In [4]:

```
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
import seaborn as sns
```

In [5]:

```
diabetes = pd.read_csv('C:/Users/Administrator/Downloads/diabetes.csv')
```

In [6]:

```
diabetes
```

Out[6]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
0	6	148	72	35	0	33.6	0.627	50
1	1	85	66	29	0	26.6	0.351	31
2	8	183	64	0	0	23.3	0.672	32
3	1	89	66	23	94	28.1	0.167	21
4	0	137	40	35	168	43.1	2.288	33
...	...	...	...	...	...	...	...	...
763	10	101	76	48	180	32.9	0.171	63
764	2	122	70	27	0	36.8	0.340	27
765	5	121	72	23	112	26.2	0.245	30
766	1	126	60	0	0	30.1	0.349	47
767	1	93	70	31	0	30.4	0.315	23

768 rows × 9 columns

In [7]:

```
diabetes.head()
```

Out[7]:

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

In [8]:

```
diabetes.tail()
```

Out[8]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age

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

In [9]:

```
diabetes.shape
```

Out[9]:

```
(768, 9)
```

In [10]:

```
diabetes.info
```

Out[10]:

```
<bound method DataFrame.info of      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  

[768 rows x 9 columns]>
```

In [11]:

```
diabetes.describe()
```

Out[11]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	76
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

In [12]:

```
diabetes.columns
```

Out[12]:

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

In [13]:

```
diabetes.groupby('Outcome').mean()
```

Out[13]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigr
Outcome							
0	3.298000	109.980000	68.184000	19.664000	68.792000	30.304200	
1	4.865672	141.257463	70.824627	22.164179	100.335821	35.142537	

In [14]:

```
#Check if any null value is present
diabetes.isnull().values.any()
```

Out[14]:

```
False
```

In [15]:

```
diabetes.corr()
```

Out[15]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Dia
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.017683	
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.221071	
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.281805	
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.392573	
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.197859	
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.000000	
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.140647	
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.036242	
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.292695	

In [16]:

```
# separating  the data and labels
X = diabetes.drop(columns = 'Outcome',axis = 1)
Y = diabetes['Outcome']
```

In [17]:

```
print(X)
```

```
     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  
0                       0.627   50  
1                       0.351   31  
2                       0.672   32  
3                       0.167   21  
4                       2.288   33  
..                        ...  ...  
763                     0.171   63  
764                     0.340   27  
765                     0.245   30  
766                     0.349   47  
767                     0.315   23  

[768 rows x 8 columns]
```

In [18]:

```
print(Y)
```

```
0      1
1      0
2      1
3      0
4      1
      ..
763    0
764    0
765    0
766    1
767    0
Name: Outcome, Length: 768, dtype: int64
```

# Check the number of zeros value in dataset

In [19]:

```
print('No. of zero value in Glucose ',diabetes[diabetes ['Glucose']==0].shape[0])
```

```
No. of zero value in Glucose  5
```

In [20]:
```
print('No. of zero value in BloodPressure ',diabetes[diabetes ['BloodPressure']==0].sha
```

```
No. of zero value in BloodPressure  35
```

In [21]:
```
print('No. of zero value in SkinThickness ',diabetes[diabetes ['SkinThickness']==0].sha
```

```
No. of zero value in SkinThickness  227
```

In [22]:
```
print('No. of zero value in Insulin ',diabetes[diabetes ['Insulin']==0].shape[0])
```

```
No. of zero value in Insulin  374
```

