In [1]:
```
import numpy  as np
import pandas as pd
import matplotlib.pyplot  as plt
import seaborn  as sns
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import MinMaxScaler

from sklearn.model_selection import train_test_split
from sklearn import svm
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score ,classification_report ,confusion_matrix
from sklearn.ensemble import RandomForestRegressor
from sklearn.neighbors import KNeighborsClassifier
# import sklearn.ensemble.RandomForestClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression

from sklearn.cluster import KMeans
from sklearn.metrics import accuracy_score


import graphviz
import warnings
import missingno as msno
import sklearn
```

In [4]:
```
df_diabetes = pd.read_csv("diabetes.csv")
df_diabetes
```

Out[4]:

	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
...	...	...	...	...	...	...	...	...	...
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

768 rows × 9 columns

In [6]:
```
df_diabetes.head()
```

Out[6]:

	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 [7]:
```
df_diabetes.describe().T
```

Out[7]:

	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

In [8]:
```
df_diabetes.isna().sum()
```

Out[8]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [9]:
```
df_diabetes.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int64  
 1   Glucose                   768 non-null    int64  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int64  
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64  
 8   Outcome                   768 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

In [10]:
```
df_diabetes['Outcome'].value_counts()
```

Out[10]:
```
0    500
1    268
Name: Outcome, dtype: int64
```

In [11]:
```
for col in df_diabetes.columns:
    if col not in ( "Outcome","Pregnancies", "DiabetesPedigreeFunction"):
        df_diabetes[col] = df_diabetes[col].replace(to_replace=0, value=np.NaN)
    else:
        df_diabetes[col]
```

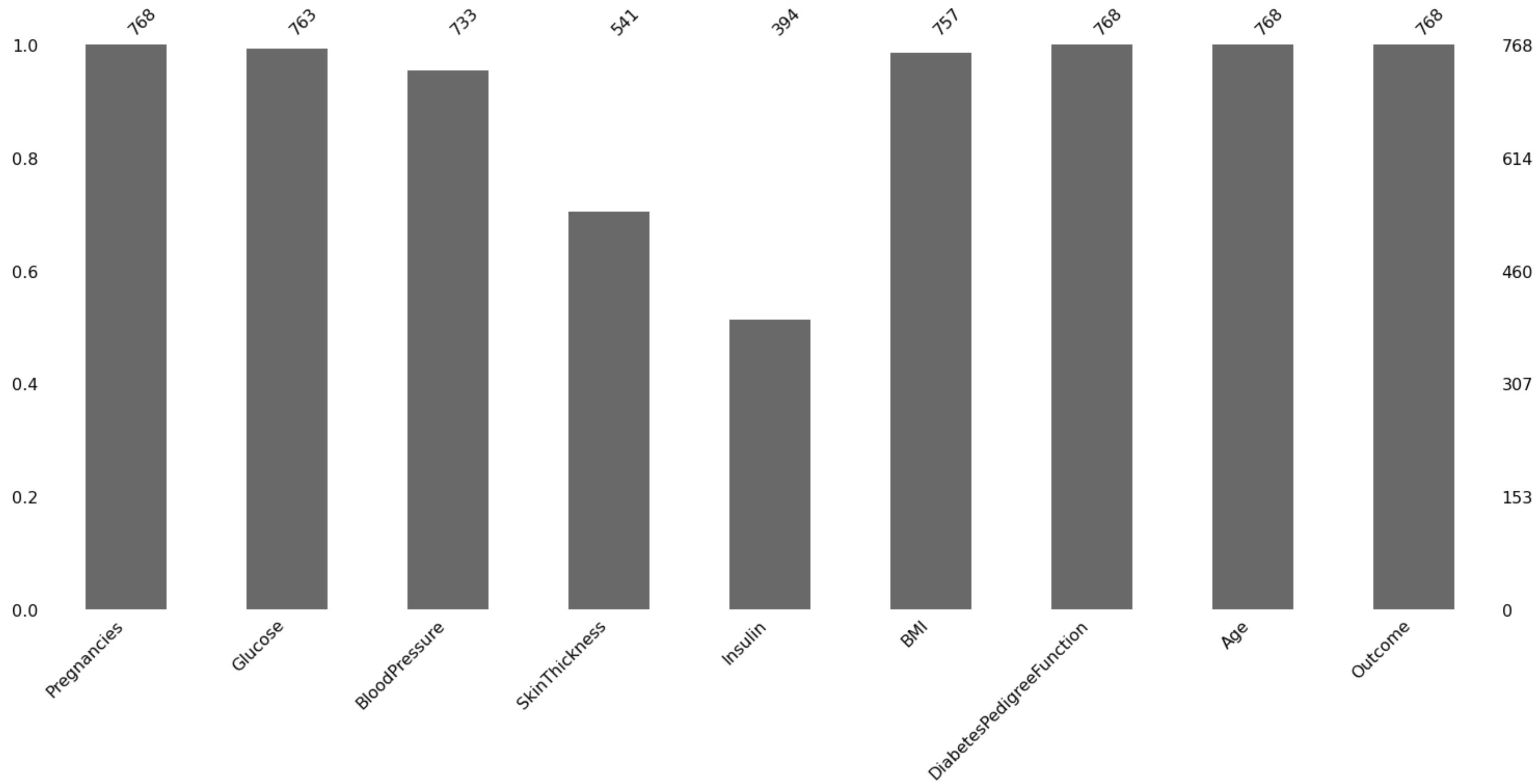
In [12]:
```
df_diabetesk1 =df_diabetes
```

In [13]:
```
df_diabetes.isnull().sum()
```

Out[13]:
```
Pregnancies                   0
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
Outcome                       0
dtype: int64
```

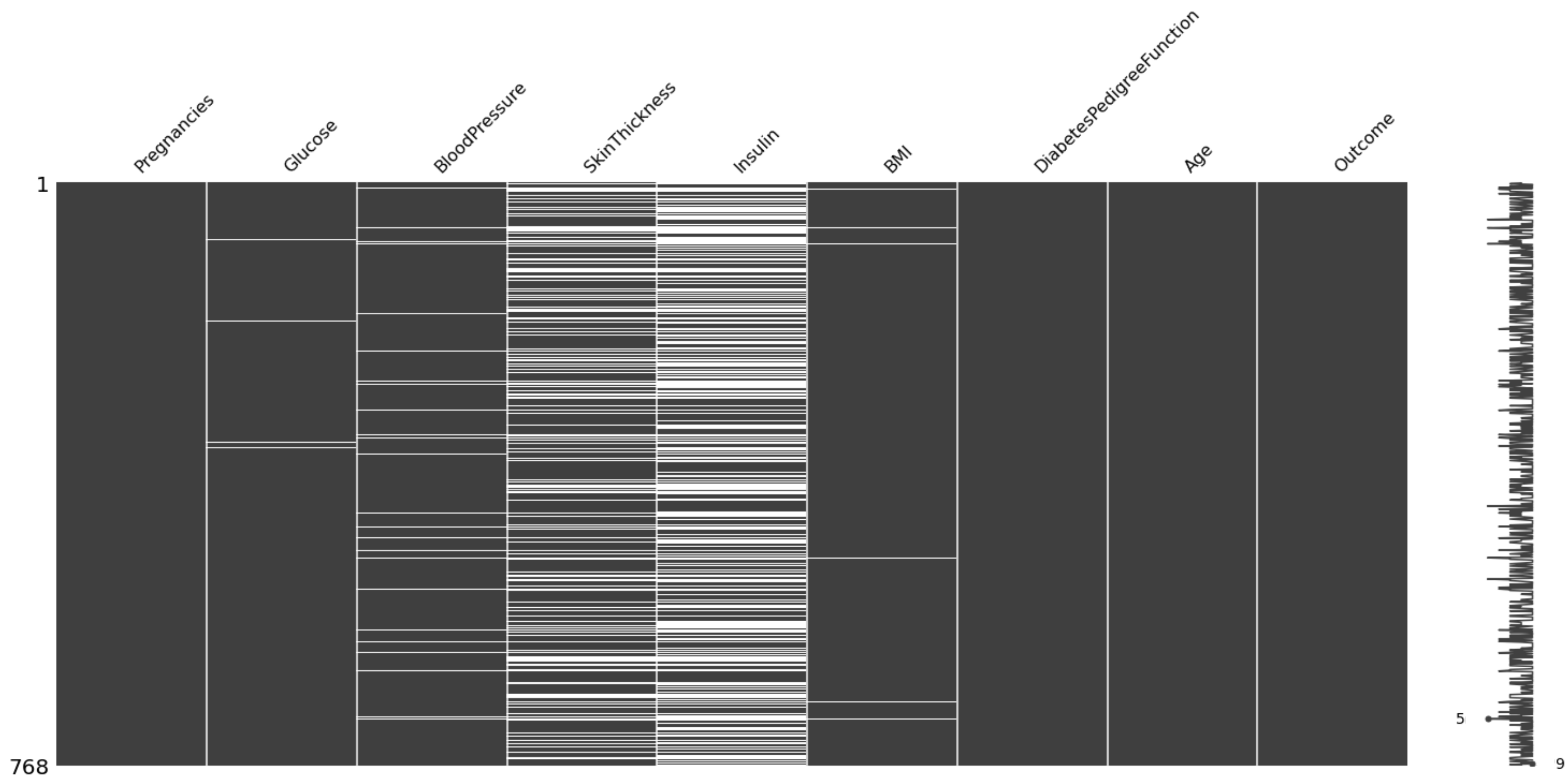
In [14]:
```
msno.bar(df_diabetes)
```

Out[14]: <AxesSubplot:>

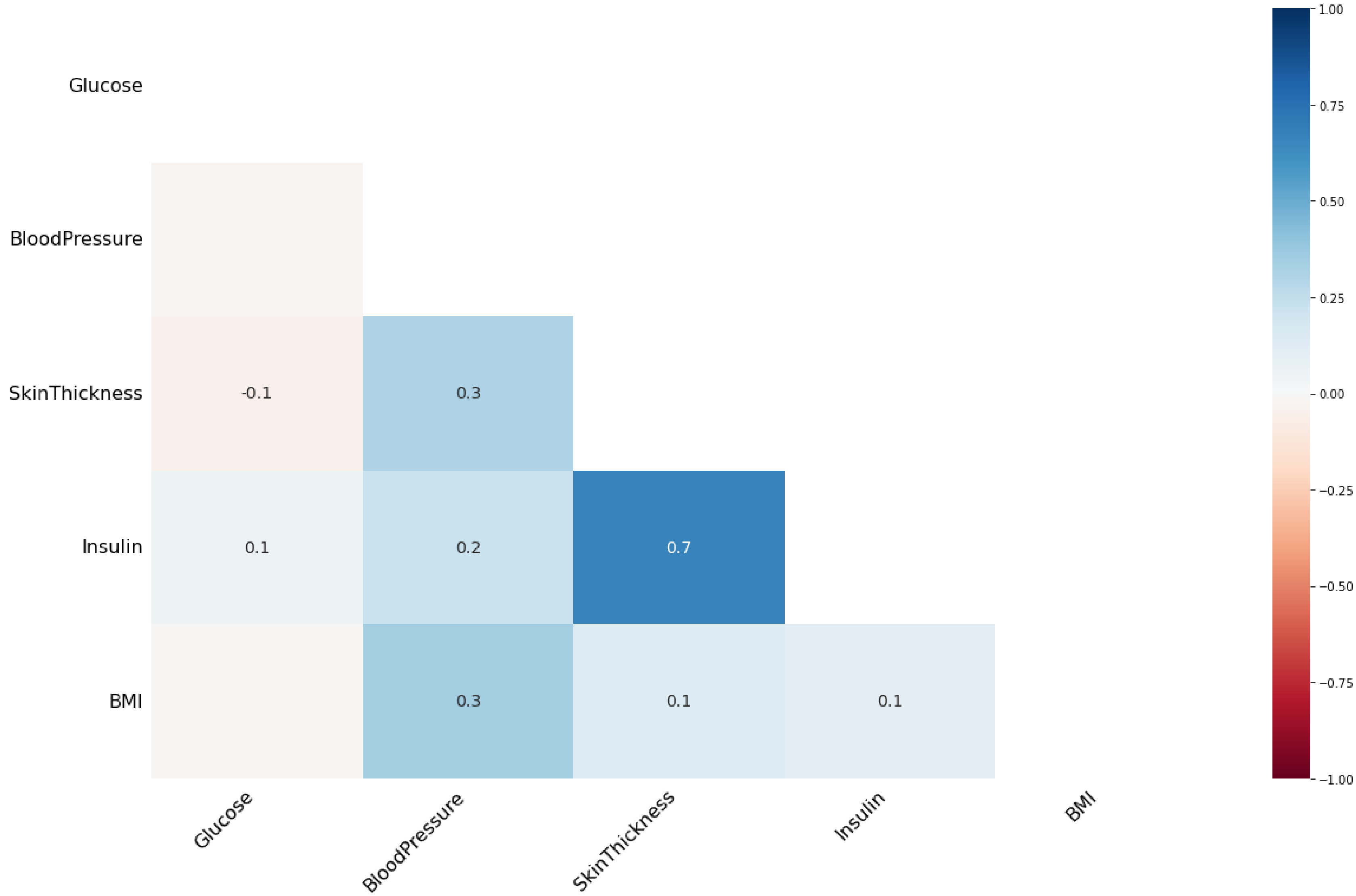


In [15]:
```
msno.matrix(df_diabetes)
```

Out[15]: <AxesSubplot:>



In [16]:
```
msno.heatmap(df_diabetes)
plt.show()
```

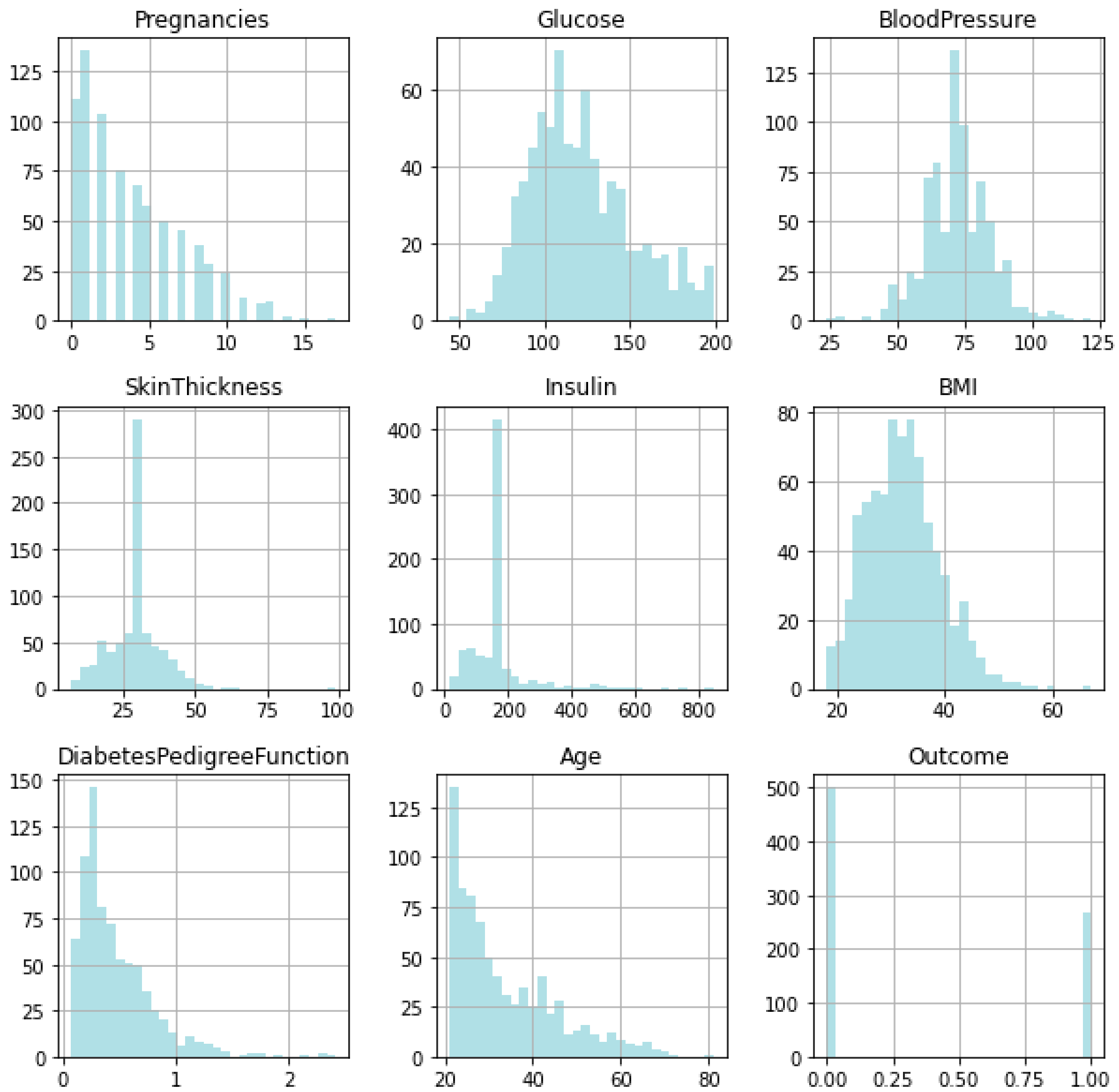


In [17]:
```
df_diabetes["Glucose"].fillna(df_diabetes["Glucose"].mean(), inplace = True)
df_diabetes["BloodPressure"].fillna(df_diabetes["BloodPressure"].mean(), inplace = True)
df_diabetes["SkinThickness"].fillna(df_diabetes["SkinThickness"].mean(), inplace = True)
df_diabetes["Insulin"].fillna(df_diabetes["Insulin"].mean(), inplace = True)
df_diabetes["BMI"].fillna(df_diabetes["BMI"].mean(), inplace = True)
```

In [18]:
```
df_diabetes.isna().sum()
```

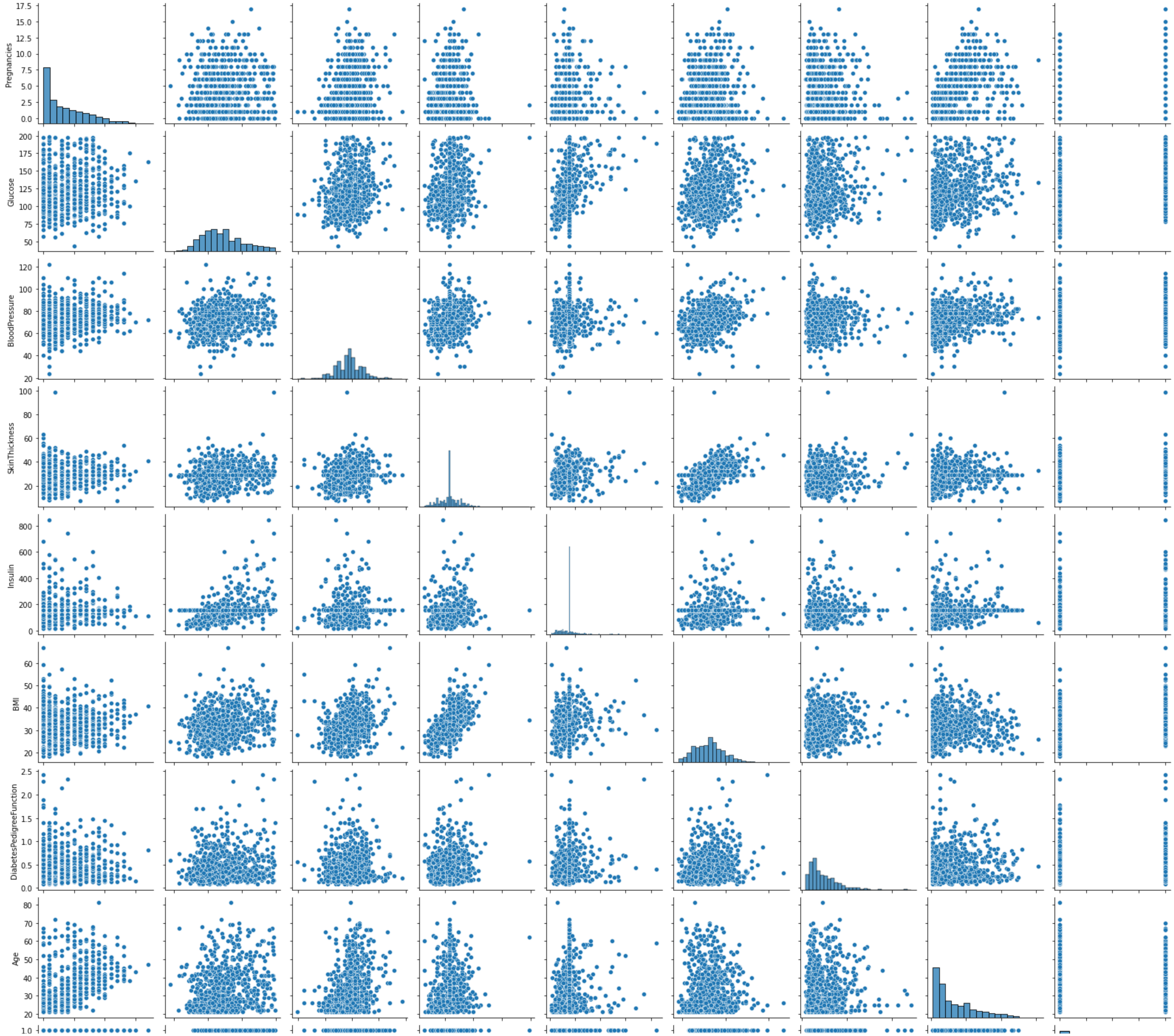
Out[18]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

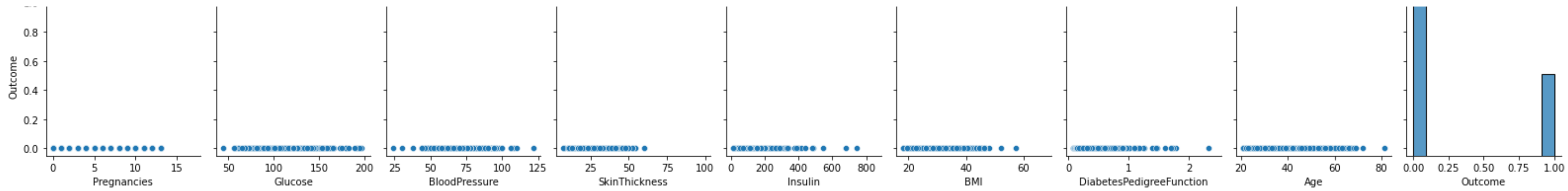
In [19]:
```
df_diabetes.hist(figsize = (10,10) , bins = 30 ,color='#b0e0e6' ,alpha = 1)
plt.show()
```



