

# MJohnsonCapstone

August 26, 2023

## CAPSTONE FINAL PROJECT: Submitted by Maureen K. Johnson on August 27, 2023

Problem Statement • NIDDK (National Institute of Diabetes and Digestive and Kidney Diseases) research creates knowledge about and treatments for the most chronic, costly, and consequential diseases. • The dataset used in this project is originally from NIDDK. The objective is to predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. • Build a model to accurately predict whether the patients in the dataset have diabetes or not.

Dataset Description The datasets consists of several medical predictor variables and one target variable (Outcome). Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and more.

Variables Description Pregnancies Number of times pregnant Glucose Plasma glucose concentration in an oral glucose tolerance test BloodPressure Diastolic blood pressure (mm Hg) SkinThickness Triceps skinfold thickness (mm) Insulin Two hour serum insulin BMI Body Mass Index DiabetesPedigreeFunction Diabetes pedigree function Age Age in years Outcome Class variable (either 0 or 1). 268 of 768 values are 1, and the others are

Pregnancies: Number of times pregnant

Glucose: Plasma glucose concentration over 2 hours in an oral glucose tolerance test

BloodPressure: Diastolic blood pressure (mm Hg) SkinThickness: Triceps skin fold thickness (mm) Insulin: 2-Hour serum insulin (mu U/ml) BMI: Body mass index (weight in kg/(height in m)<sup>2</sup>) DiabetesPedigreeFunction: Diabetes pedigree function (a function which scores likelihood of diabetes based on family history) Age: Age (years) Outcome: Class variable (0 if non-diabetic, 1 if diabetic)

### Data Exploration

1. Perform descriptive analysis. Understand the variables and their corresponding values. On the columns below, a value of zero does not make sense and thus indicates missing value:
  - Glucose
  - BloodPressure
  - SkinThickness
  - Insulin
  - BMI
2. Visually explore these variables using histograms. Treat the missing values accordingly.

```
[5]: # 1. Importing Python Libraries and CSV Data Set
# The following libraries are imported:
# 1.1 Pandas is a Python library for data manipulation and analysis.
# 1.2 NumPy is a package that contains a multidimensional array object
# 1.3 Matplotlib is a Python visualization package for 2D array plots.
# 1.4 SciKit
```

```
# 1.5 Seaborn is built on top of Matplotlib. It's used for exploratory data analysis
```

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
import time
import datetime
from sklearn import model_selection
from sklearn.ensemble import AdaBoostClassifier
from sklearn import linear_model
```

```
[6]: #Loading the health care diabetes.csv dataset
#C:\Users\maure\OneDrive\Documents\CalTech Data Science Bootcamp\Capstone\Project\Instructions and Data Set
diabetes = pd.read_csv('health care diabetes.csv')
```

Checking first five rows

```
[8]: diabetes.head()
```

```
[8]:    Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin  BMI \
0            6        148             72            35          0  33.6
1            1         85             66            29          0  26.6
2            8        183             64            0          0  23.3
3            1         89             66            23         94  28.1
4            0        137             40            35        168  43.1

   DiabetesPedigreeFunction  Age  Outcome
0                  0.627    50       1
1                  0.351    31       0
2                  0.672    32       1
3                  0.167    21       0
4                  2.288    33       1
```

```
[9]: diabetes.shape
```

```
[9]: (768, 9)
```

```
[10]: diabetes.isnull().sum()
```

```
[10]: Pregnancies          0
Glucose              0
BloodPressure        0
SkinThickness        0
Insulin              0
```

```
BMI          0  
DiabetesPedigreeFunction 0  
Age          0  
Outcome      0  
dtype: int64
```

```
[11]: diabetes.nunique()
```

```
[11]: Pregnancies      17  
Glucose          136  
BloodPressure    47  
SkinThickness    51  
Insulin          186  
BMI              248  
DiabetesPedigreeFunction 517  
Age              52  
Outcome          2  
dtype: int64
```

```
[12]: #Identify and drop observations with missing values for more than one variable.  
diabetes.value_counts()
```

```
[12]: Pregnancies Glucose BloodPressure SkinThickness Insulin BMI  
DiabetesPedigreeFunction Age Outcome  
0           57       60           0           0     21.7  0.735  
67          0        1           67       76           0           0     45.3  0.194  
46          0        1           103      108          37           0     39.2  0.305  
5           0        1           104      74           0           0     28.8  0.153  
65          0        1           105      72           29          325     36.9  0.159  
48          0        1           1           ..           0           0     21.0  0.159  
28          0        1           84       50           23          76     30.4  0.968  
21          0        1           85       65           0           0     39.6  0.930  
27          0        1           87       0            23          0     28.9  0.773  
25          0        1           1           ..           16          52     32.7  0.166  
25          0        1           163      72           41          114    40.9  0.817  
17           1        1           1           ..           0           0     24.3  0.159  
47           1        1           1           ..           0           0     20.9  0.159  
Length: 768, dtype: int64
```

```
[13]: diabetes.loc[(diabetes['BloodPressure']==0) & (diabetes['SkinThickness']==0) &  
↳(diabetes['Insulin']==0)]
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
7	10	115	0	0	0	35.3	
15	7	100	0	0	0	30.0	
49	7	105	0	0	0	0.0	
60	2	84	0	0	0	0.0	
78	0	131	0	0	0	43.2	
81	2	74	0	0	0	0.0	
193	11	135	0	0	0	52.3	
222	7	119	0	0	0	25.2	
261	3	141	0	0	0	30.0	
266	0	138	0	0	0	36.3	
269	2	146	0	0	0	27.5	
300	0	167	0	0	0	32.3	
332	1	180	0	0	0	43.3	
336	0	117	0	0	0	33.8	
347	3	116	0	0	0	23.5	
426	0	94	0	0	0	0.0	
430	2	99	0	0	0	22.2	
435	0	141	0	0	0	42.4	
453	2	119	0	0	0	19.6	
468	8	120	0	0	0	30.0	
484	0	145	0	0	0	44.2	
494	3	80	0	0	0	0.0	
522	6	114	0	0	0	0.0	
533	6	91	0	0	0	29.8	
535	4	132	0	0	0	32.9	
589	0	73	0	0	0	21.1	
601	6	96	0	0	0	23.7	
604	4	183	0	0	0	28.4	
619	0	119	0	0	0	32.4	
643	4	90	0	0	0	28.0	
697	0	99	0	0	0	25.0	
703	2	129	0	0	0	38.5	
706	10	115	0	0	0	0.0	

	DiabetesPedigreeFunction	Age	Outcome
7	0.134	29	0
15	0.484	32	1
49	0.305	24	0
60	0.304	21	0
78	0.270	26	1
81	0.102	22	0
193	0.578	40	1
222	0.209	37	0

261	0.761	27	1
266	0.933	25	1
269	0.240	28	1
300	0.839	30	1
332	0.282	41	1
336	0.932	44	0
347	0.187	23	0
426	0.256	25	0
430	0.108	23	0
435	0.205	29	1
453	0.832	72	0
468	0.183	38	1
484	0.630	31	1
494	0.174	22	0
522	0.189	26	0
533	0.501	31	0
535	0.302	23	1
589	0.342	25	0
601	0.190	28	0
604	0.212	36	1
619	0.141	24	1
643	0.610	31	0
697	0.253	22	0
703	0.304	41	0
706	0.261	30	1

```
[14]: diabetes1 = diabetes[ (diabetes['BloodPressure']== 0) &
    ~(diabetes['SkinThickness'] == 0) & (diabetes['Insulin'] == 0)].index
diabetes.drop(diabetes1 , inplace=True)
diabetes
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	6	148	72	35	0	33.6	
1	1	85	66	29	0	26.6	
2	8	183	64	0	0	23.3	
3	1	89	66	23	94	28.1	
4	0	137	40	35	168	43.1	
..	...	...	...	...	...	...	
763	10	101	76	48	180	32.9	
764	2	122	70	27	0	36.8	
765	5	121	72	23	112	26.2	
766	1	126	60	0	0	30.1	
767	1	93	70	31	0	30.4	
	DiabetesPedigreeFunction	Age	Outcome				
0	0.627	50	1				
1	0.351	31	0				

```

2          0.672   32      1
3          0.167   21      0
4          2.288   33      1
..
..       ...  ...
763         0.171   63      0
764         0.340   27      0
765         0.245   30      0
766         0.349   47      1
767         0.315   23      0

```

[735 rows x 9 columns]

[15]: diabetes.shape

[15]: (735, 9)

[16]: diabetes.loc[diabetes["Glucose"] == 0.0, "Glucose"] = np.NAN  
diabetes.loc[diabetes["BloodPressure"] == 0.0, "BloodPressure"] = np.NAN  
diabetes.loc[diabetes["SkinThickness"] == 0.0, "SkinThickness"] = np.NAN  
diabetes.loc[diabetes["Insulin"] == 0.0, "Insulin"] = np.NAN  
diabetes.loc[diabetes["BMI"] == 0.0, "BMI"] = np.NAN

diabetes.isnull().sum()[1:6]

[16]: Glucose 5  
BloodPressure 2  
SkinThickness 194  
Insulin 341  
BMI 4  
dtype: int64

[17]: missing\_columns = ["Glucose", "BloodPressure", "SkinThickness", "Insulin",  
"BMI"]

[18]: `def random_imputation(diabetes, feature):`

