Pima Indians Diabetes Dataset - SEN4018 Project

Importing Libraries and Utilities:

In [ ]:
```python
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 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)

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

In [ ]:
```python
df = pd.read_csv("diabetes.csv")
df.head()
```

Out[ ]:

	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

In [ ]:
```python
df.describe().T
```

Out[ ]:

	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:

minimum value of the following variables can not be zero:

1. Glucose
2. BloodPressure
3. SkinThickness
4. Insulin
5. BMI
 Therefore we're replacing zeros with NAN for these variables, until we find more suitable values to replace them with.

In [ ]:
```python
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())
```

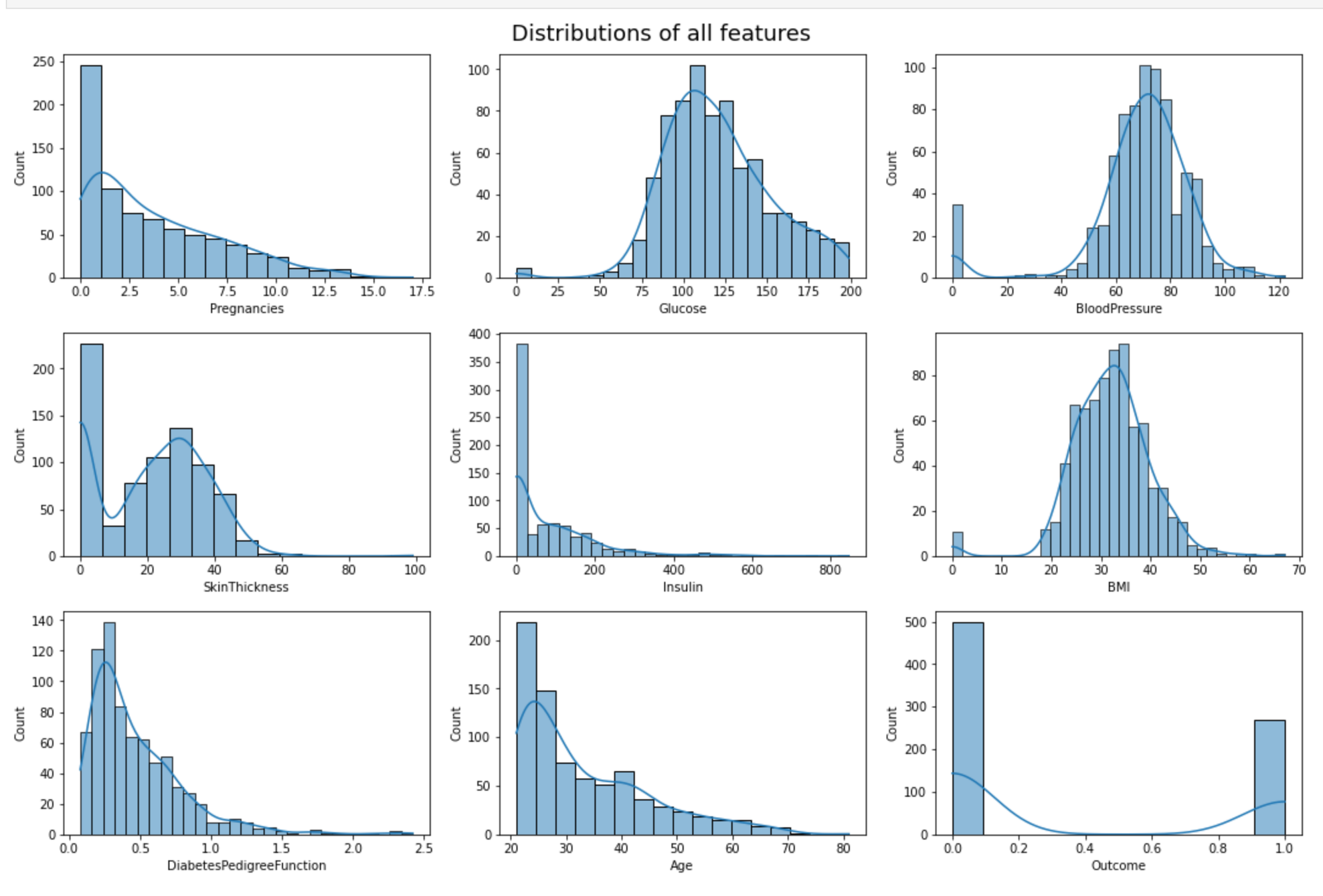
```
Pregnancies                   0
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
Outcome                       0
dtype: int64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