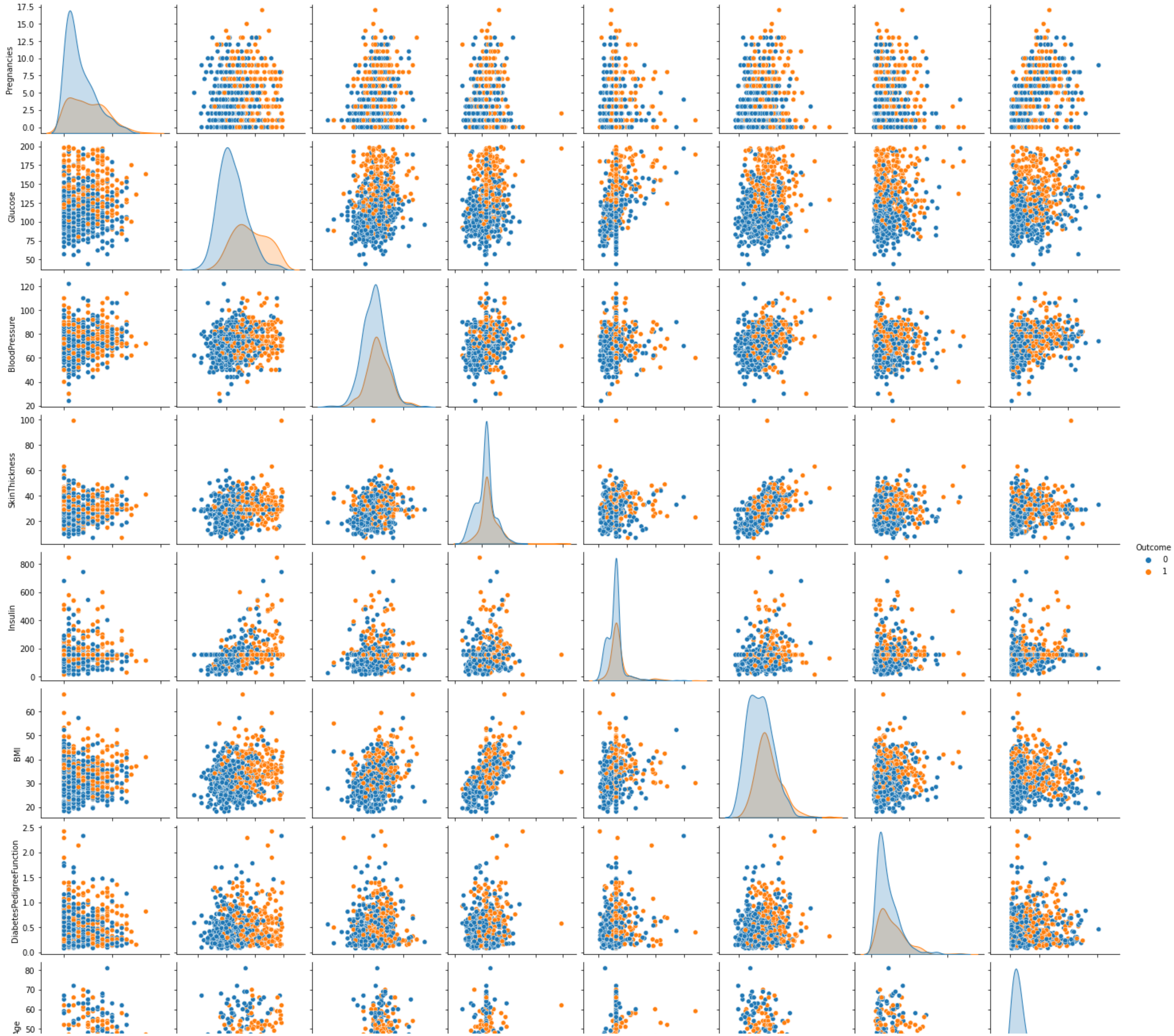
In [20]:
```
sns.pairplot(df_diabetes)
```

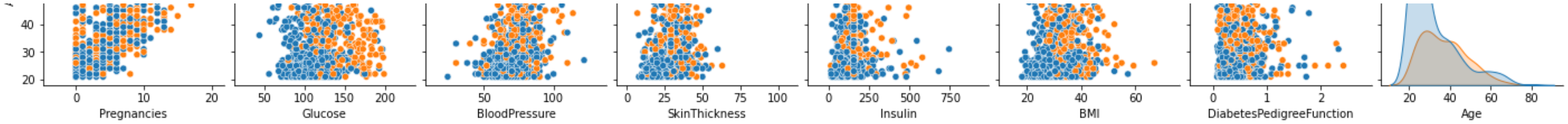
Out[20]:
```
<seaborn.axisgrid.PairGrid at 0x7ff28841caf0>
```


Pregnancies
Glucose
BloodPressure
SkinThickness
Insulin
BMI
DiabetesPedigreeFunction
Age


Outcome
0.8
0.6
0.4
0.2
0.0
Pregnancies
Glucose
BloodPressure
SkinThickness
Insulin
BMI
DiabetesPedigreeFunction
Age
Outcome

In [21]:
```
sns.pairplot(df_diabetes ,hue='Outcome')
plt.show()
```


Pregnancies
Glucose
BloodPressure
SkinThickness
Insulin
BMI
DiabetesPedigreeFunction
Age
Outcome
0
1



In [22]:
```
df_diabetes.corr()
```

Out[22]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
Pregnancies	1.000000	0.127911	0.208522	0.082989	0.056027	0.021565	-0.033523	0.544341
Glucose	0.127911	1.000000	0.218367	0.192991	0.420157	0.230941	0.137060	0.266534
BloodPressure	0.208522	0.218367	1.000000	0.192816	0.072517	0.281268	-0.002763	0.324595
SkinThickness	0.082989	0.192991	0.192816	1.000000	0.158139	0.542398	0.100966	0.127872
Insulin	0.056027	0.420157	0.072517	0.158139	1.000000	0.166586	0.098634	0.136734
BMI	0.021565	0.230941	0.281268	0.542398	0.166586	1.000000	0.153400	0.025519
DiabetesPedigreeFunction	-0.033523	0.137060	-0.002763	0.100966	0.098634	0.153400	1.000000	0.033561
Age	0.544341	0.266534	0.324595	0.127872	0.136734	0.025519	0.033561	1.000000
Outcome	0.221898	0.492928	0.166074	0.215299	0.214411	0.311924	0.173844	0.238356

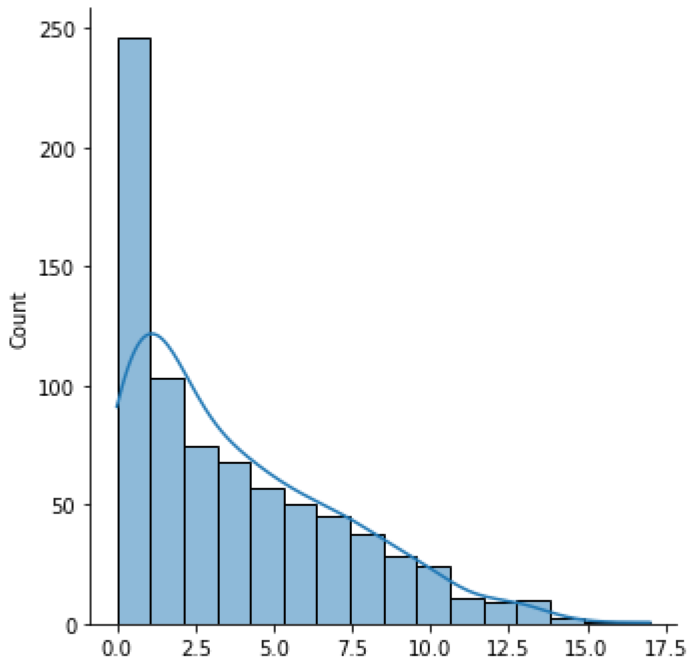
In [23]:
```
df_diabetes.corr()['Outcome'].sort_values(ascending=False)
```

Out[23]:
```
Outcome                     1.000000
Glucose                     0.492928
