In [1]:
```
########
# Student ID: 10724837
# In this notebook, I carry out some basic observation of the data, as well
# before moving over to R to develop the regression models.
########
```

In [2]:
```
# import packages we will be using
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from scipy import stats
```

In [3]:
```
# load the data and observe basic info
diabetes = pd.read_csv("PimaDiabetes.csv")
diabetes.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 750 entries, 0 to 749
Data columns (total 9 columns):
 #   Column            Non-Null Count  Dtype  
---  ------            --------------  -----  
 0   Pregnancies       750 non-null    int64  
 1   Glucose           750 non-null    int64  
 2   BloodPressure     750 non-null    int64  
 3   SkinThickness     750 non-null    int64  
 4   Insulin           750 non-null    int64  
 5   BMI               750 non-null    float64
 6   DiabetesPedigree  750 non-null    float64
 7   Age               750 non-null    int64  
 8   Outcome           750 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 52.9 KB
```

In [4]:
```
# check for null values
diabetes.isna().sum(axis = 0)
```

Out[4]:
```
Pregnancies         0
Glucose             0
BloodPressure       0
SkinThickness       0
Insulin             0
BMI                 0
DiabetesPedigree    0
Age                 0
Outcome             0
dtype: int64
```

In [5]:
```
# there are no null values!
```

In [6]:
```
# calculate some key summary statistics, mainly interested in the min and mo
diabetes.describe()
```

Out[6]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Diab
count	750.000000	750.000000	750.000000	750.000000	750.000000	750.000000	
mean	3.844000	120.737333	68.982667	20.489333	80.378667	31.959067	
std	3.370085	32.019671	19.508814	15.918828	115.019198	7.927399	
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	36.500000	32.000000	
75%	6.000000	140.750000	80.000000	32.000000	129.750000	36.575000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

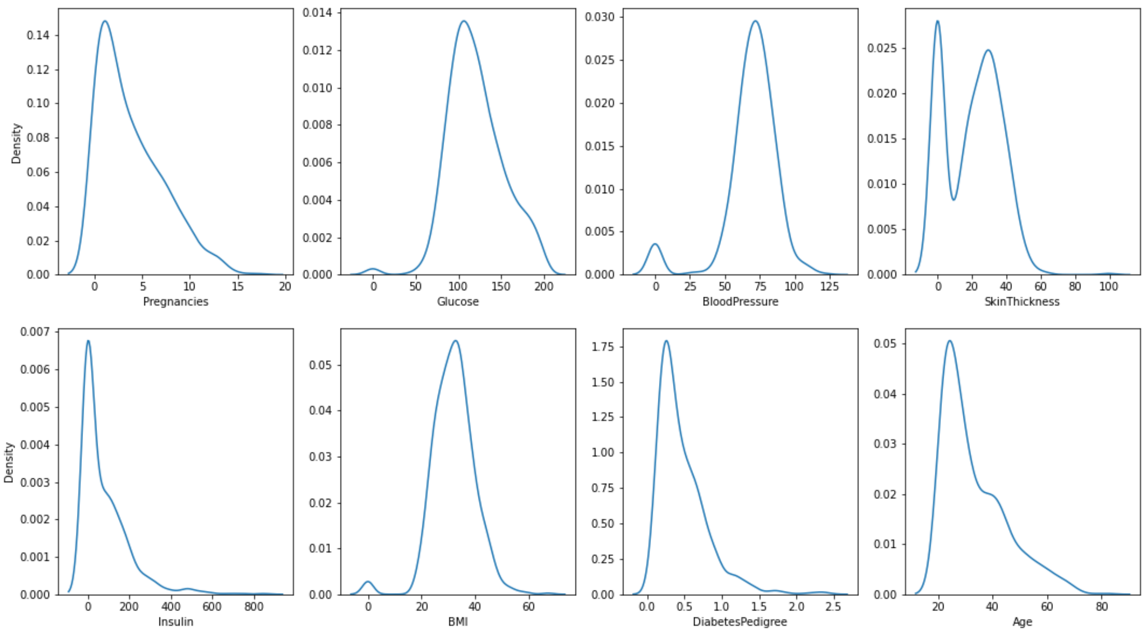
In [7]:
```
# there are no negative min values, a good sign
# there are some very large max values, such as 846 in the Insulin columns
# we will deal with such outliers later
```

