SEN4018 Project

Pima Indians Diabetes

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Dataset Description

The Pima Indians Diabetes Databas is provided by The National Institute of Diabetes and Digestive and Kidney Diseases. This dataset is a subset of the larger dataset. In this dataset, all of the patients, are Pima Indian women who are at least 21 years old. The dataset contains 8 medical predictor factors.

Medical Factors:

1. Number of times pregnant
2. Plasma glucose concentration a 2 hours in an oral glucose tolerance test
3. Diastolic blood pressure (mm Hg)
4. Triceps skin fold thickness (mm)
5. 2-Hour serum insulin (mu U/ml)
6. Body mass index (weight in kg/(height in m)^2)
7. Diabetes pedigree function
8. Age (years)

Statistical Description

	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

Data Preprocessing

01

Step 1

Visualize raw data

02

Step 2

Preprocess data

03

Step 3

Visualize Preprocessed data

Missing Data

These values can't be zero, so missing data is converted to NAN:

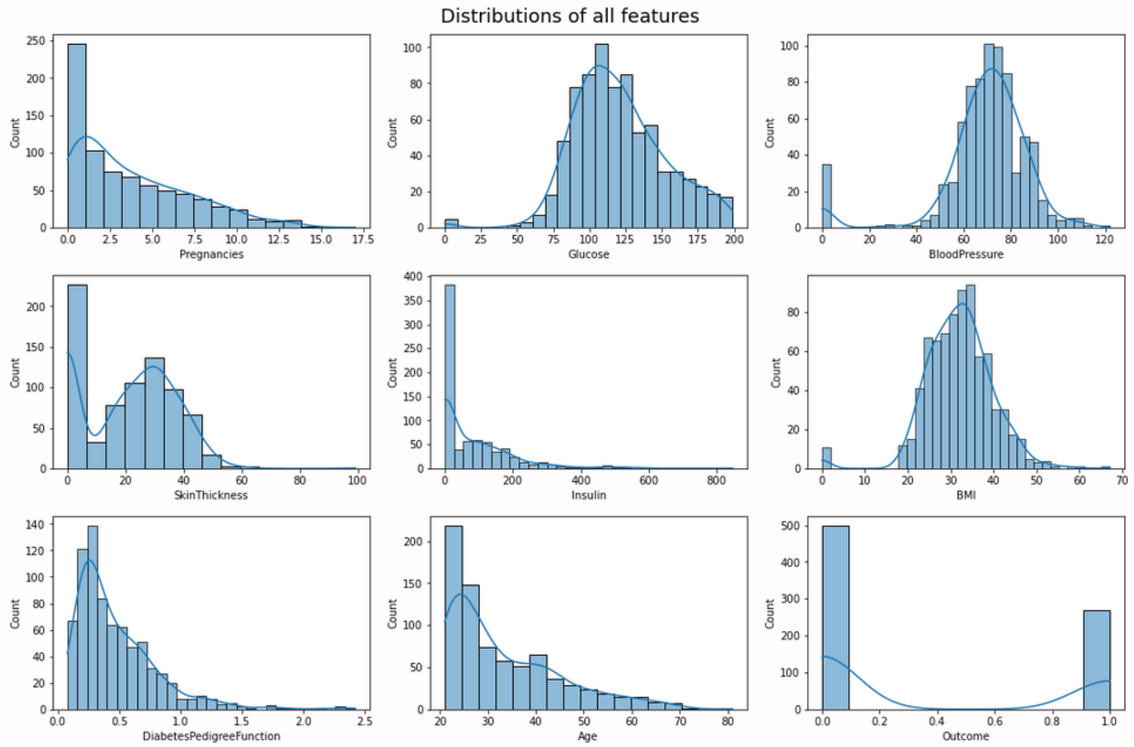
- Glucose
- BloodPressure
- SkinThickness
- Insuling
- BMI

```
Pregnancies                 0
Glucose                     5
BloodPressure              35
SkinThickness             227
Insulin                   374
BMI                        11
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

Number of NAN values for each feature

Features Distribution

This is the distributions of all features **before** imputation:



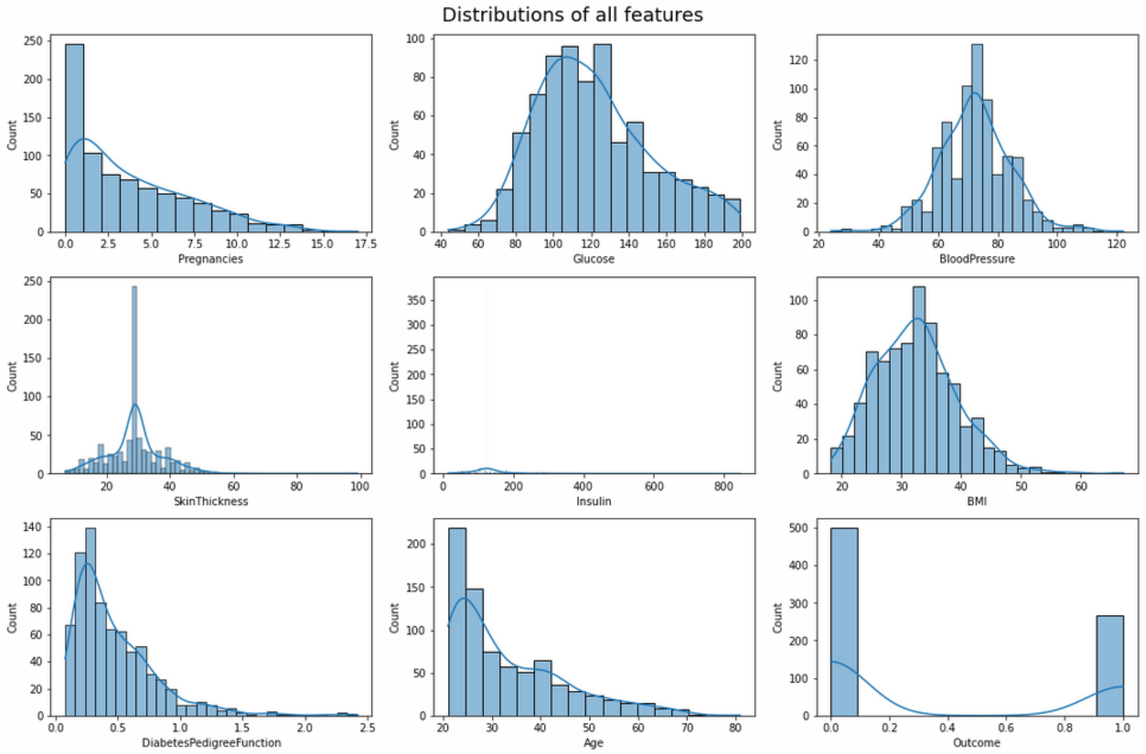
Features Distribution

NAN values were replaced with more suitable values:

- Glucose -> mean
- BloodPressure -> mean
- SkinThickness -> median
- Insulin -> mean
- BMI -> median

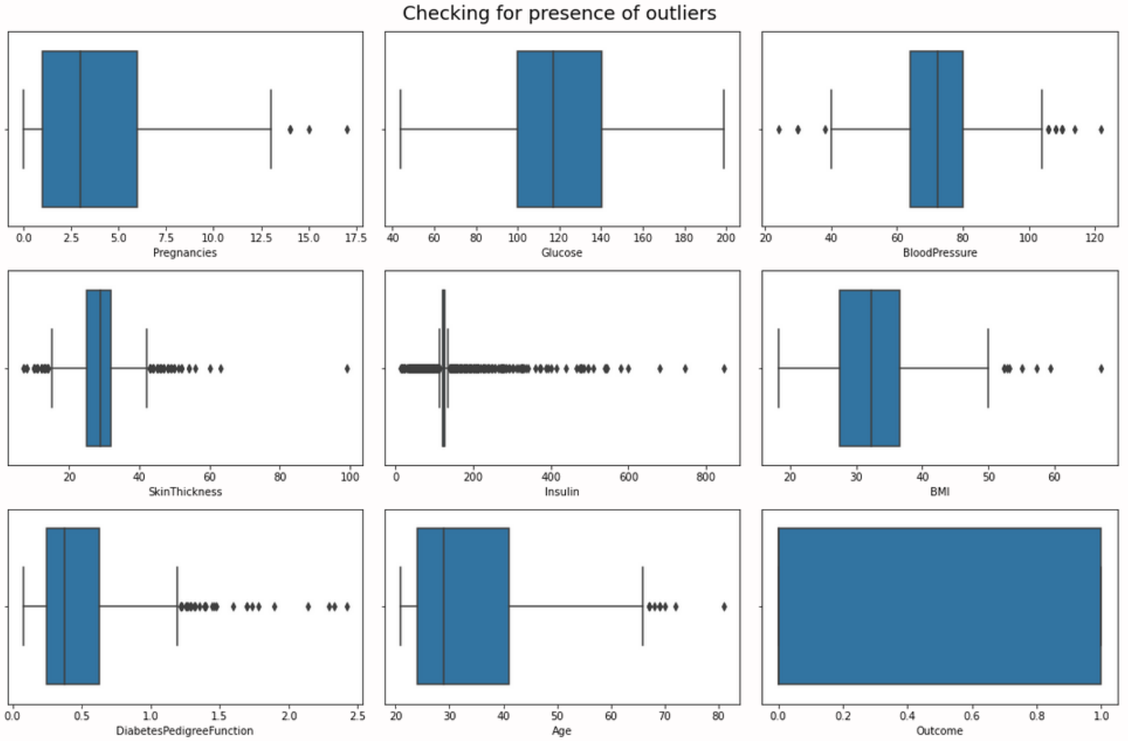
Features Distribution

This is the distributions of all features **after** imputation:



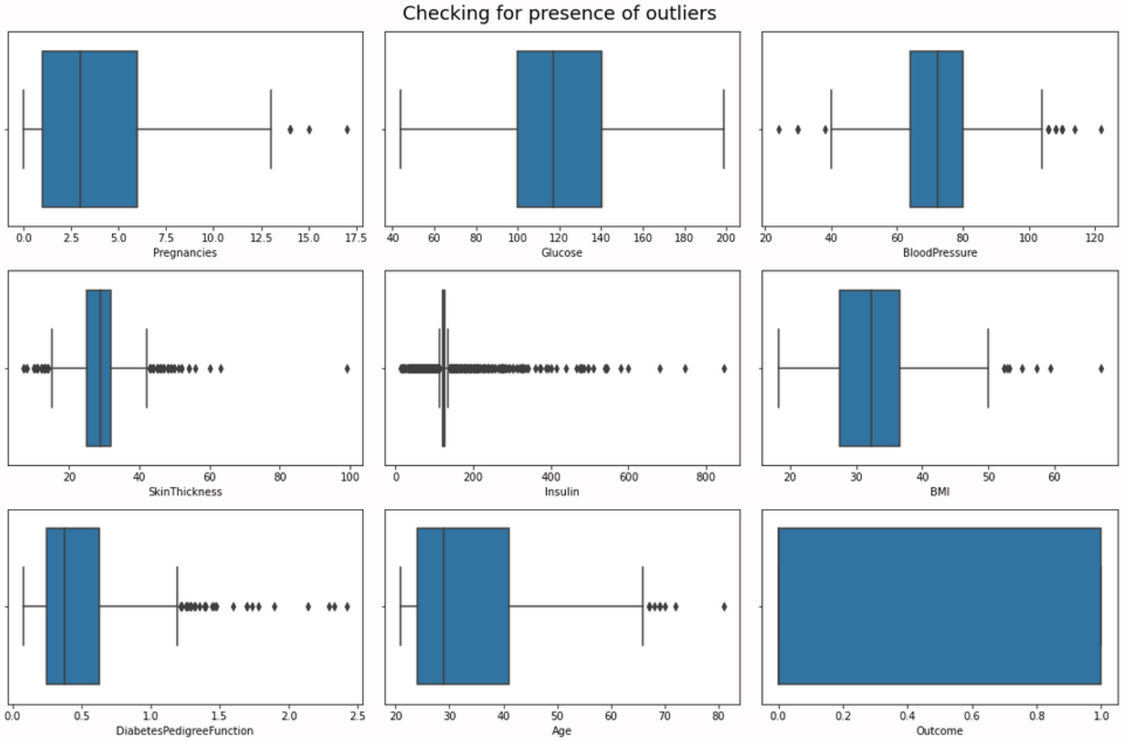
Checking for Outliers

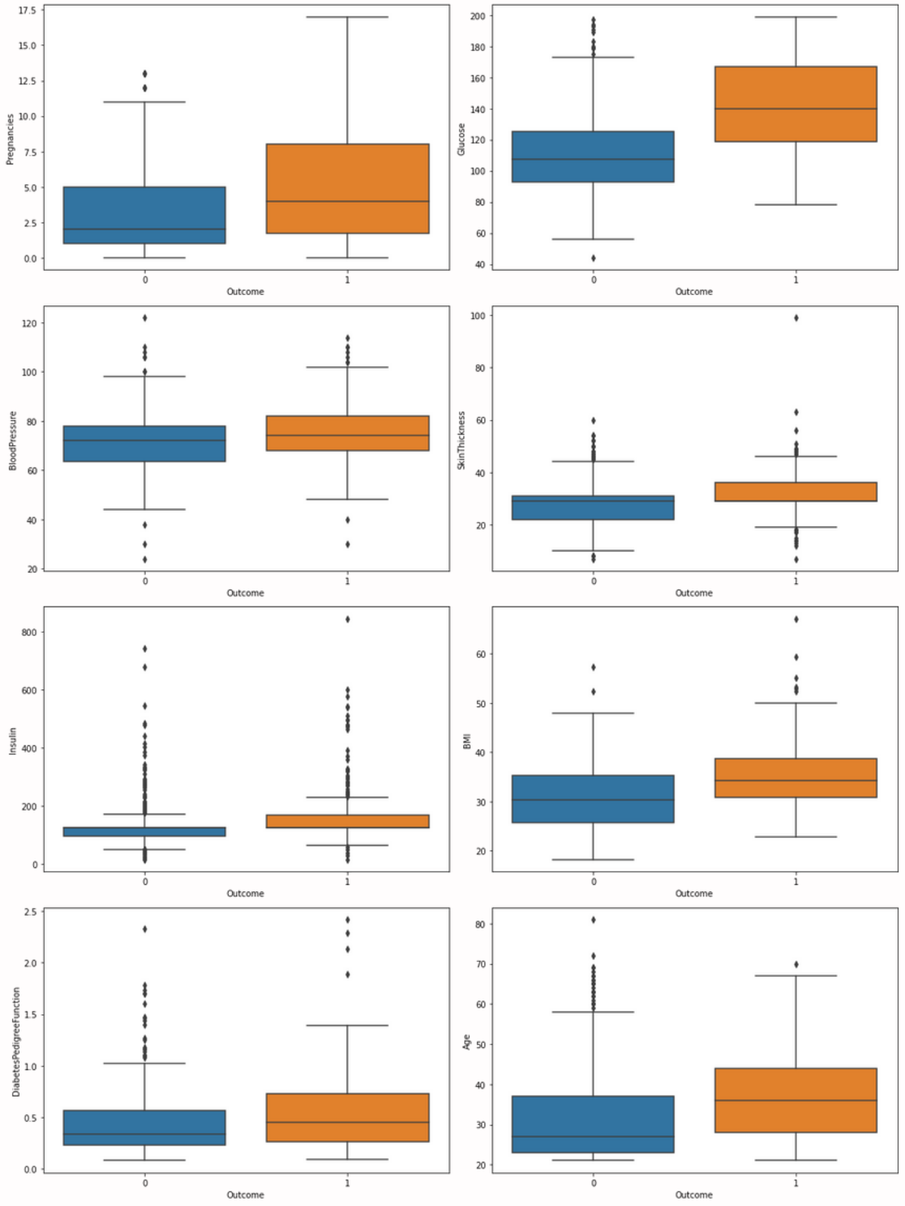
We then used Box plots to visualize the outliers in our dataset.



Checking for Outliers

In our case, the outliers help improve the prediction accuracy of the logistic regression model, therefore we do not remove them.



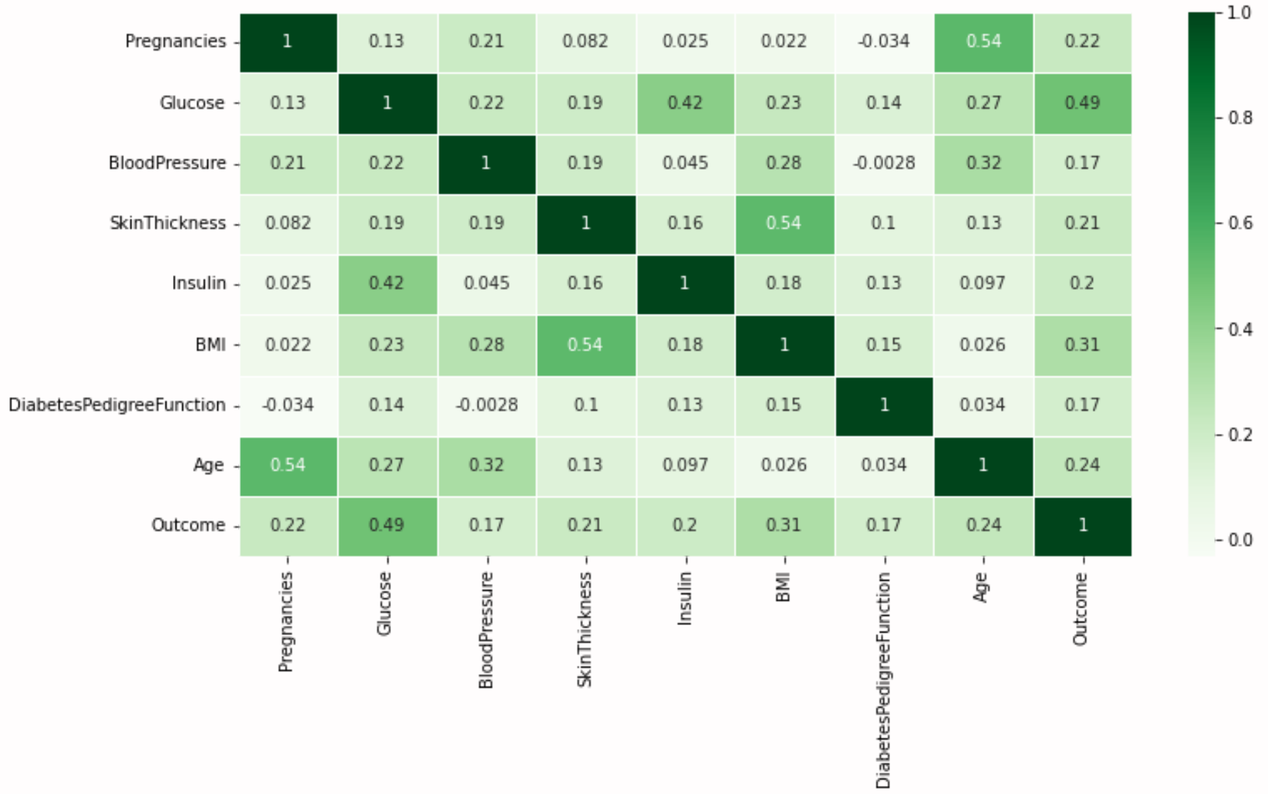


Predictor Features

We then plotted the predictor features against the dependent variable (Outcome) to check for correlations

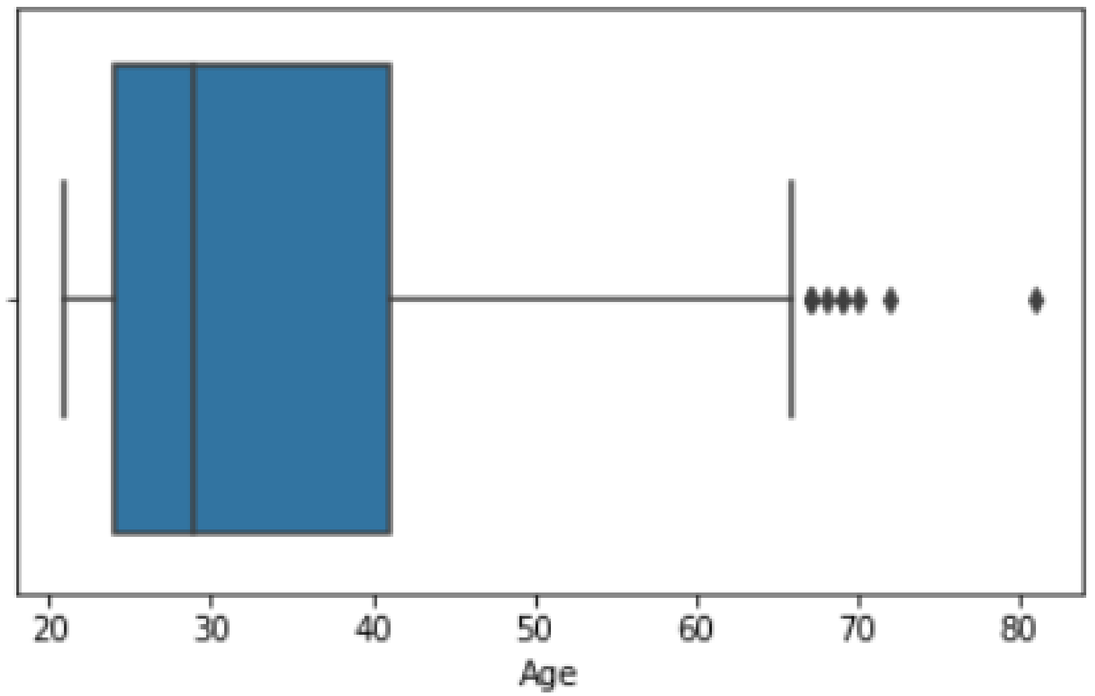
Heatmap

A heatmap of the correlation matrix:



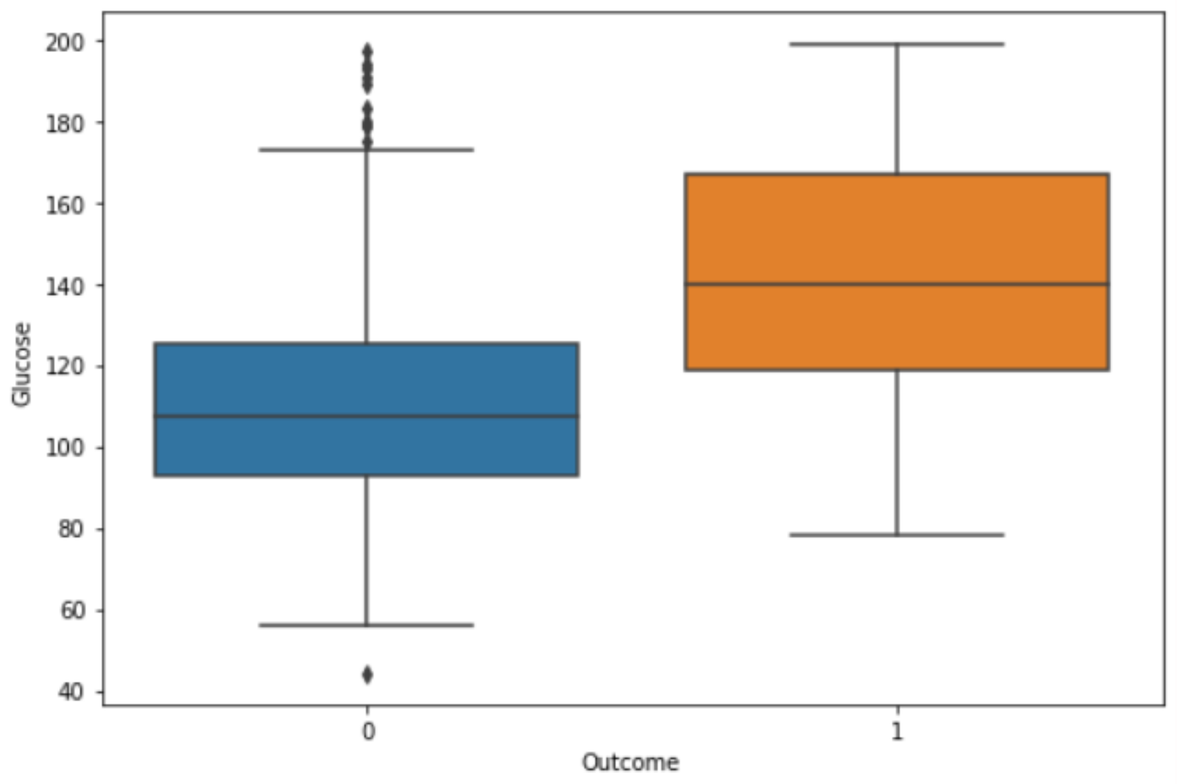
Major Findings

Outliers in terms of age, are usually women over 65.



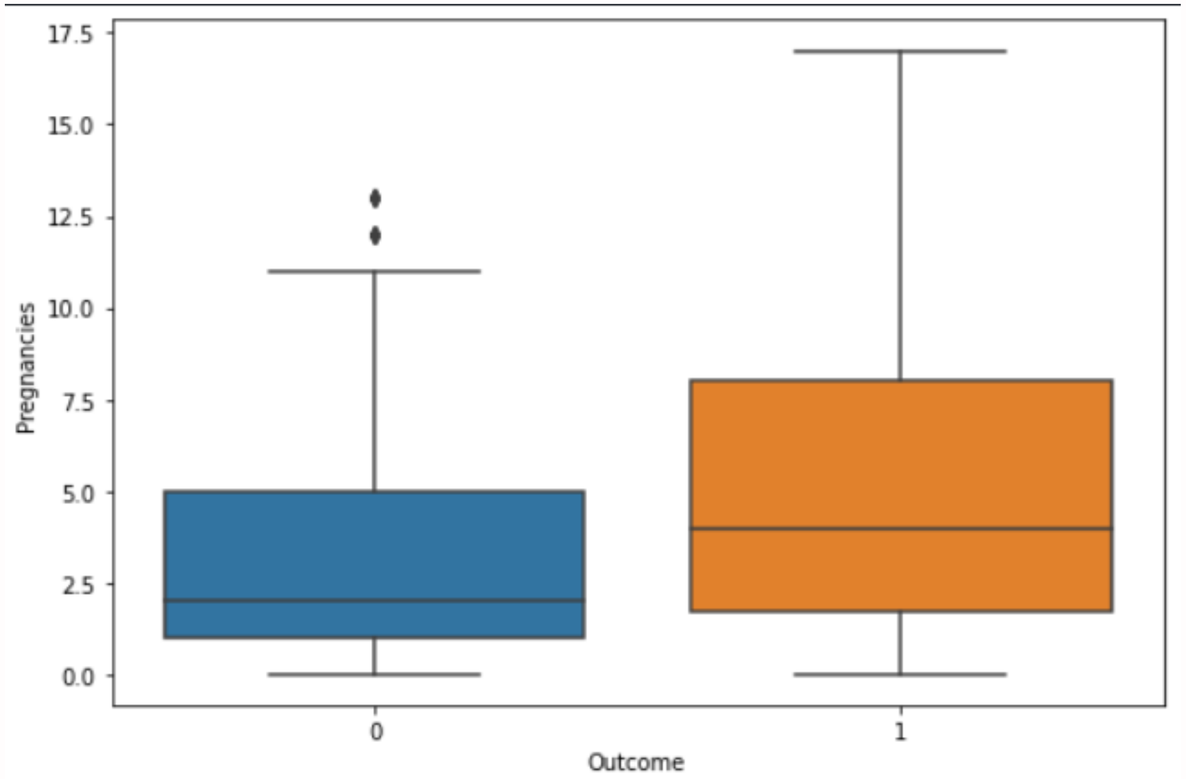
Major Findings

Glucose is a significant predictor for the outcome, especially positive cases.



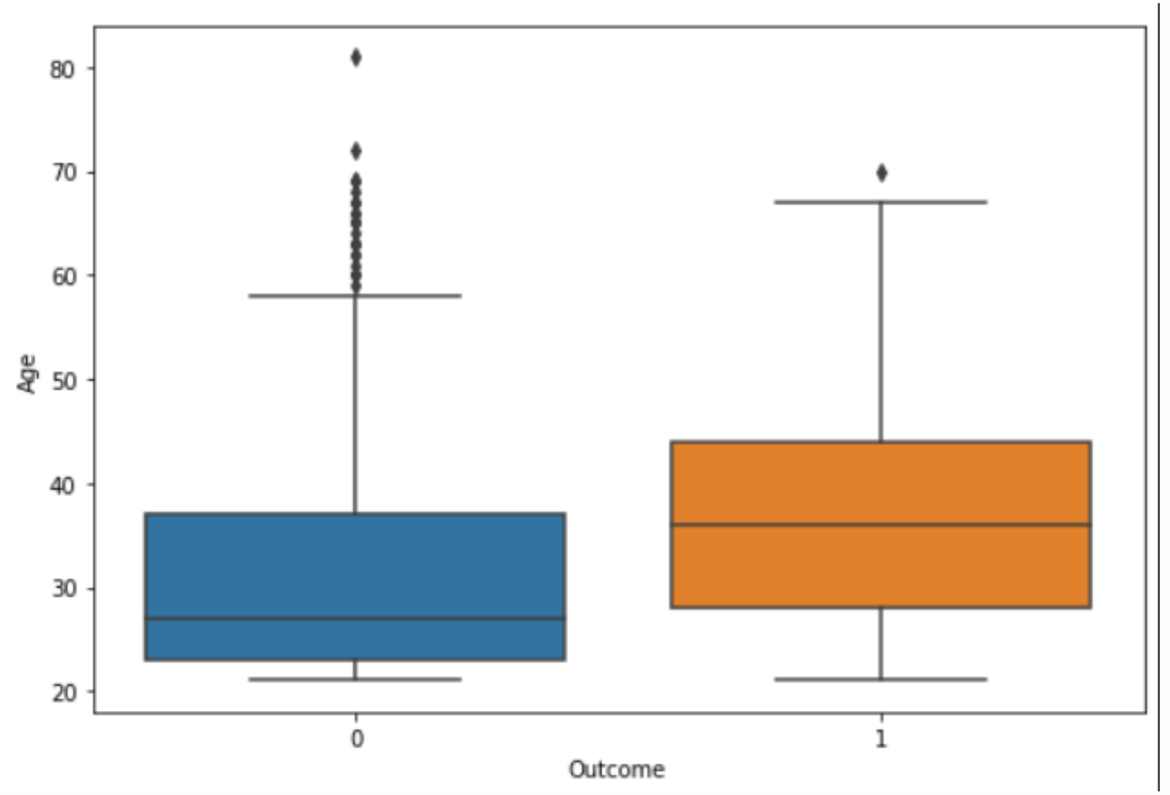
Major Findings

Number of pregnancies is a major predictor, especially when the number is high.



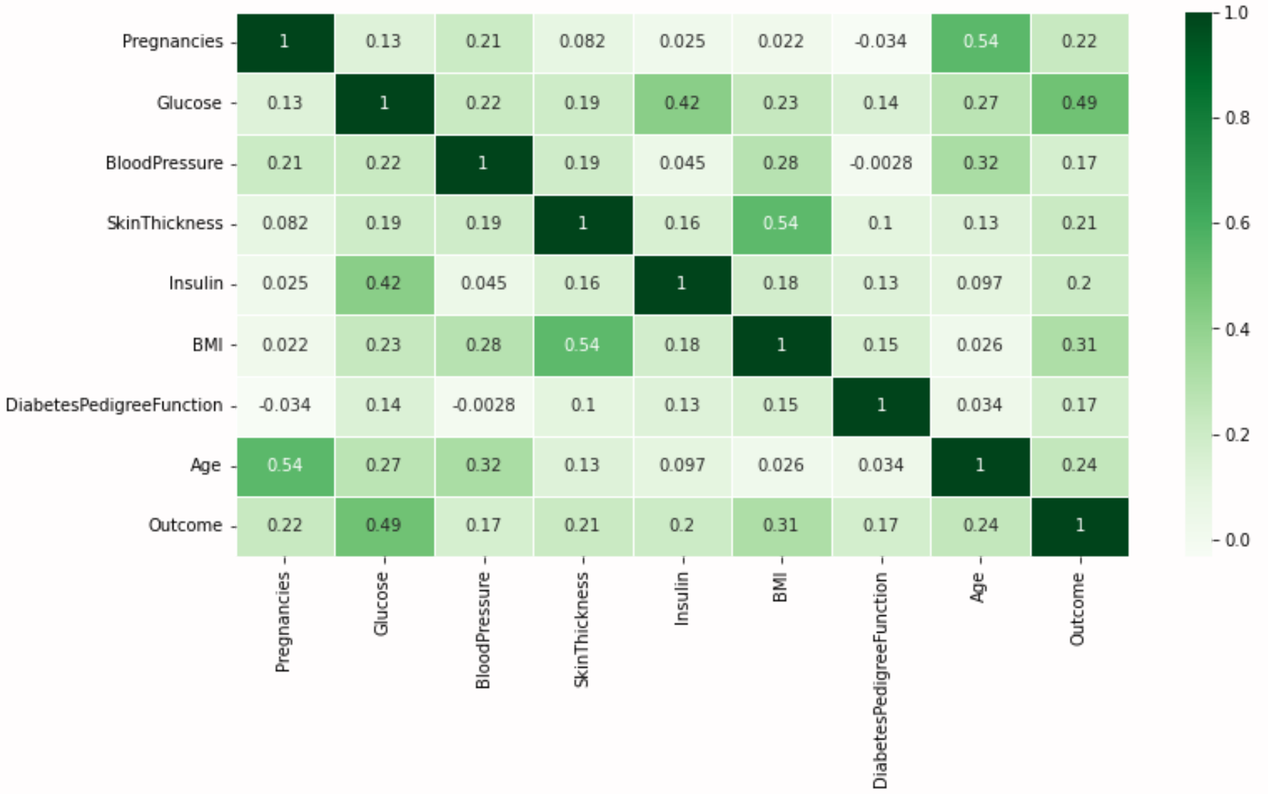
Major Findings

Age is a strong predictor. Women aged 38+ are more likely to be positive with an exception of numerous negative outliers.



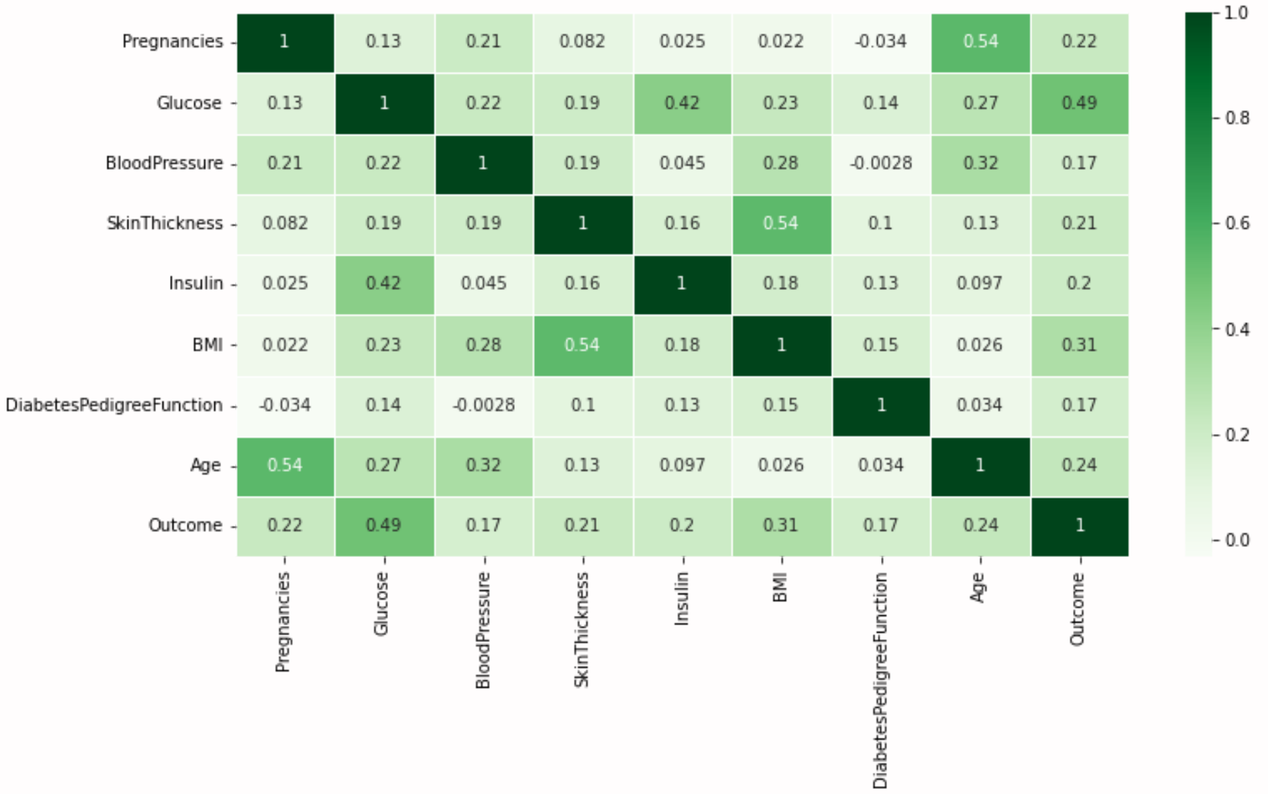
Major Findings

Skin thickness and BMI are **positively** correlated.



Major Findings

Glucose and the outcome are **positively** correlated.



Dataset Splitting

01

Step 1

Splitting the dataset into dependent and independent features

02

Step 2

Scaling the independent features

03

Step 3

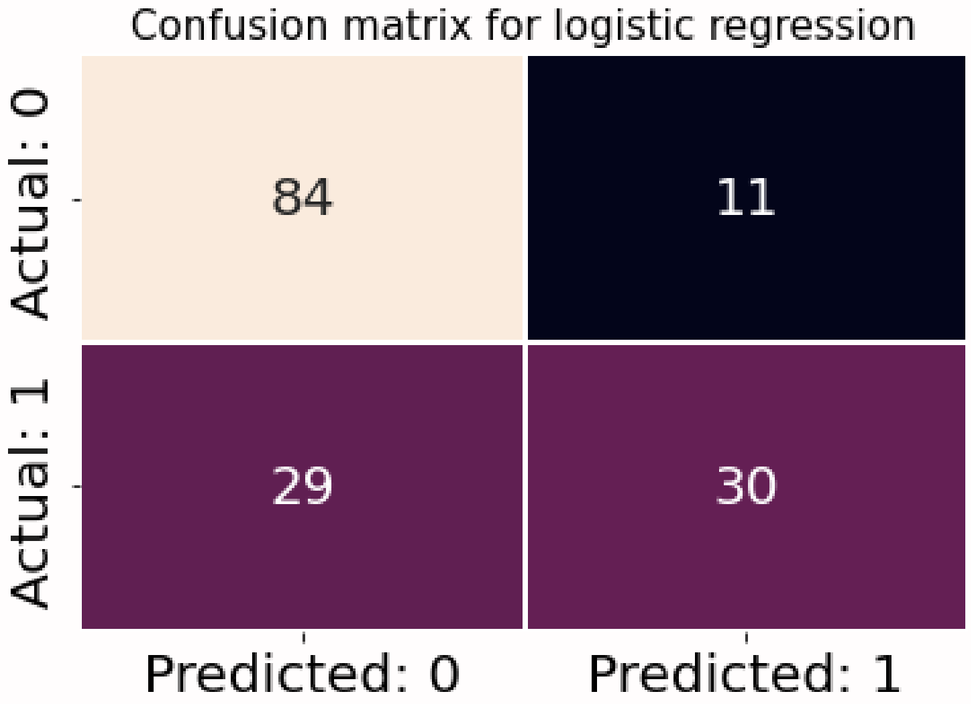
Splitting the dataset into training and testing set

Modeling:

*Since the dependent variable is binary in nature, **logistic regression** would be a suitable model to train.*

```
#Fitting the data on the logistic regression model and making predictions:
Logit_Model = LogisticRegression()
Logit_Model.fit(X_train,y_train)
Logit_Prediction = Logit_Model.predict(X_test)
```

Confusion Matrix:



Accuracy Score:

```
accuracy_score(y_test, Logit_Prediction)
```

✓ 0.8s

```
0.7402597402597403
```

Classification Report:

	precision	recall	f1-score	support
0	0.74	0.88	0.81	95
1	0.73	0.51	0.60	59
accuracy			0.74	154
macro avg	0.74	0.70	0.70	154
weighted avg	0.74	0.74	0.73	154

K-Fold Cross Validation:

By using the K-Fold cross validation technique, we can see that the average accuracy of the logistic regression model is about 77.03% with a 3.89% standard deviation.

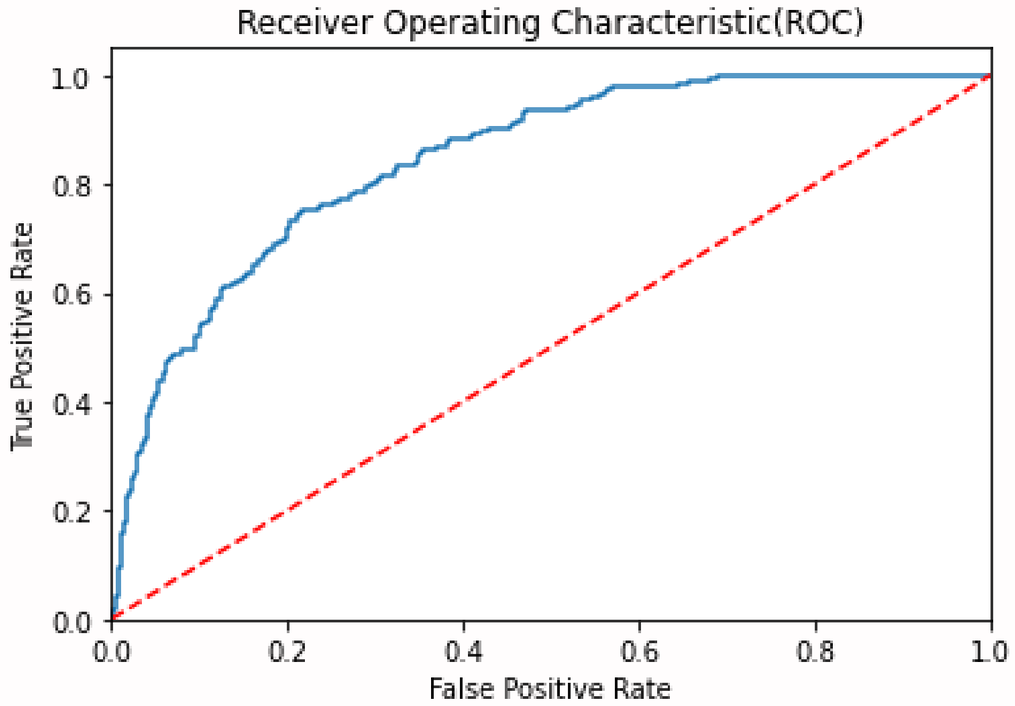
```
Average Accuracy: 77.03 %
Standard Deviation of Accuracy: 3.89 %
```

Test Data

Some outputs of applying the logistic regression model on the test data:

	Possibility of 0	Possibility of 1	Class
0	0.447662	0.552338	1
1	0.753327	0.246673	0
2	0.520646	0.479354	0
3	0.916930	0.083070	0
4	0.896715	0.103285	0
5	0.958550	0.041450	0
6	0.921040	0.078960	0
7	0.683426	0.316574	0
8	0.947893	0.052107	0
9	0.677712	0.322288	0

Receiver Operating Characteristic



THANK YOU

References:

Pima Indians Diabetes Dataset: https://www.kaggle.com/datasets/uciml/pima-indians-diabetes-database

Pima Indians Diabetes Dataset - SEN4018 Project

Importing Libraries and Utilities:

```
import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.preprocessing import MinMaxScaler, StandardScaler
from sklearn.model_selection import train_test_split, cross_val_score, cross_val_predict
from sklearn.linear_model import LogisticRegression, SGDClassifier
from sklearn.metrics import confusion_matrix, classification_report, accuracy_score, roc_auc_score, roc_curve
```

Dataset Description:

The Pima Indians Diabetes Database is provided by The National Institute of Diabetes and Digestive and Kidney Diseases. This dataset is a subset of the larger dataset. In this dataset, all of the patients, are Pima Indian women who are at least 21 years old. The dataset contains 8 medical predictor factors:

1. Number of times pregnant
2. Plasma glucose concentration at 2 hours in an oral glucose tolerance test
3. Diastolic blood pressure (mm Hg)
4. Triceps skin fold thickness (mm)
5. 2-Hour serum insulin (mu U/ml)
6. Body mass index (weight in kg/(height in m)^2)
7. Diabetes pedigree function
8. Age (years)

And there is also the dependent variable, the "Outcome" which is either equal to 1 or 0.

```
df = pd.read_csv("diabetes.csv")
df.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

```
df.describe().T
```

	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62500	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

Data preprocessing:

minimum value of the following variables can not be zero

1. Glucose
2. BloodPressure
3. SkinThickness
4. Insulin
5. BMI

<list> Therefore we're replacing zeros with NAN for these variables, until we find more suitable values to replace them with.

```
df_copy= df.copy(deep = True)
```

```
df_copy[['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']] = df_copy[
    ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']].replace(0, np.NaN)

print(df_copy.isnull().sum())
```

```
Pregnancies                 0
Glucose                     5
BloodPressure              35
SkinThickness             227
Insulin                   374
BMI                        11
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

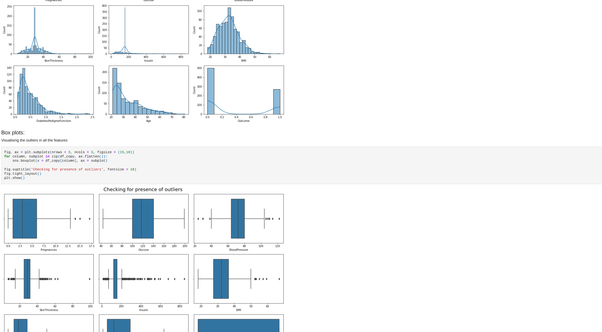
Data Visualization:

Histograms:

Checking data distribution to understand what to fill the NAN values with

```
fig, ax = plt.subplots(ncols= 3, nrows = 3, figsize = (15,15))
for column, subplot in zip(df.columns, ax.flatten()):
    sns.histplot(x = df[column], kde = True, ax = subplot)

fig.suptitle('Distributions of all features', fontsize = 14)
fig.tight_layout()
plt.show()
```



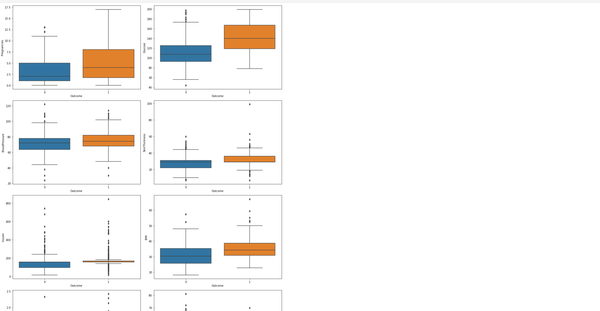
Data imputation:

Now we replace the NAN values with more suitable values according to observing the

```
df_copy['Glucose'].fillna(df_copy['Glucose'].mean(), inplace = True)
df_copy['BloodPressure'].fillna(df_copy['BloodPressure'].mean(), inplace = True)
df_copy['SkinThickness'].fillna(df_copy['SkinThickness'].median(), inplace = True)
df_copy['Insulin'].fillna(df_copy['Insulin'].median(), inplace = True)
df_copy['BMI'].fillna(df_copy['BMI'].median(), inplace = True)
```

```
fig, ax = plt.subplots(ncols= 3, nrows = 3, figsize = (15,15))
for column, subplot in zip(df_copy, ax.flatten()):
    sns.histplot(x = df_copy[column], kde = True, ax = subplot)

fig.suptitle('Distributions of all features', fontsize = 14)
fig.tight_layout()
plt.show()
```

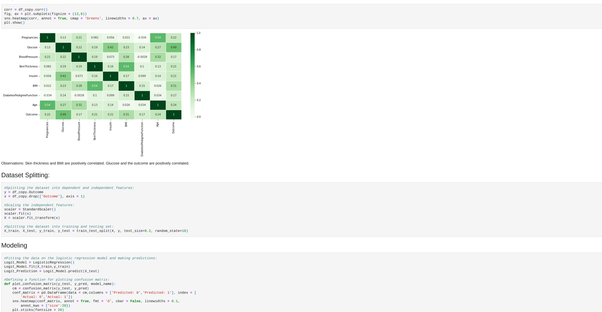


Box plots:

Visualizing the outliers in all the features

```
fig, ax = plt.subplots(ncols= 3, nrows = 3, figsize = (15,15))
for column, subplot in zip(df.copy, ax.flatten()):
    sns.boxplot(x = df[column], ax = subplot)

fig.suptitle('Checking for presence of outliers', fontsize = 14)
fig.tight_layout()
plt.show()
```

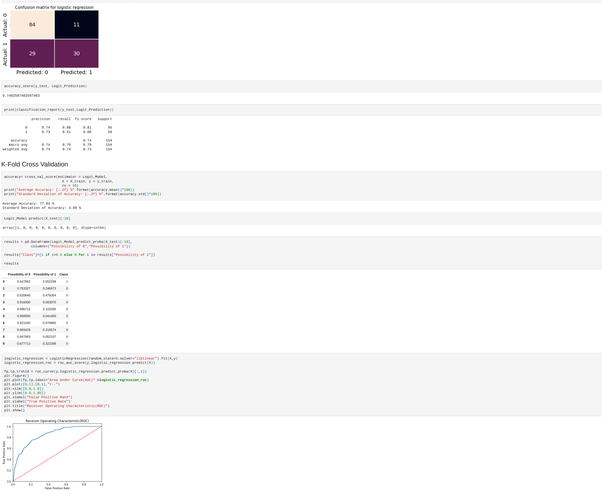


the outliers actually help improve the prediction accuracy of the logistic regression model in this particular case and therefore we do not remove them.

Plotting the predictor features against the target variable to check for correlations

```
fig, ax = plt.subplots(ncols= 4, nrows = 2, figsize = (15,20))
for column, subplot in zip(df.copy, ax.flatten()):
    if column == 'Outcome':
        continue
    sns.boxplot(x = df.copy.Outcome, y = df.copy[column], ax = subplot)

fig.tight_layout()
plt.show()
```



Heatmap:

Plotting a heatmap correlation matrix

```
corr = df.copy.corr()
plt.figure(figsize=(12,8))
sns.heatmap(corr, annot = True, cmap = 'Greens', linewidths = 0.7, ax = ax)
plt.show()
```


Observations: Skin thickness and BMI are positively correlated. Glucose and the outcome are positively correlated.

Dataset Splitting:

```
#Splitting the dataset into dependent and independent features:
X = df_copy.Outcome
Y = df_copy.drop('Outcome', axis = 1)

#Dividing the independent features:
from sklearn.model_selection import train_test_split
scaler.fit(X_trainfeats)

#Splitting the dataset into training and testing set:
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=10)
```

Modeling

```
#Fitting the data on the logistic regression model and making predictions:
Logit_Model = LogisticRegression()
Logit_Model.fit(X_train,y_train)
Logit_Prediction = Logit_Model.predict(X_test)

#defining a function for plotting confusion matrix:
def plot_confusion_matrix(y_test, y_pred, model_name):
    cm = confusion_matrix(y_test, y_pred)
    df_cm = pd.DataFrame(cm, columns = ['Predicted: 0','Predicted: 1'], index = [
        'Actual: 0','Actual: 1'])
    sns.heatmap(df_cm, annot = True, fmt = 'g', char = False, linewidths = 0.5,
                annot_kws = {'size':20})
    plt.title('Confusion Matrix for ' + model_name, fontsize = 15)
    plt.xticks(fontsize = 15)
    plt.yticks(fontsize = 15)
    plt.show()
```

```
#Getting confusion matrix:
plot_confusion_matrix(y_test, Logit_Prediction, "logistic regression")
```



```
accuracy_score(y_test, Logit_Prediction)
```

```
0.7402597402597403
```

```
print(classification_report(y_test,Logit_Prediction))
```

```
              precision    recall  f1-score   support

           0       0.74      0.88      0.81        95
           1       0.73      0.51      0.60        59

    accuracy                           0.74       154
   macro avg       0.74      0.70      0.71       154
weighted avg       0.74      0.74      0.73       154
```

K-Fold Cross Validation

```
accuracy= cross_val_score(Logit_Model,
                          X, y, cv = 5)
print("Average Accuracy: {}".format(accuracy.mean()*100))
print("Standard Deviation of Accuracy: {}".format(accuracy.std()*100))
```

```
Average Accuracy: 77.47 %
Standard Deviation of Accuracy: 2.89 %
```

```
Logit_Model.predict(X_test)[:10]
```

```
array([1, 0, 0, 0, 0, 0, 0, 0, 0, 0], dtype=int64)
```

```
results = pd.DataFrame(Logit_Model.predict_proba(X_test)[:10],
                       columns=['Possibility of 0','Possibility of 1'])

results['Class'][:].if_else(0 else 1 for i in results['Possibility of 1'])

results
```

	Possibility of 0	Possibility of 1	Class
0	0.447562	0.552438	1
1	0.755507	0.244675	0
2	0.525548	0.474354	0
3	0.610360	0.389270	0
4	0.696715	0.103285	0
5	0.800960	0.041492	0
6	0.821540	0.078460	0
7	0.609436	0.038974	0
8	0.947955	0.052107	0
9	0.977712	0.022288	0

```
logistic_regression = LogisticRegression(random_state=0,solver='liblinear').fit(X,y)
logistic_regression_roc = roc_auc_score(y_test,Logit_Regression_prediction)
```

```
fp,tp,treshold = roc_curve(y_test,Logit_Regression_prediction[:,1])
plt.figure()
plt.plot(fp,tp,label="Area Under Curve(AUC)" %logistic_regression_roc)
plt.plot([0,1],[0,1],'r--')
plt.xlim([0.0,1.0])
plt.ylim([0.0,1.05])
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Receiver Operating Characteristic(ROC)")
plt.show()
```