Data Visualization:

Histograms:

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

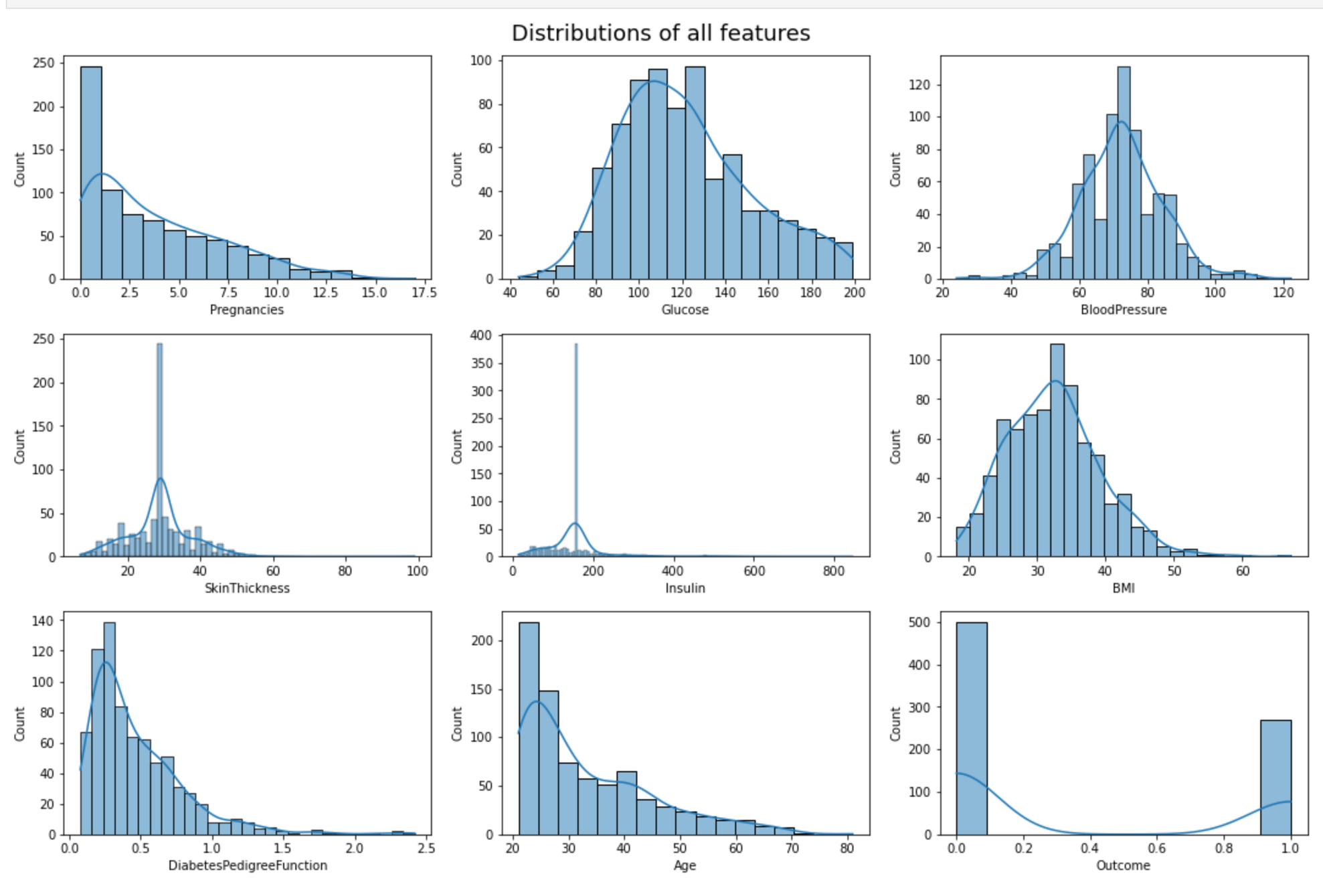
In [ ]:
```python
fig, ax = plt.subplots(nrows = 3, ncols = 3, figsize = (15,10))
for column, subplot in zip(df, ax.flatten()):
    sns.histplot(x = df[column], kde = True, ax = subplot)

fig.suptitle('Distributions of all features', fontsize = 18)
fig.tight_layout()
plt.show()
```



Data imputation:

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

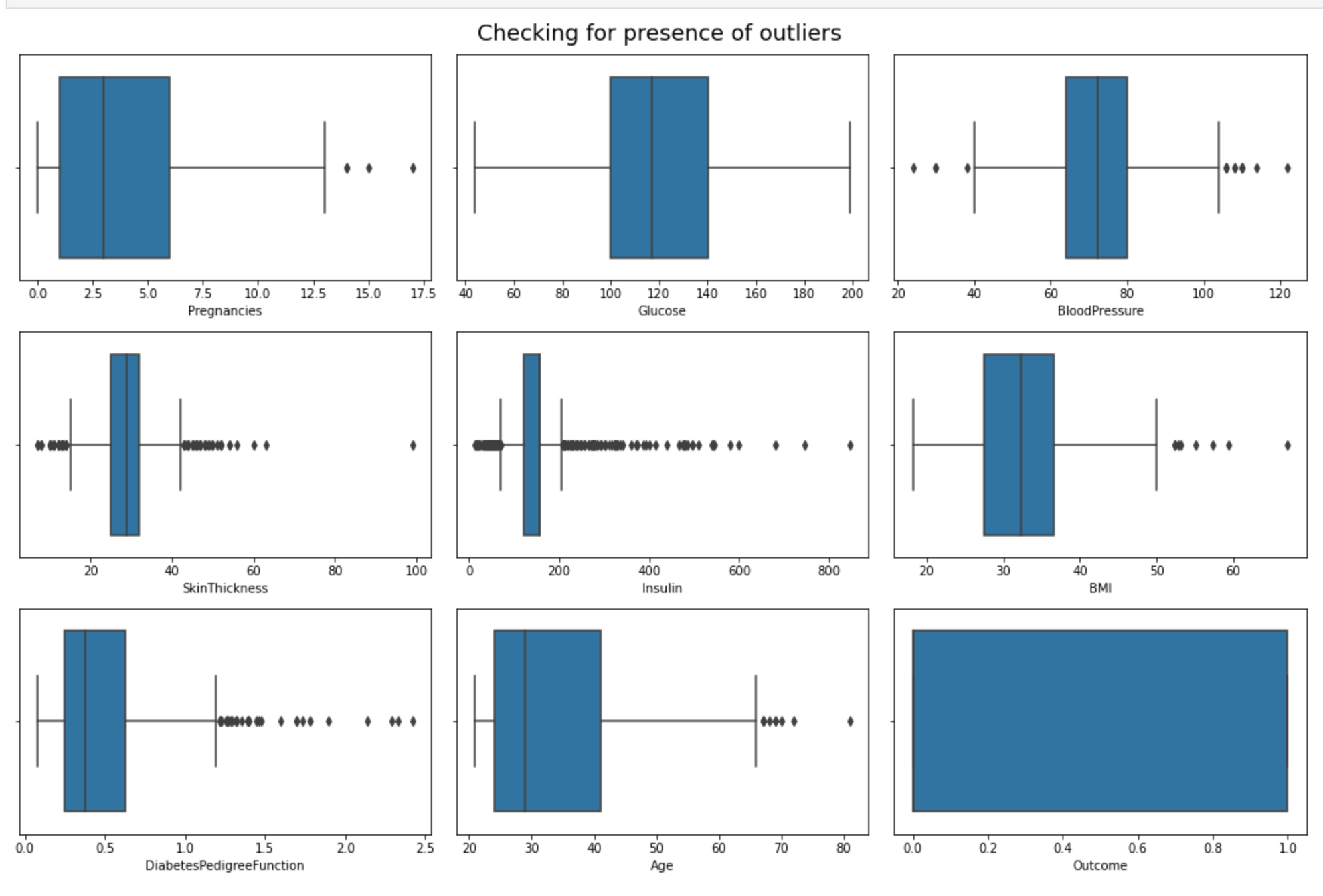
In [ ]:
```python
df_copy['Glucose'].fillna(df_copy['Glucose'].mean(), inplace = True)
df_copy['BloodPressure'].fillna(df_copy['BloodPressure'].mean(), inplace = True)
df_copy['SkinThickness'].fillna(df_copy['SkinThickness'].median(), inplace = True)
df_copy['Insulin'].fillna(df_copy['Insulin'].mean(),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

fig, ax = plt.subplots(nrows = 3, ncols = 3, figsize = (15,10))
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 = 18)
fig.tight_layout()
plt.show()
```



Box plots:

Visualising the outliers in all the features:

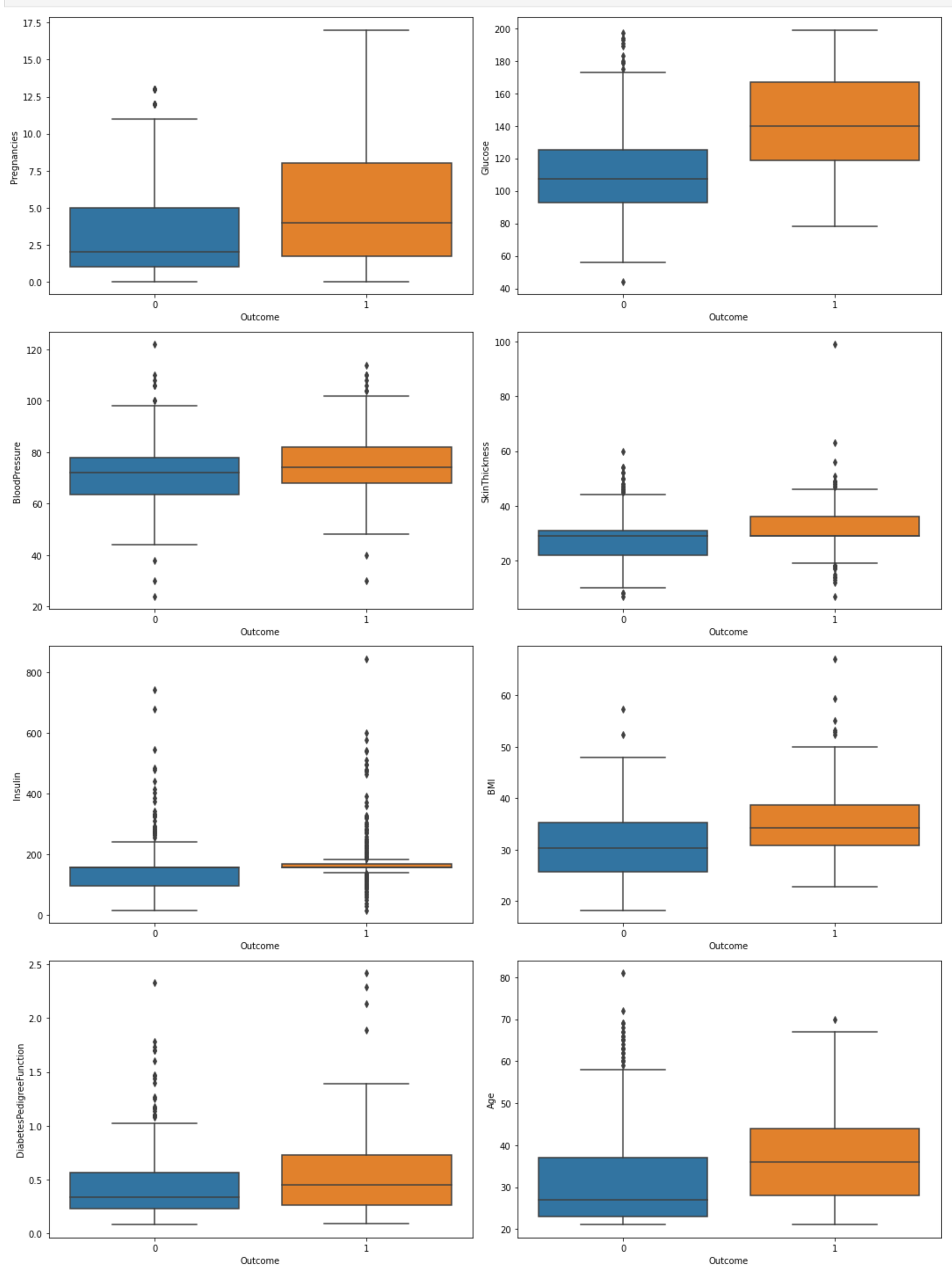
In [ ]:
```python
fig, ax = plt.subplots(nrows = 3, ncols = 3, figsize = (15,10))
for column, subplot in zip(df_copy, ax.flatten()):
    sns.boxplot(x = df_copy[column], ax = subplot)

fig.suptitle('Checking for presence of outliers', fontsize = 18)
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:

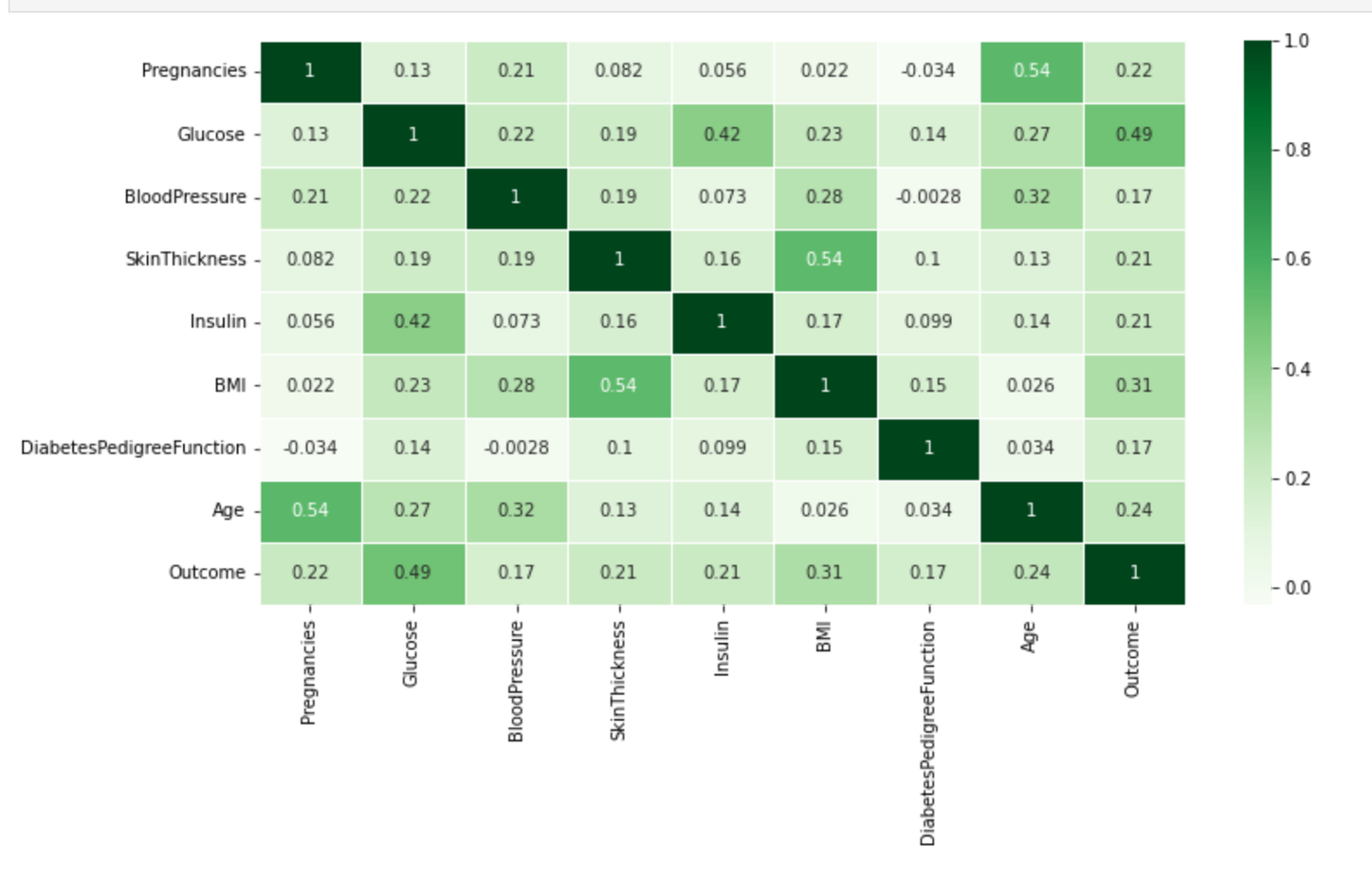
In [ ]:
```python
fig, ax = plt.subplots(nrows = 4, ncols = 2, figsize = (15,20))
for column, subplot in zip(df_copy, ax.flatten()):
    if column == 'Outcome':
        continue
    sns.boxplot(x = df_copy.Outcome, y = df_copy[column], ax = subplot)

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



Heatmap:

Plotting a heatmap correlation matrix

In [ ]:
```python
corr = df_copy.corr()
fig, ax = plt.subplots(figsize = (12,6))
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.

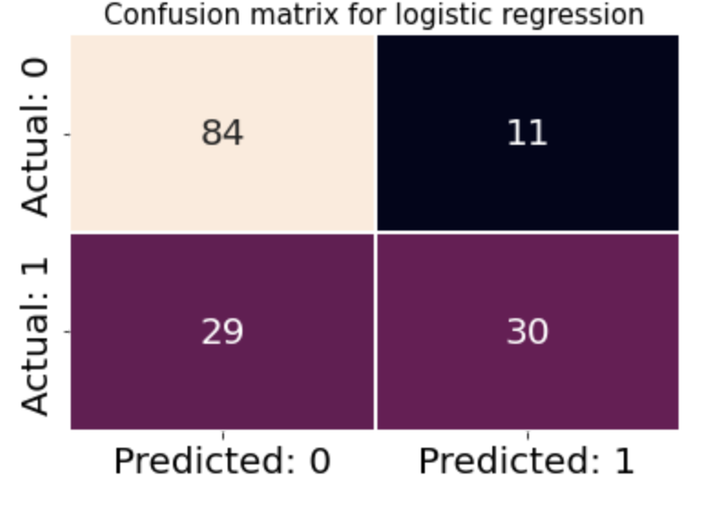
Dataset Splitting:

In [ ]:
```python
#Splitting the dataset into dependent and independent features:
y = df_copy.Outcome
x = df_copy.drop(['Outcome'], axis = 1)

#Scaling the independent features:
scaler = StandardScaler()
scaler.fit(x)
X = scaler.fit_transform(x)

#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

In [ ]:
```python
#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)
    conf_matrix = pd.DataFrame(data = cm,columns = ['Predicted: 0','Predicted: 1'], index = [
        'Actual: 0','Actual: 1'])
    sns.heatmap(conf_matrix, annot = True, fmt = 'd', cbar = False, linewidths = 0.1,
        annot_kws = {'size':20})
    plt.xticks(fontsize = 20)
    plt.yticks(fontsize = 20)
    plt.title("Confusion matrix for " + model_name, fontsize = 15)
    plt.show()
```

In [ ]:
```python
#Plotting confusion matrix:
plot_confusion_matrix(y_test, Logit_Prediction, "logistic regression")
```



In [ ]:
```python
accuracy_score(y_test, Logit_Prediction)
```

Out[ ]:
```
0.7402597402597403
```

In [ ]:
```python
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      0.70       154
weighted avg       0.74      0.74      0.73       154
```

K-Fold Cross Validation

In [ ]:
```python
accuracy= cross_val_score(estimator = Logit_Model,
                          X = X_train, y = y_train,
                          cv = 10)
print("Average Accuracy: {:.2f} %".format(accuracy.mean()*100))
print("Standard Deviation of Accuracy: {:.2f} %".format(accuracy.std()*100))
```

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

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

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

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

results["Class"]=[1 if i>0.5 else 0 for i in results["Possibility of 1"]]

results
```

Out[ ]:

	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

In [ ]:
```python
logistic_regression = LogisticRegression(random_state=0,solver="liblinear").fit(X,y)
logistic_regression_roc = roc_auc_score(y,logistic_regression.predict(X))

fp,tp,trshld = roc_curve(y,logistic_regression.predict_proba(X)[:,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()
```