In [8]:
```
# check the number of zero values in each column
diabetes.isin([0]).sum(axis = 0)
```

Out[8]:
```
Pregnancies          109
Glucose                5
BloodPressure         35
SkinThickness        221
Insulin              362
BMI                   11
DiabetesPedigree       0
Age                    0
Outcome              490
dtype: int64
```

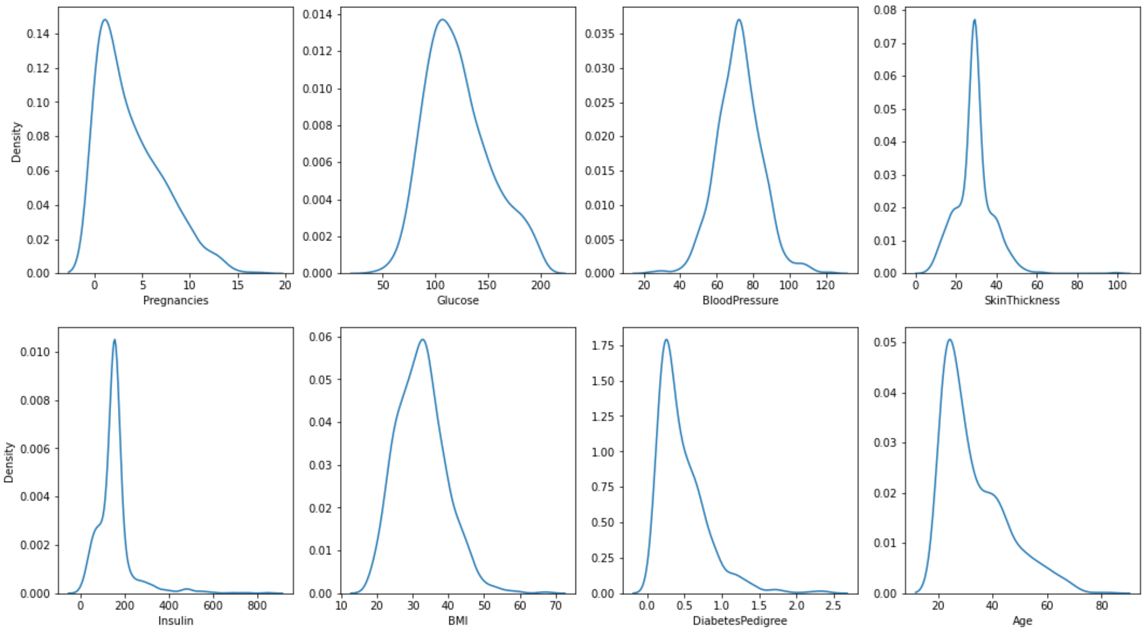
In [9]:
```
# there are lots of zeroes in columns where it doesn't make sense
# for example, you definitely cannot have a SkinThickness or BMI of 0
# the columns which have zeroes when they should not are: Glucose, BloodPres
# this is a problem with the data and we need to look at how these 0s are di
```

In [10]:
```python
# plot the distributions of each column
plt.figure(figsize = (18,10),facecolor=(1, 1, 1))

plt.subplot(2,4,1)
sns.kdeplot(data = diabetes['Pregnancies'])

plt.subplot(2,4,2)
sns.kdeplot(data = diabetes['Glucose'])
plt.ylabel("")

plt.subplot(2,4,3)
sns.kdeplot(data = diabetes['BloodPressure'])
plt.ylabel("")

plt.subplot(2,4,4)
sns.kdeplot(data = diabetes['SkinThickness'])
plt.ylabel("")

plt.subplot(2,4,5)
sns.kdeplot(data = diabetes['Insulin'])

plt.subplot(2,4,6)
sns.kdeplot(data = diabetes['BMI'])
plt.ylabel("")

plt.subplot(2,4,7)
sns.kdeplot(data = diabetes['DiabetesPedigree'])
plt.ylabel("")

plt.subplot(2,4,8)
sns.kdeplot(data = diabetes['Age'])
plt.ylabel("")

plt.savefig(fname = "diabetesfig1")
```



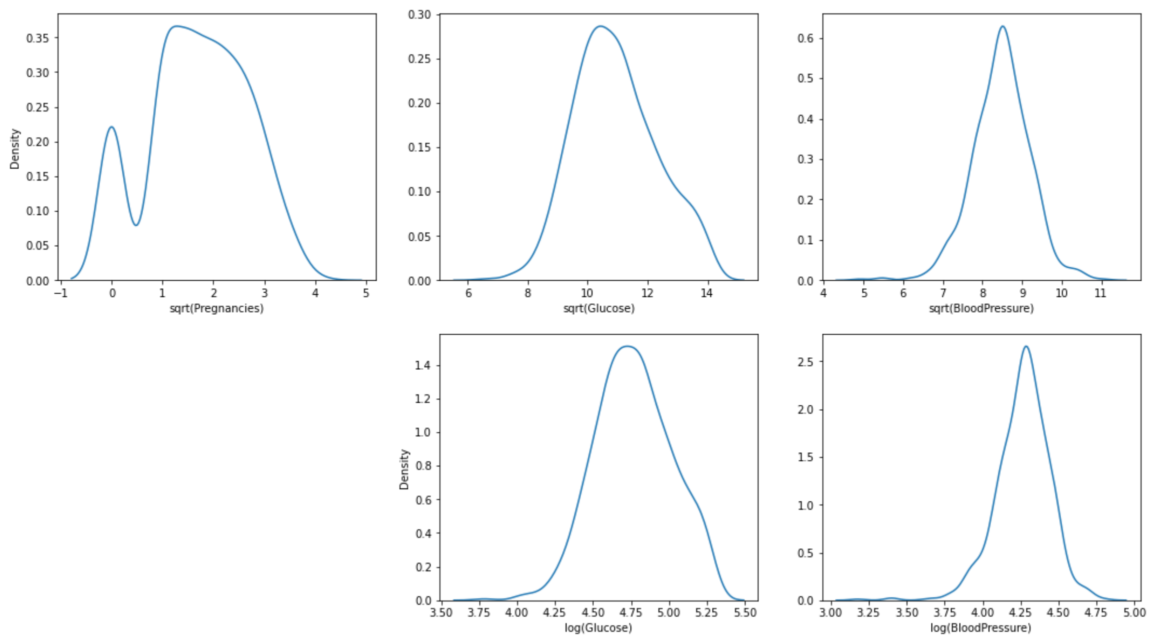
In [11]:
```
# ignoring the zero values, these columns resemble normal distributions
# use mean value imputation to replace all zero values
# apply the mean value imputations
meanImputationColumns = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insul
for column in meanImputationColumns:
    mean = diabetes[diabetes[column] != 0][column].mean()
    diabetes[column] = diabetes[column].replace(0, mean)
```

In [12]:
```
# observe the distributions now that we have imputed zero values
plt.figure(figsize = (18,10),facecolor=(1, 1, 1))

plt.subplot(2,4,1)
sns.kdeplot(data = diabetes['Pregnancies'])

plt.subplot(2,4,2)
sns.kdeplot(data = diabetes['Glucose'])
plt.ylabel("")

plt.subplot(2,4,3)
sns.kdeplot(data = diabetes['BloodPressure'])
plt.ylabel("")

plt.subplot(2,4,4)
sns.kdeplot(data = diabetes['SkinThickness'])
plt.ylabel("")

plt.subplot(2,4,5)
sns.kdeplot(data = diabetes['Insulin'])

plt.subplot(2,4,6)
sns.kdeplot(data = diabetes['BMI'])
plt.ylabel("")

plt.subplot(2,4,7)
sns.kdeplot(data = diabetes['DiabetesPedigree'])
plt.ylabel("")

plt.subplot(2,4,8)
sns.kdeplot(data = diabetes['Age'])
plt.ylabel("")

plt.savefig(fname = "diabetesfig2")
```