```

number_missing = diabetes[feature].isnull().sum()
observed_values = diabetes.loc[diabetes[feature].notnull(), feature]
diabetes.loc[diabetes[feature].isnull(), feature + '_imp'] = np.random.
choice(observed_values, number_missing, replace = True)

return diabetes

```

[19]: `for feature in missing_columns:`  
diabetes[feature + '\_imp'] = diabetes[feature]  
diabetes = random\_imputation(diabetes, feature)

```
[20]: deter_data = pd.DataFrame(columns = ["Det" + name for name in missing_columns])

for feature in missing_columns:

    deter_data["Det" + feature] = diabetes[feature + "_imp"]
    parameters = list(set(diabetes.columns) - set(missing_columns) - {feature + '_imp'})

#Create a Linear Regression model to estimate the missing data
model = linear_model.LinearRegression()
model.fit(X = diabetes[parameters], y = diabetes[feature + '_imp'])

#observe that I preserve the index of the missing data from the original dataframe
deter_data.loc[diabetes[feature].isnull(), "Det" + feature] = model.predict(diabetes[parameters])[diabetes[feature].isnull()]
```

```
[21]: deter_data.head()
```

```
[21]:   DetGlucose  DetBloodPressure  DetSkinThickness  DetInsulin  DetBMI
0        148.0              72.0      35.00000  187.048788     33.6
1         85.0              66.0      29.00000 110.552764     26.6
2        183.0              64.0      24.85059 223.708919     23.3
3         89.0              66.0      23.00000  94.000000     28.1
4        137.0              40.0      35.00000 168.000000     43.1
```

```
[22]: diabetes.head()
```

```
[22]:   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin  BMI \
0            6    148.0          72.0        35.0       NaN  33.6
1            1     85.0          66.0        29.0       NaN  26.6
2            8    183.0          64.0        NaN       NaN  23.3
3            1     89.0          66.0        23.0     94.0  28.1
4            0    137.0          40.0        35.0     168.0  43.1

   DiabetesPedigreeFunction  Age  Outcome  Glucose_imp  BloodPressure_imp \
0                  0.627  50       1      148.0             72.0
1                  0.351  31       0      85.0             66.0
2                  0.672  32       1     183.0             64.0
3                  0.167  21       0      89.0             66.0
4                  2.288  33       1     137.0             40.0

   SkinThickness_imp  Insulin_imp  BMI_imp
0            35.0      183.0     33.6
1            29.0      105.0     26.6
2            41.0      185.0     23.3
3            23.0      94.0     28.1
```

```
4           35.0      168.0      43.1
```

```
[23]: diabetes
```

```
[23]:    Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin  BMI  \
0            6       148.0          72.0        35.0      NaN  33.6
1            1       85.0          66.0        29.0      NaN  26.6
2            8      183.0          64.0        NaN      NaN  23.3
3            1       89.0          66.0        23.0      94.0  28.1
4            0      137.0          40.0        35.0     168.0  43.1
..
763          10      101.0          76.0        48.0     180.0  32.9
764          2       122.0          70.0        27.0      NaN  36.8
765          5       121.0          72.0        23.0     112.0  26.2
766          1       126.0          60.0        NaN      NaN  30.1
767          1       93.0          70.0        31.0      NaN  30.4

    DiabetesPedigreeFunction  Age  Outcome  Glucose_imp  BloodPressure_imp  \
0             0.627    50         1      148.0              72.0
1             0.351    31         0      85.0              66.0
2             0.672    32         1      183.0              64.0
3             0.167    21         0      89.0              66.0
4             2.288    33         1      137.0              40.0
..
763          0.171    63         0      101.0              ...
764          0.340    27         0      122.0              70.0
765          0.245    30         0      121.0              72.0
766          0.349    47         1      126.0              60.0
767          0.315    23         0      93.0              70.0

    SkinThickness_imp  Insulin_imp  BMI_imp
0            35.0       183.0     33.6
1            29.0       105.0     26.6
2            41.0       185.0     23.3
3            23.0       94.0     28.1
4            35.0       168.0     43.1
..
763          48.0       180.0     32.9
764          27.0       155.0     36.8
765          23.0       112.0     26.2
766          32.0       579.0     30.1
767          31.0       155.0     30.4
```

```
[735 rows x 14 columns]
```

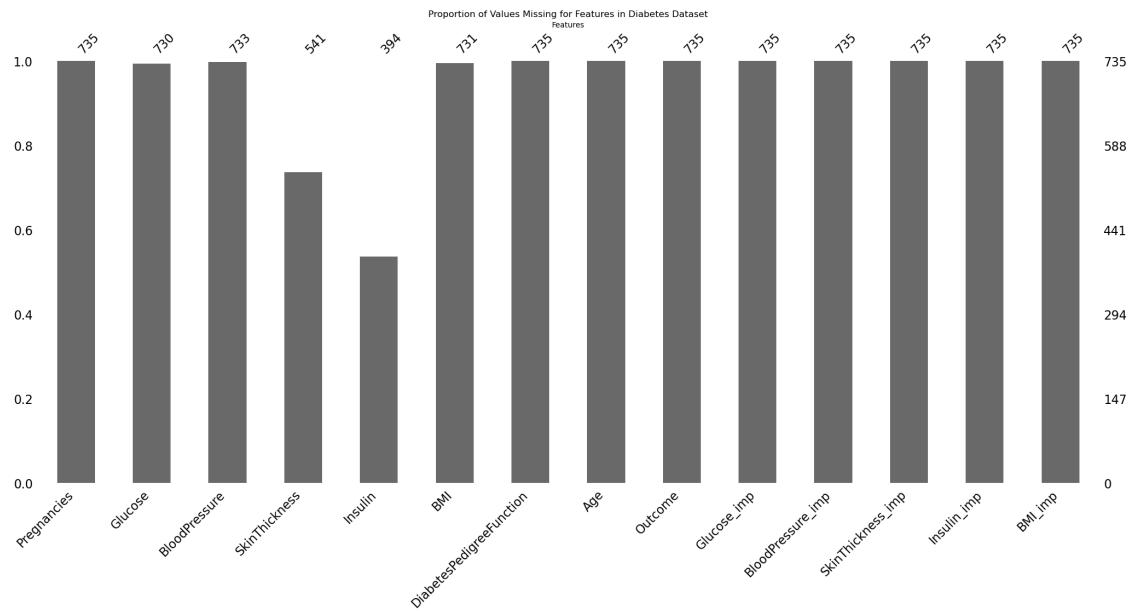
```
[24]: pip install missingno
```

```
Defaulting to user installation because normal site-packages is not writeable
Looking in links: /usr/share/pip-wheels
Requirement already satisfied: missingno in
/home/8d4c0998-ac1c-4c5c-9c72-25b20502cf79/.local/lib/python3.11/site-packages
(0.5.2)
Requirement already satisfied: numpy in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from missingno) (1.24.3)
Requirement already satisfied: matplotlib in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from missingno) (3.7.1)
Requirement already satisfied: scipy in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from missingno) (1.10.1)
Requirement already satisfied: seaborn in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from missingno) (0.12.2)
Requirement already satisfied: contourpy>=1.0.1 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from matplotlib->missingno)
(1.0.5)
Requirement already satisfied: cycler>=0.10 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from matplotlib->missingno)
(0.11.0)
Requirement already satisfied: fonttools>=4.22.0 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from matplotlib->missingno)
(4.25.0)
Requirement already satisfied: kiwisolver>=1.0.1 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from matplotlib->missingno)
(1.4.4)
Requirement already satisfied: packaging>=20.0 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from matplotlib->missingno)
(23.0)
Requirement already satisfied: pillow>=6.2.0 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from matplotlib->missingno)
(9.4.0)
Requirement already satisfied: pyparsing>=2.3.1 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from matplotlib->missingno)
(3.0.9)
Requirement already satisfied: python-dateutil>=2.7 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from matplotlib->missingno)
(2.8.2)
Requirement already satisfied: pandas>=0.25 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from seaborn->missingno)
(1.5.3)
Requirement already satisfied: pytz>=2020.1 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from
pandas>=0.25->seaborn->missingno) (2022.7)
Requirement already satisfied: six>=1.5 in /opt/conda/envs/anaconda-
panel-2023.05-py310/lib/python3.11/site-packages (from python-
dateutil>=2.7->matplotlib->missingno) (1.16.0)
Note: you may need to restart the kernel to use updated packages.
```

```
[25]: import missingno as msno
```

```
[26]: msno.bar(diabetes)
plt.xlabel('Features')
plt.ylabel('Proportion of Values Missing')
plt.title('Proportion of Values Missing for Features in Diabetes Dataset')
plt.show
```

```
[26]: <function matplotlib.pyplot.show(close=None, block=None)>
```



Dropping the original glucose, blood pressure, skin thickness, insulin, and BMI variables

```
[28]: diabetes2=diabetes.drop(['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI'], axis=1)
```

```
[29]: diabetes2.head()
```

```
[29]:   Pregnancies  DiabetesPedigreeFunction  Age  Outcome  Glucose_imp \
0            6              0.627    50        1      148.0
1            1              0.351    31        0      85.0
2            8              0.672    32        1     183.0
3            1              0.167    21        0      89.0
4            0              2.288    33        1     137.0

