In [2]:
```python
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
data=pd.read_csv("pima.csv")
data
```

Out[2]:

	num_preg	glucose_conc	diastolic_bp	thickness	insulin	bmi	diab_pred	age	diabetes
0	1	85	66	29	0	26.6	0.351	31	0
1	8	183	64	0	0	23.3	0.672	32	1
2	1	89	66	23	94	28.1	0.167	21	0
3	0	137	40	35	168	43.1	2.288	33	1
4	5	116	74	0	0	25.6	0.201	30	0
...	...	...	...	...	...	...	...	...	...
762	10	101	76	48	180	32.9	0.171	63	0
763	2	122	70	27	0	36.8	0.340	27	0
764	5	121	72	23	112	26.2	0.245	30	0
765	1	126	60	0	0	30.1	0.349	47	1
766	1	93	70	31	0	30.4	0.315	23	0

767 rows × 9 columns

In [3]:
```python
print("Diabetes data set dimensions : {}".format(data.shape))
```

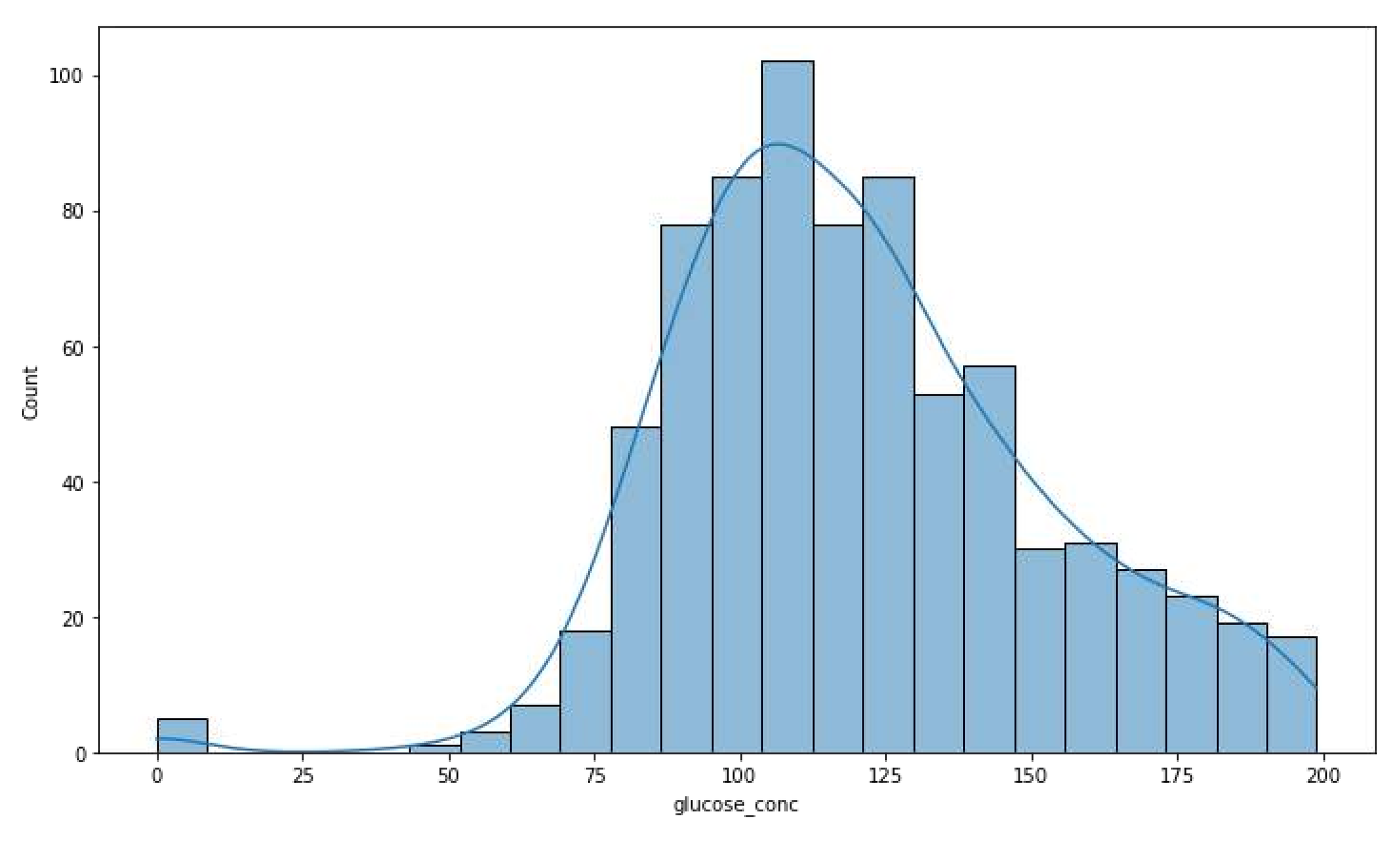
```
Diabetes data set dimensions : (767, 9)
```