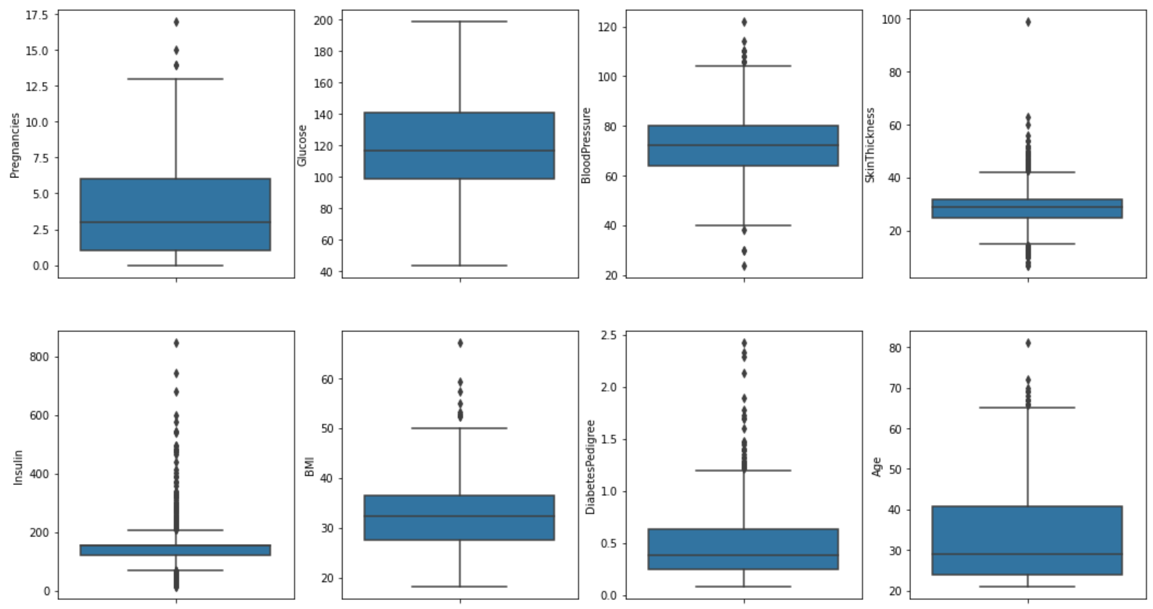
In [13]:
```
# some of the distributions are right-skewed, particularly Pregnancies, Diab
# to fix this, we can use either log or square root transformations
# since Pregnancies has zero values, log transform will not work
# as for DiabetesPedigree and Age, we can try both log and square root trans
```

In [14]:
```
# plot the square root transforms of all three columns
plt.figure(figsize = (18,10),facecolor=(1, 1, 1))

plt.subplot(2,3,1)
sns.kdeplot(data = np.sqrt(diabetes['Pregnancies']))
plt.xlabel("sqrt(Pregnancies)")

plt.subplot(2,3,2)
sns.kdeplot(data = np.sqrt(diabetes['Glucose']))
plt.xlabel("sqrt(Glucose)")
plt.ylabel("")

plt.subplot(2,3,3)
sns.kdeplot(data = np.sqrt(diabetes['BloodPressure']))
plt.xlabel("sqrt(BloodPressure)")
plt.ylabel("")


# plot the log transforms of Glucose and BloodPressure
plt.subplot(2,3,5)
sns.kdeplot(data = np.log(diabetes['Glucose']))
plt.xlabel("log(Glucose)")

plt.subplot(2,3,6)
sns.kdeplot(data = np.log(diabetes['BloodPressure']))
plt.xlabel("log(BloodPressure)")
plt.ylabel("")


plt.savefig(fname = "diabetesfig3")
```



In [15]:
```python
# the square root transform made Pregnancies bimodal, so leave Pregnancies w
# both sqrt and log transforms worked well on Glucose and BloodPressure
# so consider using log(Glucose) and log(BloodPressure) in our later models
```

In [16]:
```python
# we move onto dealing with outliers
# plot boxplots to see how outliers are distributed visually
plt.figure(figsize = (18,10),facecolor=(1, 1, 1))

plt.subplot(2,4,1)
sns.boxplot(y = diabetes['Pregnancies'])

plt.subplot(2,4,2)
sns.boxplot(y = diabetes['Glucose'])

plt.subplot(2,4,3)
sns.boxplot(y = diabetes['BloodPressure'])

plt.subplot(2,4,4)
sns.boxplot(y = diabetes['SkinThickness'])

plt.subplot(2,4,5)
sns.boxplot(y = diabetes['Insulin'])

plt.subplot(2,4,6)
sns.boxplot(y = diabetes['BMI'])

plt.subplot(2,4,7)
sns.boxplot(y = diabetes['DiabetesPedigree'])

plt.subplot(2,4,8)
sns.boxplot(y = diabetes['Age'])

# save the figure
plt.savefig(fname = "diabetesfig4")
```



In [17]:
```
# z-score or IQR methods would be more methodical to remove outliers, but sc
# and some have barely any
# we do not want to remove too much data, so remove outliers by observation

# remove Pregnancies above 13
# define the condition for removal
condition = diabetes['Pregnancies'] > 13
# remove the entries where this is true
diabetes = diabetes[~condition]

# remove the obvious outlier for SkinThickness
condition = diabetes['SkinThickness'] > 80
diabetes = diabetes[~condition]

# remove Insulin above 620
condition = diabetes['Insulin'] > 620
diabetes = diabetes[~condition]

# remove the top outlier for BMI
condition = diabetes['BMI'] > 65
diabetes = diabetes[~condition]

# remove the top outlier for Age
condition = diabetes['Age'] > 80
diabetes = diabetes[~condition]

diabetes.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 740 entries, 0 to 749
Data columns (total 9 columns):
 #   Column            Non-Null Count  Dtype  
---  ------            --------------  -----  
 0   Pregnancies       740 non-null    int64  
 1   Glucose           740 non-null    float64
 2   BloodPressure     740 non-null    float64
 3   SkinThickness     740 non-null    float64
 4   Insulin           740 non-null    float64
 5   BMI               740 non-null    float64
 6   DiabetesPedigree  740 non-null    float64
 7   Age               740 non-null    int64  
 8   Outcome           740 non-null    int64  
dtypes: float64(6), int64(3)
memory usage: 57.8 KB
```

In [18]:
```
# we have removed only 10 entries in total, a small amount, but it will impr
```

In [19]:
```python
# calculate the covariance matrix
diabetes.cov()
```

Out[19]:

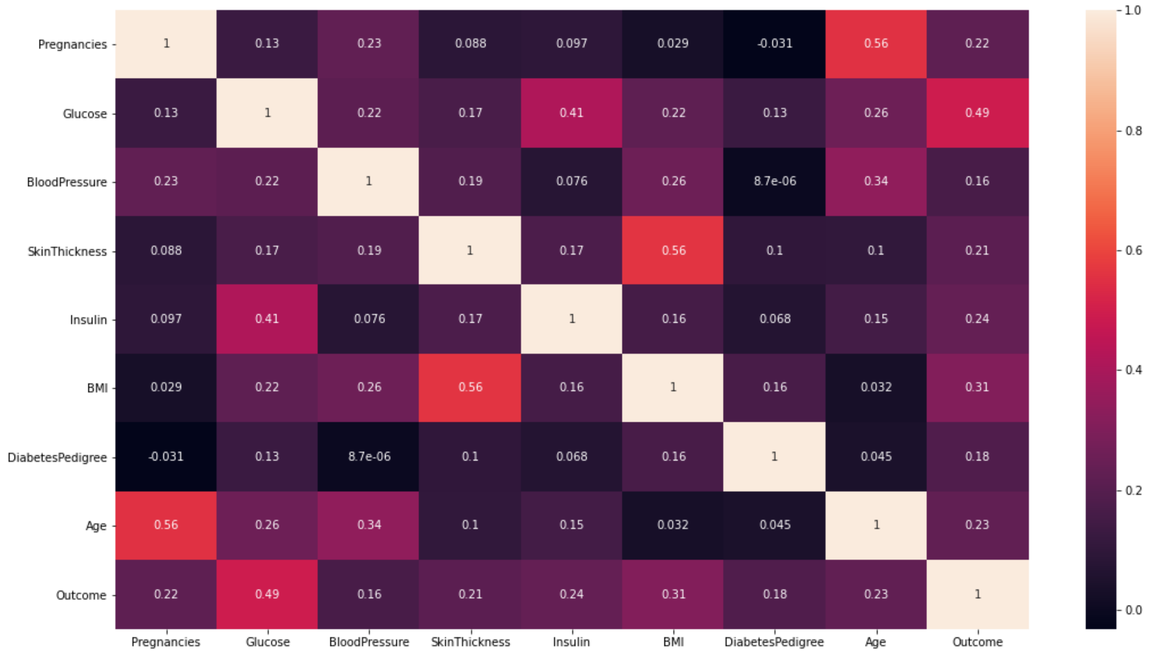
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	
Pregnancies	10.735272	12.504876	9.082032	2.447829	24.190580	0.64
Glucose	12.504876	908.084944	79.560776	43.060065	945.514805	45.11
BloodPressure	9.082032	79.560776	146.576174	19.311283	70.400334	21.19
SkinThickness	2.447829	43.060065	19.311283	71.356030	112.342561	32.26
Insulin	24.190580	945.514805	70.400334	112.342561	5779.974721	81.16
BMI	0.645843	45.115947	21.199835	32.261255	81.160529	45.84
DiabetesPedigree	-0.033573	1.250934	0.000034	0.278894	1.690199	0.36
Age	20.983482	88.719892	47.644872	9.960717	132.732698	2.51
Outcome	0.341420	7.006599	0.945726	0.847734	8.566895	0.99

In [20]:
```python
# calculate the correlation matrix
diabetes.corr()
```

Out[20]:

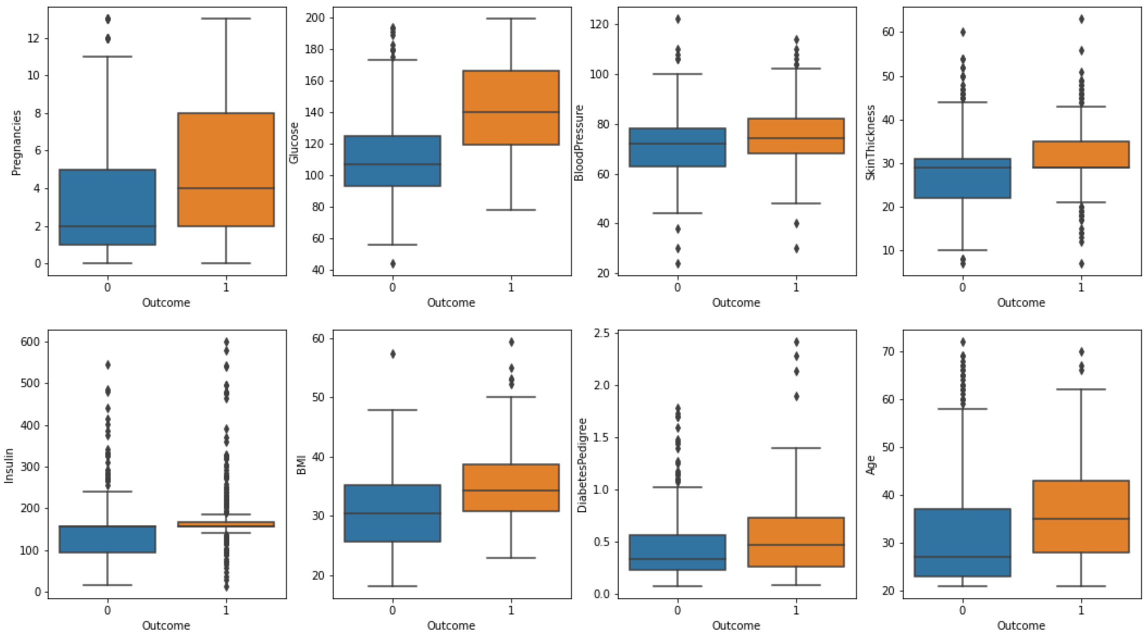
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI
Pregnancies	1.000000	0.126651	0.228952	0.088442	0.097113	0.029112
Glucose	0.126651	1.000000	0.218074	0.169159	0.412707	0.221112
BloodPressure	0.228952	0.218074	1.000000	0.188827	0.076486	0.258611
SkinThickness	0.088442	0.169159	0.188827	1.000000	0.174931	0.564042
Insulin	0.097113	0.412707	0.076486	0.174931	1.000000	0.157662
BMI	0.029112	0.221112	0.258611	0.564042	0.157662	1.000000
DiabetesPedigree	-0.031372	0.127095	0.000009	0.101084	0.068066	0.162814
Age	0.555447	0.255346	0.341315	0.102270	0.151421	0.032204
Outcome	0.219531	0.489844	0.164569	0.211426	0.237396	0.308122

In [21]:
```
# alternatively, show as a heatmap
plt.figure(figsize = (18,10),facecolor=(1, 1, 1))
sns.heatmap(data = diabetes.corr(), annot = True)

plt.savefig(fname = "diabetesfig5")
```



In [22]:
```
# the strongest correlations are between BMI and SkinThickness and Age and P
# none of these correlations are strong enough to instantly remove anything,
# are less likely to keep these pairs in the model together
# Glucose has a higher correlation with Outcome than the other predictors, s
# BloodPressure has the lowest, so we are less likely to keep this
```

