y,test_size=0.3,random_state=189)
X_val,X_test,y_val,y_test = train_test_split(X_test, y_test,test_size=0.3,random_state=189)
```

1. Decision Tree

In [203…
```
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 [204…
```
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 [205…
```
plt.plot(depths,ac,label='Test_accuracy')
plt.xlabel('Maximum depth')
plt.ylabel('Accuracy')
plt.show()
```



In [206…
```
#Finding the depth for which Accuracy is maximum

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

```
86.72566371681415 10
```

In [207…
```
#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[207]:

▾ DecisionTreeClassifier

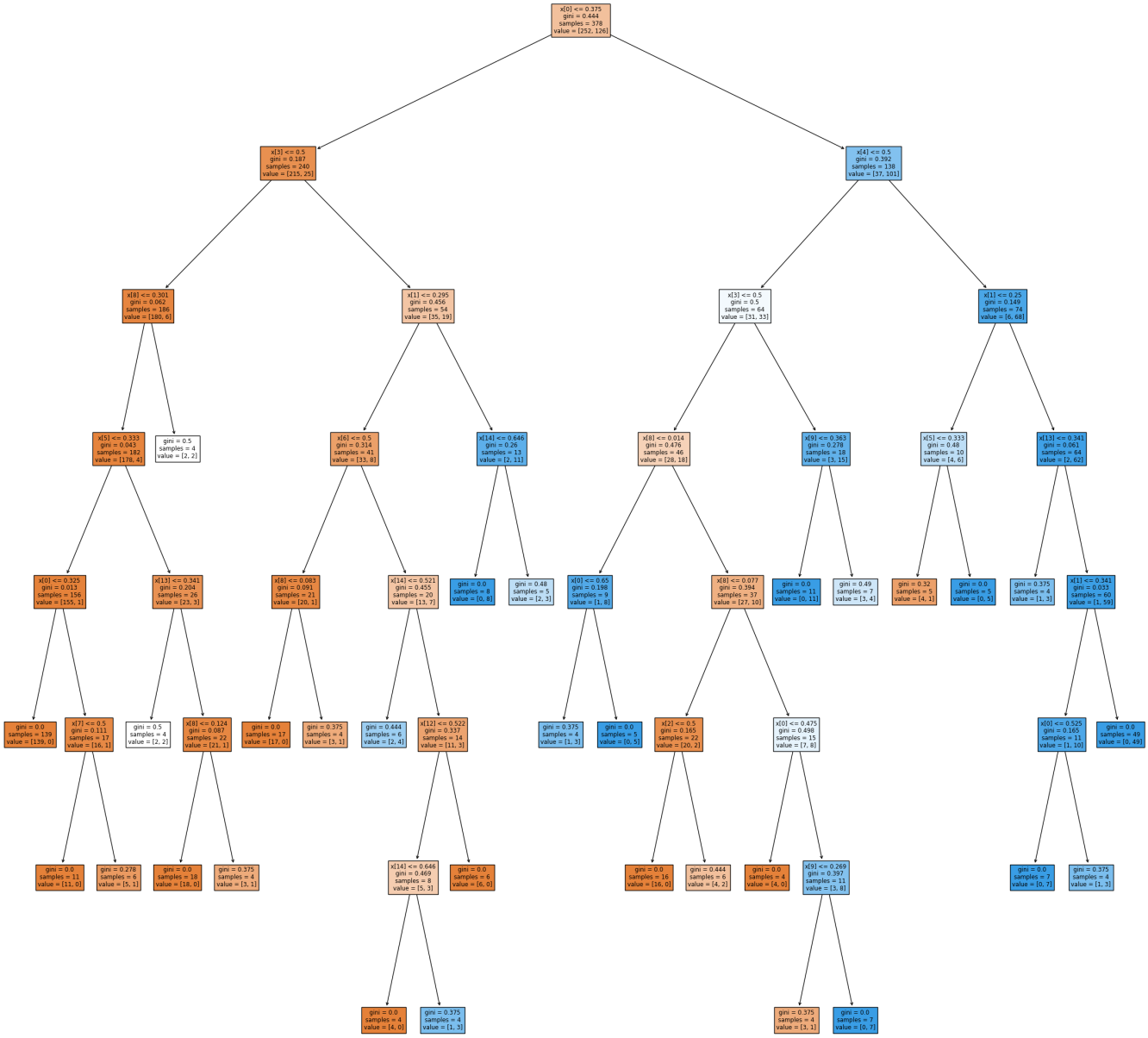
```
DecisionTreeClassifier(max_depth=10, min_samples_leaf=4)
```

In [208…
```
y_pred_dtree = dtree_clf.predict(X_val)
```

In [209…
```
acc_dtree = accuracy_score(y_val,y_pred_dtree)
print(acc_dtree)
```