In [10]:
```python
data.groupby('diabetes').size()
```

Out[10]:
```
diabetes
0    500
1    267
dtype: int64
```

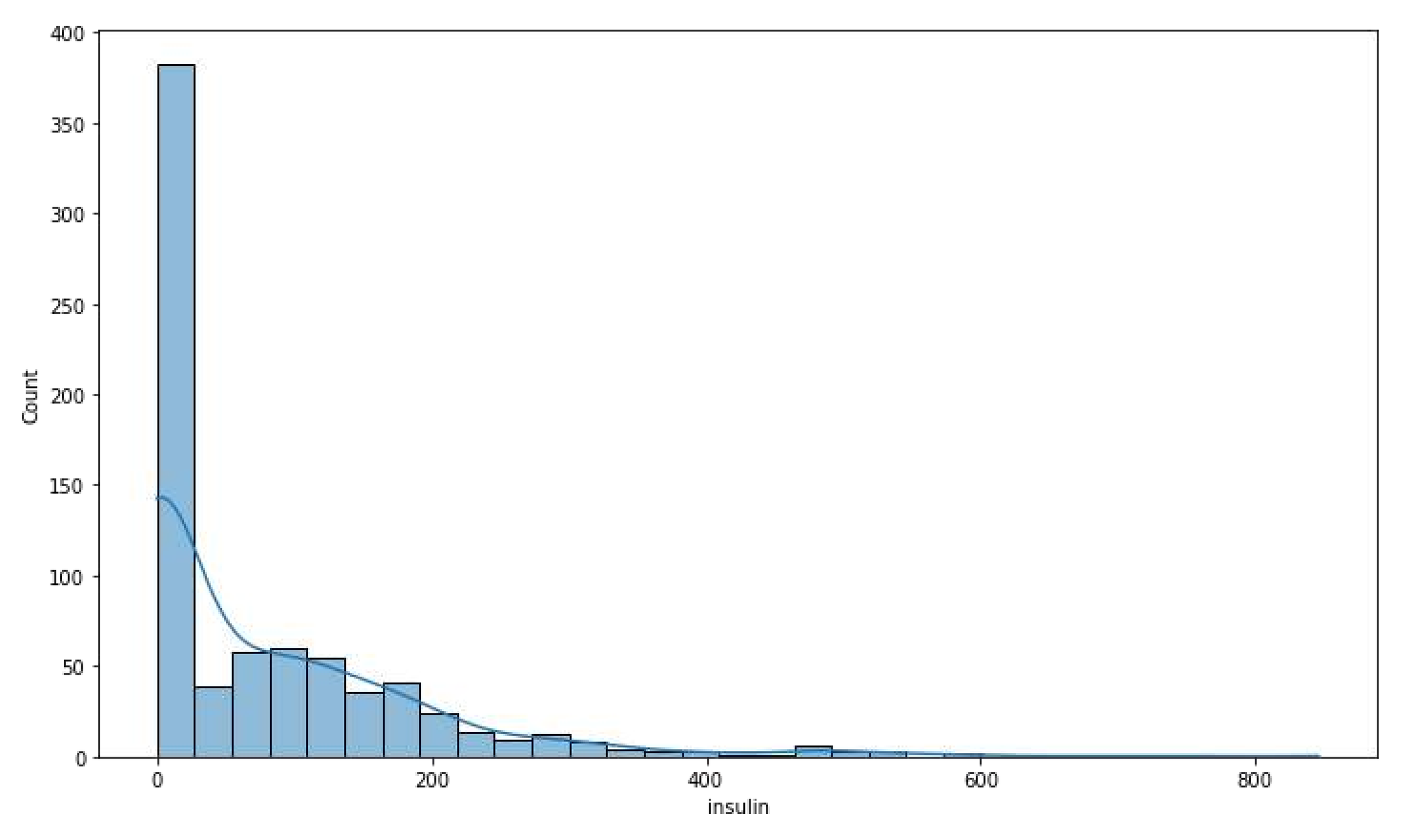
In [3]:
```python
plt.figure(figsize=(12,7))
sns.histplot(data['glucose_conc'],kde=True)
```