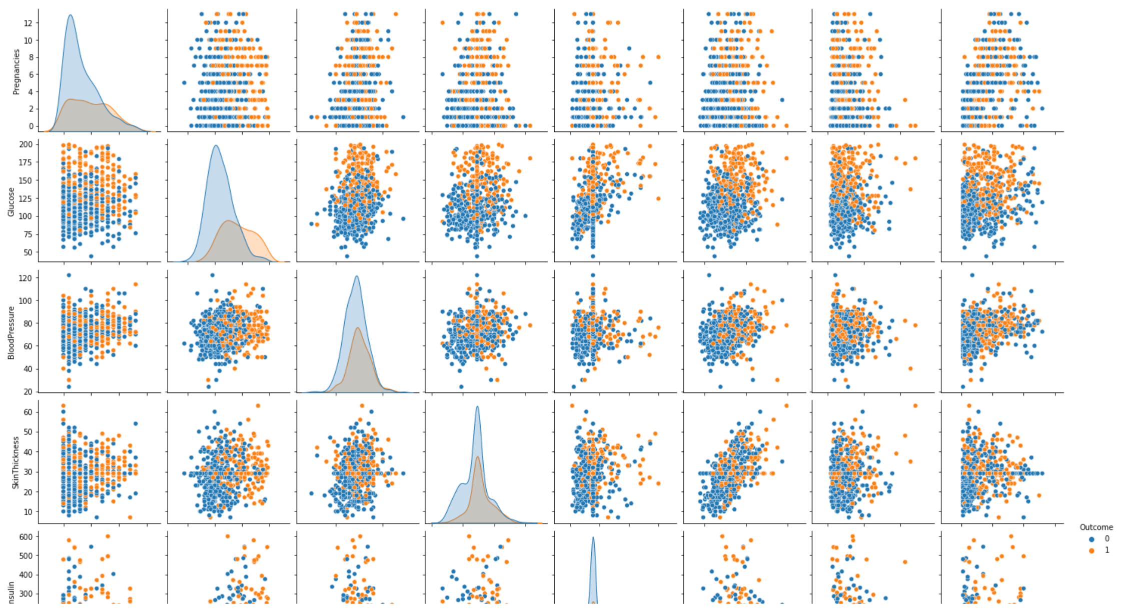
In [23]:
```python
# boxplots for the sake of seeing how each predictor impacts the Outcome
plt.figure(figsize = (18,10), facecolor=(1, 1, 1))

plt.subplot(2,4,1)
sns.boxplot(x = diabetes['Outcome'], y = diabetes['Pregnancies'])

plt.subplot(2,4,2)
sns.boxplot(x = diabetes['Outcome'], y = diabetes['Glucose'])

plt.subplot(2,4,3)
sns.boxplot(x = diabetes['Outcome'], y = diabetes['BloodPressure'])

plt.subplot(2,4,4)
sns.boxplot(x = diabetes['Outcome'], y = diabetes['SkinThickness'])

plt.subplot(2,4,5)
sns.boxplot(x = diabetes['Outcome'], y = diabetes['Insulin'])

plt.subplot(2,4,6)
sns.boxplot(x = diabetes['Outcome'], y = diabetes['BMI'])

plt.subplot(2,4,7)
sns.boxplot(x = diabetes['Outcome'], y = diabetes['DiabetesPedigree'])

plt.subplot(2,4,8)
sns.boxplot(x = diabetes['Outcome'], y = diabetes['Age'])

# save the figure
plt.savefig(fname = "diabetesfig6")
```



In [24]:
```python
# due to the high number of imputations carried out on Insulin and SkinThick
# BloodPressure does not change very much between the two, which was also re
# again, it is likely a candidate for removal
```

In [25]:
```python
# pairplots for all predictors
plt.figure(figsize = (18,10),facecolor=(1, 1, 1))

sns.pairplot(data = diabetes, hue = "Outcome")

plt.savefig(fname = "diabetesfig7.jpg")
```

```
<Figure size 1296x720 with 0 Axes>
```



In [26]:
```python
# these pairplots do not show any major patterns, it is not very informative
```

In [27]:
```python
# add the column 7 or more pregnancies
diabetes['SevenOrMorePregnancies'] = np.where(diabetes['Pregnancies'] >= 7,
```

In [28]:
```python
# save the diabetes dataset as a .csv and move over to R to carry on analysi
diabetes.to_csv("PimaDiabetes2.csv", index = False)
```