```
0.8495575221238938
```

In [210…
```
fig = plt.figure(figsize=(30,30))
dtree_plot = tree.plot_tree(dtree_clf,filled=True)
```



Analyzation of the model

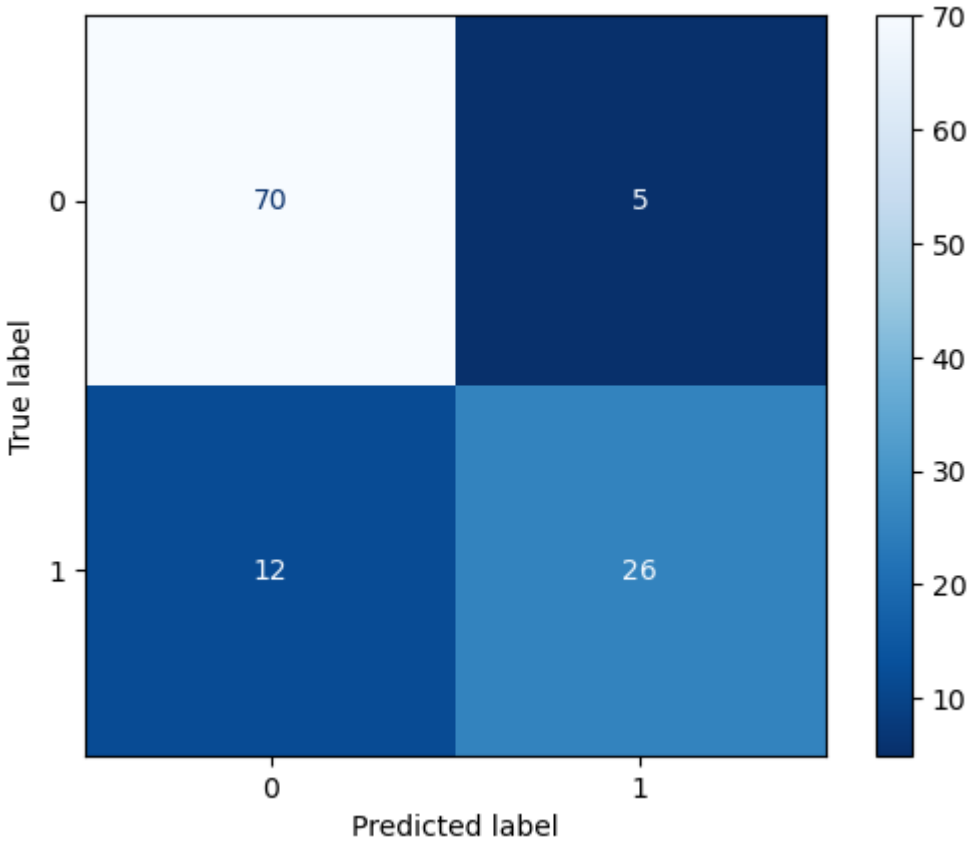
In [211…

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

```
              precision    recall  f1-score   support

         0.0       0.85      0.93      0.89        75
         1.0       0.84      0.68      0.75        38

    accuracy                           0.85       113
   macro avg       0.85      0.81      0.82       113
weighted avg       0.85      0.85      0.85       113
```

In [212…

```
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()
```

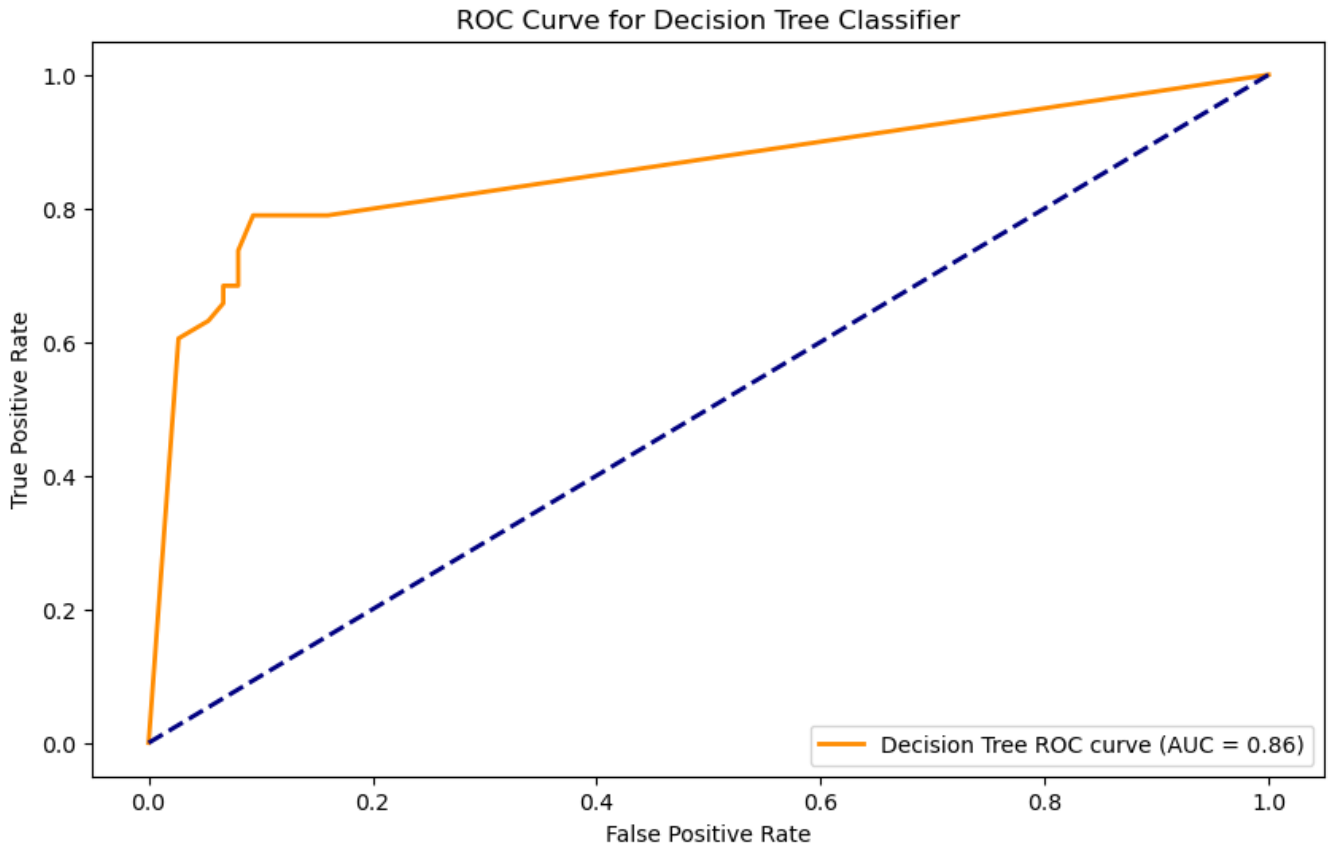


In [213…

```
from sklearn.metrics import roc_curve, auc
# Use the trained Decision Tree model (dtree_clf) and X_val for predictions
y_prob_dtree = dtree_clf.predict_proba(X_val)[:, 1]

# Calculate ROC curve
fpr_dtree, tpr_dtree, thresholds_dtree = roc_curve(y_val, y_prob_dtree)

# Calculate Area Under the Curve (AUC)
roc_auc_dtree = auc(fpr_dtree, tpr_dtree)
```

In [214…

```
# Plot ROC curve
plt.figure(figsize=(10, 6))
plt.plot(fpr_dtree, tpr_dtree, color='darkorange', lw=2, label=f'Decision Tree ROC curve (AUC
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve for Decision Tree Classifier')
plt.legend(loc='lower right')
plt.show()
```



In [215…
```
# Print the AUC value
print(f'AUC for Decision Tree: {roc_auc_dtree:.4f}')
```

```
AUC for Decision Tree: 0.8567
```

2.SVM

In [216…
```
S = SVC(kernel = 'linear')
S.fit(X_train,y_train)
```

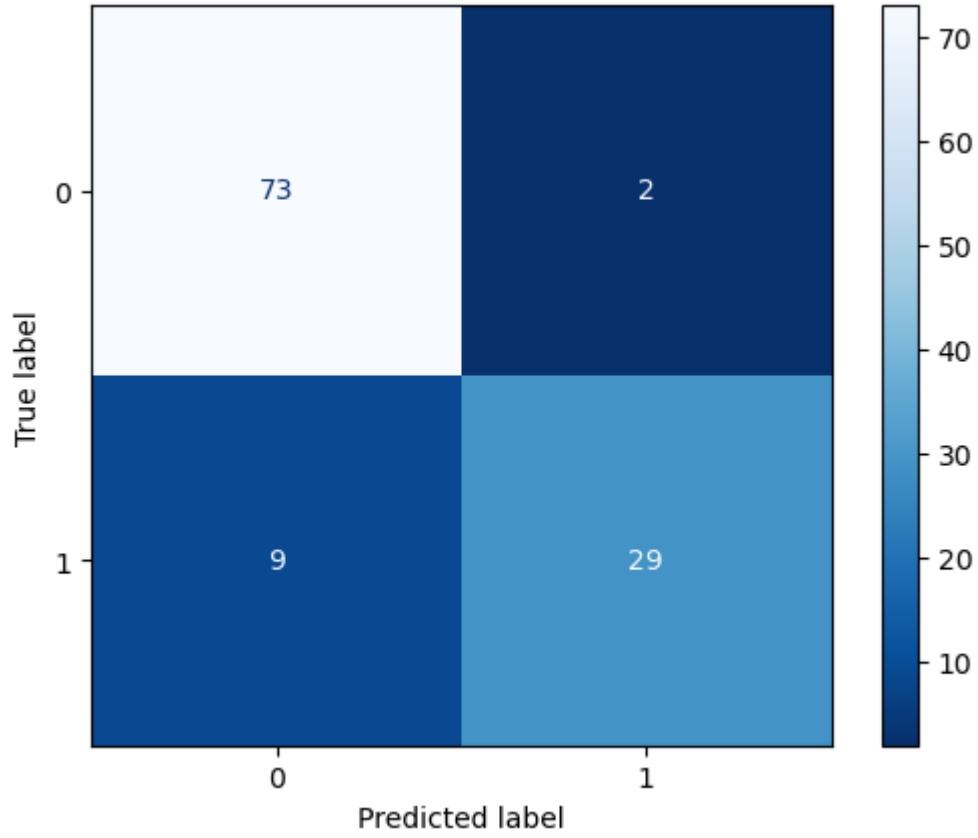
Out[216]:
```
SVC(kernel='linear')
```

In [217…
```
y_pred_svm = S.predict(X_val)
```

In [218…
```
acc_svm = accuracy_score(y_val,y_pred_svm)
print(acc_svm)
```

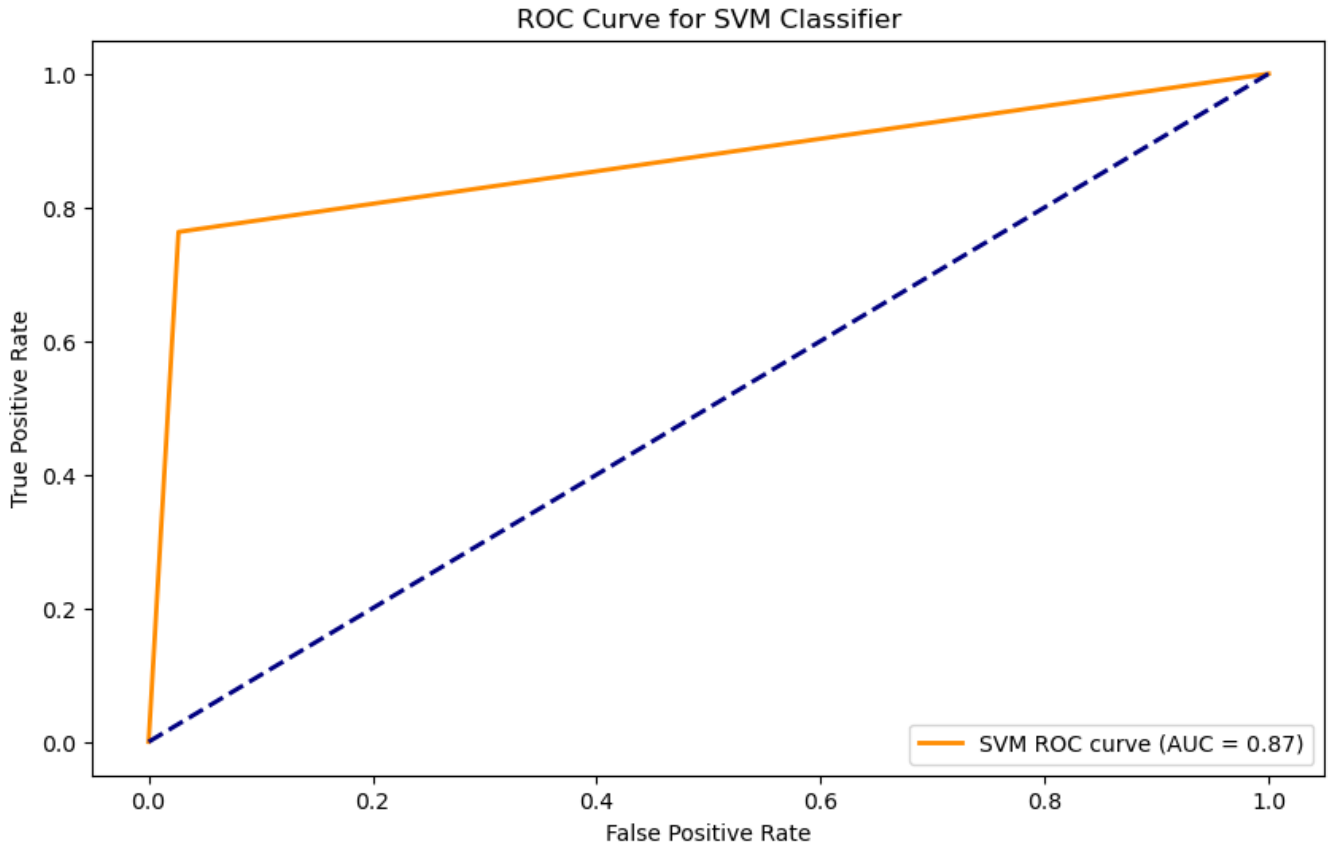
```
0.9026548672566371
```

In [219…
```
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()
```



In [220…