Out[3]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x2e7f2e49fa0>
```



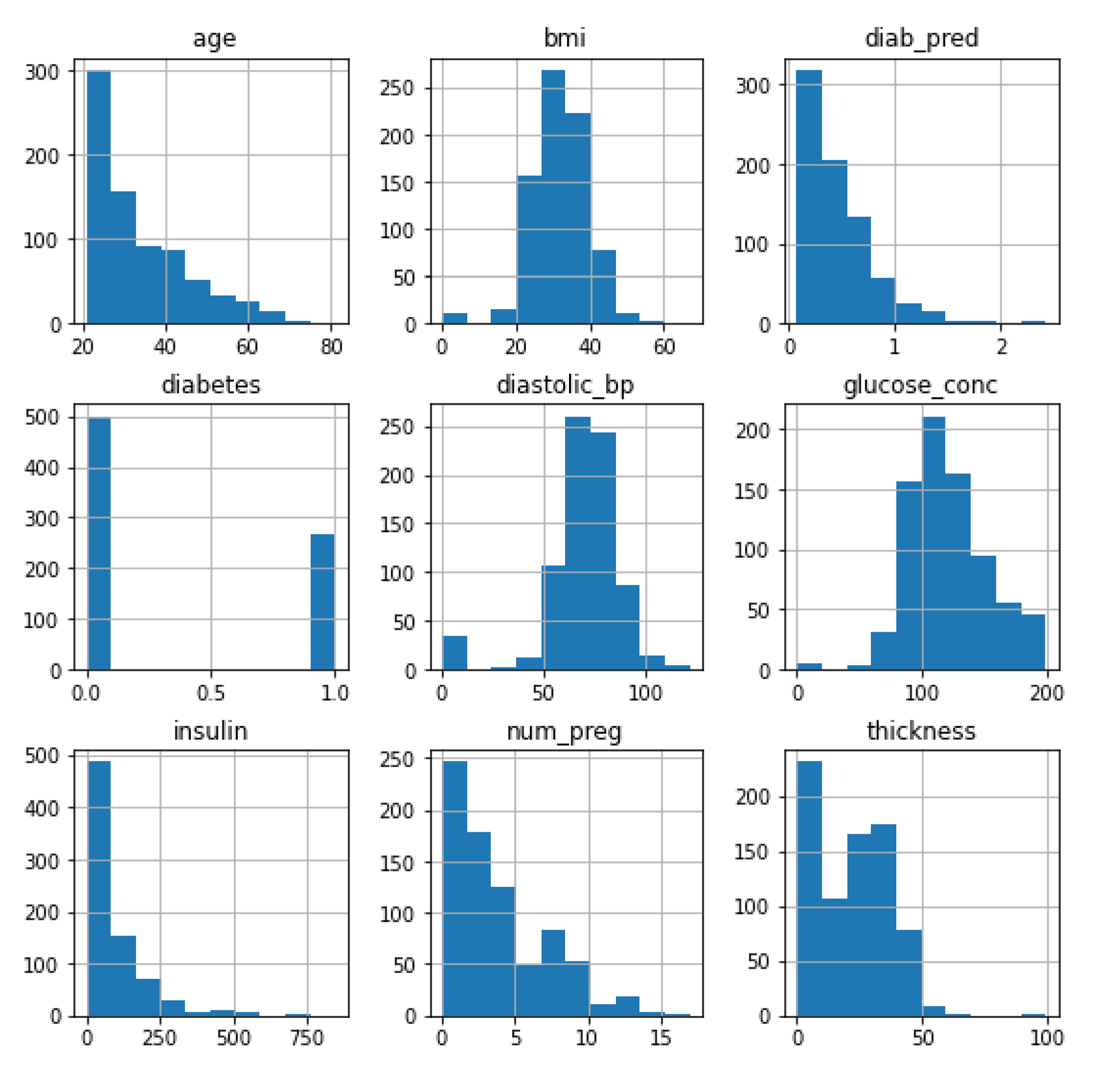
In [6]:
```python
plt.figure(figsize=(12,7))
sns.histplot(data['insulin'],kde=True)
```

Out[6]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x2e7f31d3940>
```