BMI                         0.311924
Age                         0.238356
Pregnancies                 0.221898
SkinThickness               0.215299
Insulin                     0.214411
DiabetesPedigreeFunction    0.173844
BloodPressure               0.166074
Name: Outcome, dtype: float64
```

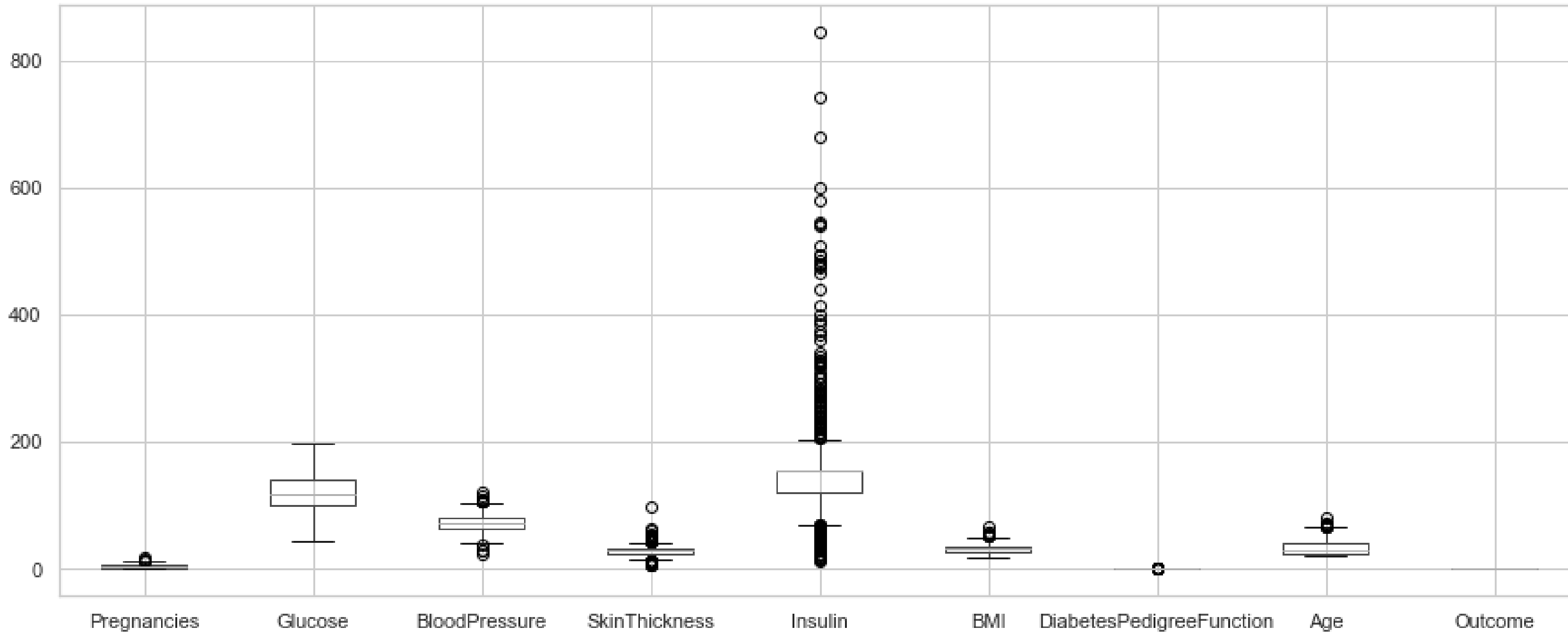
In [24]:
```
df_diabetes.columns
```

Out[24]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [25]:
```
for i in df_diabetes.columns[0:-1] :
    sns.displot(data=df_diabetes, x=i, kde=True)
```



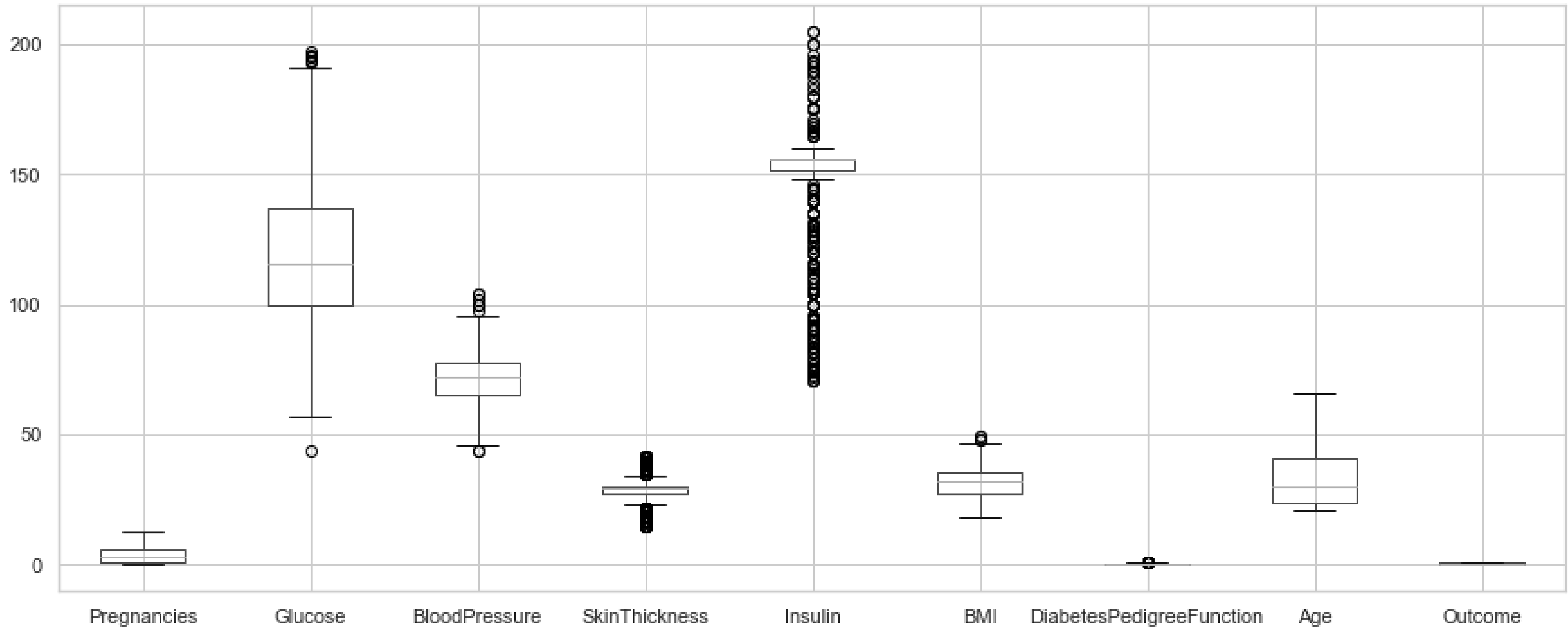
In [26]:
```
sns.set(style="whitegrid")
df_diabetes.boxplot(figsize=(15,6))
plt.show()
```



In [27]:
```
Q1=df_diabetes.quantile(0.25)
Q3=df_diabetes.quantile(0.75)
IQR=Q3-Q1
#outlier remove
df_out = df_diabetes[~((df_diabetes < (Q1 - 1.5 * IQR)) |(df_diabetes > (Q3 + 1.5 * IQR))).any(axis=1
df_diabetes.shape,df_out.shape
```

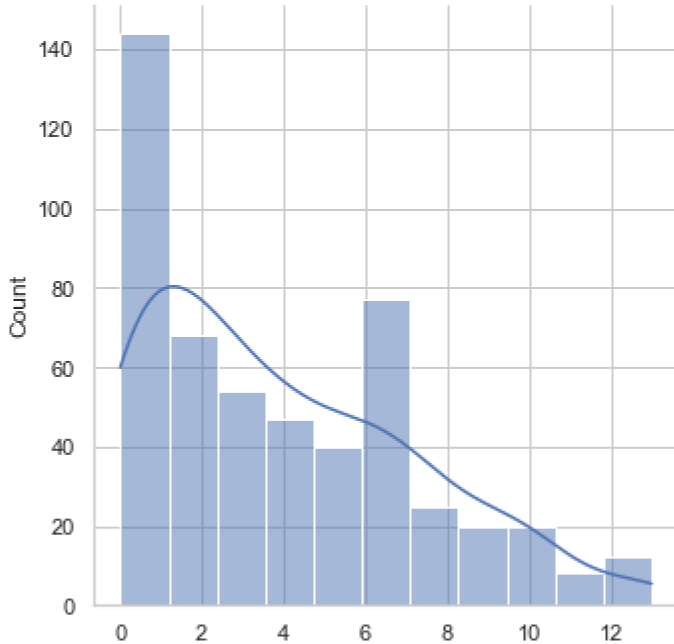
Out[27]:
```
((768, 9), (515, 9))
```

In [28]:
```
sns.set(style="whitegrid")
df_out.boxplot(figsize=(15,6))
plt.show()
```



In [29]:
```
df_diabetes =df_out
```

In [30]:
```
for i in df_diabetes.columns[0:-1] :
    sns.displot(data=df_diabetes, x=i, kde=True)
```



In [31]:
```
df_diabetes.corr().T
```

Out[31]:

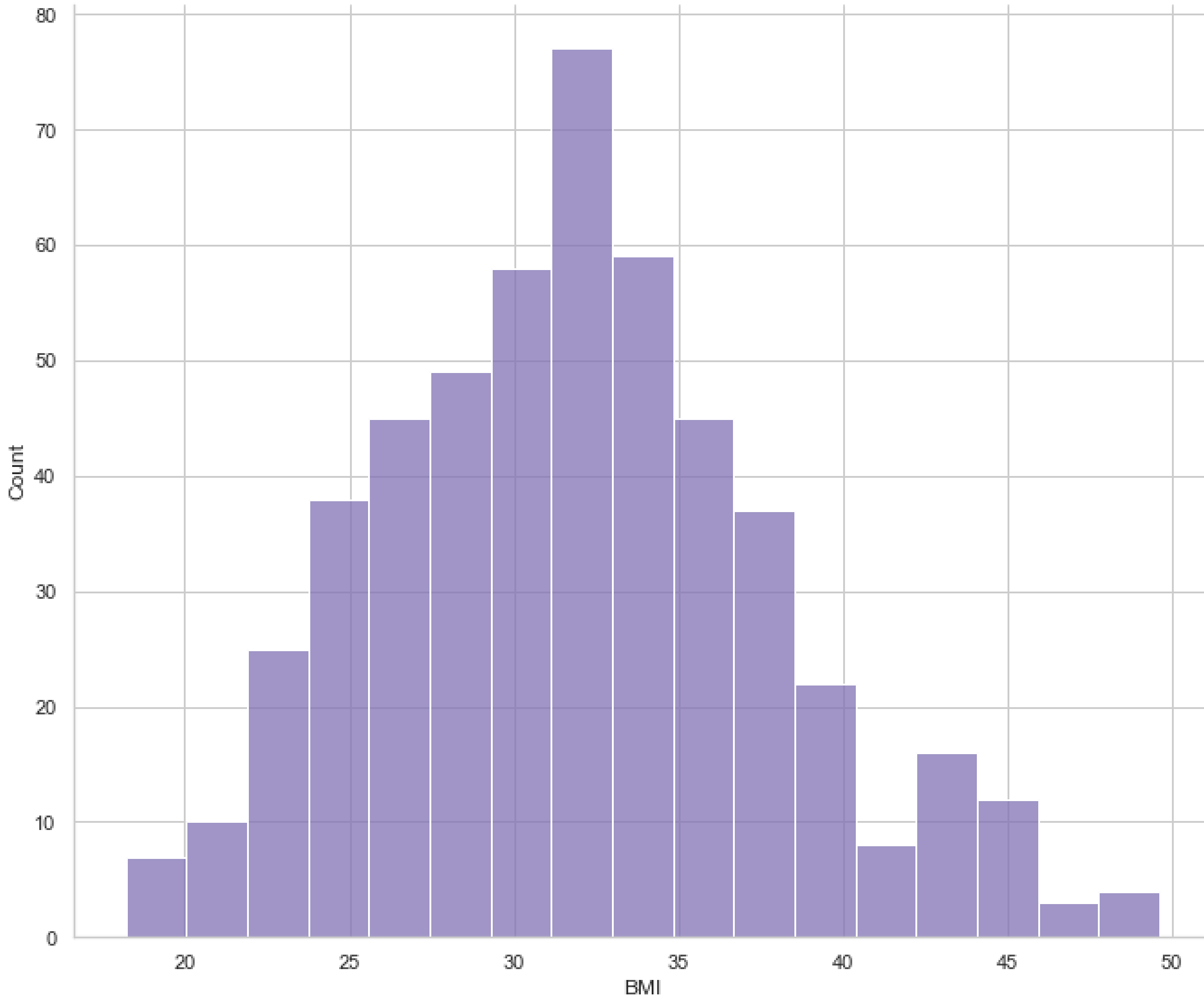
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
Pregnancies	1.000000	0.110622	0.201698	0.129082	0.119618	0.028829	0.014969	0.513640
Glucose	0.110622	1.000000	0.214924	0.069066	0.180899	0.152330	0.068436	0.266073
BloodPressure	0.201698	0.214924	1.000000	0.128661	0.107820	0.229477	0.025405	0.352452
SkinThickness	0.129082	0.069066	0.128661	1.000000	0.125630	0.415246	0.051262	0.074935