```
fpr_svm, tpr_svm, thresholds_svm = roc_curve(y_val, y_pred_svm)
roc_auc_svm = auc(fpr_svm, tpr_svm)

plt.figure(figsize=(10, 6))
plt.plot(fpr_svm, tpr_svm, color='darkorange', lw=2, label=f'SVM ROC curve (AUC = {roc_auc_sv
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve for SVM Classifier')
plt.legend(loc='lower right')
plt.show()
```



In [221…

```
print(f'AUC for SVM: {roc_auc_svm:.4f}')
```

```
AUC for SVM: 0.8682
```

3.Naive Bayes classifier

In [222…]
```
import numpy as np
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import KFold
from sklearn.metrics import accuracy_score
```

In [223…]
```
# K-fold cross validation
kf = KFold(n_splits=5, shuffle=True)

accuracy_scores = []

for train_index, test_index in kf.split(X):

    X_train, X_test = X[train_index], X[test_index]
    y_train, y_test = y[train_index], y[test_index]

    # Gaussian Naive Bayes model
    gnb = GaussianNB()

    # Fit model with Laplace smoothing
    gnb.fit(X_train, y_train, sample_weight=None)

    # Make predictions
    y_pred = gnb.predict(X_test)

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

In [224…]
```
# Print average accuracy
print("Accuracy:", np.mean(accuracy_scores)*100,"%")
```

```
Accuracy: 87.77777777777779 %
```

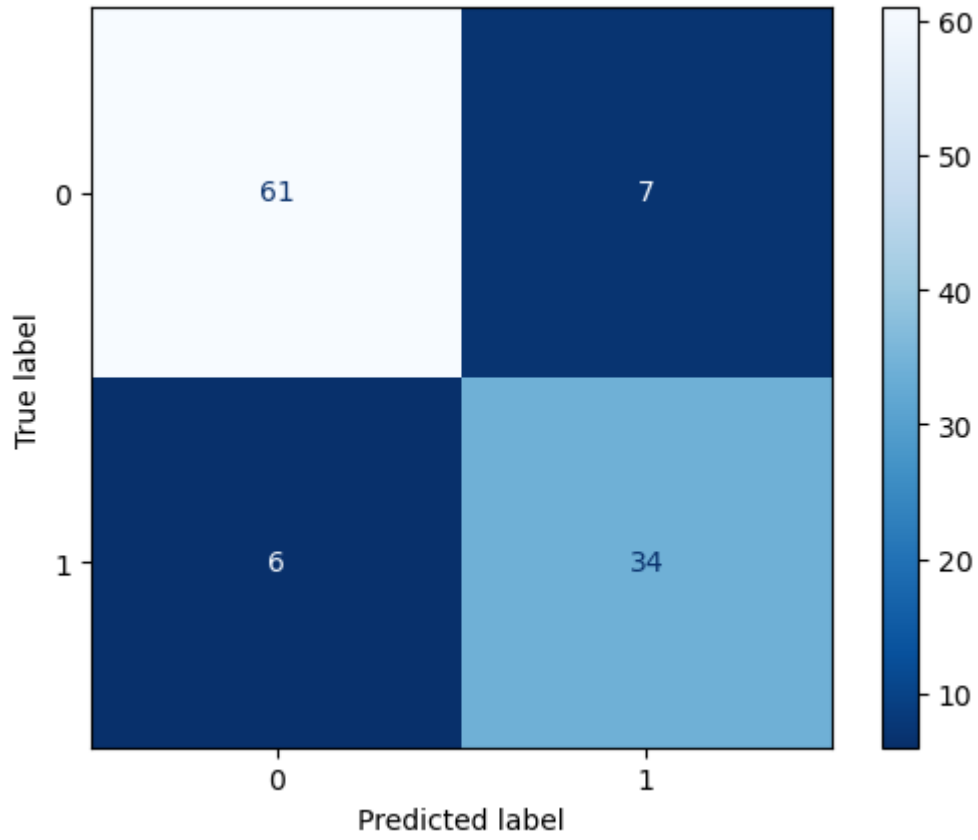
In [225…]
```
# Evaluate the accuracy
acc_nb = accuracy_score(y_test, y_pred)
print("Accuracy:", acc_nb * 100, "%")
```

```
Accuracy: 87.96296296296296 %
```

In [226…]
```
# Evaluate overall performance
print("Overall Classification Report:")
print(classification_report(y_test, y_pred))
```

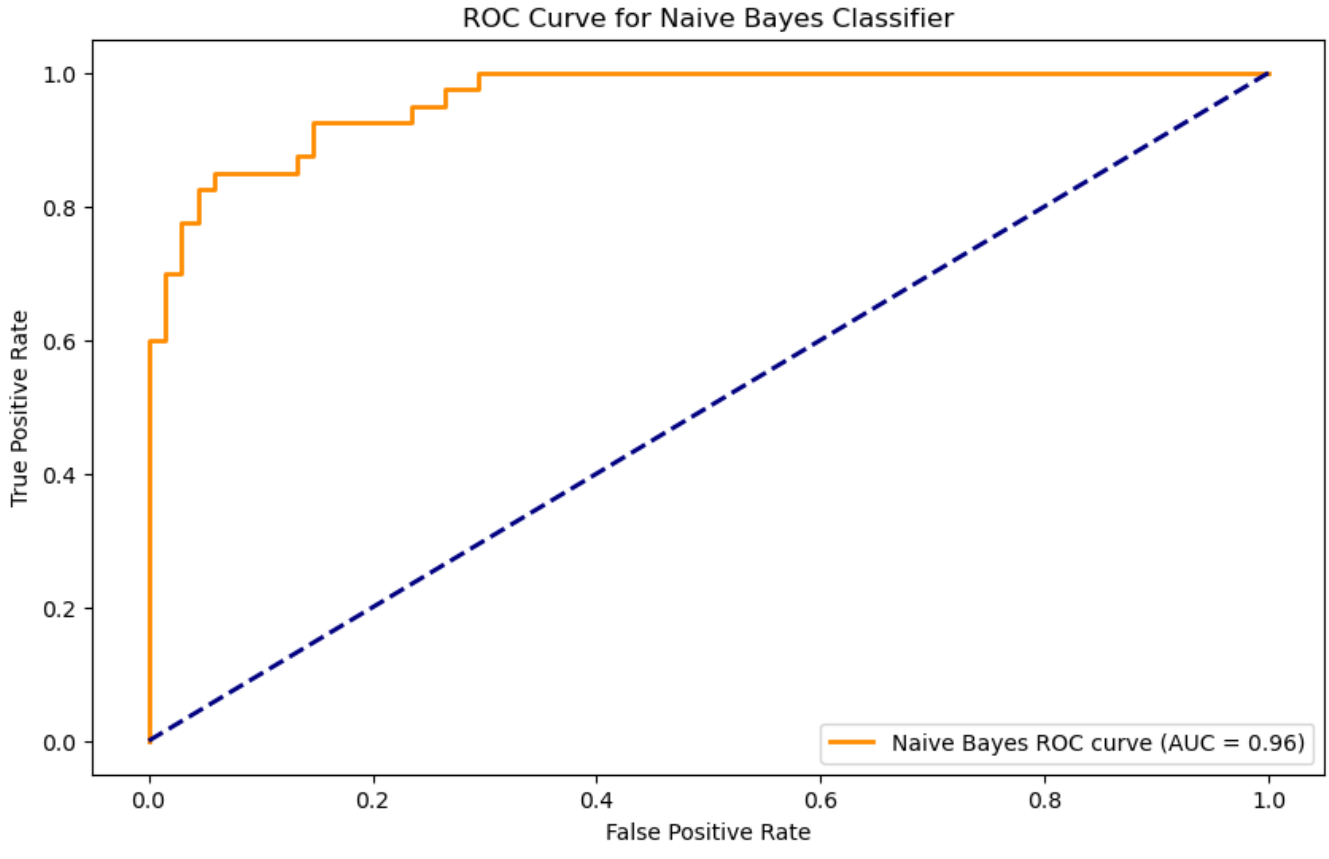
```
Overall Classification Report:
              precision    recall  f1-score   support

         0.0       0.91      0.90      0.90        68
         1.0       0.83      0.85      0.84        40

    accuracy                           0.88       108
   macro avg       0.87      0.87      0.87       108
weighted avg       0.88      0.88      0.88       108
```

In [227…]
```
# Assuming y_true_all and y_pred_all are your true and predicted labels
cm = confusion_matrix(y_test, y_pred)

# Plotting confusion matrix
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=['0', '1'])
disp.plot(cmap="Blues_r")
plt.show()
```



In [228…

```
# ROC Curve and AUC for Naive Bayes
y_prob_nb = gnb.predict_proba(X_test)[:, 1]
fpr_nb, tpr_nb, thresholds_nb = roc_curve(y_test, y_prob_nb)
roc_auc_nb = auc(fpr_nb, tpr_nb)

plt.figure(figsize=(10, 6))
plt.plot(fpr_nb, tpr_nb, color='darkorange', lw=2, label=f'Naive Bayes ROC curve (AUC = {roc_
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve for Naive Bayes Classifier')
plt.legend(loc='lower right')
plt.show()
```



In [229…
```
print(f'AUC for Naive Bayes: {roc_auc_nb:.4f}')
```

```
AUC for Naive Bayes: 0.9621
```

4.XG Boost

In [230…
```
pip install xgboost
```

```
Requirement already satisfied: xgboost in c:\users\vinay\anaconda3\lib\site-packages (2.0.3)N
ote: you may need to restart the kernel to use updated packages.

Requirement already satisfied: numpy in c:\users\vinay\anaconda3\lib\site-packages (from xgbo
ost) (1.24.3)
Requirement already satisfied: scipy in c:\users\vinay\anaconda3\lib\site-packages (from xgbo
ost) (1.11.1)
```

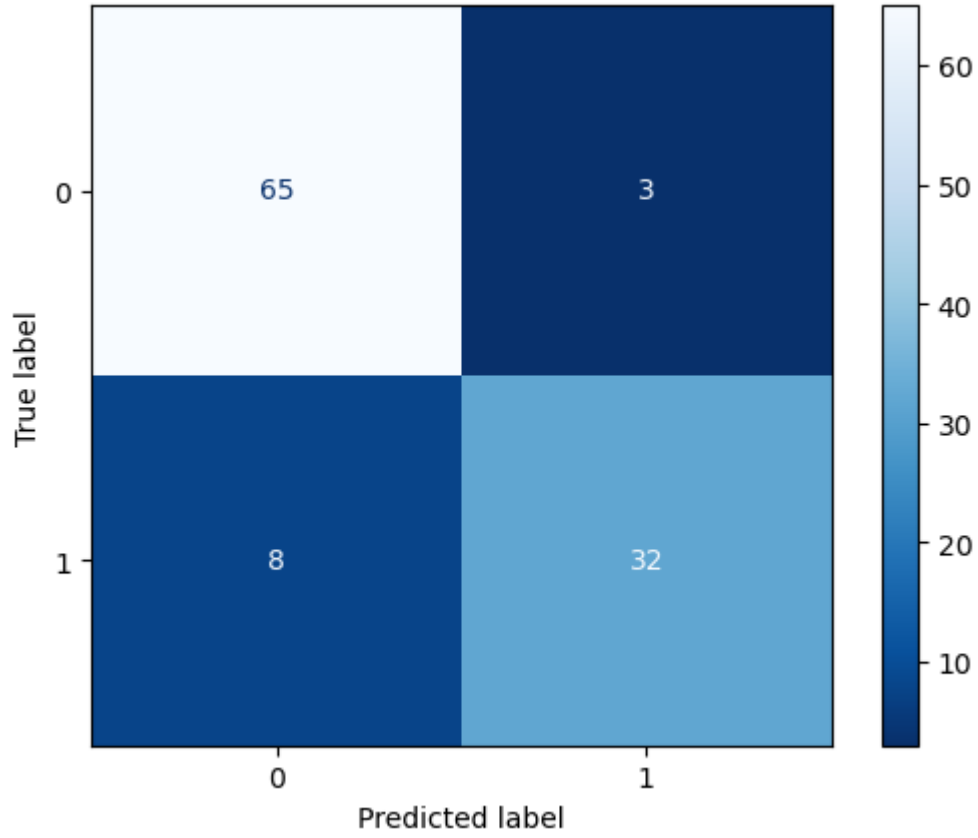
In [231…
```
# Train XGBoost model
model = XGBClassifier()
model.fit(X_train, y_train)

# Make predictions
y_pred = model.predict(X_test)

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

```
Accuracy: 89.81%
```

In [232…
```
# Print classification report
print("Classification Report:")
print(classification_report(y_test, y_pred))
```

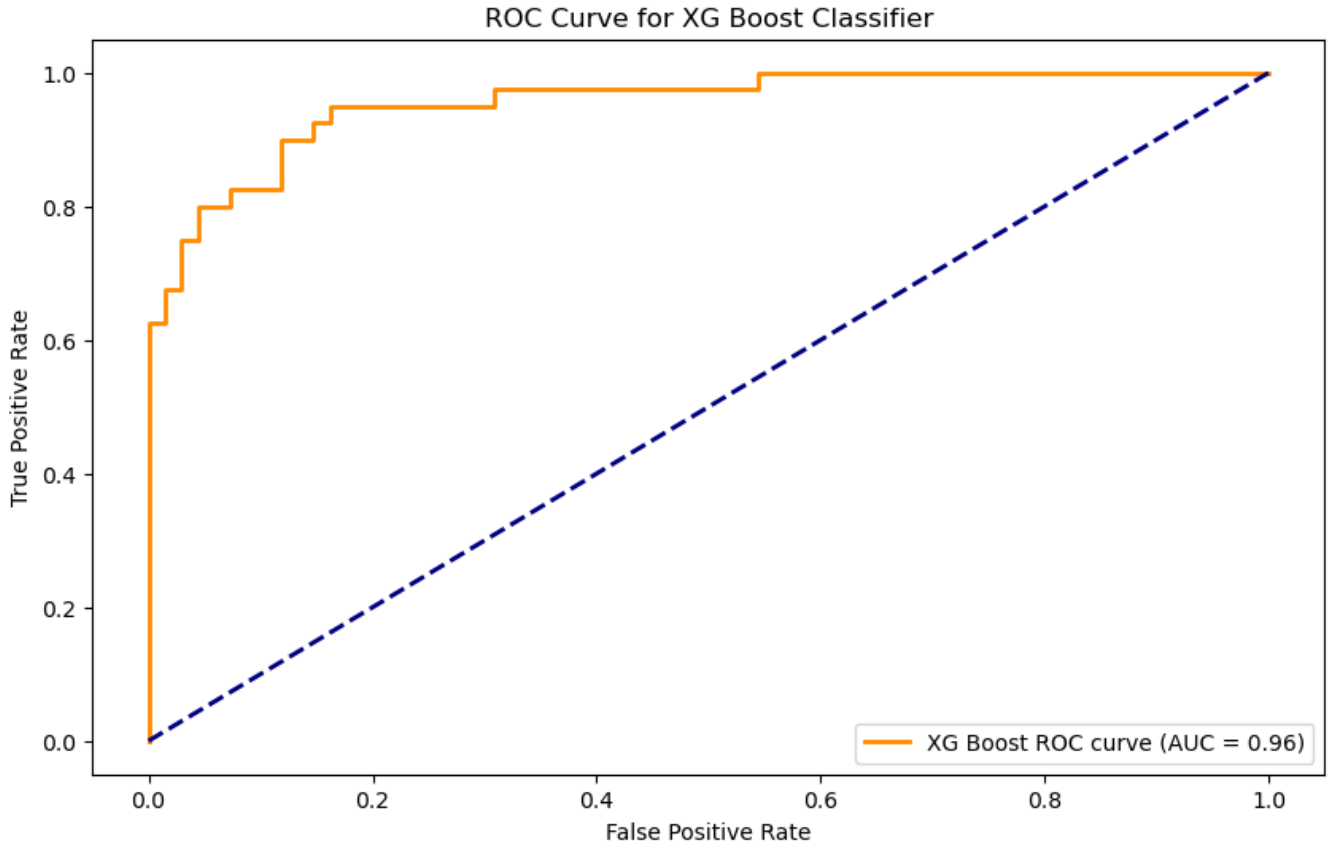
```
Classification Report:
              precision    recall  f1-score   support

         0.0       0.89      0.96      0.92        68
         1.0       0.91      0.80      0.85        40

    accuracy                           0.90       108
   macro avg       0.90      0.88      0.89       108
weighted avg       0.90      0.90      0.90       108
```

In [233…
```
# Confusion Matrix
cm_xgb = confusion_matrix(y_test, y_pred)

# Plotting Confusion Matrix
disp_xgb = ConfusionMatrixDisplay(confusion_matrix=cm_xgb, display_labels=['0', '1'])
disp_xgb.plot(cmap="Blues_r")
plt.show()
```



In [234…

```
# ROC Curve and AUC for XG Boost
y_prob_xgb = model.predict_proba(X_test)[:, 1]
fpr_xgb, tpr_xgb, thresholds_xgb = roc_curve(y_test, y_prob_xgb)
roc_auc_xgb = auc(fpr_xgb, tpr_xgb)

plt.figure(figsize=(10, 6))
plt.plot(fpr_xgb, tpr_xgb, color='darkorange', lw=2, label=f'XG Boost ROC curve (AUC = {roc_a
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve for XG Boost Classifier')
plt.legend(loc='lower right')
plt.show()
```



In [235…]
```
print(f'AUC for XG Boost: {roc_auc_xgb:.4f}')
```

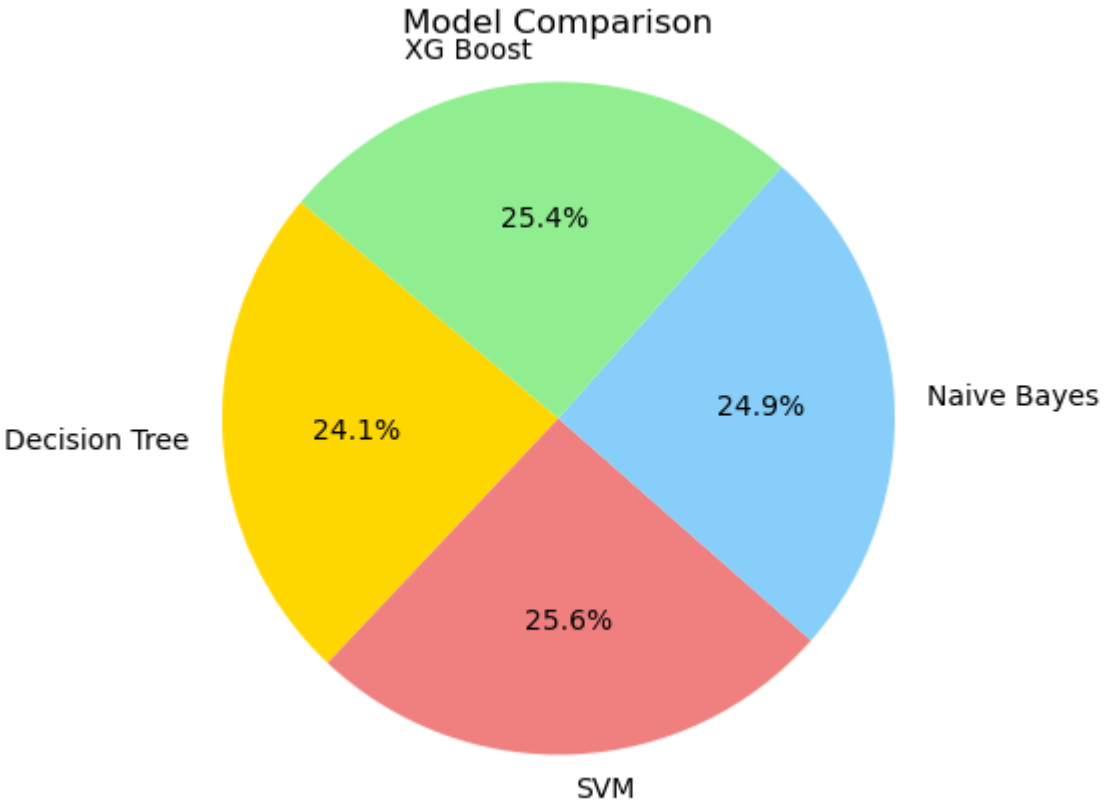
```
AUC for XG Boost: 0.9551
```

Comparing Different Models

Using a box plot

In [236…]
```
# 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)
}
```

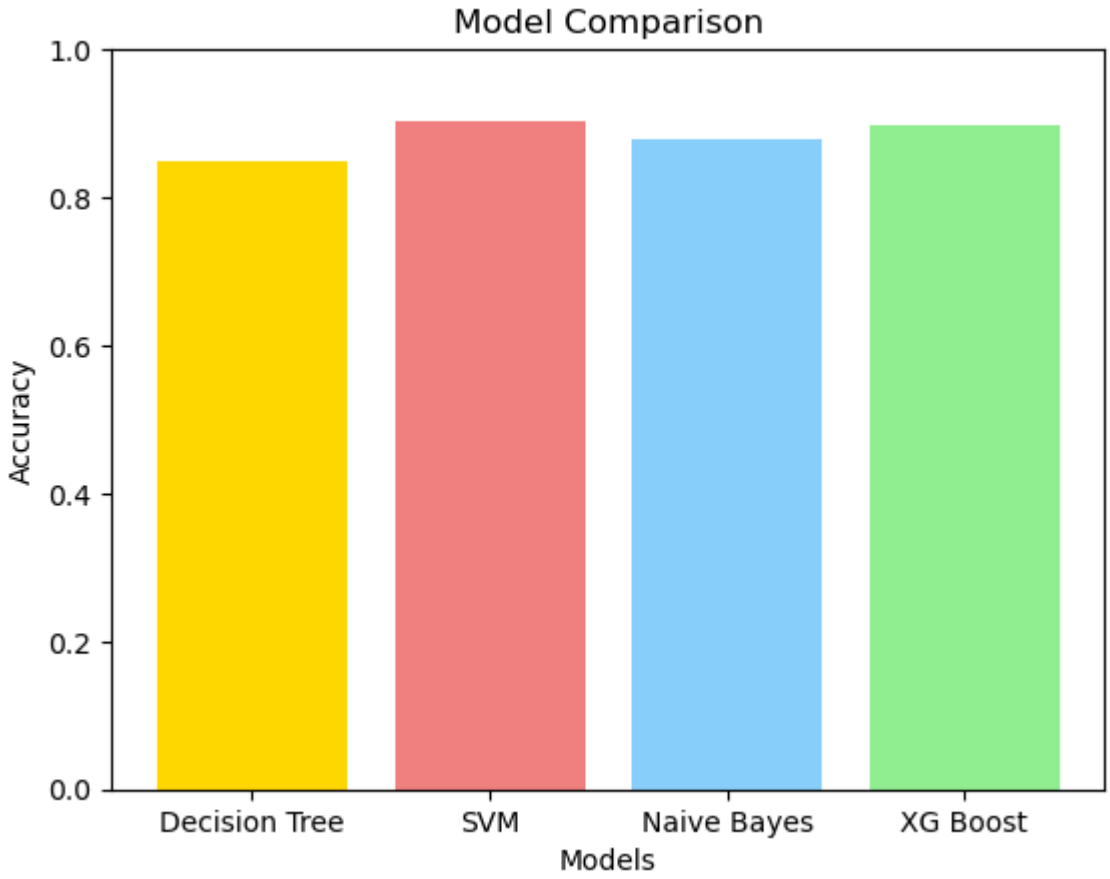
In [237…]
```
# Plotting the pie chart
labels = model_accuracies.keys()
sizes = model_accuracies.values()
colors = ['gold', 'lightcoral', 'lightskyblue', 'lightgreen']

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 [238…]
```
# 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 [239…

```
# 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 [240…

```
# 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: 84.95575221238938
SVM Accuracy: 90.2654867256637
Naive Bayes Accuracy: 87.96296296296296
XG Boost Accuracy: 89.81481481481481
```