In [8]:
```python
data.hist(figsize=(9, 9))
```

Out[8]:
```
array([[<matplotlib.axes._subplots.AxesSubplot object at 0x0000024BAD927E50>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x0000024BAD983580>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x0000024BAD9B3A00>],
       [<matplotlib.axes._subplots.AxesSubplot object at 0x0000024BAD9E0E50>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x0000024BADA182E0>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x0000024BADA43670>],
       [<matplotlib.axes._subplots.AxesSubplot object at 0x0000024BADA43760>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x0000024BADA6FC10>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x0000024BADAD5460>]],
      dtype=object)
```



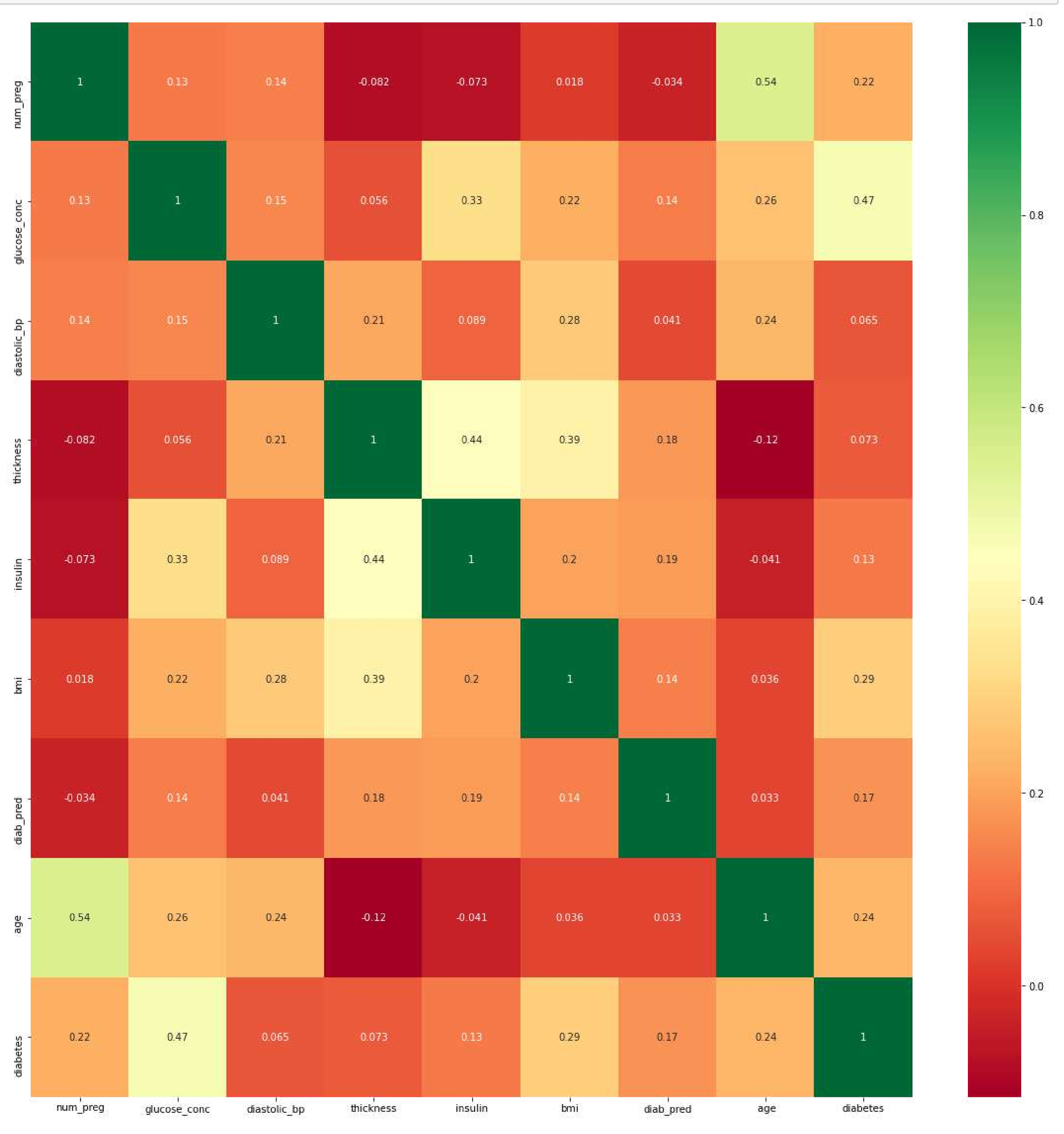
In [11]:
```python
data.isnull().sum()
data.isna().sum()
```