Insulin	0.119618	0.180899	0.107820	0.125630	1.000000	0.029492	-0.032920	0.193573
BMI	0.028829	0.152330	0.229477	0.415246	0.029492	1.000000	0.138813	0.013666
DiabetesPedigreeFunction	0.014969	0.068436	0.025405	0.051262	-0.032920	0.138813	1.000000	0.021202
Age	0.513640	0.266073	0.352452	0.074935	0.193573	0.013666	0.021202	1.000000
Outcome	0.187868	0.478218	0.162221	0.151155	0.140253	0.267172	0.182401	0.228587

In [32]:
```
df_diabetes.corr()['Outcome'].sort_values(ascending=False)
```

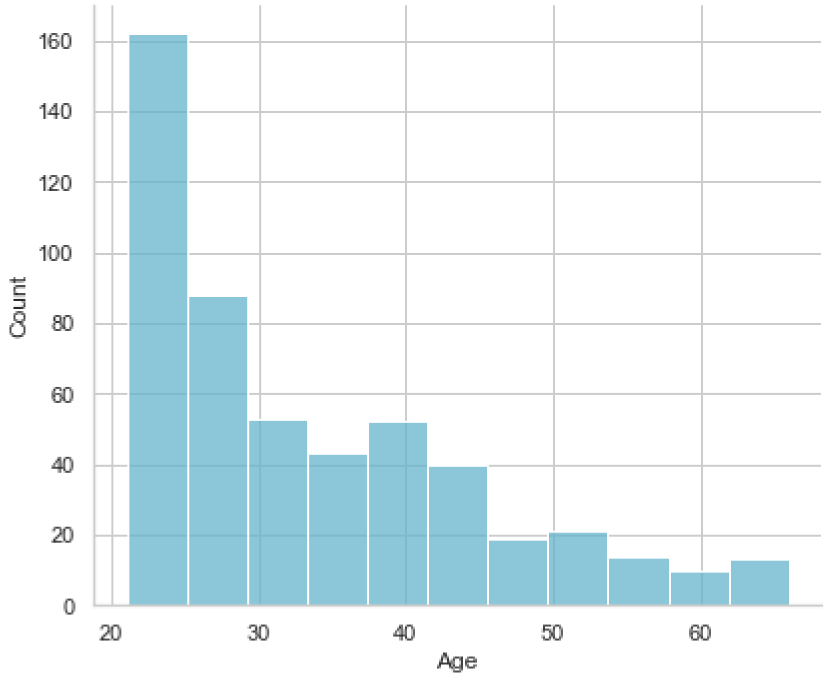
Out[32]:
```
Outcome                     1.000000
Glucose                     0.478218
BMI                         0.267172
Age                         0.228587
Pregnancies                 0.187868
DiabetesPedigreeFunction    0.182401
BloodPressure               0.162221
SkinThickness               0.151155
Insulin                     0.140253
Name: Outcome, dtype: float64
```

In [33]:
```
plt.figure(figsize=(12, 6))
sns.heatmap(df_diabetes.corr(), annot=True, cmap='Blues')  ## symmetric matrix
plt.show()
```

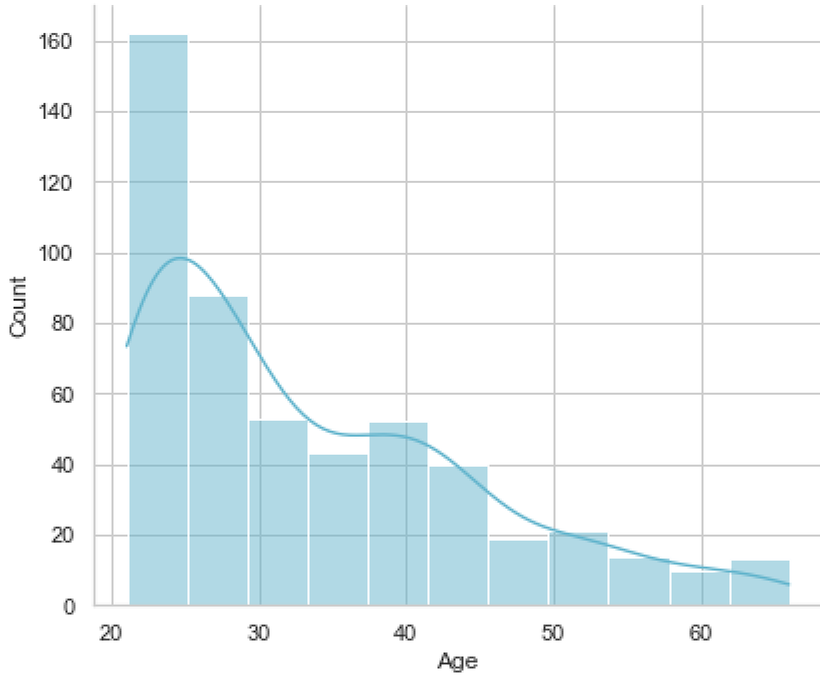
In [34]:
```
sns.displot(df_diabetes['BMI'],kde = False, color='m',height=8,aspect=1.2)
plt.show()
```



In [35]:
```
sns.displot(df_diabetes['Age'], color='c',height=5,aspect=1.2 )
plt.show()
```



In [36]:
```
sns.displot(df_diabetes['Age'], color='c',kde =True,height=5,aspect=1.2)
plt.show()
```

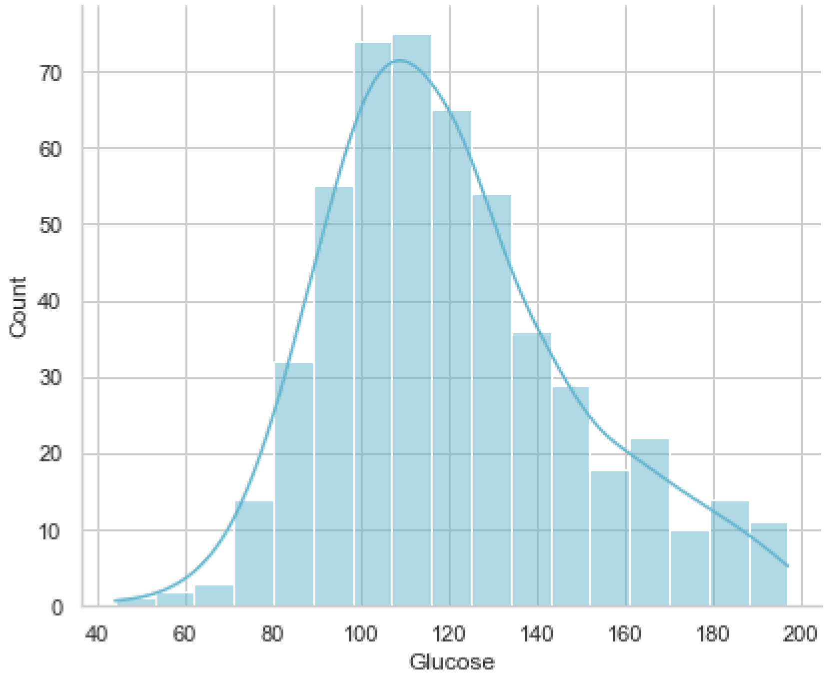


In [37]:
```
df_diabetes.head(10)
```

Out[37]:

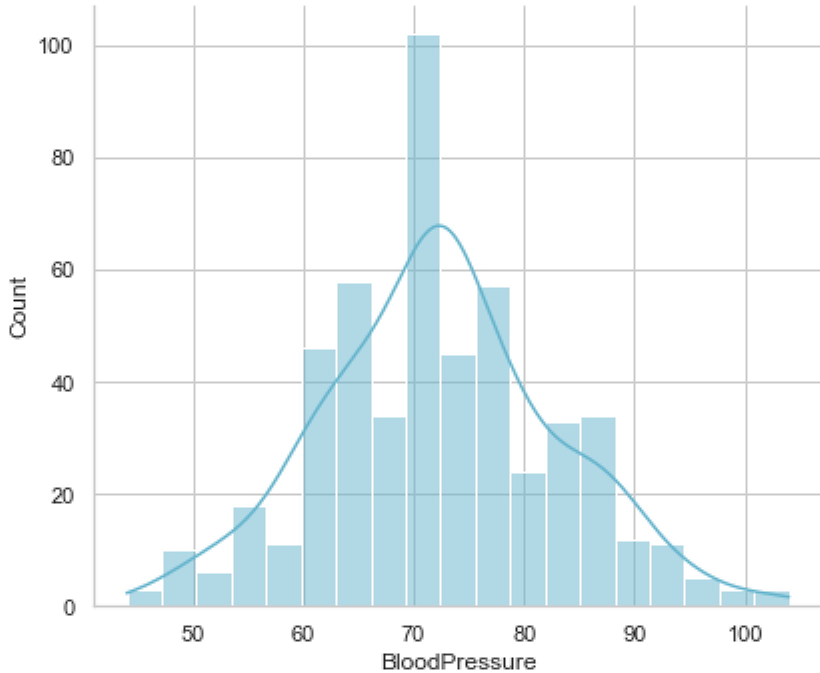
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.000000	35.00000	155.548223	33.600000	0.627	50	1
1	1	85.0	66.000000	29.00000	155.548223	26.600000	0.351	31	0
2	8	183.0	64.000000	29.15342	155.548223	23.300000	0.672	32	1
3	1	89.0	66.000000	23.00000	94.000000	28.100000	0.167	21	0
5	5	116.0	74.000000	29.15342	155.548223	25.600000	0.201	30	0
6	3	78.0	50.000000	32.00000	88.000000	31.000000	0.248	26	1
7	10	115.0	72.405184	29.15342	155.548223	35.300000	0.134	29	0
9	8	125.0	96.000000	29.15342	155.548223	32.457464	0.232	54	1
10	4	110.0	92.000000	29.15342	155.548223	37.600000	0.191	30	0
11	10	168.0	74.000000	29.15342	155.548223	38.000000	0.537	34	1

In [38]:
```
sns.displot(df_diabetes.Glucose, color='c',kde =True,height=5,aspect=1.2)
plt.show()
```



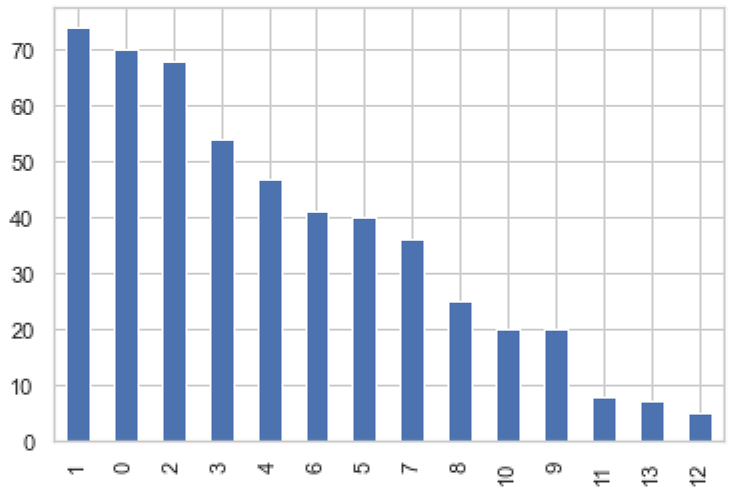
In [39]:
```
sns.displot(df_diabetes.BloodPressure, color='c',kde =True,height=5,aspect=1.2)
```

Out[39]: <seaborn.axisgrid.FacetGrid at 0x7ff2acf81700>



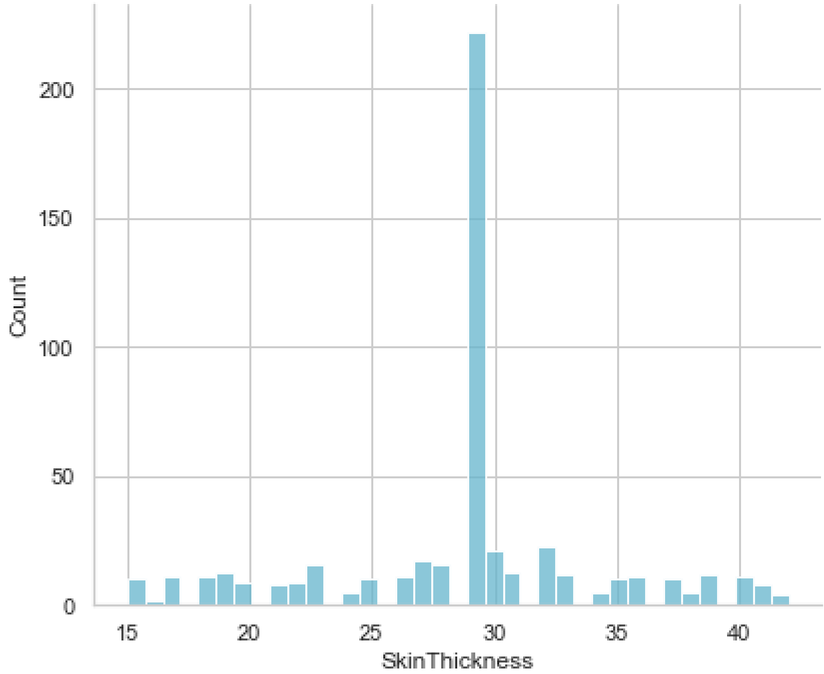
In [40]:
```
df_diabetes['Pregnancies'].value_counts().plot(kind='bar')
```

Out[40]: <AxesSubplot:>



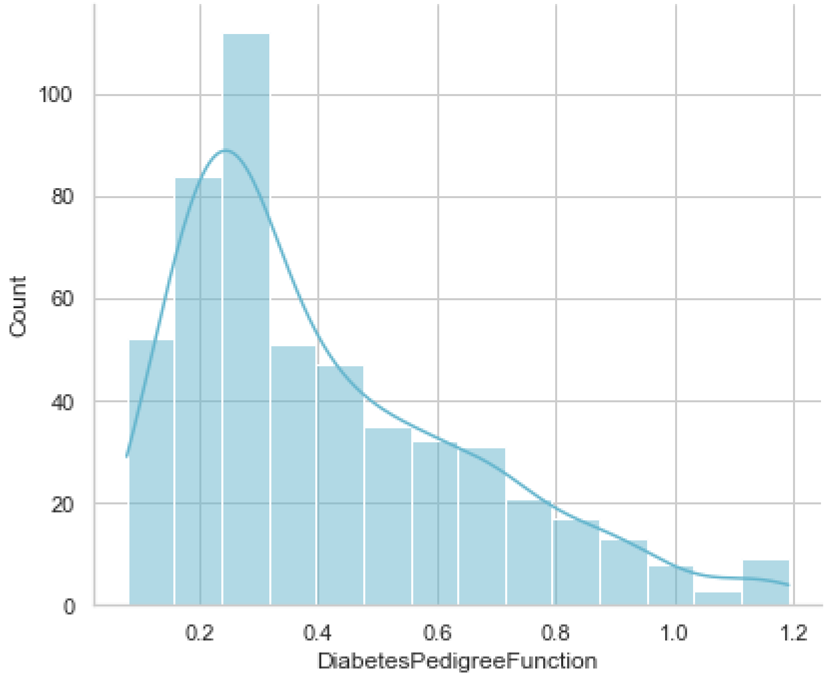
In [41]:
```
sns.displot(df_diabetes.SkinThickness, color='c',height=5,aspect=1.2)
```

Out[41]: <seaborn.axisgrid.FacetGrid at 0x7ff2adadad30>



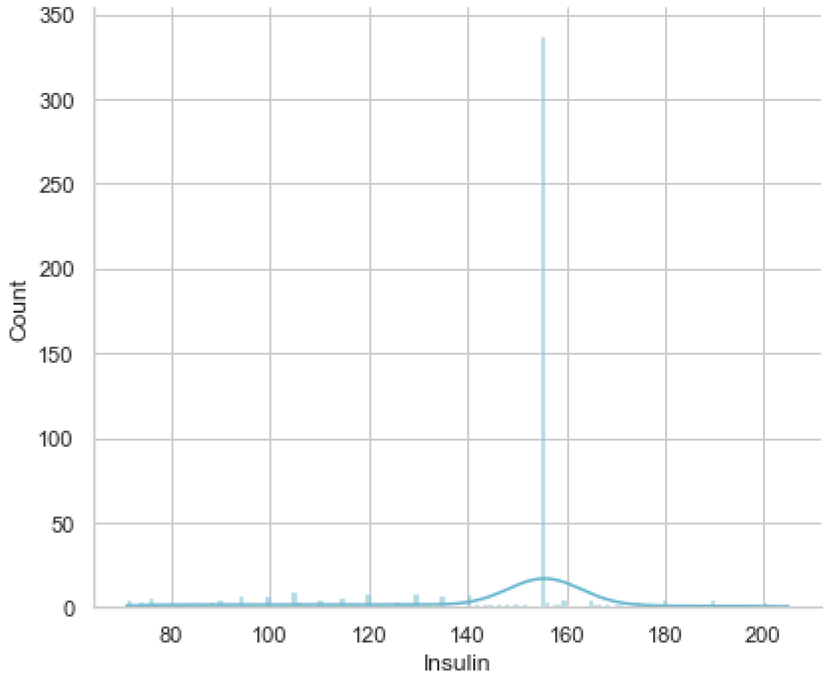
In [42]:
```
sns.displot(df_diabetes.DiabetesPedigreeFunction, color='c',kde =True,height=5,aspect=1.2)
```

Out[42]: <seaborn.axisgrid.FacetGrid at 0x7ff293805b50>

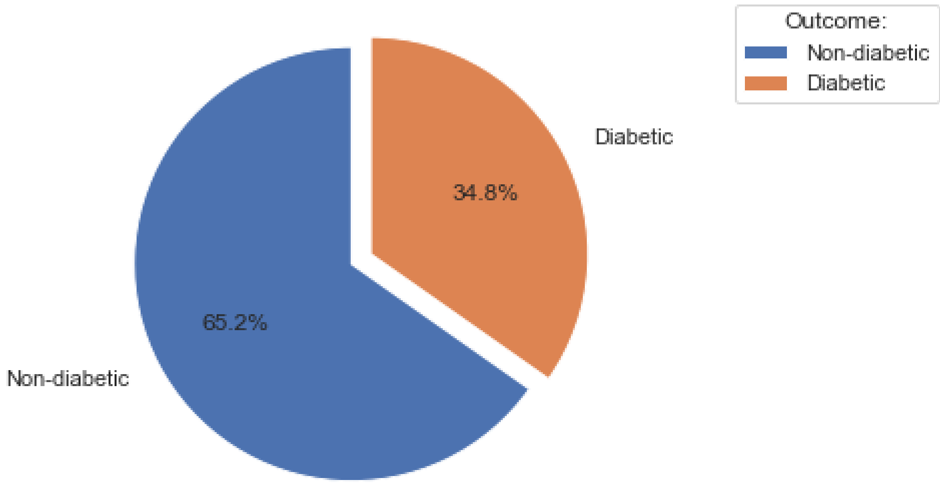


In [43]:
```
sns.displot(df_diabetes.Insulin, color='c',kde =True,height=5,aspect=1.2)
```

Out[43]: <seaborn.axisgrid.FacetGrid at 0x7ff2adadadf0>



In [44]:
```
plt.figure(figsize=(5,5))

plt.pie(df_diabetes['Outcome'].value_counts(),labels=['Non-diabetic','Diabetic'],radius=1,
        autopct='%1.1f%%',explode = [0,0.1],labeldistance=1.15,startangle = 90)

plt.legend(title = 'Outcome:',loc='upper right', bbox_to_anchor=(1.6,1))
plt.show()
```



In [45]:
```
data = df_diabetes.iloc[:,0:8]
outcome = df_diabetes.iloc[:,8]
X , Y = data,outcome
```

In [46]:
```
print(X.shape)
print(Y.shape)
```

```
(515, 8)
(515,)
```

In [47]:
```
scaler = StandardScaler()
newx = scaler.fit_transform(X)
print(newx)
```

```
[[ 0.59980785  0.98895509 -0.03283239 ...  0.28690136  0.85924683
   1.4695238 ]
 [-0.92487648 -1.25325879 -0.59529548 ... -0.87955789 -0.25291665
  -0.22634722]
 [ 1.20968159  2.23462946 -0.78278318 ... -1.42946011  1.04057783
  -0.13709085]
 ...
 [ 0.29487099  0.02800628 -0.03283239 ... -0.94621271 -0.68005189
  -0.31560359]
 [-0.92487648  0.20595976 -1.15775857 ... -0.29632827 -0.2609758
   1.20175469]
 [-0.92487648 -0.96853322 -0.22032008 ... -0.24633716 -0.39798145
  -0.94039817]]
```

In [48]:
```
X = newx
print(X)
```

```
[[ 0.59980785  0.98895509 -0.03283239 ...  0.28690136  0.85924683
   1.4695238 ]
 [-0.92487648 -1.25325879 -0.59529548 ... -0.87955789 -0.25291665
  -0.22634722]
 [ 1.20968159  2.23462946 -0.78278318 ... -1.42946011  1.04057783
  -0.13709085]
 ...
 [ 0.29487099  0.02800628 -0.03283239 ... -0.94621271 -0.68005189
  -0.31560359]
 [-0.92487648  0.20595976 -1.15775857 ... -0.29632827 -0.2609758
   1.20175469]
 [-0.92487648 -0.96853322 -0.22032008 ... -0.24633716 -0.39798145
  -0.94039817]]
```

In [49]:
```
X_train , X_test , y_train , y_test = train_test_split(X ,Y ,random_state=42, stratify=Y,test_size=0.
```

In [50]:
```
X_train.shape , X_test.shape , y_train.shape ,  y_test.shape
```

Out[50]:
```
((412, 8), (103, 8), (412,), (103,))
```

In [51]:
```
linear_svc = svm.SVC(kernel='linear')
linear_svc.fit(X_train,y_train)
```

Out[51]:
```
SVC(kernel='linear')
```

In [53]:
```
X_train_prediction = linear_svc.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, y_train)
```

In [54]:
```
print('Accuracy Scores -- ', round(accuracy_score(X_train_prediction, y_train)*100),'%')
```

```
Accuracy Scores --  75 %
```

In [55]:
```
y_pred = linear_svc.predict(X_test)
```

In [56]:
```
print('Accuracy Scores -- ', round(accuracy_score(y_test, y_pred)*100),'%')
```

```
Accuracy Scores --  79 %
```

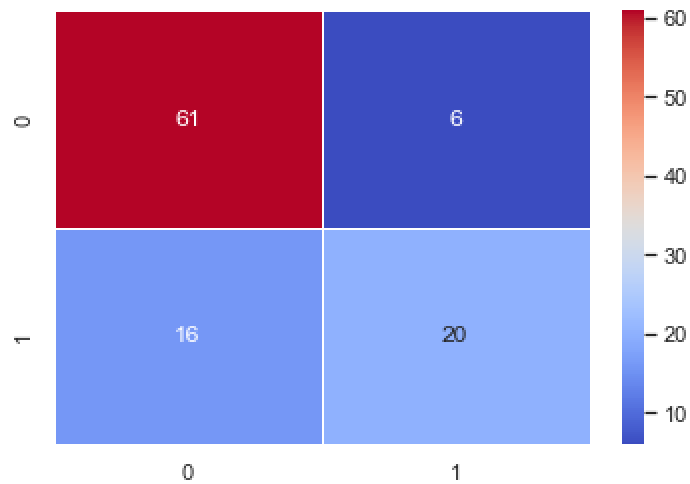
In [57]:
```
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.79      0.91      0.85        67
           1       0.77      0.56      0.65        36

    accuracy                           0.79       103
   macro avg       0.78      0.73      0.75       103
weighted avg       0.78      0.79      0.78       103
```

In [58]:
```
cm =confusion_matrix(y_test,y_pred)
print("confusion_matrix " , cm )
sns.heatmap(cm, cmap='coolwarm',annot = True ,linewidths=1,fmt="d")
```

```
confusion_matrix  [[61  6]
 [16 20]]
```

Out[58]:
```
<AxesSubplot:>
```



In [59]:
```
import pickle
pickle_file = 'Diabetes_plk.pickle'
pickle.dump(linear_svc , open(pickle_file,'wb'))
```

In [60]:
```
loaded_model = pickle.load(open(pickle_file ,'rb'))
loaded_model.predict(X_test)
```

Out[60]:
```
array([0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,
       0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0,
       0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 1, 0, 1, 1, 0, 1, 1, 0, 1, 0, 0, 0,
       0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 1, 0])
```

In [61]:
```
result = loaded_model.predict([(5,166,72,19,175,25.8,0.587,51)])
```

In [62]:
```
if (result == 0):
    print('The person is not diabetic')
else:
    print('The person is diabetic')
```

```
The person is diabetic
```

In [63]:
```
RF  = RandomForestClassifier(random_state=42, n_estimators=100,  max_depth=50,n_jobs=-1)
'''(n_estimators=100, max_depth=3, max_leaf_nodes=20,
                                    criterion='gini', max_features=1.0, max_samples=0.8)'''
```

Out[63]:
```
"(n_estimators=100, max_depth=3, max_leaf_nodes=20, \n                                    criterion
='gini', max_features=1.0, max_samples=0.8)"
```

In [64]:
```
RF.fit(X_train,y_train)
```

Out[64]:
```
RandomForestClassifier(max_depth=50, n_jobs=-1, random_state=42)
```

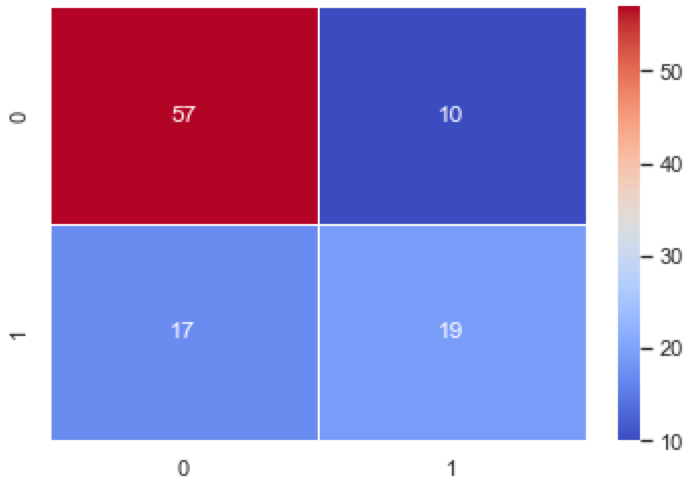
In [65]:
```
y_pred = RF.predict(X_test)
```

In [66]:
```
print('Accuracy Scores -- ', round(accuracy_score(y_test, y_pred)*100),'%')
```

```
Accuracy Scores --  74 %
```

In [67]:
```
cmrf =confusion_matrix(y_test,y_pred)
print("confusion_matrix " , cmrf )
sns.heatmap(cmrf, cmap='coolwarm',annot = True ,linewidths=1,fmt="d")
plt.show()
```

```
confusion_matrix  [[57 10]
 [17 19]]
```



In [68]:
```
logmodel = LogisticRegression()
logmodel.fit(X_train,y_train)
```

Out[68]: LogisticRegression()

In [69]:
```
X_train_prediction_log = logmodel.predict(X_train)
training_data_accuracy_log = accuracy_score(X_train_prediction_log, y_train)
```

In [70]:
```
print('Accuracy Scores -- ', round(accuracy_score(X_train_prediction_log, y_train)*100),'%')
```

```
Accuracy Scores --  75 %
```

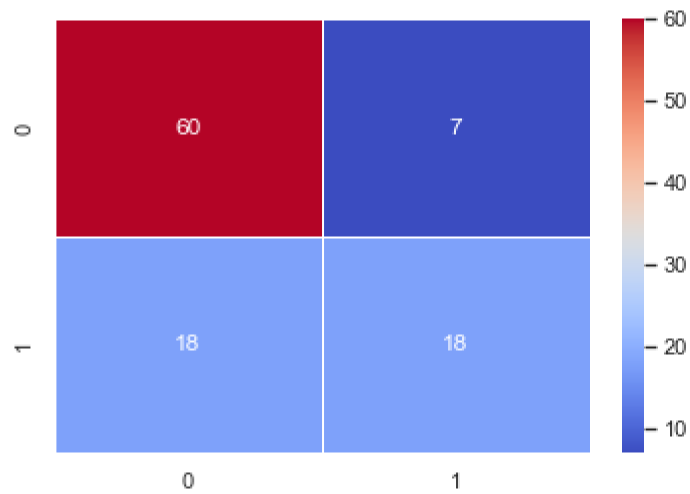
In [71]:
```
y_pred_log =logmodel.predict(X_test)
print('Accuracy Scores -- ', round(accuracy_score(y_test, y_pred_log)*100),'%')
```

```
Accuracy Scores --  76 %
```

In [72]:
```
cmlog =confusion_matrix(y_test,y_pred_log)
print("confusion_matrix " , cmlog )
sns.heatmap(cmlog, cmap='coolwarm',annot = True ,linewidths=1,fmt="d")
```

```
confusion_matrix  [[60  7]
 [18 18]]
```

Out[72]: <AxesSubplot:>



In [73]:
```
knn=KNeighborsClassifier(n_neighbors=5,metric='euclidean',p=2)
knn.fit(X_train,y_train)
```

Out[73]: KNeighborsClassifier(metric='euclidean')

In [74]:
```
y_pred=knn.predict(X_test)
y_pred
```

Out[74]:
```
array([0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 0, 1, 1, 0, 0, 0, 0, 0,
       0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 1, 0, 0,
       1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0,
       0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 0])
```

In [75]:
```
knn.score(X_test,y_test)
```

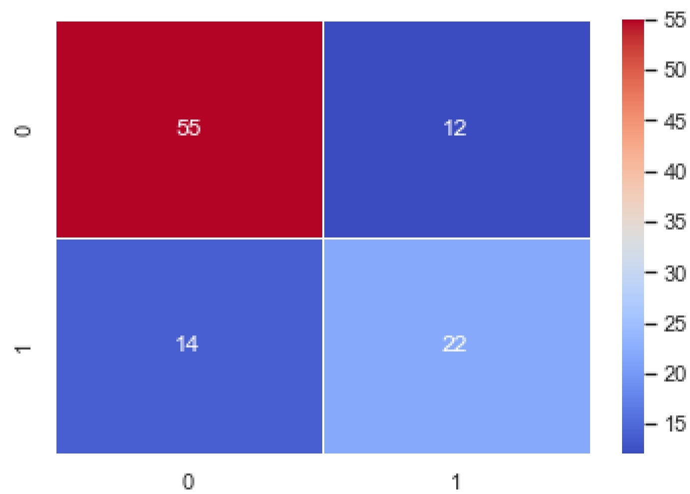
Out[75]:
```
0.7475728155339806
```

In [76]:
```
print(round(accuracy_score(y_test,y_pred)*100),"%")
```

```
75 %
```

In [77]:
```
mat = confusion_matrix(y_test, y_pred)
mat
print("confusion_matrix " , mat )
sns.heatmap(mat, cmap='coolwarm',annot = True ,linewidths=1,fmt="d")
plt.show()
```

```
confusion_matrix  [[55 12]
 [14 22]]
```



In [78]:
```
from sklearn.ensemble import RandomForestClassifier
```

In [79]:
```
modelRan = RandomForestClassifier(n_estimators=80,criterion='gini')
modelRan.fit(X_train,y_train)
```

Out[79]:
```
RandomForestClassifier(n_estimators=80)
```

In [80]:
```
print(round(modelRan.score(X_test,y_test)*100),"%")
```

```
74 %
```

In [81]:
```
sc = MinMaxScaler(feature_range = (0, 1))
dataset_scaled = sc.fit_transform(df_diabetesk1)
```

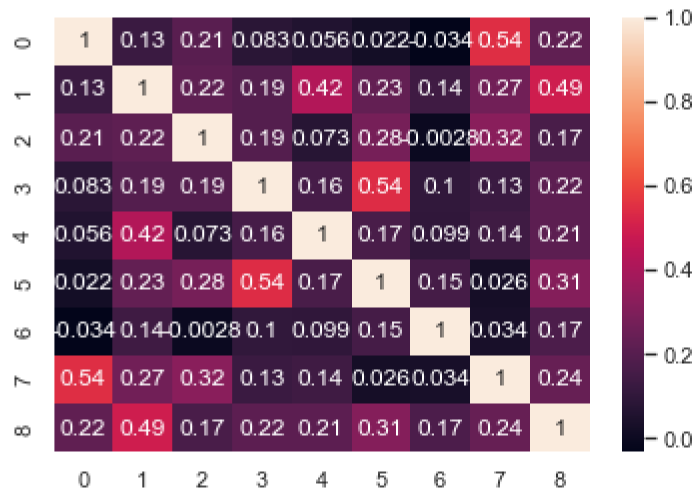
In [82]:
```
data1 = pd.DataFrame(dataset_scaled)
data1
```

Out[82]:

	0	1	2	3	4	5	6	7	8
0	0.352941	0.670968	0.489796	0.304348	0.170130	0.314928	0.234415	0.483333	1.0
1	0.058824	0.264516	0.428571	0.239130	0.170130	0.171779	0.116567	0.166667	0.0
2	0.470588	0.896774	0.408163	0.240798	0.170130	0.104294	0.253629	0.183333	1.0
3	0.058824	0.290323	0.428571	0.173913	0.096154	0.202454	0.038002	0.000000	0.0
4	0.000000	0.600000	0.163265	0.304348	0.185096	0.509202	0.943638	0.200000	1.0
...	...	...	...	...	...	...	...	...	...
763	0.588235	0.367742	0.530612	0.445652	0.199519	0.300613	0.039710	0.700000	0.0
764	0.117647	0.503226	0.469388	0.217391	0.170130	0.380368	0.111870	0.100000	0.0
765	0.294118	0.496774	0.489796	0.173913	0.117788	0.163599	0.071307	0.150000	0.0
766	0.058824	0.529032	0.367347	0.240798	0.170130	0.243354	0.115713	0.433333	1.0
767	0.058824	0.316129	0.469388	0.260870	0.170130	0.249489	0.101196	0.033333	0.0

768 rows × 9 columns

In [83]:
```
sns.heatmap(data1.corr(), annot = True)
plt.show()
```



In [84]:
```
X = data1.iloc[:, [1, 5, 5]].values
Y = data1.iloc[:, 8].values
```

In [85]:
```
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size = 0.20, random_state = 42, strati
```

In [86]:
```
print("X_train shape:", X_train.shape)
print("X_test shape:", X_test.shape)
print("Y_train shape:", Y_train.shape)
print("Y_test shape:", Y_test.shape)
```

```
X_train shape: (614, 3)
X_test shape: (154, 3)
Y_train shape: (614,)
Y_test shape: (154,)
```

In [87]:
```
KMeans_Clustering = KMeans(n_clusters=2, n_init=10, algorithm='auto', init='k-means++', random_state=
#KMeans(n_clusters =2, random_state=0)
KMeans_Clustering.fit(X_train)
```

Out[87]:
```
KMeans(n_clusters=2, random_state=42)
```

In [88]:
```
print(KMeans_Clustering.cluster_centers_)
```

```
[[0.68556447 0.38164466 0.38164466]
 [0.39093369 0.23733383 0.23733383]]
```

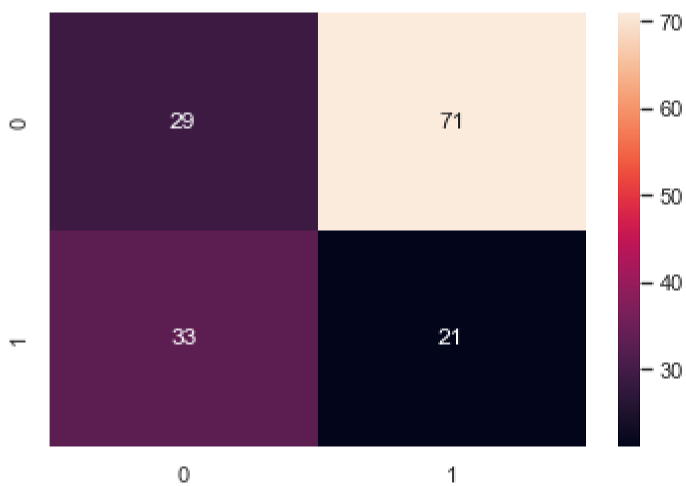
In [89]:
```
kpred = KMeans_Clustering.predict(X_test)

print('Classification report:\n\n', sklearn.metrics.classification_report(Y_test,kpred))
```

```
Classification report:

               precision    recall  f1-score   support

         0.0       0.47      0.29      0.36       100
         1.0       0.23      0.39      0.29        54

    accuracy                           0.32       154
   macro avg       0.35      0.34      0.32       154
weighted avg       0.38      0.32      0.33       154
```

In [90]:
```
print("Confusion Matrix :")
outcome_labels = sorted(df_diabetes.Outcome.unique())
sns.heatmap(
    confusion_matrix(Y_test, kpred),
    annot=True,
    xticklabels=outcome_labels,
    yticklabels=outcome_labels
)
```

```
Confusion Matrix :
```

Out[90]: <AxesSubplot:>

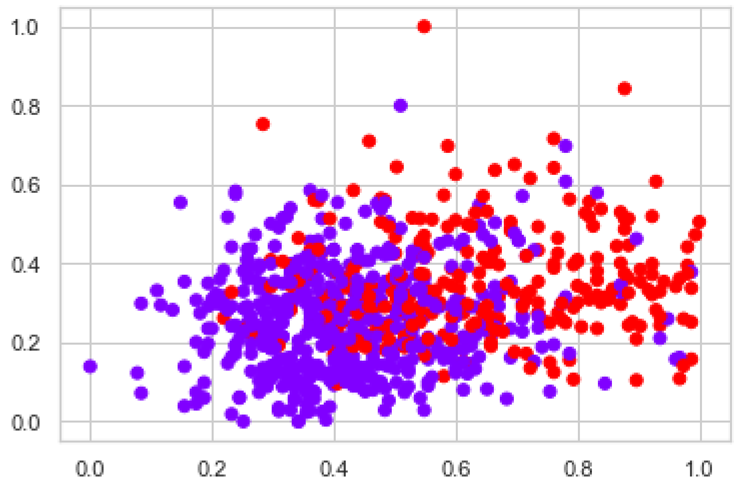


In [91]:
```
out = KMeans_Clustering.predict([[0.53,0.54,0.5253]])
if (out==0):
    print("No Diabetes")
else:
    print("Diabetes")
```

```
No Diabetes
```

In [92]:
```
plt.scatter(data1.iloc[:, [1]].values,data1.iloc[:, [5]].values, c=df_diabetesk1['Outcome'], cmap='ra
```

Out[92]:
```
<matplotlib.collections.PathCollection at 0x7ff2938e03d0>
```



In [93]:
```
KMeans_Clustering = KMeans(n_clusters =2, random_state=0)
KMeans_Clustering.fit(X)
```

Out[93]:
```
KMeans(n_clusters=2, random_state=0)
```

In [94]:
```
plt.scatter(data1.iloc[:, [1]].values,data1.iloc[:, [5]].values, c=KMeans_Clustering.labels_, cmap='r
```

Out[94]:
```
<matplotlib.collections.PathCollection at 0x7ff2ad083d00>
```