

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)²)

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

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           76           0           0           45.3  0.194
46    0           1           108          37           0           39.2  0.305
5           103           74           0           0           28.8  0.153
65    0           1           105           29          325           36.9  0.159
48    0           1           ..           ..           ..           ..
2           84           50           23           76           30.4  0.968
21    0           1           65           0           0           39.6  0.930
27    0           1           23           0           0           28.9  0.773
25    0           1           58           16          52           32.7  0.166
25    0           1           72           41          114           40.9  0.817
47    1           1
Length: 768, dtype: int64

```

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

```
[13]:      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
```

```
[14]:
```

	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           76.0
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]
```

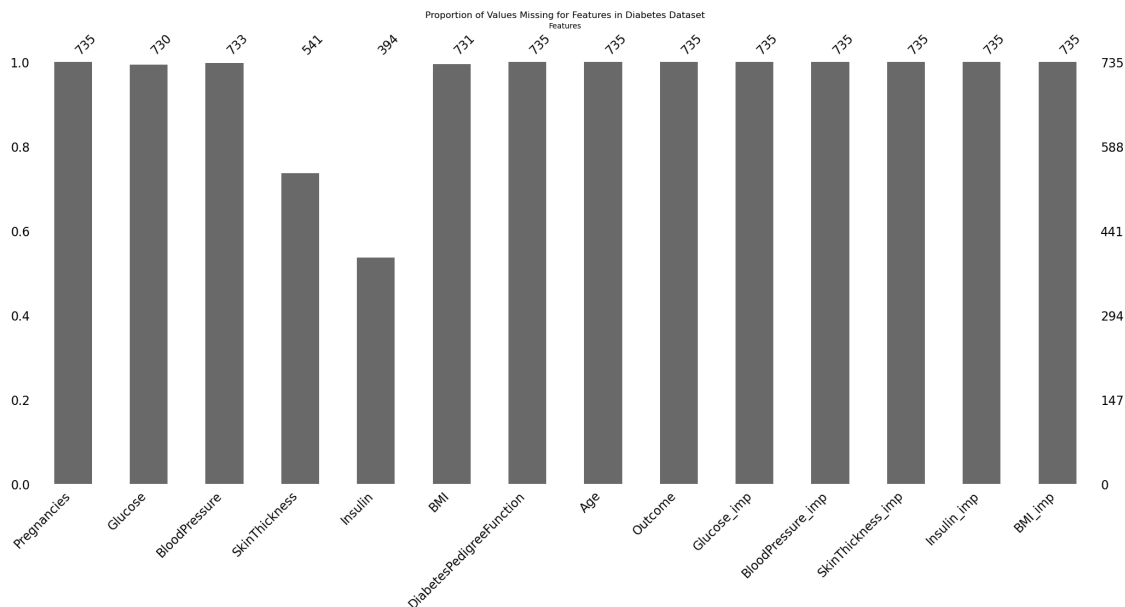
```
[24]: pip install missingno
```


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()
```

```
[30]:
```

	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	

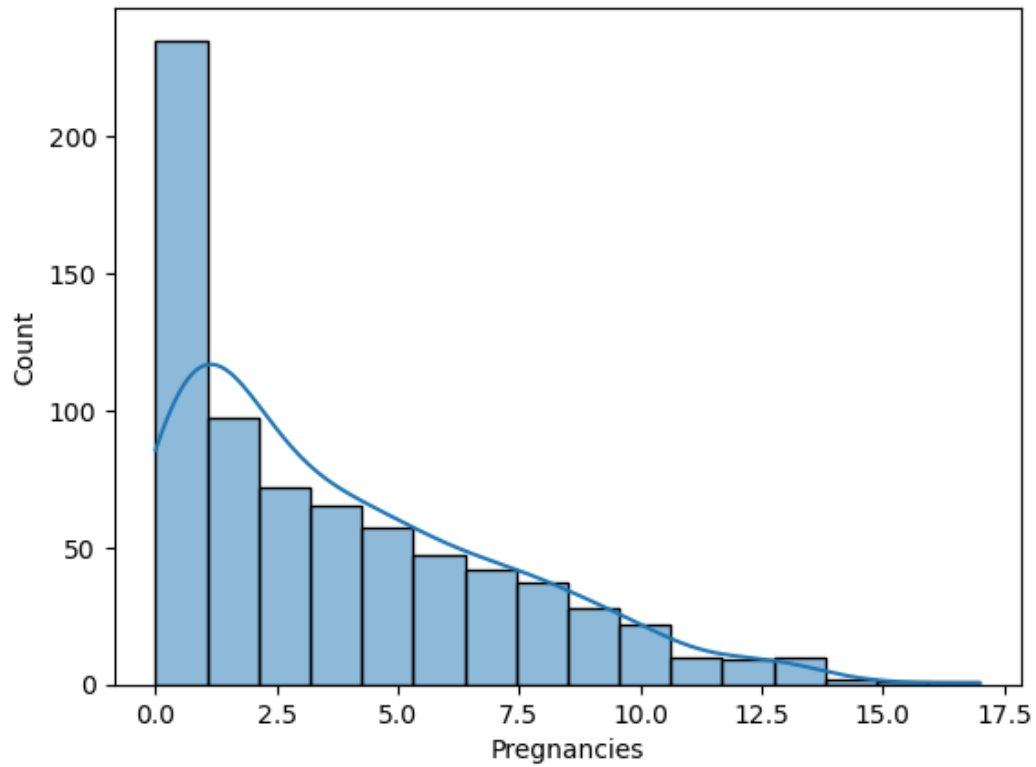
	BMI_imp
count	735.000000
mean	32.470748
std	6.891538
min	18.200000
25%	27.500000
50%	32.400000
75%	36.650000
max	67.100000

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

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

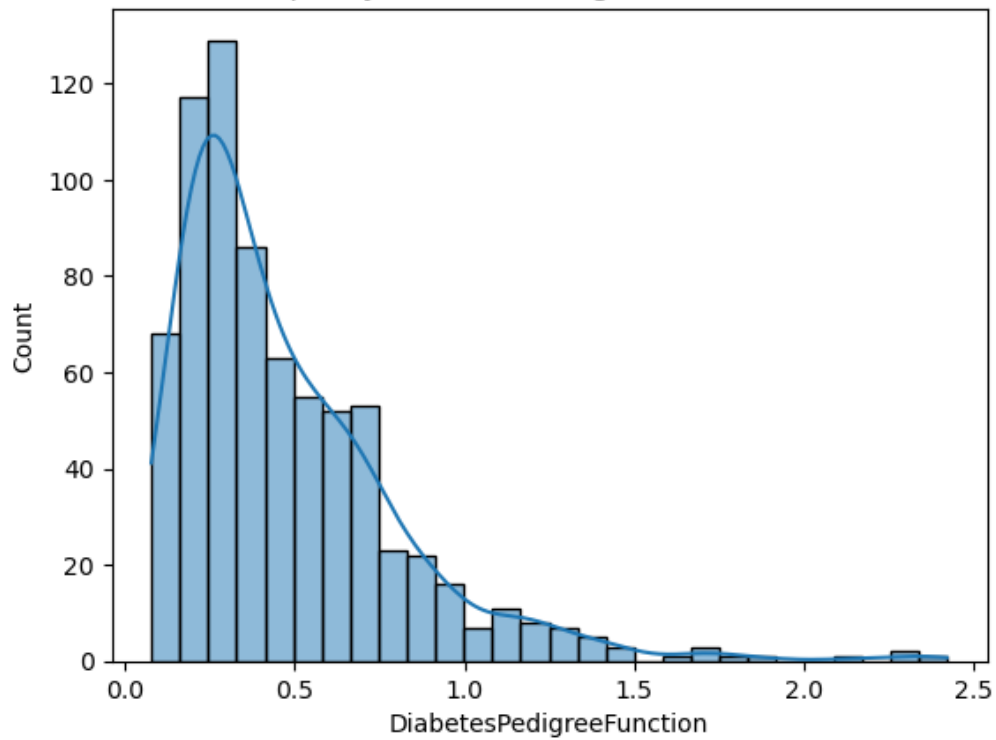
```
[33]: sns.histplot(data=diabetes2, x='Pregnancies', kde=True)
plt.title('Distribution of Sample by Number of Pregnancies in Diabetes Dataset')
plt.show()
```

Distribution of Sample by Number of Pregnancies in Diabetes Dataset

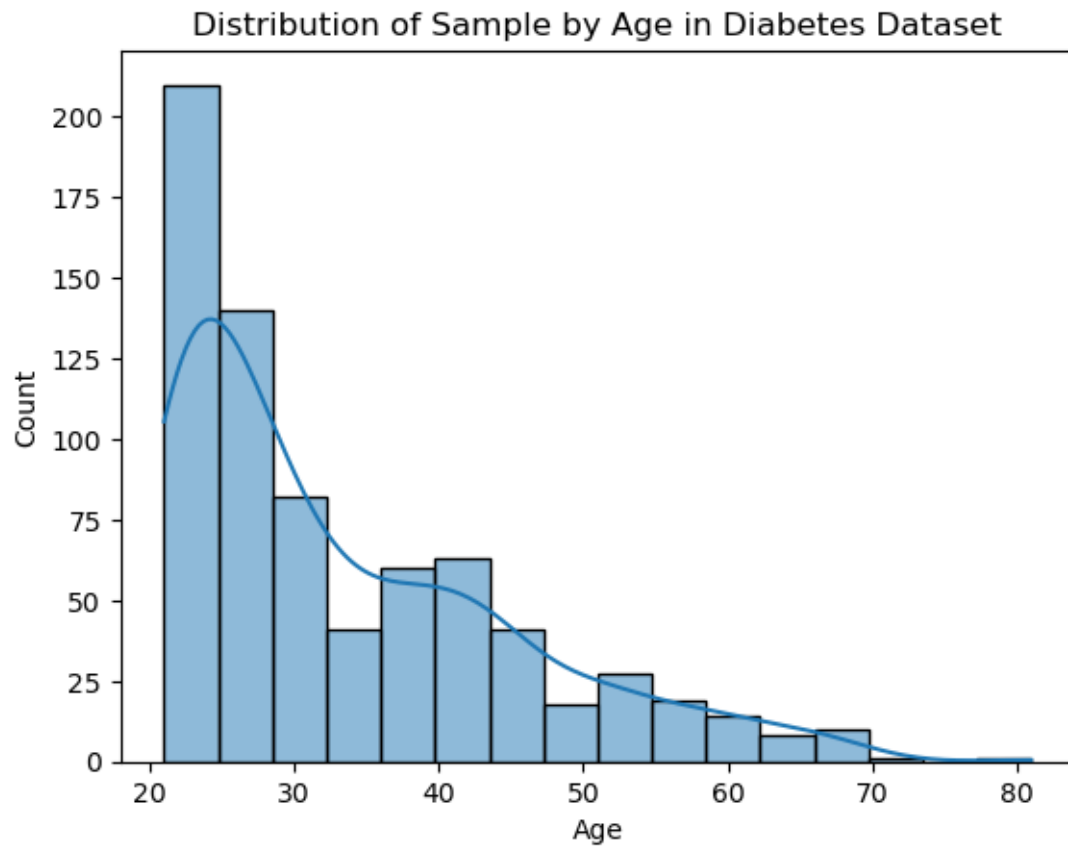


```
[34]: sns.histplot(data=diabetes2, x='DiabetesPedigreeFunction', kde=True)
plt.title('Distribution of Sample by Diabetes Pedigree Function in Diabetes_
↳Dataset')
plt.show()
```

Distribution of Sample by Diabetes Pedigree Function in Diabetes Dataset

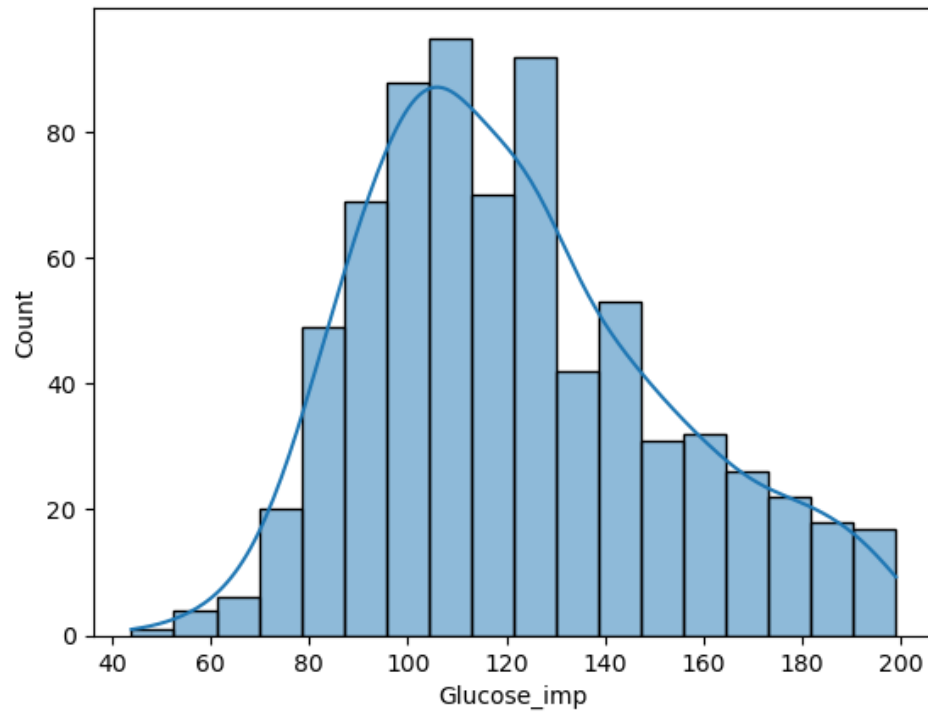


```
[35]: sns.histplot(data=diabetes2, x='Age', kde=True)
plt.title('Distribution of Sample by Age in Diabetes Dataset')
plt.show()
```



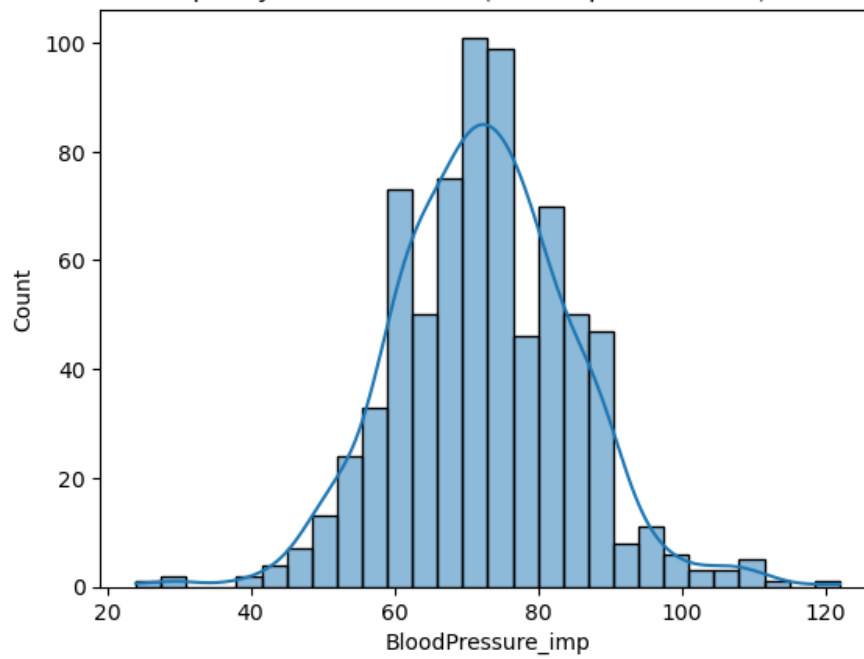
```
[36]: sns.histplot(data=diabetes2, x='Glucose_imp', kde=True)
plt.title('Distribution of Sample by Glucose (with Imputed Values) in Diabetes_
↳Dataset')
plt.show()
```

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



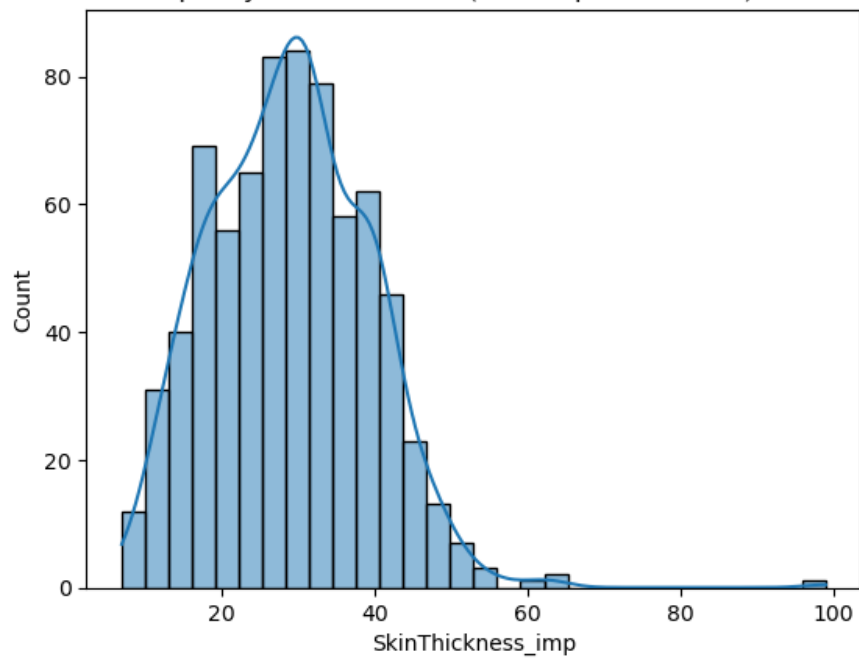
```
[37]: sns.histplot(data=diabetes2, x='BloodPressure_imp', kde=True)
plt.title('Distribution of Sample by Blood Pressure (with Imputed Values) in_
↳Diabetes Dataset')
plt.show()
```

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



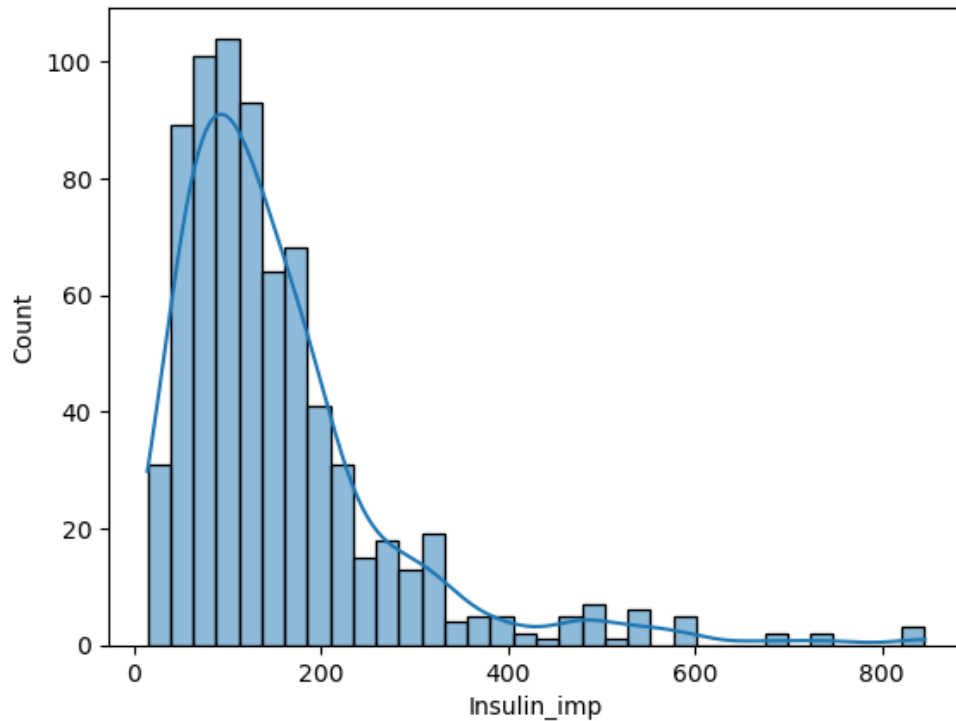
```
[38]: sns.histplot(data=diabetes2, x='SkinThickness_imp', kde=True)
plt.title('Distribution of Sample by Skin Thickness (with Imputed Values) in_
↳Diabetes Dataset')
plt.show()
```

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



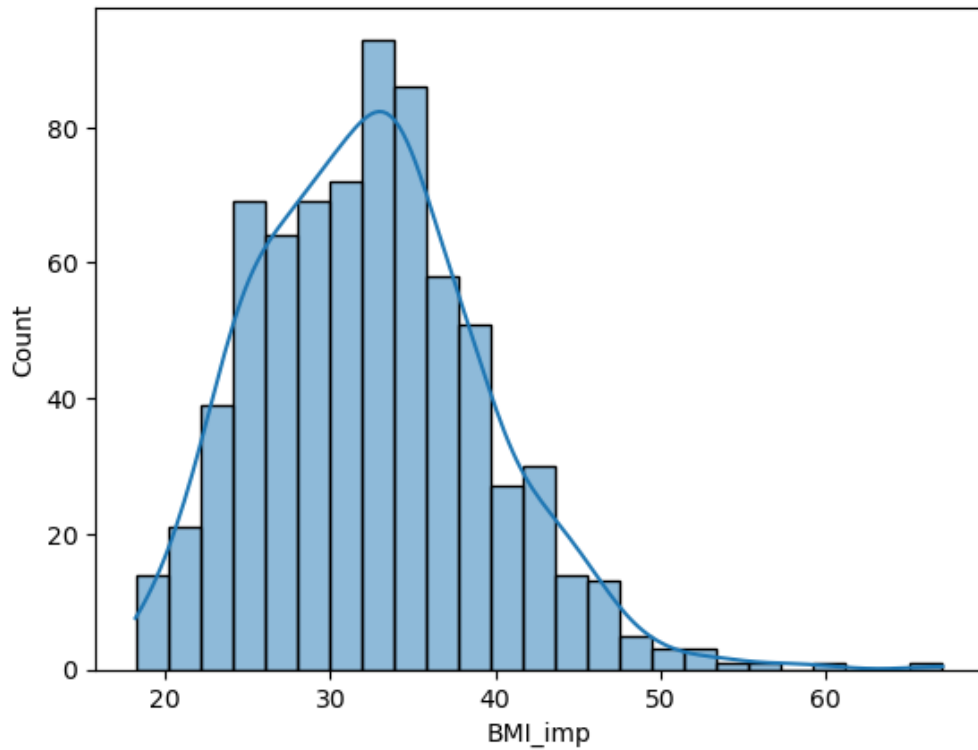

```
[39]: sns.histplot(data=diabetes2, x='Insulin_imp', kde=True)
plt.title('Distribution of Sample by Insulin (with Imputed Values) in Diabetes_
↳Dataset')
plt.show()
```

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



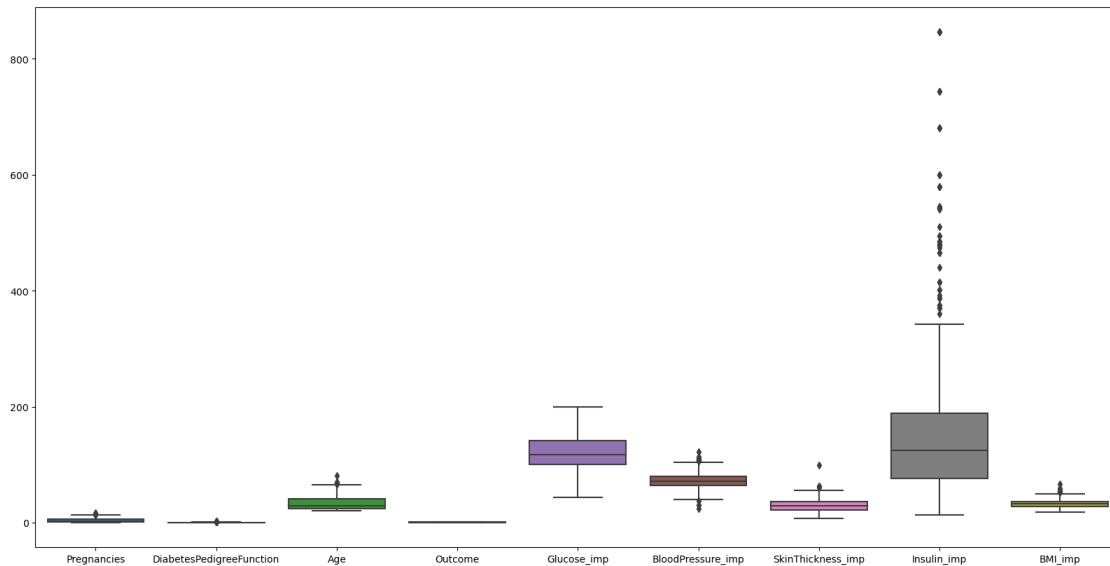
```
[40]: sns.histplot(data=diabetes2, x='BMI_imp', kde=True)
plt.title('Distribution of Sample by BMI (with Imputed Values) in Diabetes_
↳Dataset')
plt.show()
```

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 tranformation 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

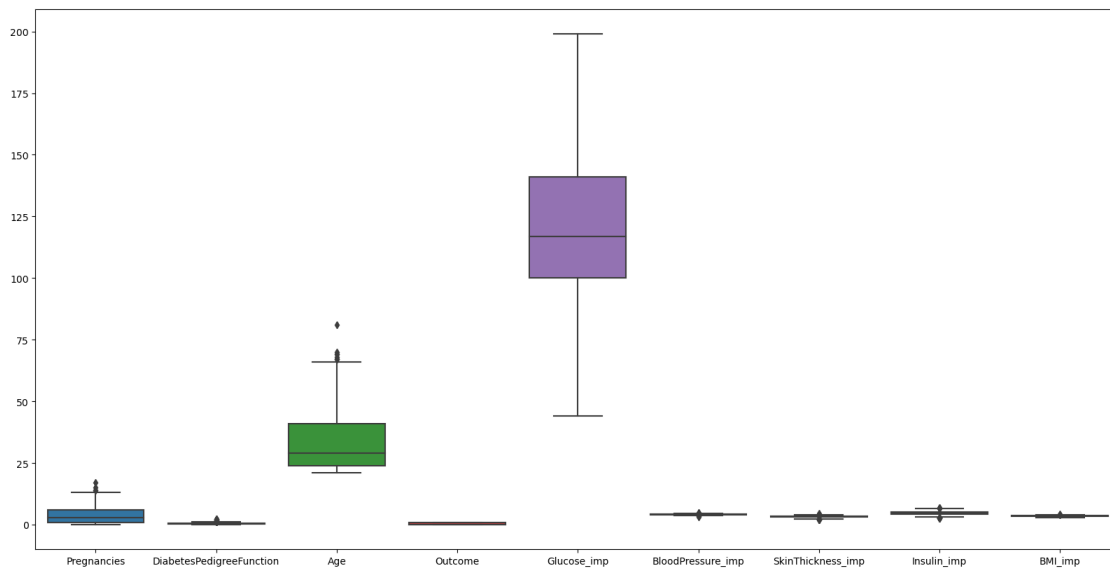
	BloodPressure_imp	SkinThickness_imp	Insulin_imp	BMI_imp
0	4.276666	3.555348	5.209486	3.514526
1	4.189655	3.367296	4.653960	3.280911
2	4.158883	3.713572	5.220356	3.148453
3	4.189655	3.135494	4.543295	3.335770
4	3.688879	3.555348	5.123964	3.763523
..
763	4.330733	3.871201	5.192957	3.493473
764	4.248495	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.

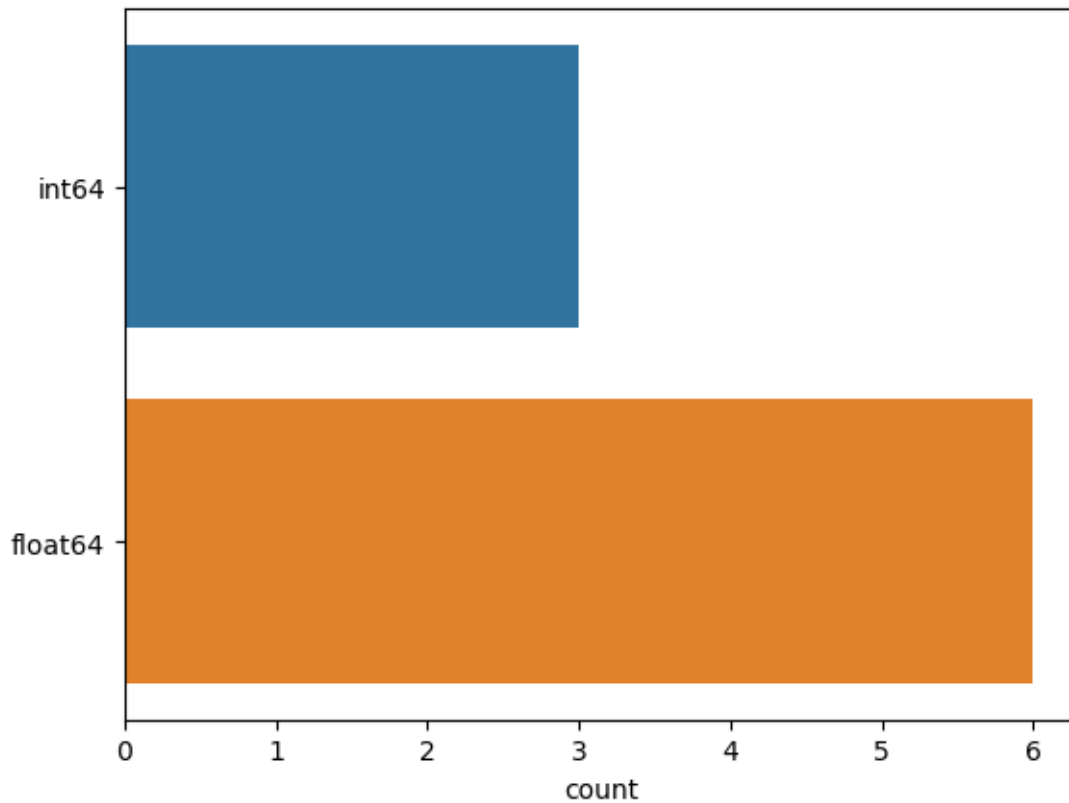
```
[46]: plt.figure(figsize=(20, 10))
sns.boxplot(data=diabetes2)
plt.show()
```



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.

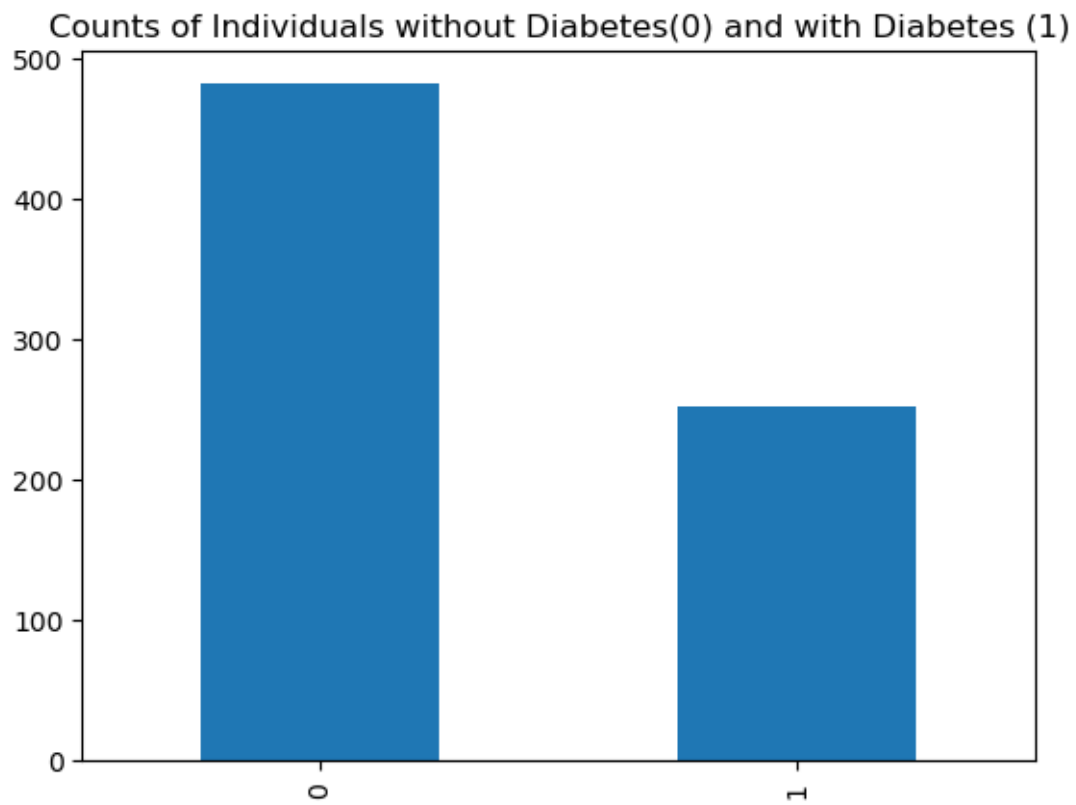
The below table and chart both indicate an imbalanced dataset based on the distribution of the sample by outcome (e.g., individuals with no diabetes responded with “0”, and individuals with diabetes responded with “1”). The number of individuals without diabetes is almost twice as great as the number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

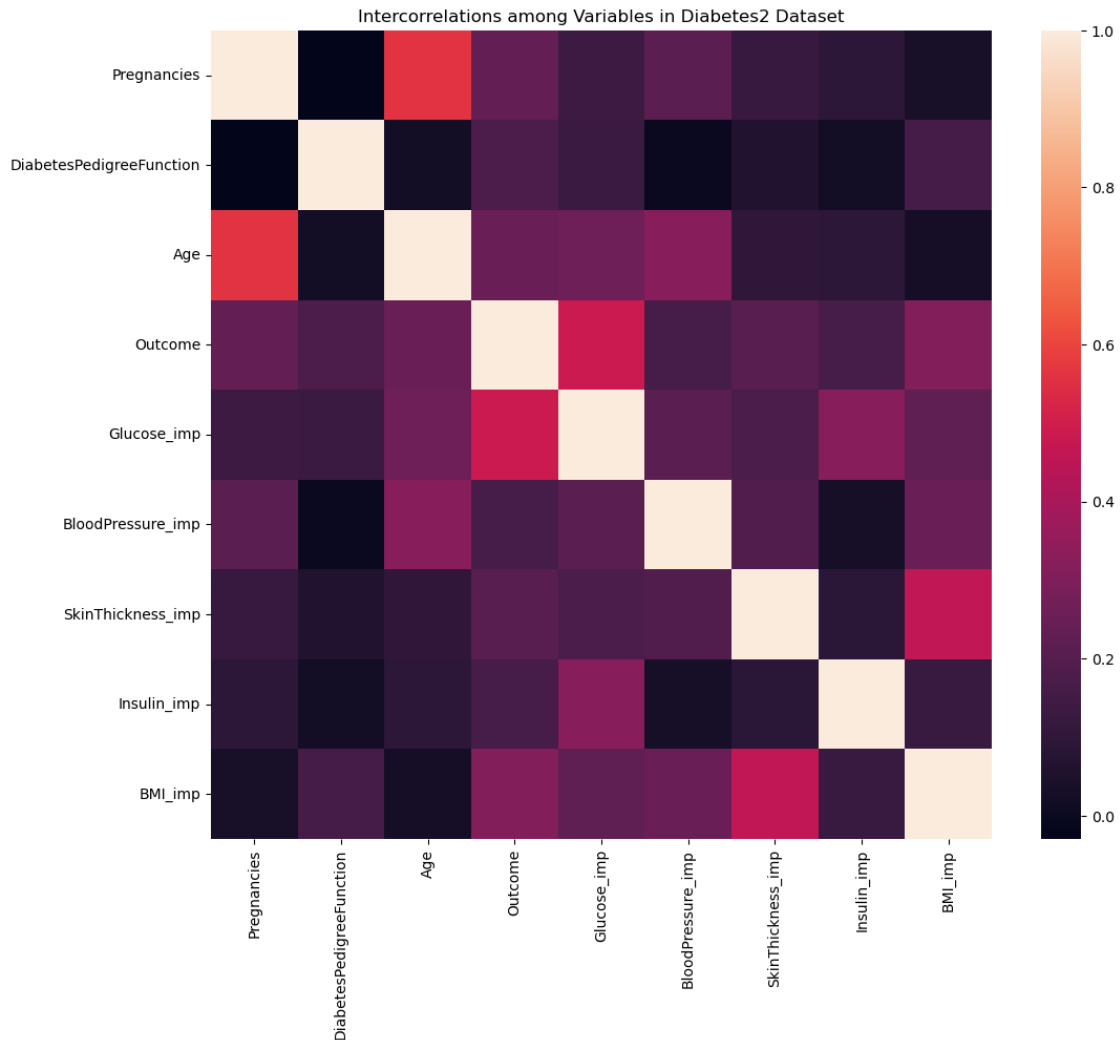
```
[57]:
```

	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')
```

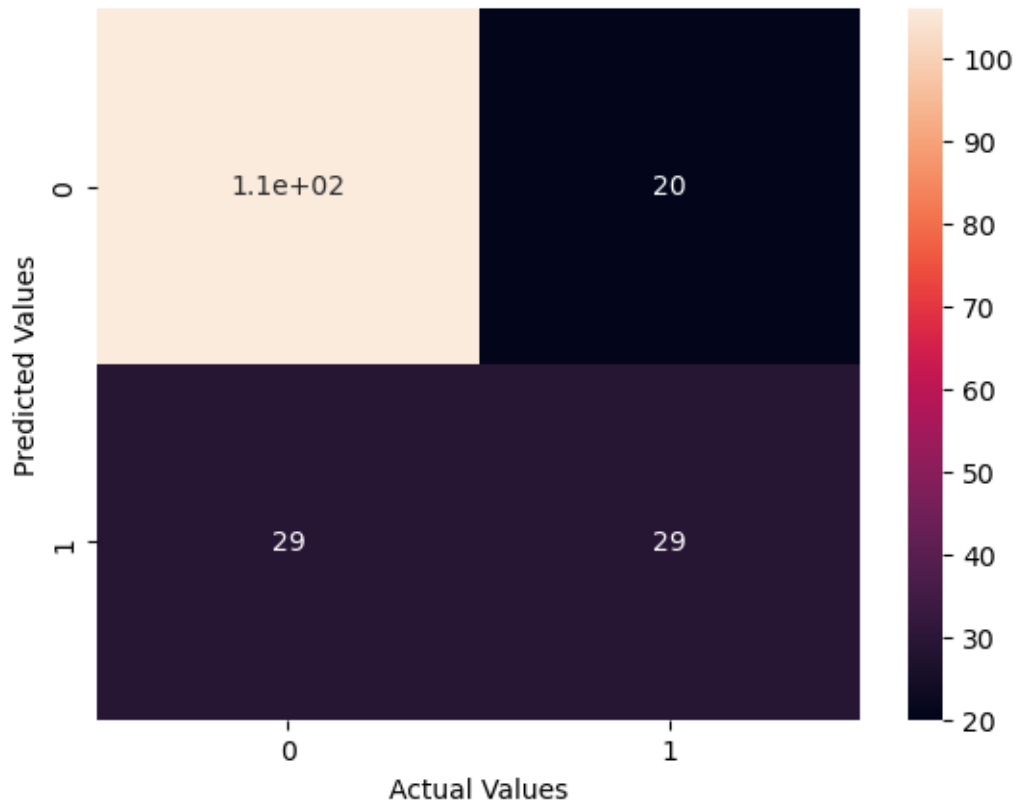
```
[70]: # Step 6 - Predicting logistic regression model on x_test
y_pred = classifier.predict(X_test)
```

```
[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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```

```

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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

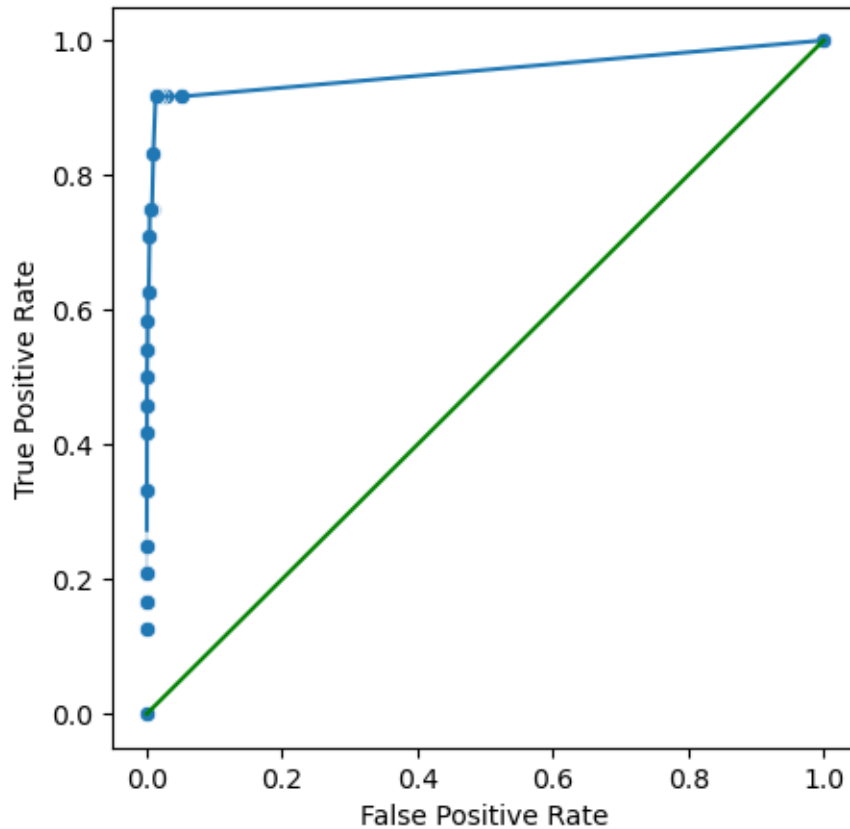
    return tpr, fpr
```

```
[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.