Out[11]:
```
num_preg        0
glucose_conc    0
diastolic_bp    0
thickness       0
insulin         0
bmi             0
diab_pred       0
 age            0
diabetes        0
dtype: int64
```

In [12]:
```python
data.isnull().values.any()
```

Out[12]:
```
False
```

In [13]:
```python
corrmat = data.corr()
top_corr_features = corrmat.index
plt.figure(figsize=(20,20))
#plot heat map
g=sns.heatmap(data[top_corr_features].corr(),annot=True,cmap="RdYlGn")
```



In [14]:
```python
data.corr()
```

Out[14]:

	num_preg	glucose_conc	diastolic_bp	thickness	insulin	bmi	diab_pred	age	diabetes
num_preg	1.000000	0.128846	0.141197	-0.082495	-0.072999	0.017518	-0.033927	0.544018	0.221087
glucose_conc	0.128846	1.000000	0.152498	0.056381	0.332383	0.220955	0.136903	0.262408	0.465856
diastolic_bp	0.141197	0.152498	1.000000	0.207308	0.089098	0.281777	0.041180	0.239571	0.064882
thickness	-0.082495	0.056381	0.207308	1.000000	0.437974	0.392553	0.183498	-0.115873	0.073265
insulin	-0.072999	0.332383	0.089098	0.437974	1.000000	0.198111	0.185579	-0.040942	0.131984
bmi	0.017518	0.220955	0.281777	0.392553	0.198111	1.000000	0.140546	0.035911	0.292695
diab_pred	-0.033927	0.136903	0.041180	0.183498	0.185579	0.140546	1.000000	0.032738	0.173245
age	0.544018	0.262408	0.239571	-0.115873	-0.040942	0.035911	0.032738	1.000000	0.236417
diabetes	0.221087	0.465856	0.064882	0.073265	0.131984	0.292695	0.173245	0.236417	1.000000

In [19]:
```python
diabetes_map = {True: 1, False: 0}
```

In [20]:
```python
data['diabetes'] = data['diabetes'].map(diabetes_map)
```

In [21]:
```python
data.head(5)
```

Out[21]:

	num_preg	glucose_conc	diastolic_bp	thickness	insulin	bmi	diab_pred	age	diabetes
0	1	85	66	29	0	26.6	0.351	31	0
1	8	183	64	0	0	23.3	0.672	32	1
2	1	89	66	23	94	28.1	0.167	21	0
3	0	137	40	35	168	43.1	2.288	33	1
4	5	116	74	0	0	25.6	0.201	30	0