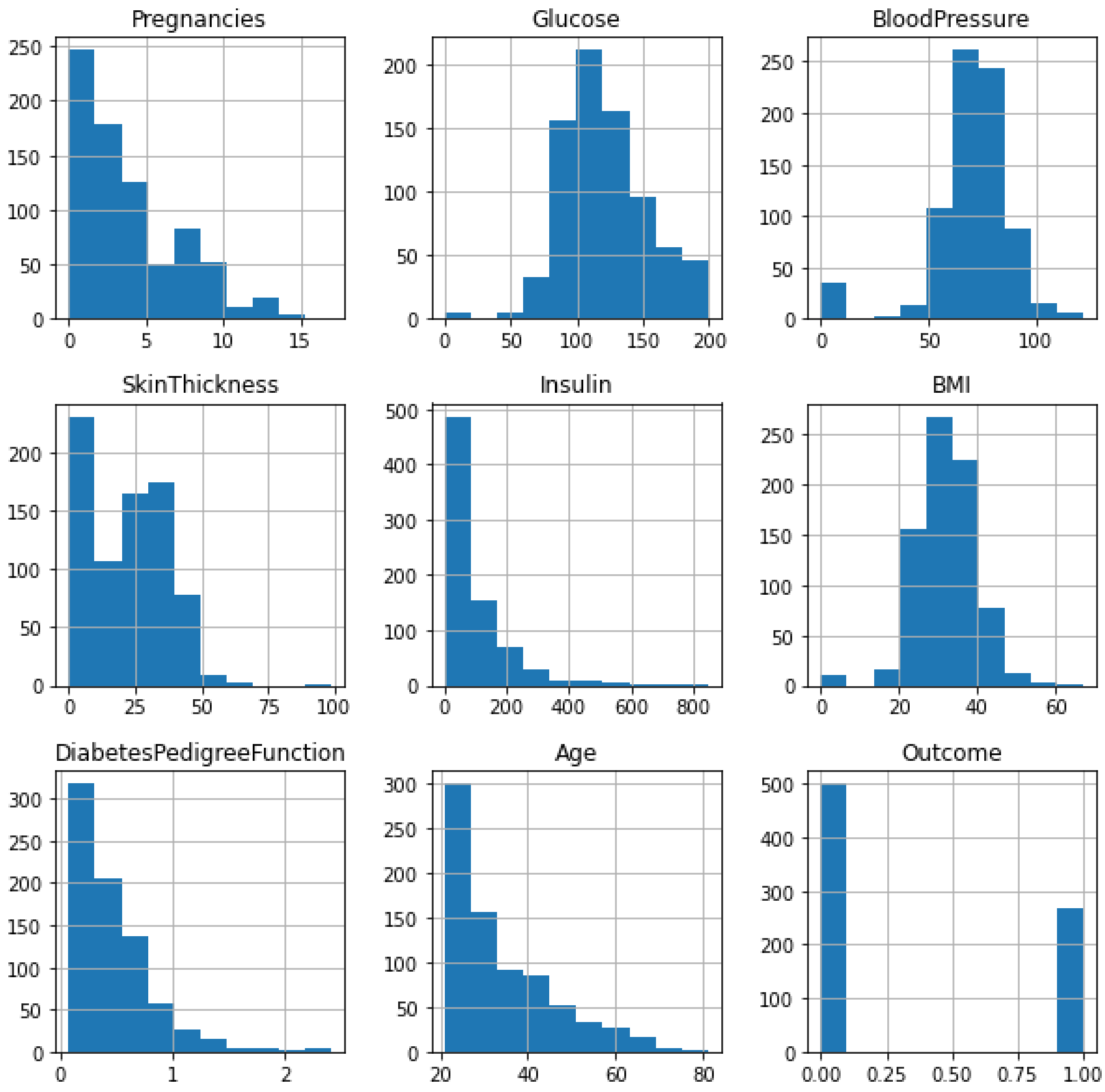
In [23]:
```
print('No. of zero value in BMI ',diabetes[diabetes ['BMI']==0].shape[0])
```

```
No. of zero value in BMI  11
```

# Data visualization

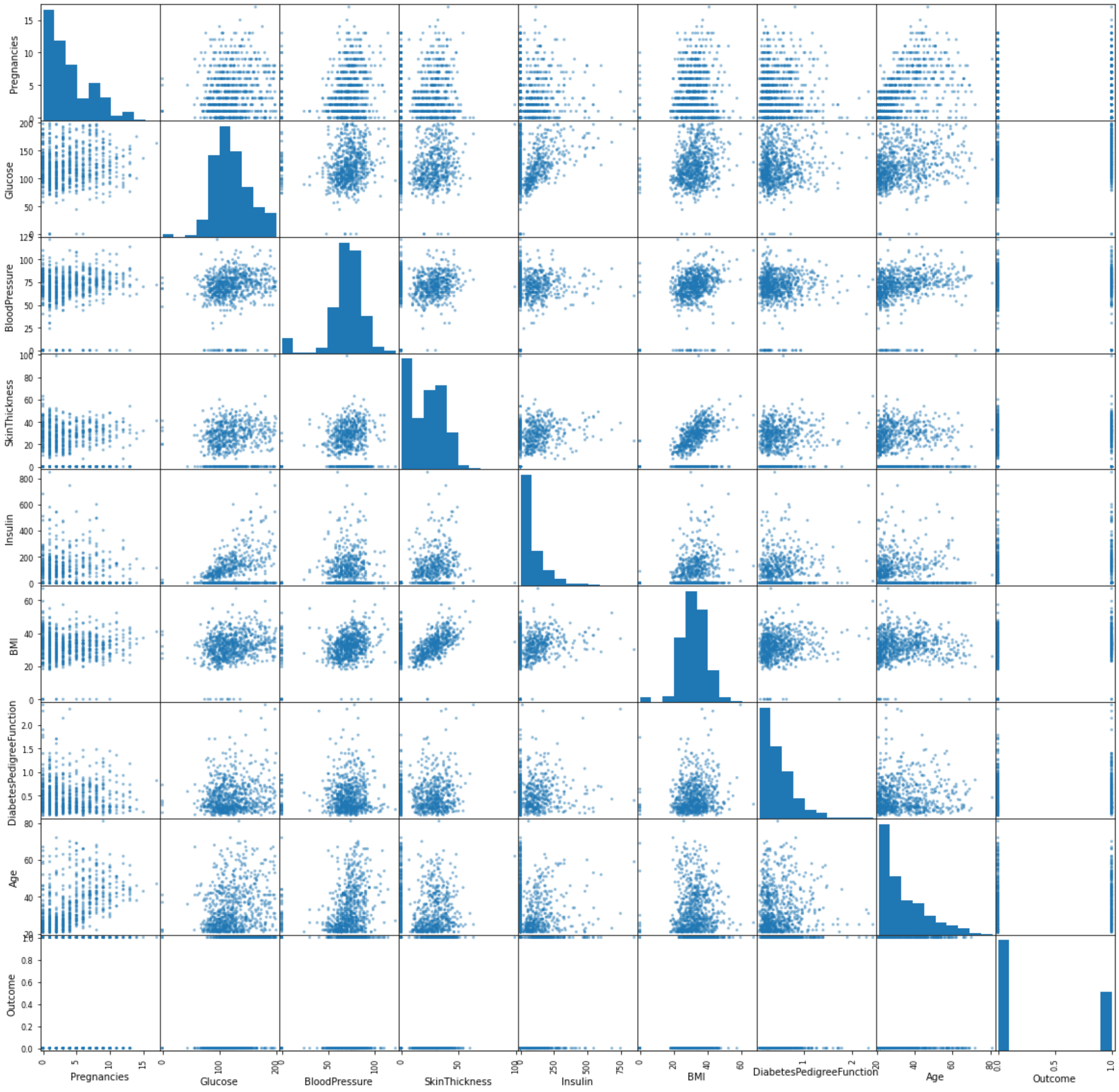
In [24]:
```
# histogram of each feature
diabetes.hist(bins=10,figsize=(10,10))
```

Out[24]:
```
array([[<AxesSubplot:title={'center':'Pregnancies'}>,
        <AxesSubplot:title={'center':'Glucose'}>,
        <AxesSubplot:title={'center':'BloodPressure'}>],
       [<AxesSubplot:title={'center':'SkinThickness'}>,
        <AxesSubplot:title={'center':'Insulin'}>,
        <AxesSubplot:title={'center':'BMI'}>],
       [<AxesSubplot:title={'center':'DiabetesPedigreeFunction'}>,
        <AxesSubplot:title={'center':'Age'}>,
        <AxesSubplot:title={'center':'Outcome'}>]], dtype=object)
```