   BloodPressure_imp  SkinThickness_imp  Insulin_imp  BMI_imp
0            72.0          35.0          183.0      33.6
1            66.0          29.0          105.0      26.6
```

```
2           64.0          41.0        185.0       23.3
3           66.0          23.0         94.0       28.1
4           40.0          35.0        168.0       43.1
```

```
[30]: diabetes2.describe()
```

```
Pregnancies  DiabetesPedigreeFunction      Age      Outcome \
count    735.000000    735.000000  735.000000  735.000000
mean     3.865306     0.476392   33.364626   0.344218
std      3.371152     0.333921   11.831485   0.475436
min      0.000000     0.078000   21.000000   0.000000
25%     1.000000     0.245000   24.000000   0.000000
50%     3.000000     0.380000   29.000000   0.000000
75%     6.000000     0.630000   41.000000   1.000000
max     17.000000    2.420000   81.000000   1.000000

Glucose_imp  BloodPressure_imp  SkinThickness_imp  Insulin_imp \
count    735.000000    735.000000  735.000000  735.000000
mean    121.810884    72.395918   29.012245  154.765986
std     30.616302    12.375472   10.276219  121.152165
min     44.000000    24.000000    7.000000  14.000000
25%    100.000000    64.000000   22.000000  76.000000
50%    117.000000    72.000000   29.000000  125.000000
75%    141.000000    80.000000   36.000000  189.000000
max    199.000000   122.000000   99.000000  846.000000

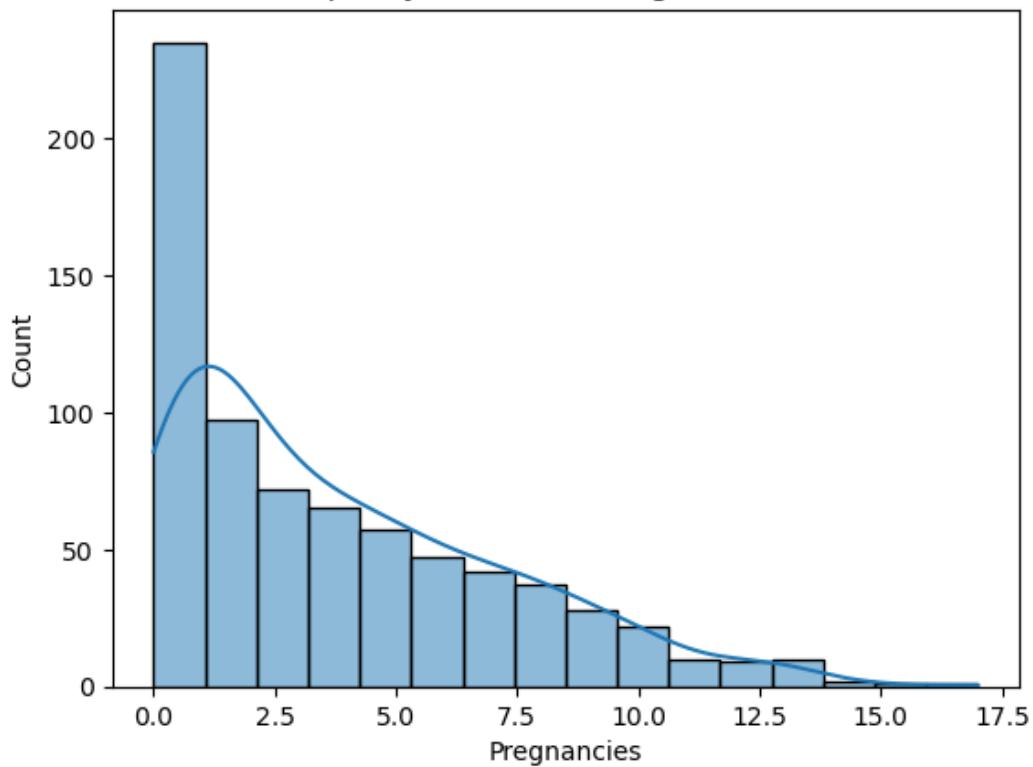
BMI_imp
count  735.000000
mean   32.470748
std    6.891538
min    18.200000
25%   27.500000
50%   32.400000
75%   36.650000
max   67.100000
```

```
[31]: df = pd.DataFrame(diabetes)
```

```
[32]: df.to_csv('diabetes.csv', encoding='utf-8', index=False)
```

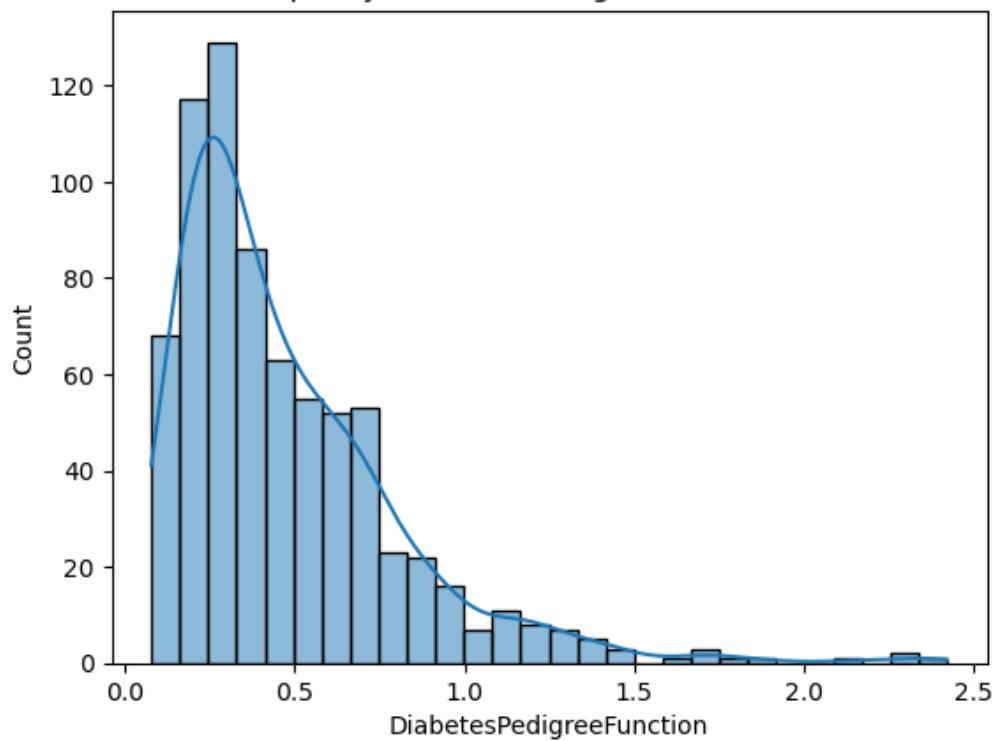
```
[33]: sns.histplot(data=diabetes2, x='Pregnancies', kde=True)
plt.title('Distribution of Sample by Number of Pregnancies in Diabetes Dataset')
plt.show()
```

Distribution of Sample by Number of Pregnancies in Diabetes Dataset

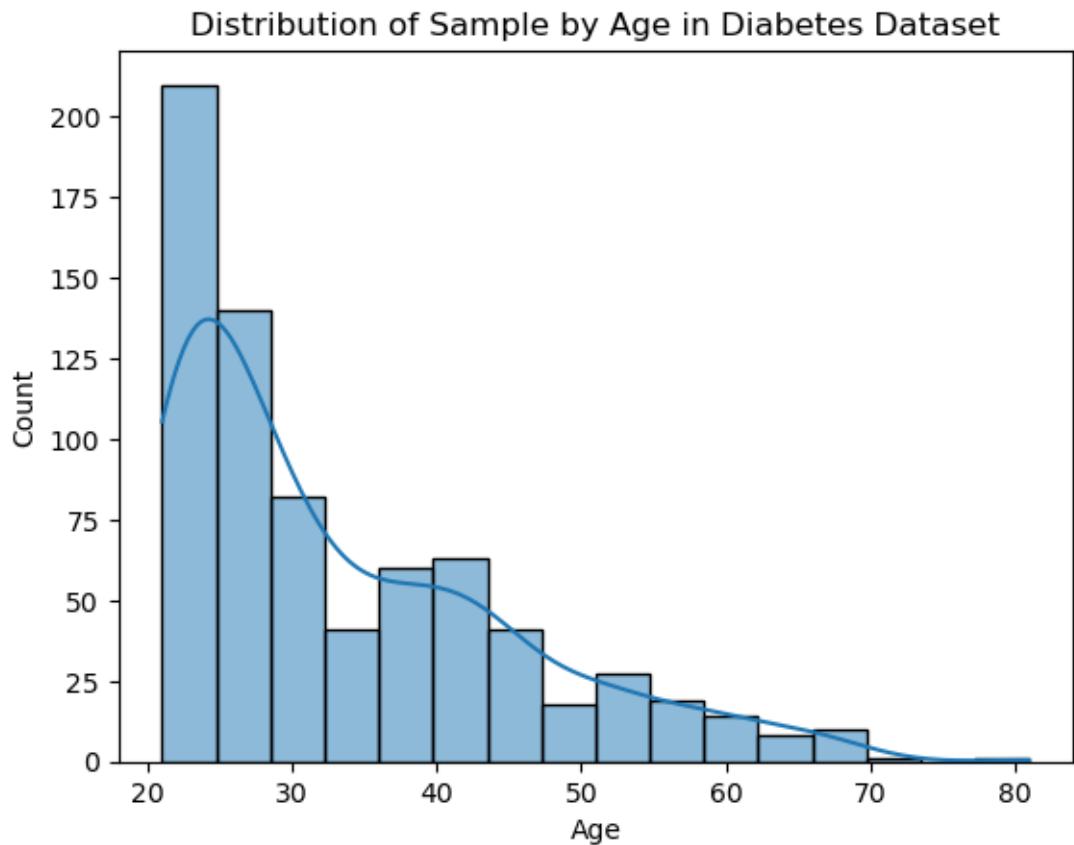