In [26]:
```python
diabetes_true_count = len(data.loc[data['diabetes'] == True])
diabetes_false_count = len(data.loc[data['diabetes'] == False])
```

In [27]:
```python
(diabetes_true_count,diabetes_false_count)
```

Out[27]:
```
(267, 500)
```

In [37]:
```python
from sklearn.model_selection import train_test_split
feature_columns = ['num_preg','glucose_conc','diastolic_bp','thickness','insulin','bmi','dia
b_pred','diabetes']
predicted_class = ['diabetes']
X = data[feature_columns].values
y = data[predicted_class].values
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.30, random_state=10)
```

In [43]:
```python
print("total number of rows : {0}".format(len(data)))
print("number of rows missing glucose_conc: {0}".format(len(data.loc[data['glucose_conc'] ==
0])))
print("number of rows missing glucose_conc: {0}".format(len(data.loc[data['glucose_conc'] ==
0])))
print("number of rows missing diastolic_bp: {0}".format(len(data.loc[data['diastolic_bp'] ==
0])))
print("number of rows missing insulin: {0}".format(len(data.loc[data['insulin'] == 0])))
print("number of rows missing bmi: {0}".format(len(data.loc[data['bmi'] == 0])))
print("number of rows missing diab_pred: {0}".format(len(data.loc[data['diab_pred'] == 0])))
```

```
total number of rows : 767
number of rows missing glucose_conc: 5
number of rows missing glucose_conc: 5
number of rows missing diastolic_bp: 35
number of rows missing insulin: 373
number of rows missing bmi: 11
number of rows missing diab_pred: 0
```

In [47]:
```python
from sklearn.impute import SimpleImputer
fill_values = SimpleImputer(missing_values=0, strategy='mean')
X_train = fill_values.fit_transform(X_train)
X_test = fill_values.fit_transform(X_test)
```

RandomForest Algorithm

In [48]:
```python
from sklearn.ensemble import RandomForestClassifier
random_forest_model = RandomForestClassifier(random_state=10)
random_forest_model.fit(X_train, y_train.ravel())
randomforest_prediction = random_forest_model.predict(X_test)
```

SVC Algorithm

In [50]:
```python
from sklearn.svm import SVC
svc_model = SVC(kernel = 'rbf', random_state = 0)
svc_model.fit(X_train, y_train.ravel())
svc_prediction = svc_model.predict(X_test)
```

KNeighborsClassifier Algorithm

In [52]:
```python
from sklearn.neighbors import KNeighborsClassifier
knn_classifier = KNeighborsClassifier(n_neighbors = 5, metric = 'minkowski', p = 2)
knn_classifier.fit(X_train, y_train.ravel())
knn_prediction = knn_classifier.predict(X_test)
```

Decision Tree Algorithm

In [54]:
```python
from sklearn.tree import DecisionTreeClassifier
decisiontree_classifier = DecisionTreeClassifier(criterion = 'entropy', random_state = 0)
decisiontree_classifier.fit(X_train, y_train.ravel())
decisiontree_prediction = decisiontree_classifier.predict(X_test)
```

In [57]:
```python
from sklearn import metrics
print('Accuracy RandomForest = {0:.3f}'.format(metrics.accuracy_score(y_test, randomforest_p
rediction)))
print('Accuracy SVC = {0:.3f}'.format(metrics.accuracy_score(y_test, svc_prediction)))
print('Accuracy KNN = {0:.3f}'.format(metrics.accuracy_score(y_test, knn_prediction)))
print('Accuracy Decision Tree = {0:.3f}'.format(metrics.accuracy_score(y_test, decisiontree_
prediction)))
```

```
Accuracy RandomForest = 0.706
Accuracy SVC = 0.706
Accuracy KNN = 0.719
Accuracy Decision Tree = 0.593
```

In [ ]:

In [ ]: