In [1]:

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

In [2]:

```
da = pd.read_csv(r"C:\Users\LENOVO\Downloads\diabetes.csv")
```

Exploratory Data Analysis

In [3]:

```
da.head(15)
```

Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFur
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	
5	5	116	74	0	0	25.6	
6	3	78	50	32	88	31.0	
7	10	115	0	0	0	35.3	
8	2	197	70	45	543	30.5	
9	8	125	96	0	0	0.0	
10	4	110	92	0	0	37.6	
11	10	168	74	0	0	38.0	
12	10	139	80	0	0	27.1	
13	1	189	60	23	846	30.1	
14	5	166	72	19	175	25.8	

In [4]:

```
da.tail()
```

Out[4]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFu
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	

In [5]:

```
da.describe().T
```

Out[5]:

	count	mean	std	min	25%	50%	
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.0
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.2
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.0
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.0
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.2
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.6
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.6
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.0
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.0

In [6]:

```
nullcount = print(da.isnull().sum())
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [7]:

```
BP = da["BloodPressure"].mean()
ST = da["SkinThickness"].mean()
BMIM = da["BMI"].mean()

da['BloodPressure'] = da['BloodPressure'].replace(0, BP)
da['SkinThickness'] = da['SkinThickness'].replace(0, ST)
da['BMI'] = da['BMI'].replace(0, BMIM)
```

```
da.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    float64
 3   SkinThickness             768 non-null    float64
 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(4), int64(5)
memory usage: 54.1 KB
```

In [8]:
```
da['Outcome'].value_counts()
```

Out[8]:
```
0    500
1    268
Name: Outcome, dtype: int64
```

In [9]:
```
# The distribution of the Outcome variable
da["Outcome"].value_counts()*100/len(da)
```

Out[9]:
```
0    65.104167
1    34.895833
Name: Outcome, dtype: float64
```

In [10]:
```
da.groupby("Outcome").agg({"Pregnancies":"mean"})
```

Out[10]:

	Pregnancies
Outcome	
0	3.298000
1	4.865672

In [11]:
```
da.groupby("Outcome").agg({"Age":"max"})
```

Out[11]:

	Age
Outcome	
0	81
1	70

In [12]:
```
da.groupby("Outcome").agg({"Insulin": "mean"})
```

Out[12]:

	Insulin
Outcome	
0	68.792000
1	100.335821

In [13]:
```
da.groupby("Outcome").agg({"Insulin": "max"})
```

Out[13]:

	Insulin
Outcome	
0	744
1	846

In [14]:
```
da.groupby("Outcome").agg({"Glucose": "mean"})
```

Out[14]:

	Glucose
Outcome	
0	109.980000
1	141.257463

In [15]:
```
da.groupby("Outcome").agg({"Glucose": "max"})
```

Out[15]:

	Glucose
Outcome	
0	197
1	199

In [16]:
```
da.groupby("Outcome").agg({"BMI": "mean"})
```

Out[16]:

	BMI
Outcome	
0	30.880066
1	35.381288

Data Preprocessing

checking duplicate values in dataset

In [17]:

```
da.duplicated().sum()
```

Out[17]:

```
0
```

In [18]:

```
# there is no duplicate values in this dataset
```

In [19]:

```
# checking null values in dataset
da.isna().sum()
# there is no null values in this dataset
```

Out[19]:

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [20]:

```
(da[da.columns] == 0).sum()
```

Out[20]:

```
Pregnancies                 111
Glucose                       5
BloodPressure                 0
SkinThickness                 0
Insulin                     374
BMI                           0
DiabetesPedigreeFunction      0
Age                           0
Outcome                     500
dtype: int64
```

In [21]:

```
# Replacing 0 values with mean

for i in ["Glucose","BMI","Insulin","BloodPressure"]:
    da[i].replace({0:da[i].mean()},inplace = True)
```

In [22]:

```
# checking again for 0 values

(da[da.columns] == 0).sum()
```

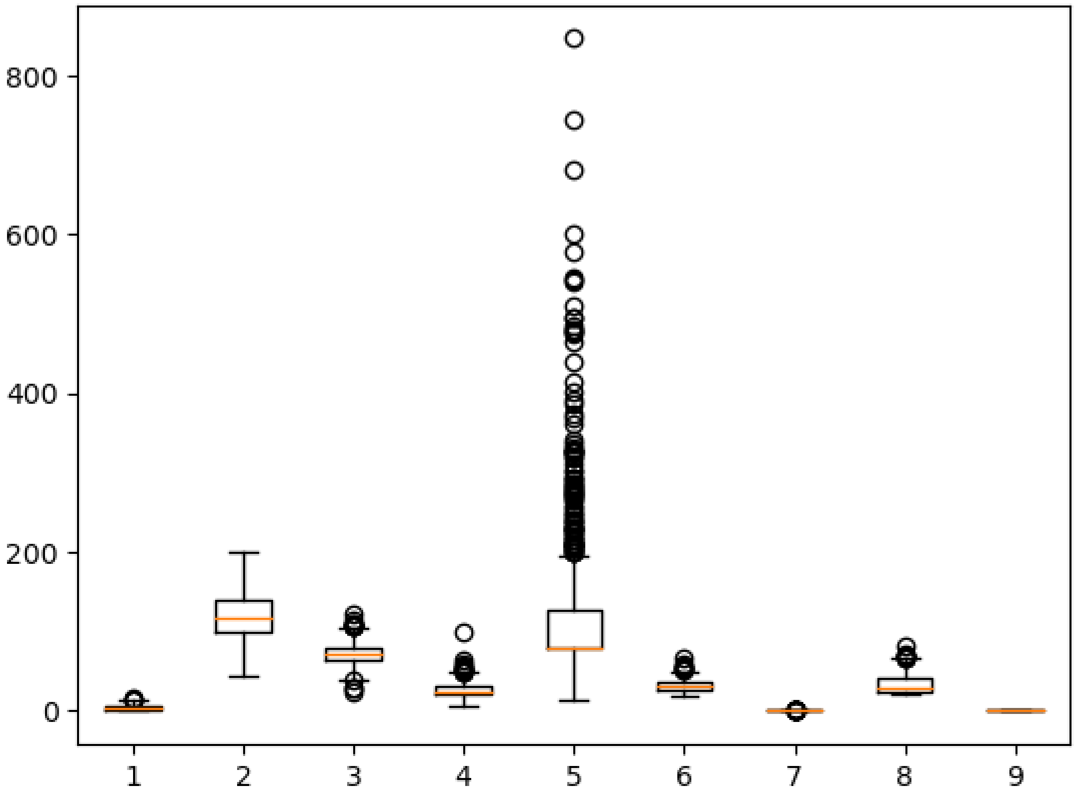
Out[22]:

```
Pregnancies                 111
Glucose                       0
BloodPressure                 0
SkinThickness                 0
Insulin                       0
BMI                           0
DiabetesPedigreeFunction      0
Age                           0
Outcome                     500
dtype: int64
```

Outlier Observation Analysis

In [23]:

```
# checking outliers in variables
plt.boxplot(da);
```



In [24]:

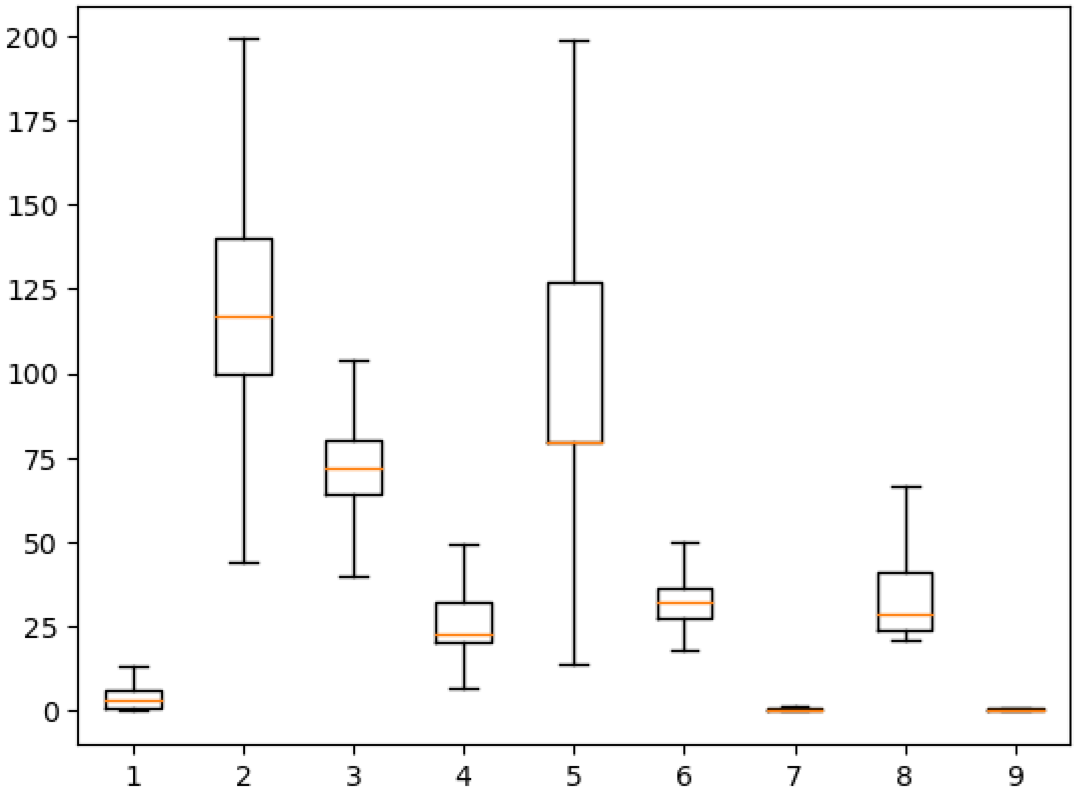
```
def outlier_treatment():
    l = ["BMI","Glucose","SkinThickness","Age","BloodPressure","Insulin","Pregnanci
    for i in l:
        x = np.quantile(da[i],[0.25,0.75])
        iqr = x[1]-x[0]
        uw = x[1]+1.5*iqr
        lw = x[0]-1.5*iqr
        da[i]  = np.where(da[i]>uw,uw,(np.where(da[i]<lw,lw,da[i])))

outlier_treatment()
```

In [25]:

```
#boxplot after treating outliers


plt.boxplot(da);
```

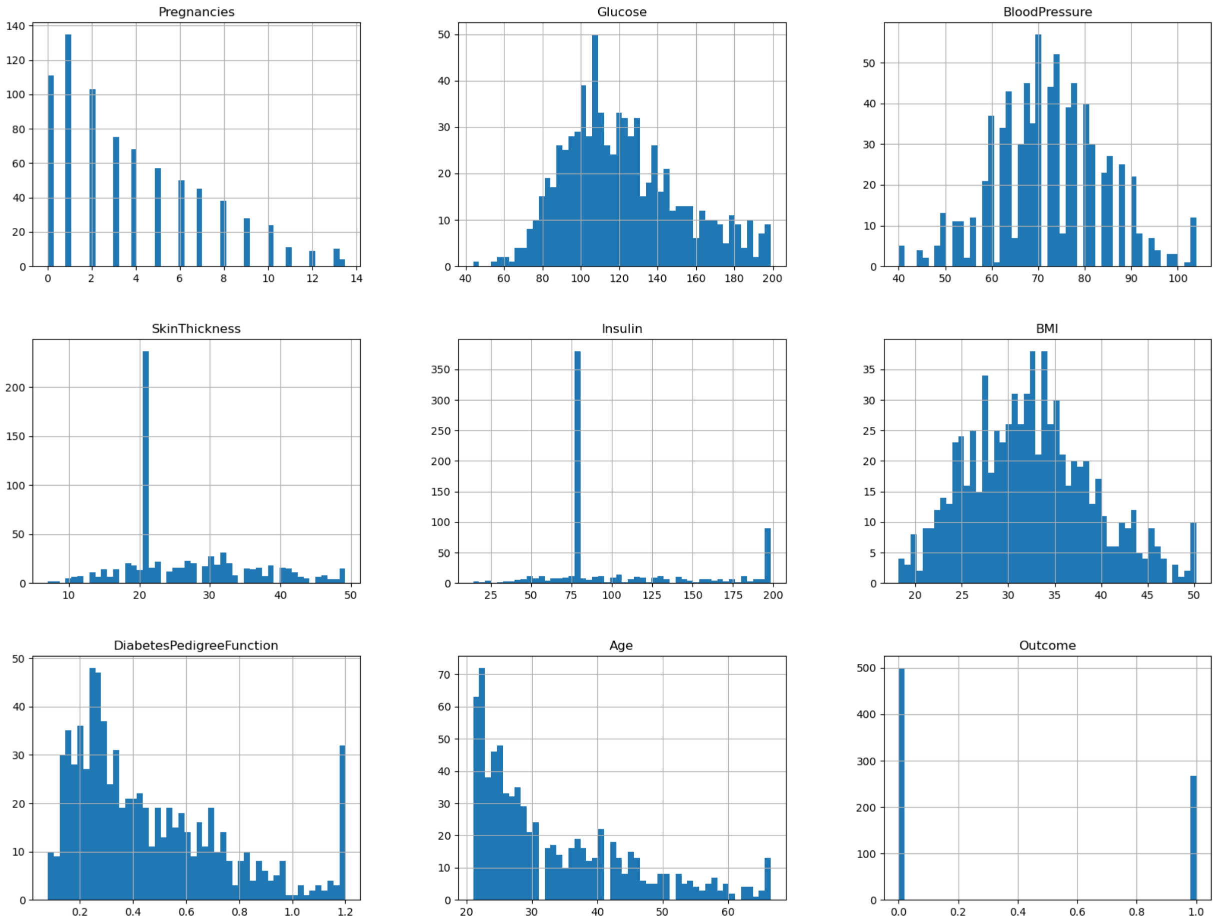


Visualization of dataset

```
        Data distribution of variables
```

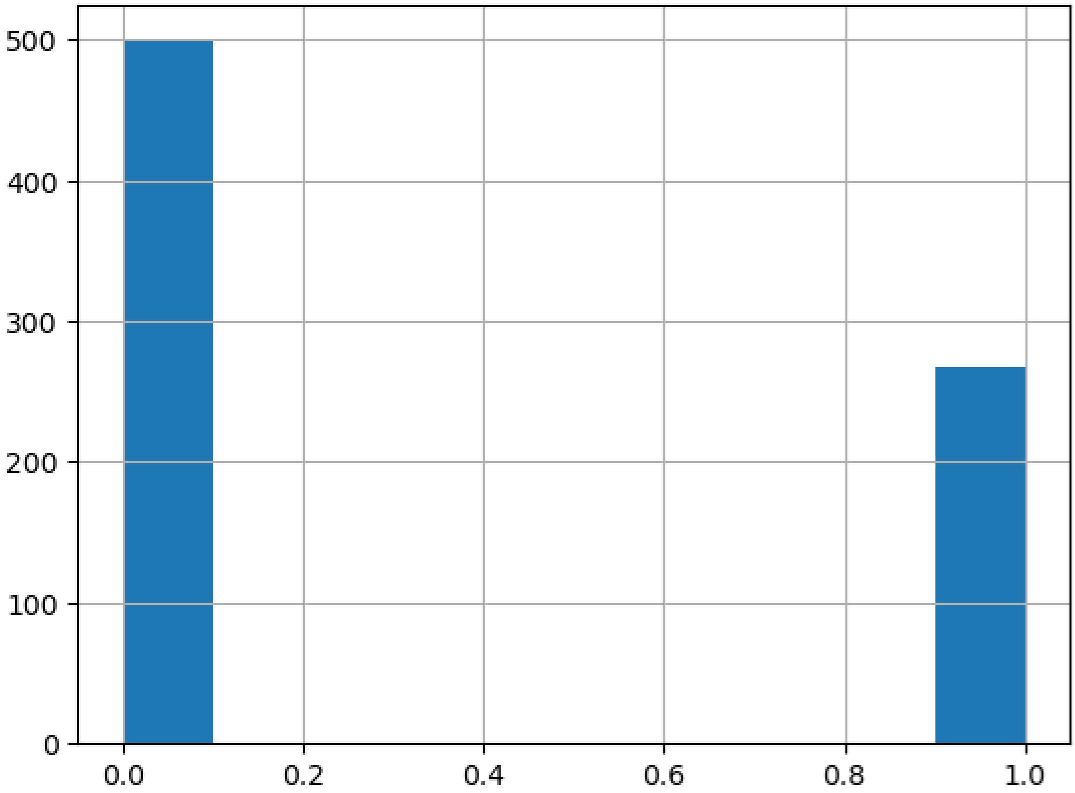
In [26]:

```
da.hist(bins=50, figsize=(20,15));
```

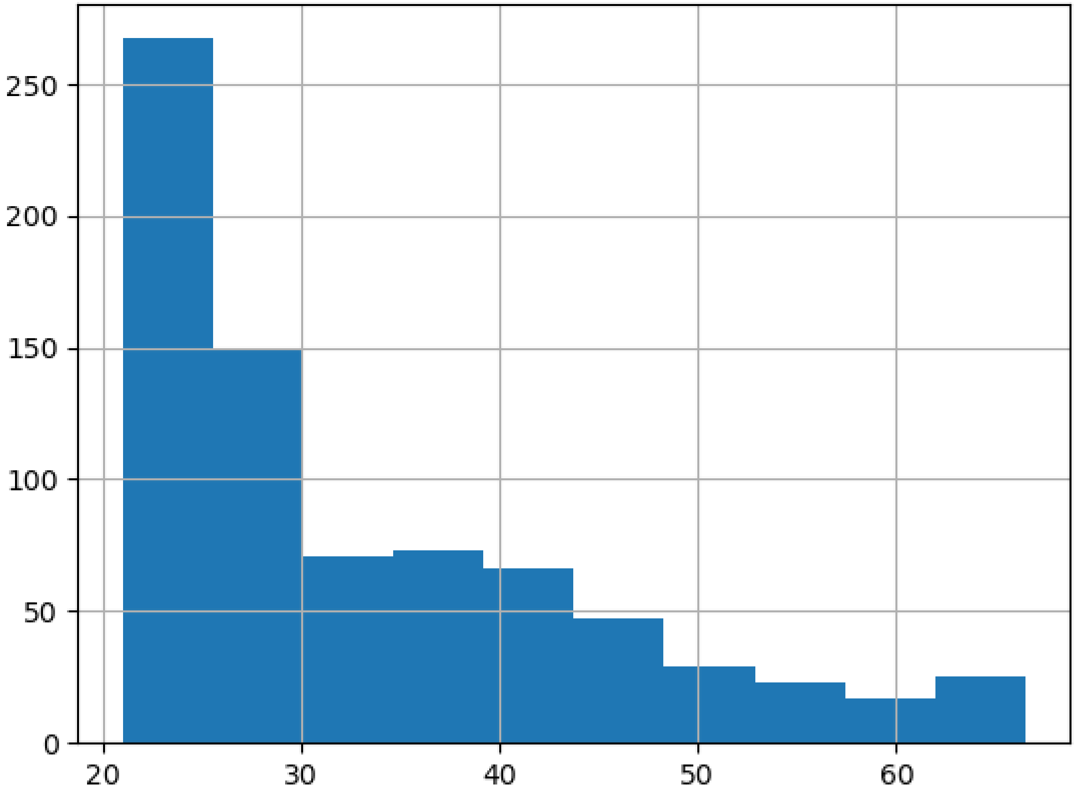


Data distribution of Output variable

```
In [27]: da['Outcome'].hist();
```

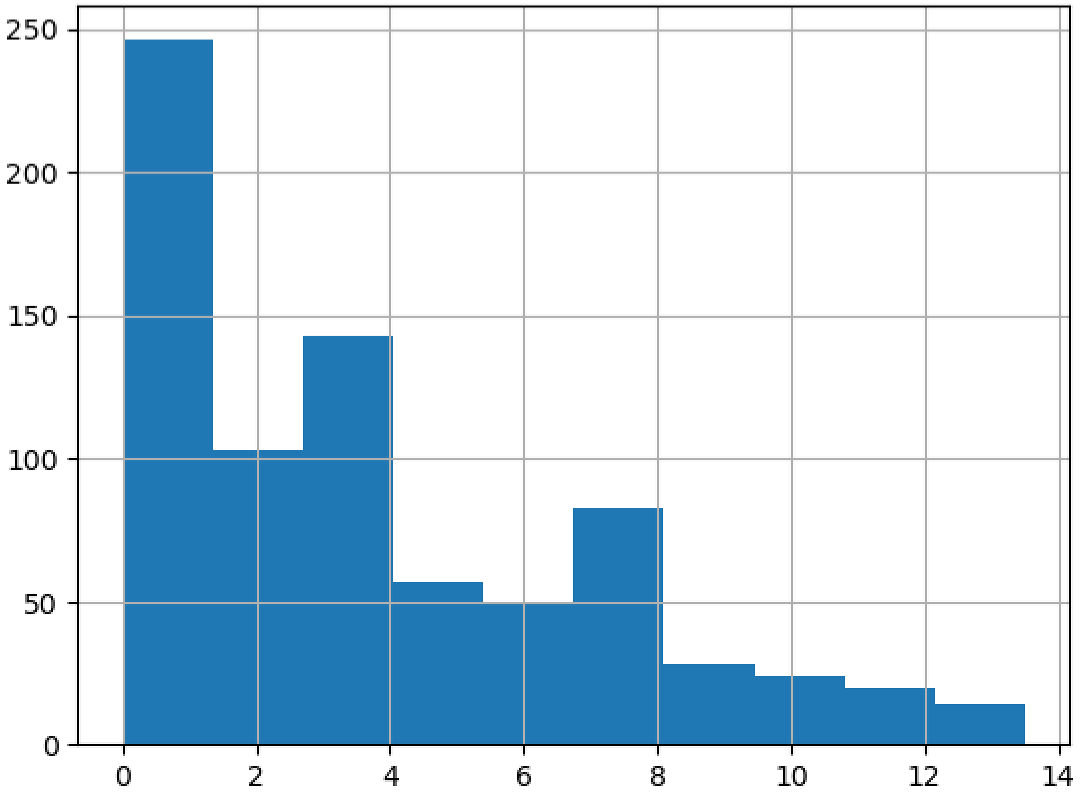


```
In [28]: # Data distribution of Age variable
         da['Age'].hist();
```



```
In [29]: # Data distribution of Pregnancies variable
```

```
da['Pregnancies'].hist();
```



In [30]:

```
#Checking correlation between variables
da.corr()
```

Out[30]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin
Pregnancies	1.000000	0.126606	0.211257	0.020722	-0.007679
Glucose	0.126606	1.000000	0.220946	0.149026	0.394778
BloodPressure	0.211257	0.220946	1.000000	0.145294	0.017952
SkinThickness	0.020722	0.149026	0.145294	1.000000	0.303747
Insulin	-0.007679	0.394778	0.017952	0.303747	1.000000
BMI	0.027144	0.234041	0.286508	0.548198	0.225814
DiabetesPedigreeFunction	-0.017398	0.118236	0.015067	0.134284	0.180001
Age	0.549695	0.268602	0.334903	0.013831	0.038798
Outcome	0.220392	0.492908	0.166131	0.173868	0.208749

In [31]:

```
da.corr()['Outcome'].sort_values(ascending=False)
```

Out[31]:

```
Outcome                     1.000000
Glucose                     0.492908
BMI                         0.313035
Age                         0.242702
Pregnancies                 0.220392
Insulin                     0.208749
DiabetesPedigreeFunction    0.184969
SkinThickness               0.173868
BloodPressure               0.166131
Name: Outcome, dtype: float64
```

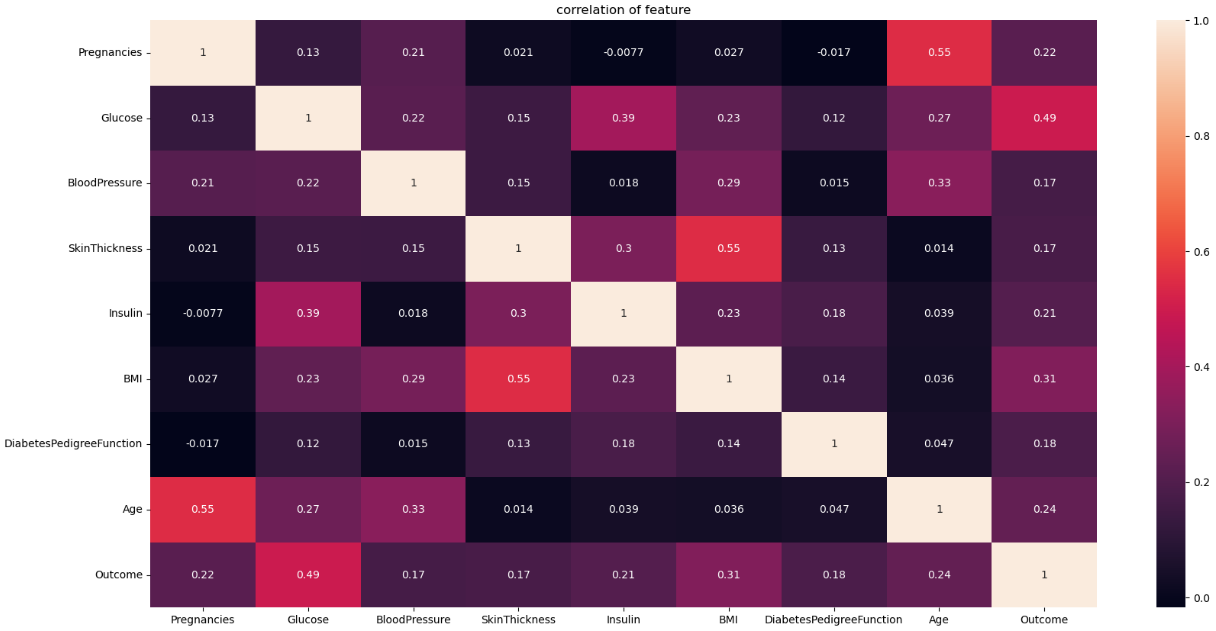
In [32]:

```
# Heatmap of correlation

plt.figure(figsize = (20,10))
sns.heatmap(da.corr(), annot=True)
plt.title("correlation of feature")
```

Out[32]:

```
Text(0.5, 1.0, 'correlation of feature')
```



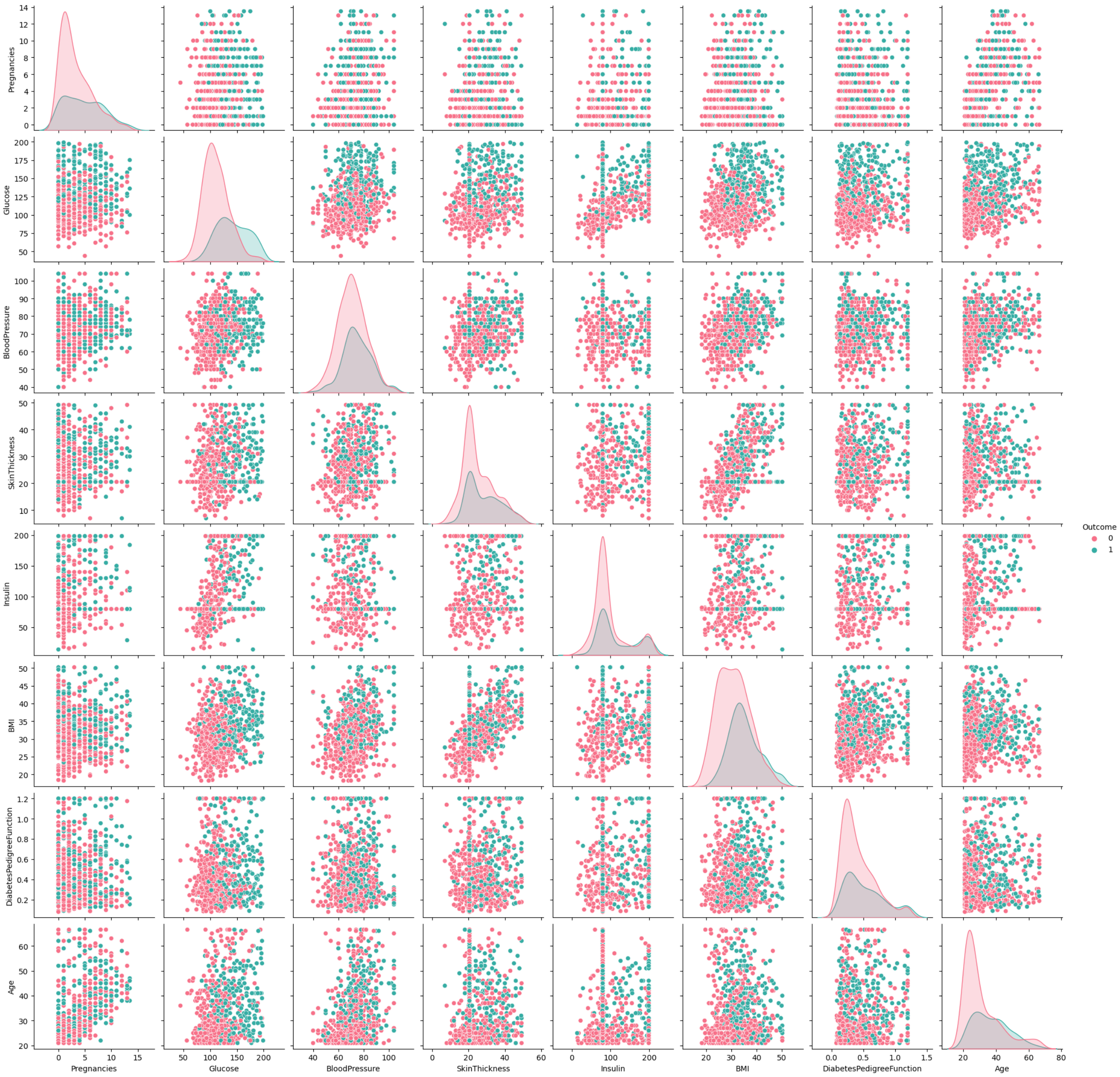
In [33]:

```
# Pairplot of dataset - variables relation with Outcome

sns.pairplot(da, hue='Outcome', palette="husl")
```

Out[33]:

```
<seaborn.axisgrid.PairGrid at 0x26c5721a250>
```



Result:

1. high Glucose level in pregnancy increase the risk of diabetes.
2. BMI Above 30 and high level of Glucose togather increase the risk of diabetes.
3. We can see here that increasing Glucose level is the key factor which increase the risk of diabetes.
4. High Glucose level along with other variables increase the risk of diabetes.

In [ ]:

```
# Histplot of dataset - variables relation with Outcome

pno = 1
plt.figure(figsize=(18,20))
for i in da.columns:
        if pno<9:
            plt.subplot(3,3,pno)
            ax = sns.histplot(data = da , x = i , hue = da.Outcome , kde = True);
            plt.xlabel(i)
            pno+=1
            for i in ax.containers:     #to set a label on top of the bars.
                ax.bar_label(i,)
```

Result:

1. When the number of pregnancies increases the risk of diabetes also increase.
2. When the level of Glucose increase above 140 the risk of diabetes also increase.
3. Blood pressure between 60 to 90 have more diabetic people then other rate.
4. Risk of diabetes increase when skin thickness increase.
5. Insulin level affect diabetes when its level increase the risk of diabetes also increase.
6. When BMI increase above 30 the risk of diabetes also increase.
7. Risk of diabetes increase when age increase.

Output variable distribution

In [ ]:

```
sns.countplot(x ='Outcome', data = da);
```

In [ ]:

```
plt.title('Outcome')
plt.pie(da['Outcome'].value_counts(),labels=['No','Yes'], autopct='%1.2f%%')
plt.show()
```

In [ ]:

```
```