```
[34]: sns.histplot(data=diabetes2, x='DiabetesPedigreeFunction', kde=True)
plt.title('Distribution of Sample by Diabetes Pedigree Function in DiabetesDataset')
plt.show()
```

Distribution of Sample by Diabetes Pedigree Function in Diabetes Dataset

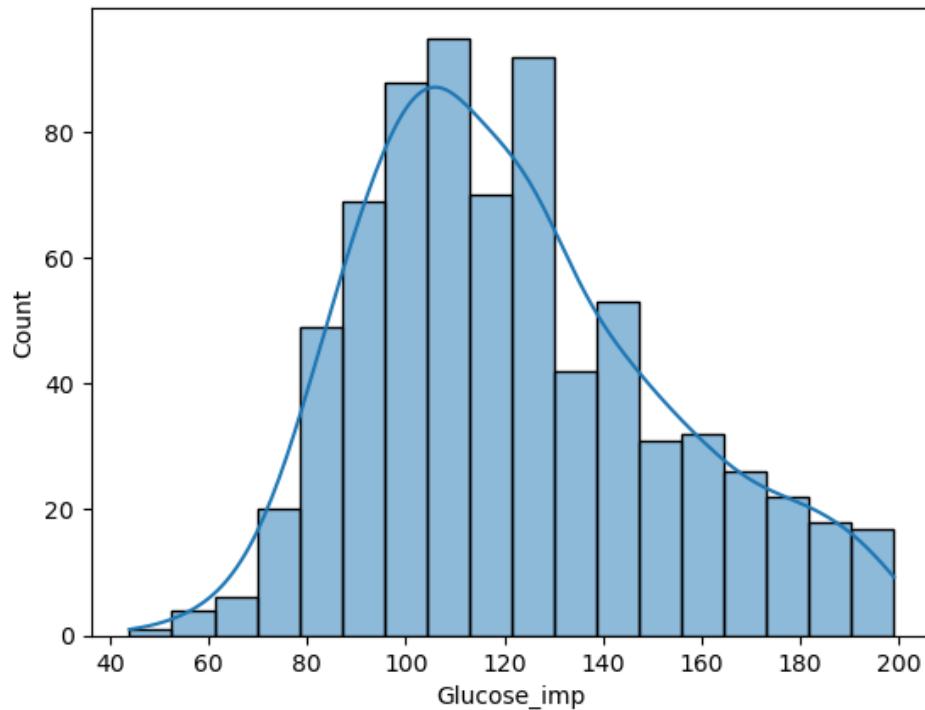


```
[35]: sns.histplot(data=diabetes2, x='Age', kde=True)
plt.title('Distribution of Sample by Age in Diabetes Dataset')
plt.show()
```



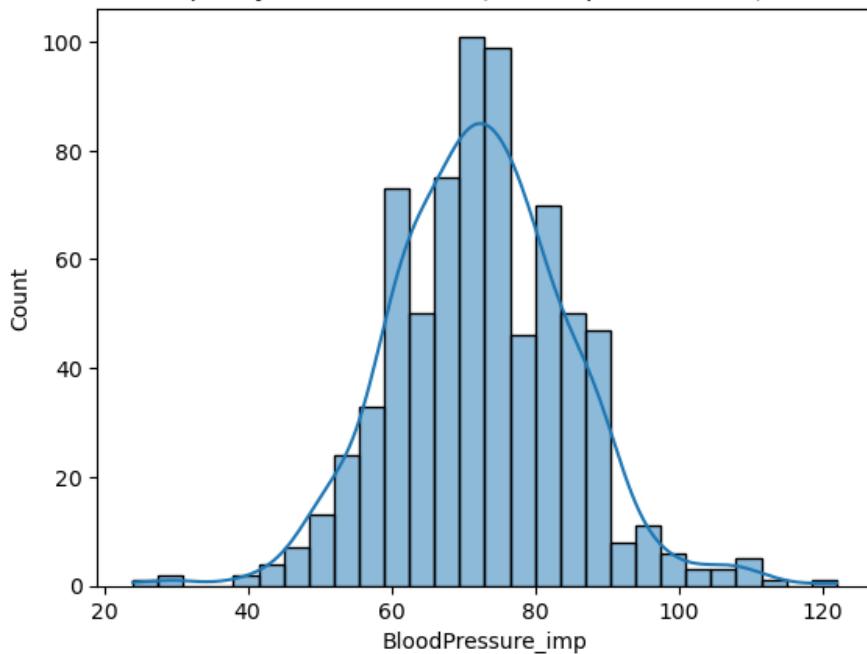
```
[36]: sns.histplot(data=diabetes2, x='Glucose_imp', kde=True)
plt.title('Distribution of Sample by Glucose (with Imputed Values) in DiabetesDataset')
plt.show()
```

Distribution of Sample by Glucose (with Imputed Values) in Diabetes Dataset



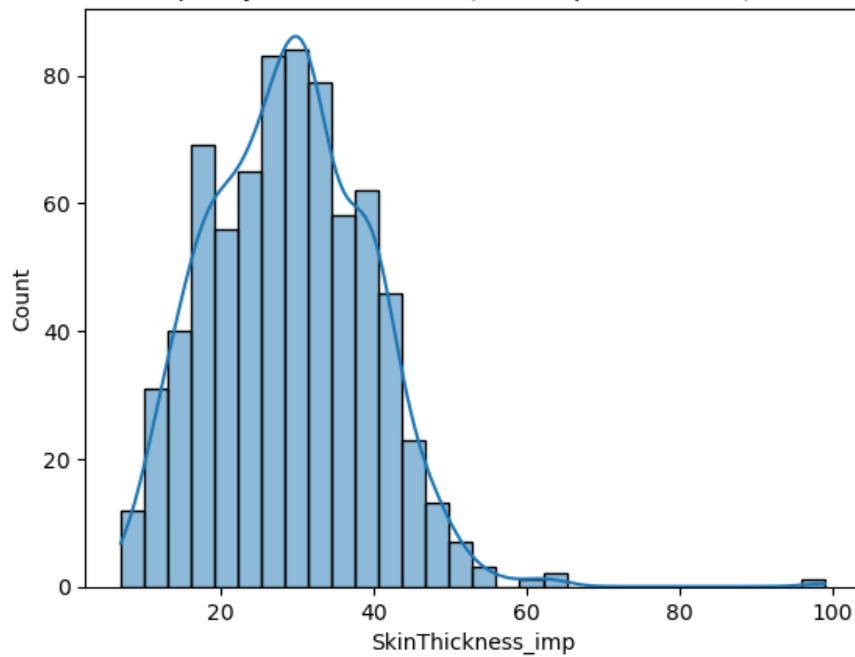
```
[37]: sns.histplot(data=diabetes2, x='BloodPressure_imp', kde=True)
plt.title('Distribution of Sample by Blood Pressure (with Imputed Values) in Diabetes Dataset')
plt.show()
```

Distribution of Sample by Blood Pressure (with Imputed Values) in Diabetes Dataset

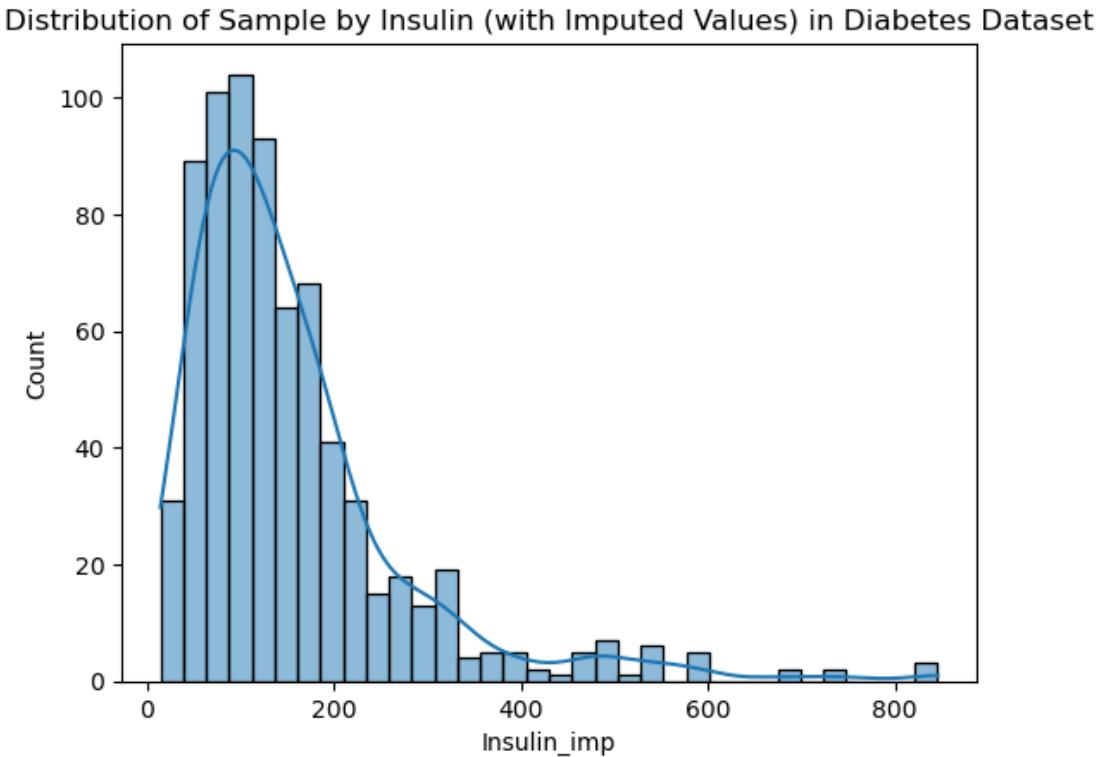


```
[38]: sns.histplot(data=diabetes2, x='SkinThickness_imp', kde=True)
plt.title('Distribution of Sample by Skin Thickness (with Imputed Values) in Diabetes Dataset')
plt.show()
```

Distribution of Sample by Skin Thickness (with Imputed Values) in Diabetes Dataset

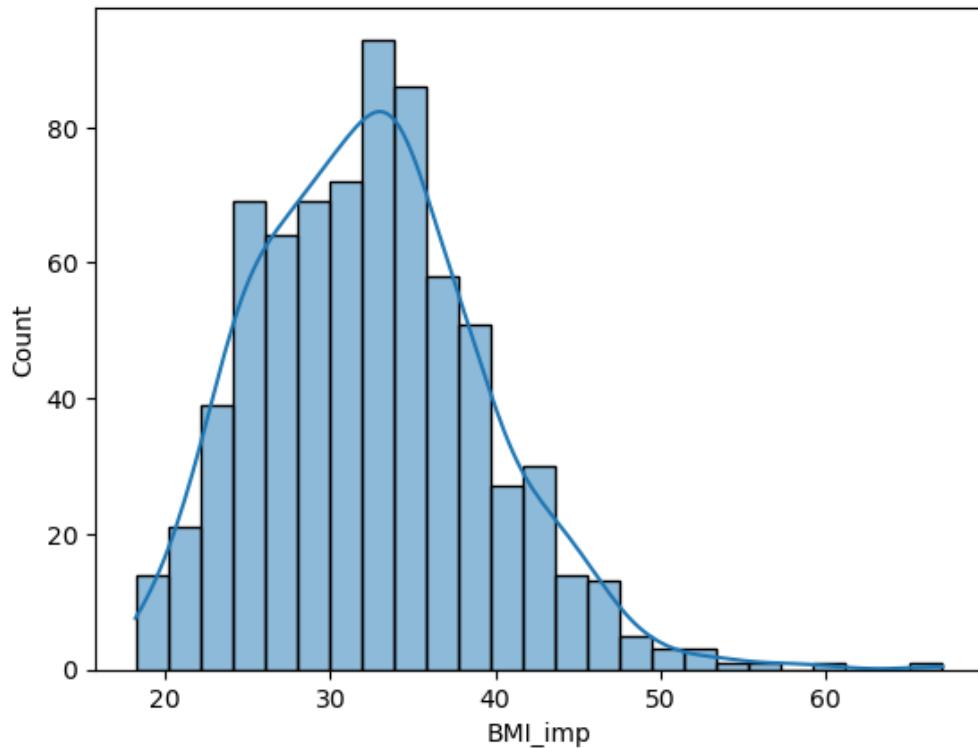


```
[39]: sns.histplot(data=diabetes2, x='Insulin_imp', kde=True)
plt.title('Distribution of Sample by Insulin (with Imputed Values) in Diabetes Dataset')
plt.show()
```



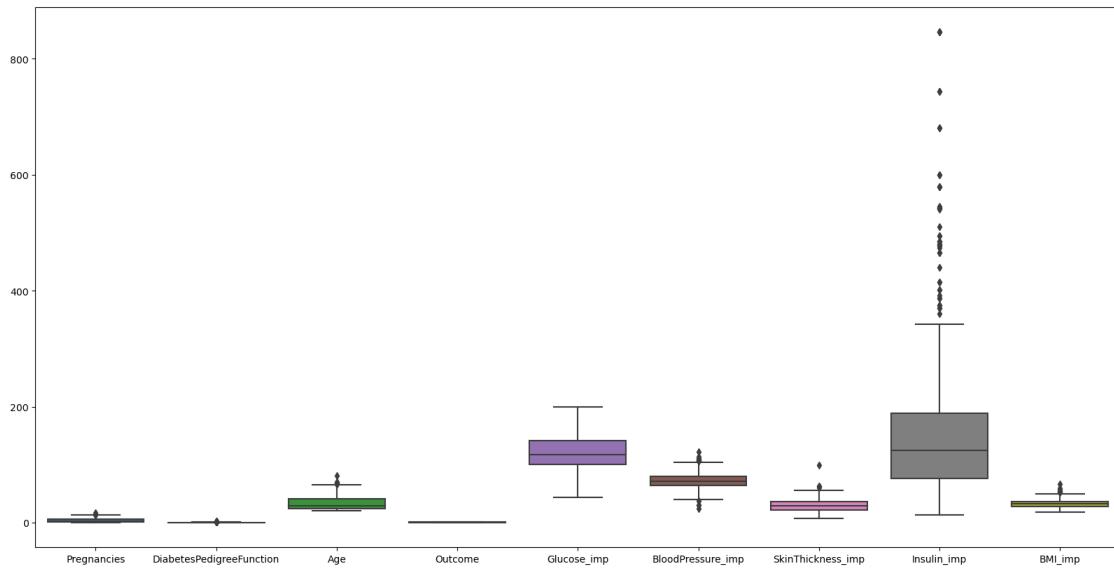
```
[40]: sns.histplot(data=diabetes2, x='BMI_imp', kde=True)
plt.title('Distribution of Sample by BMI (with Imputed Values) in Diabetes Dataset')
plt.show()
```

Distribution of Sample by BMI (with Imputed Values) in Diabetes Dataset



There are a number of distributions that are skewed. A boxplot is generated to determine if there are outliers in any of the features. The boxplots show many outliers for insulin. However, several outliers are identified for diastolic blood pressure, skin thickness, and BMI.

```
[42]: plt.figure(figsize=(20, 10))
sns.boxplot(data=diabetes2)
plt.show()
```



A log transformation is used to address the outliers.

```
[44]: diabetes2[["BloodPressure_imp", "SkinThickness_imp", "Insulin_imp", "BMI_imp"]]  
      ↵= diabetes2[["BloodPressure_imp", "SkinThickness_imp", "Insulin_imp",  
      ↵"BMI_imp"]].apply(np.log)  
      print(diabetes2)
```

	Pregnancies	DiabetesPedigreeFunction	Age	Outcome	Glucose_imp	\
0	6		0.627	50	1	148.0
1	1		0.351	31	0	85.0
2	8		0.672	32	1	183.0
3	1		0.167	21	0	89.0
4	0		2.288	33	1	137.0
..	..	..	..	..	..	..
763	10		0.171	63	0	101.0
764	2		0.340	27	0	122.0
765	5		0.245	30	0	121.0
766	1		0.349	47	1	126.0
767	1		0.315	23	0	93.0
	BloodPressure_imp	SkinThickness_imp	Insulin_imp	BMI_imp		
0	4.276666	3.555348	5.209486	3.514526		
1	4.189655	3.367296	4.653960	3.280911		
2	4.158883	3.713572	5.220356	3.148453		
3	4.189655	3.135494	4.543295	3.335770		
4	3.688879	3.555348	5.123964	3.763523		
..	..	..	..	..		
763	4.330733	3.871201	5.192957	3.493473		
764	4.248495	3.295837	5.043425	3.605498		

```

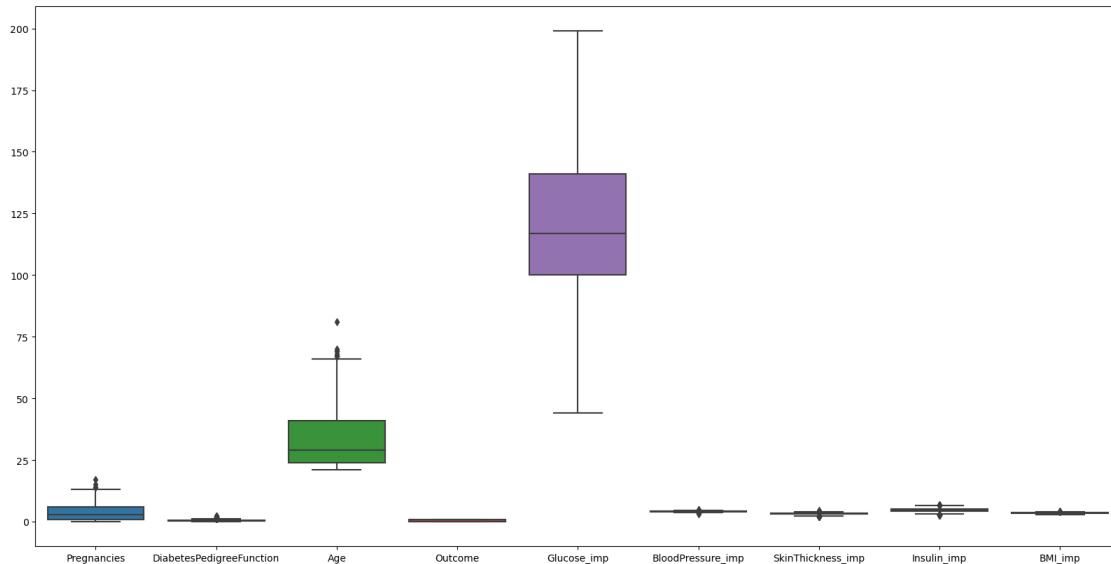
765      4.276666    3.135494    4.718499    3.265759
766      4.094345    3.465736    6.361302    3.404525
767      4.248495    3.433987    5.043425    3.414443

```

[735 rows x 9 columns]

As seen in the below boxplot, the log transformation has removed the outliers from all attributes.

```
[46]: plt.figure(figsize=(20, 10))
sns.boxplot(data=diabetes2)
plt.show()
```



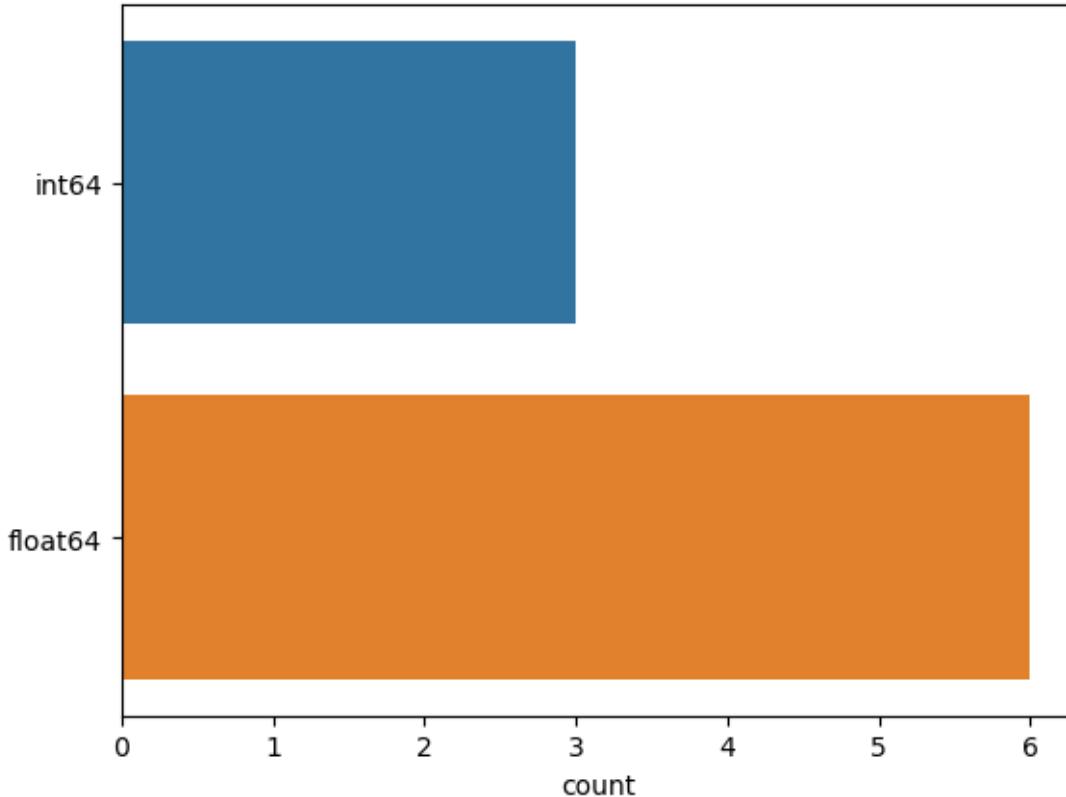
## Creation of Count Plot Describing Data Types and Count of Variables

```
[48]: print(diabetes2.dtypes)
sns.countplot(y=diabetes2.dtypes, data=diabetes2)
plt.show()
```

```

Pregnancies          int64
DiabetesPedigreeFunction float64
Age                  int64
Outcome              int64
Glucose_imp          float64
BloodPressure_imp    float64
SkinThickness_imp    float64
Insulin_imp          float64
BMI_imp              float64
dtype: object

```



## SECTION 2: DATA EXPLORATION

Check the balance of the data by plotting the count of outcomes by their value. Describe your findings and plan future course of action.

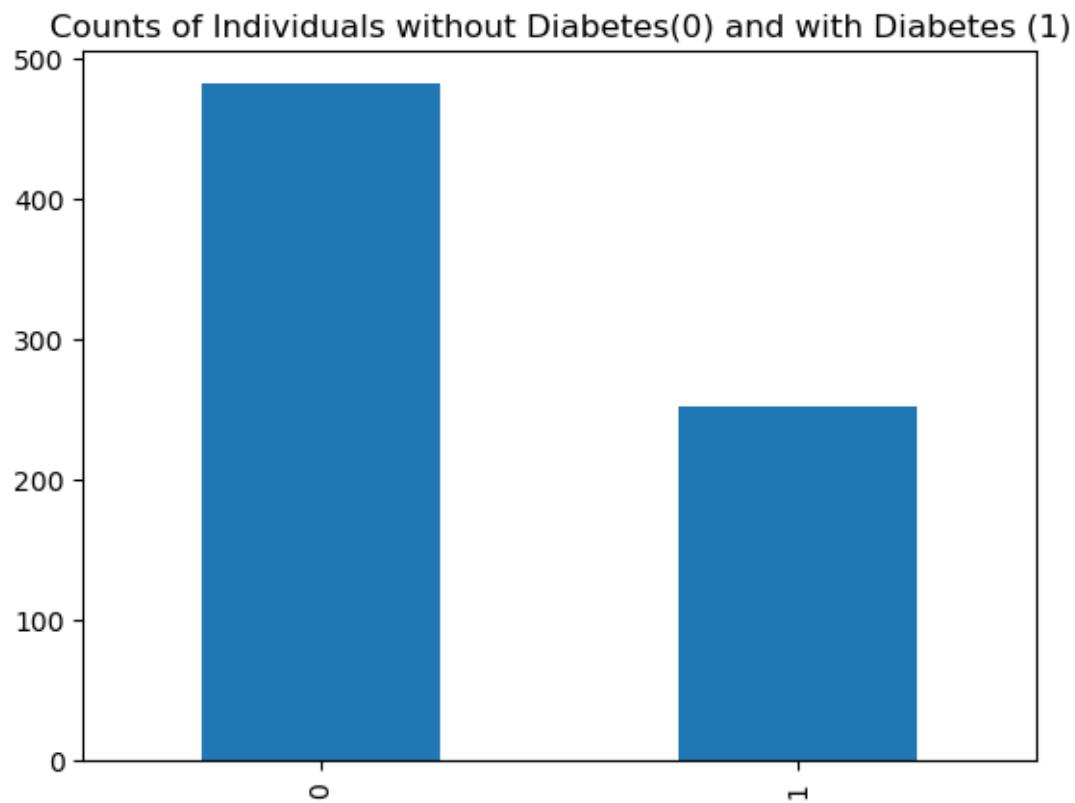
The below table and chart both indicate an imbalanced dataset based on the distribution of the sample by outcome (e.g., individuals with no diabetes responded with “0”, and individuals with diabetes responded with “1”). The number of individuals without diabetes is almost twice as great as the number of individuals with diabetes.

```
[52]: diabetes2.Outcome.value_counts()
```

```
[52]: 0    482  
1    253  
Name: Outcome, dtype: int64
```

```
[53]: diabetes2.Outcome.value_counts().plot(kind='bar')  
plt.title('Counts of Individuals without Diabetes(0) and with Diabetes (1)')
```

```
[53]: Text(0.5, 1.0, 'Counts of Individuals without Diabetes(0) and with Diabetes  
(1)')
```



```
[ ]:
```

```
[55]: sns.pairplot(diabetes2, hue = 'Outcome')
```

```
[55]: <seaborn.axisgrid.PairGrid at 0x7fa59016af10>
```



### 2c. Correlation of Features with the Outcome (no diabetes = 0, diabetes = 1)

The below correlational table indicates glucose is the most strongly associated with being diabetic, whereas insulin is indicated as having the weakest correlation with having diabetes. However, one limitation is that of error related to regression-based imputation.

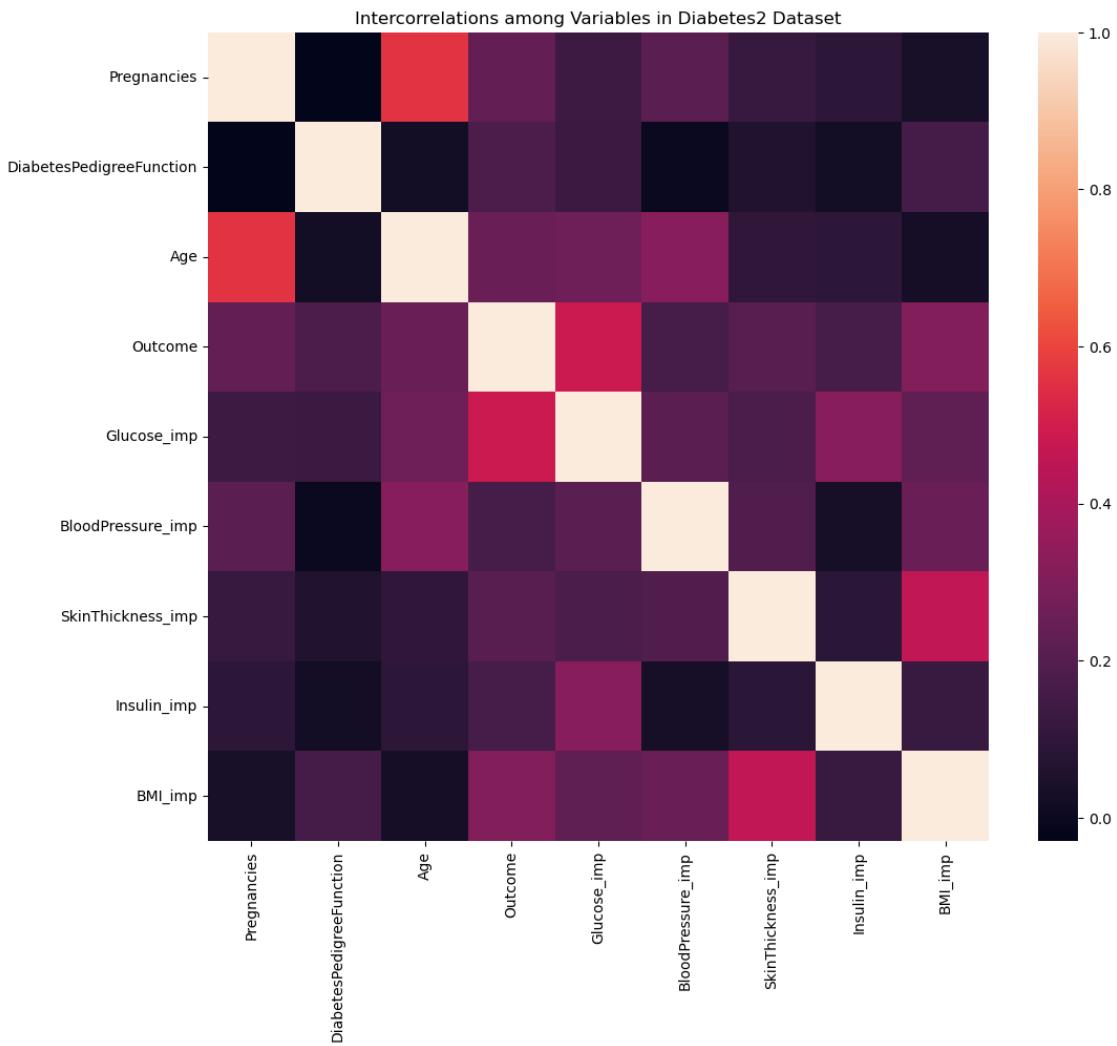
```
[57]: corr_diabetes2 = diabetes2.corrwith(diabetes2['Outcome'])
corr_diabetes2 = corr_diabetes2.to_frame(name='correlation')
corr_diabetes2 = corr_diabetes2.sort_values(by='correlation', ascending=False)
corr_diabetes2
```

	correlation
Outcome	1.000000
Glucose_imp	0.483037
BMI_imp	0.308141

Age	0.250131
Pregnancies	0.234674
SkinThickness_imp	0.204815
DiabetesPedigreeFunction	0.177518
BloodPressure_imp	0.162594
Insulin_imp	0.161442

The following is a heatmap of intercorrelations among variables. The strongest (although still moderate) correlation being between glucose and having diabetes is reflected in the below color scheme. However, moderate correlations are indicated between age and pregnancies as well as between BMI and skin thickness.

```
[59]: plt.figure(figsize=(12, 10))
sns.heatmap(diabetes2.corr())
plt.title('Intercorrelations among Variables in Diabetes2 Dataset')
plt.show()
```



## DATA MODELING

Before selecting an appropriate classification algorithm, the dataset must be split into “test” and “train” datasets.

```
[63]: #Importing Logistic Regression model
from sklearn.linear_model import LogisticRegression
```

```
[64]: lr= LogisticRegression()
```

```
[65]: #Importing "train_test-split" function to test the model
from sklearn.model_selection import train_test_split
```

```
[66]: X=diabetes2.drop(['Outcome'],axis=1)
y=diabetes2['Outcome']
y=y.astype('int')
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.
↪25,random_state=0)
```

```
[67]: #Fit the model in train and test data
lr.fit(X_train,y_train).score(X_train,y_train)

/opt/conda/envs/anaconda-panel-2023.05-py310/lib/python3.11/site-
packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed
to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression
    n_iter_i = _check_optimize_result(
```

```
[67]: 0.7695099818511797
```

```
[68]: # Step 4 - Feature scaling
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)
```

```
[69]: # Step 5 - Logistic regression classifier
from sklearn.linear_model import LogisticRegression
classifier = LogisticRegression(random_state=0, solver="liblinear")
classifier.fit(X_train, y_train)
```

```
[69]: LogisticRegression(random_state=0, solver='liblinear')
```

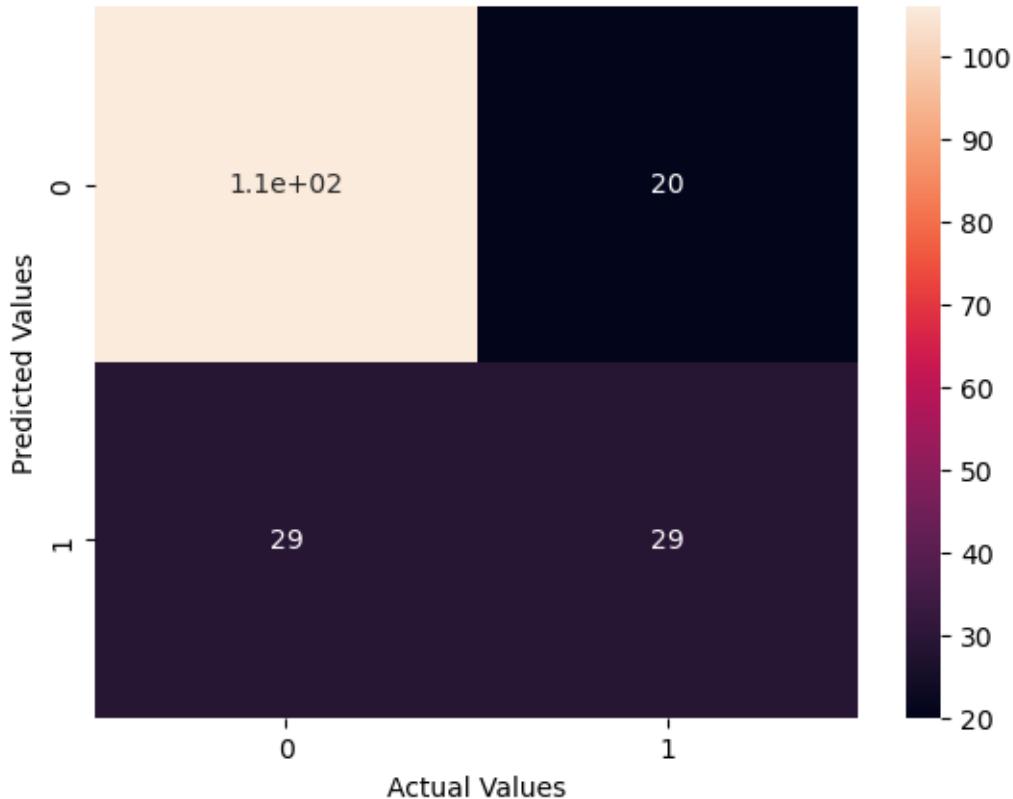
```
[70]: # Step 6 - Predicting logistic regression model on x_test  
y_pred = classifier.predict(X_test)
```

```
[71]: # Step 7 - Confusion matrix  
from sklearn import metrics  
cm = metrics.confusion_matrix(y_test, y_pred, normalize='true')  
print(cm)  
accuracy = metrics.accuracy_score(y_test, y_pred)  
print("Accuracy score:", accuracy)  
precision = metrics.precision_score(y_test, y_pred, average= 'weighted',  
zero_division="warn")  
print("Precision score:",precision)  
recall = metrics.recall_score(y_test, y_pred, zero_division='warn',average='weighted')  
print("Recall score:",recall)
```

```
[[0.84126984 0.15873016]  
 [0.5 0.5 ]]  
Accuracy score: 0.7336956521739131  
Precision score: 0.7242383910085772  
Recall score: 0.7336956521739131
```

```
[72]: from sklearn.metrics import confusion_matrix  
print(confusion_matrix(y_test,y_pred))  
sns.heatmap(confusion_matrix(y_test,y_pred),annot=True)  
plt.xlabel("Actual Values")  
plt.ylabel("Predicted Values")  
plt.show()
```

```
[[106 20]  
 [ 29 29]]
```



```
[73]: # Step 9 - Compare classification algorithms
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier
```

```
[74]: classification_models = []
classification_models.append(('Logistic Regression', LogisticRegression(solver="liblinear")))
classification_models.append(('K Nearest Neighbor', KNeighborsClassifier(n_neighbors=10,
metric="minkowski", p=2)))
classification_models.append(('Decision Tree', DecisionTreeClassifier(criterion="entropy")))
classification_models.append(('Random Forest', RandomForestClassifier(n_estimators=100,
criterion="entropy")))
```

```
[75]: for name, model in classification_models:
    kfold = KFold(n_splits=10, random_state=(7), shuffle=(True))
    result = cross_val_score(model, X, y, cv=kfold, scoring='accuracy')
    print("%s: Mean Accuracy = %.2f%% - SD Accuracy = %.2f%%" % (name, result.
        mean()*100,
        result.std()*100))
```

Logistic Regression: Mean Accuracy = 76.87% - SD Accuracy = 4.66%  
 K Nearest Neighbor: Mean Accuracy = 75.37% - SD Accuracy = 6.27%  
 Decision Tree: Mean Accuracy = 72.67% - SD Accuracy = 4.90%  
 Random Forest: Mean Accuracy = 76.19% - SD Accuracy = 5.34%

```
[76]: from catboost import CatBoostClassifier, Pool, metrics, cv
from sklearn.metrics import accuracy_score
```

While there are many techniques for addressing imbalanced datasets, techniques such as oversampling the minority class (in this case, individuals with diabetes) and undersampling the majority class (in this case, individuals without diabetes) also present challenges. Ensemble learning methods benefit from the combined strength of multiple simple models to generate the highest level of prediction accuracy. Random Forest Classifier is used below. A mean ROC AUC score of 0.865 is generated. The closer a ROC AUC score is to 1, the more accurate the model is. The ROC AUC score of 0.865 is relatively high. However, Random Forest Classifier may not have corrected the imbalance present in the data set.

```
[204]: # random forest classifier
from numpy import mean
from sklearn.datasets import make_classification
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import RepeatedStratifiedKFold
from sklearn.ensemble import RandomForestClassifier
# generate dataset
X, y = make_classification(n_samples=10000, n_features=2, n_redundant=0,
    n_clusters_per_class=1, weights=[0.99], flip_y=0, random_state=4)
# define model
model = RandomForestClassifier(n_estimators=10)
# define evaluation procedure
cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3, random_state=1)
# evaluate model
scores = cross_val_score(model, X, y, scoring='roc_auc', cv=cv, n_jobs=-1)
# summarize performance
print('Mean ROC AUC: %.3f' % mean(scores))
```

Mean ROC AUC: 0.865

To correct the imbalance in the dataset, a Balanced Random Forest Classifier is used. An AUC ROC score of 0.963 is generated. Because this is a higher score than generated by Random Forest Classifier, correcting for the imbalance seems to have positively impacted the accuracy of the model.

```
[208]: # random forest with random undersampling for imbalanced classification
from imblearn.ensemble import BalancedRandomForestClassifier
# generate dataset
X, y = make_classification(n_samples=10000, n_features=2, n_redundant=0,
                           n_clusters_per_class=1, weights=[0.99], flip_y=0, random_state=4)
# define model
model = BalancedRandomForestClassifier(n_estimators=10)
# define evaluation procedure
cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3, random_state=1)
# evaluate model
scores = cross_val_score(model, X, y, scoring='roc_auc', cv=cv, n_jobs=-1)
# summarize performance
print('Mean ROC AUC: %.3f' % mean(scores))
```

```
/opt/conda/envs/anaconda-panel-2023.05-py310/lib/python3.11/site-
packages/sklearn/utils/deprecation.py:86: FutureWarning: Function delayed is
deprecated; The function `delayed` has been moved from `sklearn.utils.fixes` to
`sklearn.utils.parallel`. This import path will be removed in 1.5.
    warnings.warn(msg, category=FutureWarning)
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```

```

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Mean ROC AUC: 0.963

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```

To envision the sensitivity (increased true positive rate) and specificity (decreased false positive rate), an ROC curve is generated below.

```

[178]: from sklearn.model_selection import train_test_split
from sklearn.naive_bayes import GaussianNB# Split train and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.25)
# Create the model object
model = GaussianNB()
# Fit the model to the training data
model.fit(X_train, y_train)
# Predict the classes on the test data
y_pred = model.predict(X_test)
# Predict the classes on the test data, and return the probabilities for each
# class
y_proba = model.predict_proba(X_test)

```

```

[184]: from sklearn.metrics import confusion_matrix
def calculate_tpr_fpr(y_real, y_pred):
    # Calculates the confusion matrix and recover each element
    cm = confusion_matrix(y_real, y_pred)
    TN = cm[0, 0]
    FP = cm[0, 1]
    FN = cm[1, 0]
    TP = cm[1, 1]
    # Calculates tpr and fpr
    tpr = TP/(TP + FN) # sensitivity - true positive rate
    fpr = 1 - TN/(TN+FP) # 1-specificity - false positive rate

    return tpr, fpr

```

```

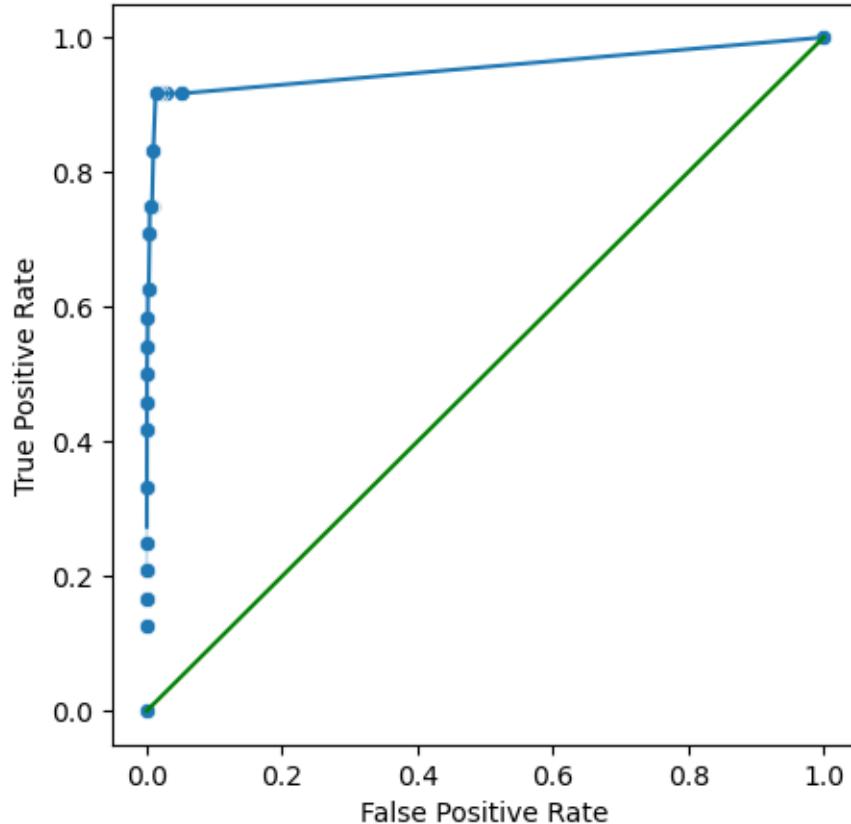
[186]: def get_n_roc_coordinates(y_real, y_proba, n = 50):
    tpr_list = [0]
    fpr_list = [0]
    for i in range(n):
        threshold = i/n
        y_pred = y_proba[:, 1] > threshold
        tpr, fpr = calculate_tpr_fpr(y_real, y_pred)
        tpr_list.append(tpr)
        fpr_list.append(fpr)
    return tpr_list, fpr_list

```

```
import seaborn as sns import matplotlib.pyplot as plt def plot_roc_curve(tpr, fpr, scatter = True):
```

```
plt.figure(figsize = (5, 5)) if scatter: sns.scatterplot(x = fpr, y = tpr) sns.lineplot(x = fpr, y = tpr) sns.lineplot(x = [0, 1], y = [0, 1], color = 'green') plt.xlim(-0.05, 1.05) plt.ylim(-0.05, 1.05)  
plt.xlabel("False Positive Rate") plt.ylabel("True Positive Rate")
```

```
[194]: # Calculates 10 coordinates of the ROC Curve  
tpr, fpr = get_n_roc_coordinates(y_test, y_proba)  
# Plots the ROC curve  
plot_roc_curve(tpr, fpr)
```



In the above ROC curve, the green line represents where the true positive rate is the same as the false positive rate. Thus, the blue line (the ROC line of the classifier) should be as far as possible (and above) from the green line. The green line represents classification accuracy which is the same as the flip of a fair coin. If the blue line falls beneath the green line, the classification is even less accurate than the flip of a fair coin. The ROC curve above clearly indicates that the model is an excellent fit, as it displays a well-defined elbow in the upper left-hand corner of the chart.