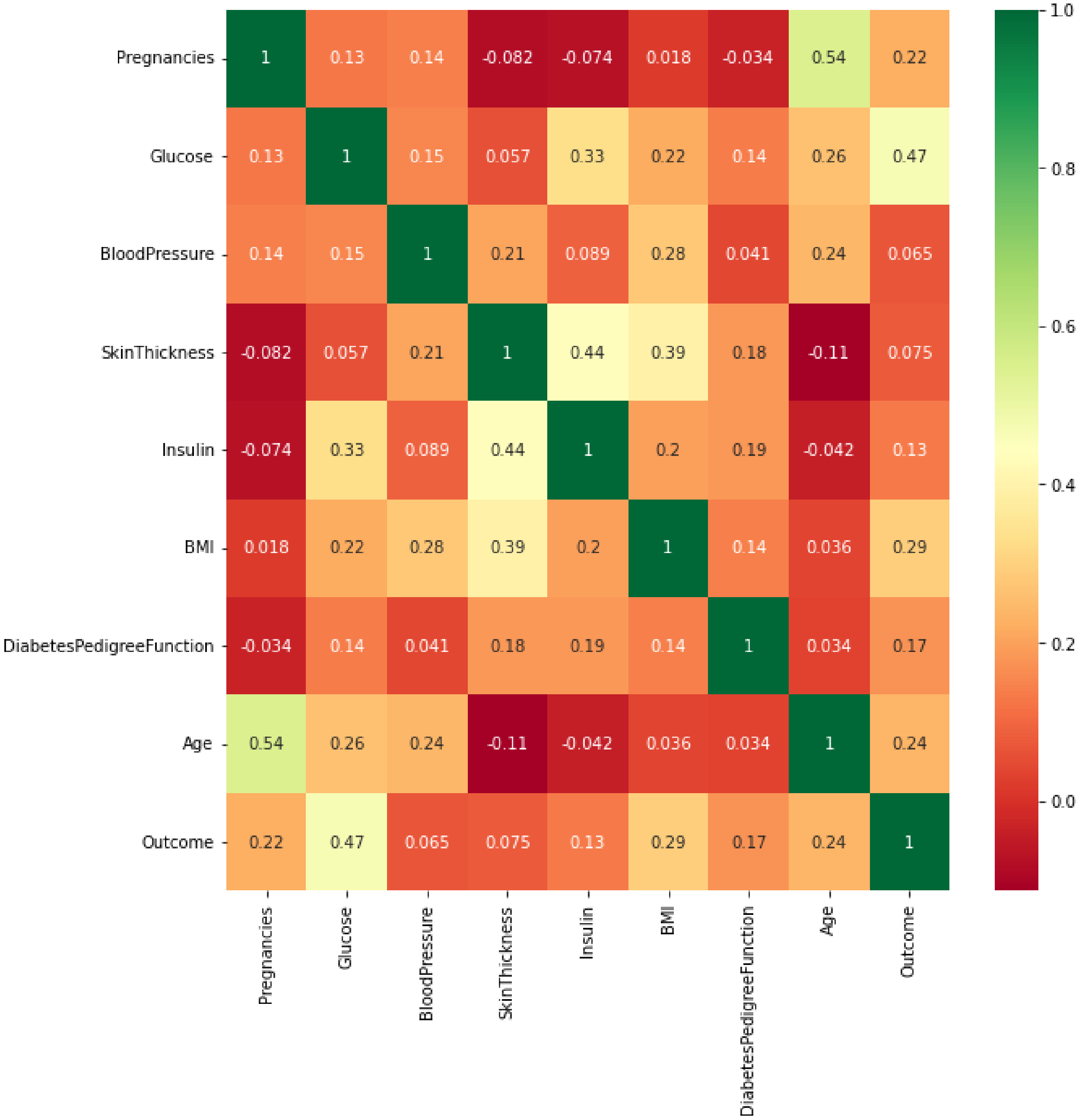
In [29]:

```
# scatter plot matrix
from pandas.plotting import scatter_matrix
scatter_matrix(diabetes,figsize = (20,20));
```



In [28]:

```python
# get correlation of each feature in dataset
corrmat= diabetes.corr()
top_corr_features = corrmat.index
plt.figure(figsize=(10,10))
#plot heat map
g=sns.heatmap(diabetes[top_corr_features].corr(),annot=True,cmap="RdYlGn")
```



In [30]:

```
target_name = 'Outcome'

#Separated object for target feature
y = diabetes[target_name]

#separated object for input features
x = diabetes.drop(target_name, axis=1)
```

In [31]:

```
x.head()
```

Out[31]:

```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  DiabetesPedigreeFunction  Age
0            6      148             72             35        0  33.6                     0.627   50
1            1       85             66             29        0  26.6                     0.351   31
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
2	8	183	64	0	0	23.3	0.672	32
3	1	89	66	23	94	28.1	0.167	21
4	0	137	40	35	168	43.1	2.288	33

In [32]:

```
y.head()
```

Out[32]:

```
0    1
1    0
2    1
3    0
4    1
Name: Outcome, dtype: int64
```

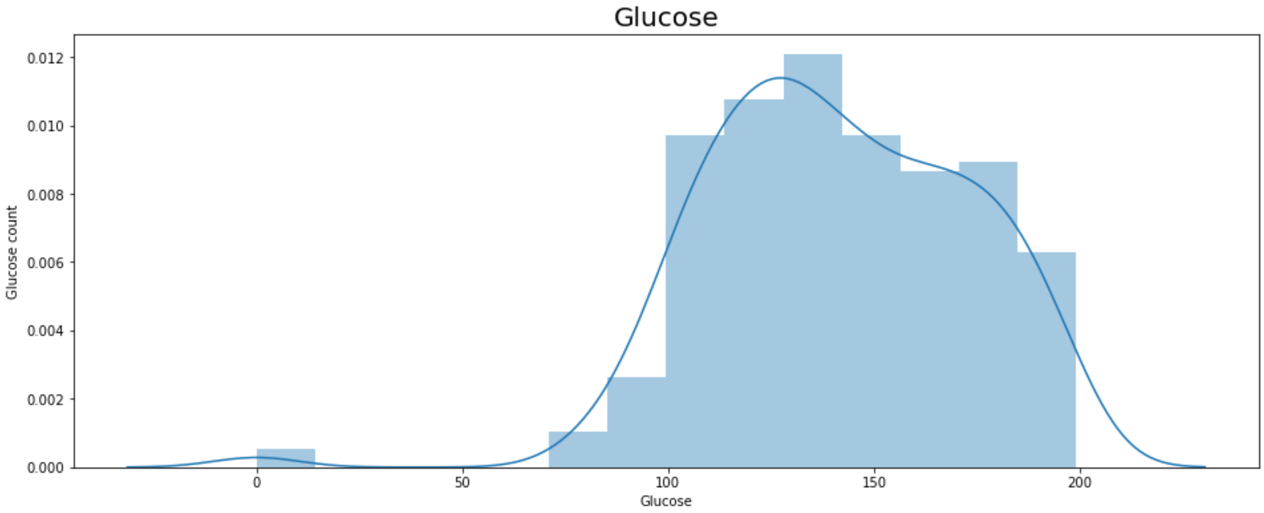
In [33]:

```
# glucose for diabetes
fig = plt.figure(figsize = (16,6))
sns.distplot(diabetes['Glucose'][diabetes['Outcome']==1])
plt.ylabel('Glucose count')
plt.title('Glucose',fontsize = 20)
```

```
C:\ProgramData\Anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please adap
t your code to use either `displot` (a figure-level function with similar flexibility) o
r `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[33]:

```
Text(0.5, 1.0, 'Glucose')
```



In [35]:

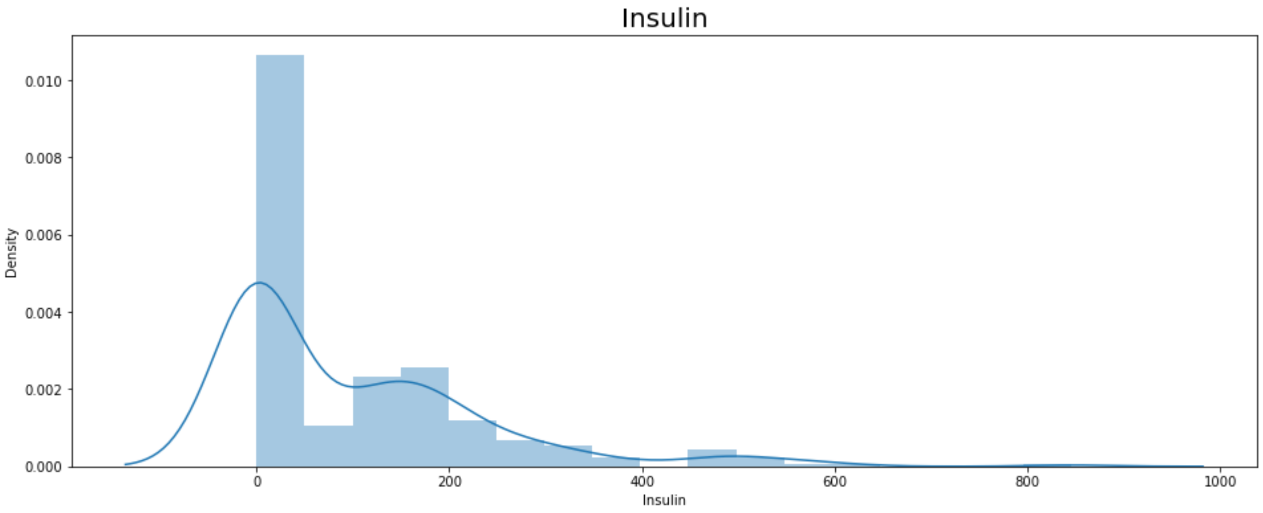
```
# Insuline for diabetes
fig = plt.figure(figsize = (16,6))
sns.distplot(diabetes["Insulin"][diabetes['Outcome']==1])
plt.xticks()
plt.title("Insulin",fontsize = 20)
```

```
C:\ProgramData\Anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please adap
t your code to use either `displot` (a figure-level function with similar flexibility) o
```

```
r `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[35]:

```
Text(0.5, 1.0, 'Insulin')
```



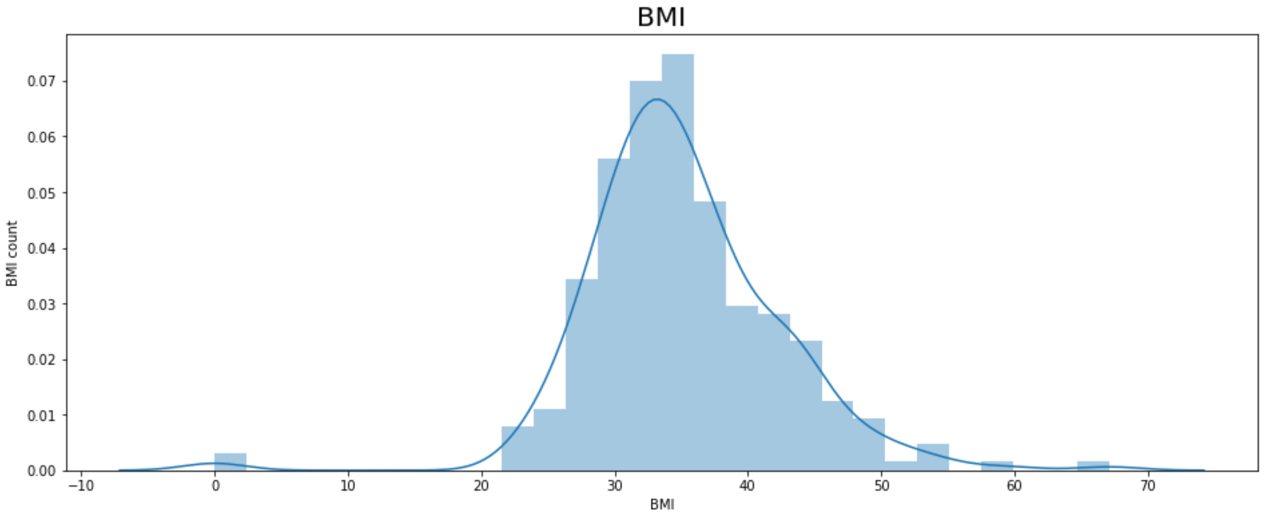
In [36]:

```
# BMI for diabetes
fig = plt.figure(figsize = (16,6))
sns.distplot(diabetes['BMI'][diabetes['Outcome']==1])
plt.ylabel('BMI count')
plt.title('BMI',fontsize = 20)
```

```
C:\ProgramData\Anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please adap
t your code to use either `displot` (a figure-level function with similar flexibility) o
r `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[36]:

```
Text(0.5, 1.0, 'BMI')
```



In [ ]: