In linear regression, the type of data we deal with is quantitative, whereas we use classification models to deal with qualitative data or categorical data. The algorithms used for solving a classification problem first predict the probability of each of the categories of the qualitative variables, as the basis for making the classification. And, as the probabilities are continuous numbers, classification using probabilities also behave like regression methods. Logistic regression is one such type of classification model which is used to classify the dependent variable into two or more classes or categories.

Why don't we use Linear regression for classification problems?

Let's suppose you took a survey and noted the response of each person as satisfied, neutral or Not satisfied. Let's map each category:

Satisfied – 2

Neutral – 1

Not Satisfied – 0

But this doesn't mean that the gap between Not satisfied and Neutral is same as Neutral and satisfied. There is no mathematical significance of these mapping. We can also map the categories like:

Satisfied – 0

Neutral – 1

Not Satisfied – 2

- It's completely fine to choose the above mapping. If we apply linear regression to both the type of mappings, we will get different sets of predictions. Also, we can get prediction values like 1.2, 0.8, 2.3 etc. which makes no sense for categorical values. So, there is no normal method to convert qualitative data into quantitative data for use in linear regression. Although, for binary classification, i.e. when there only two categorical values, using the least square method can give decent results. Suppose we have two categories Black and White and we map them as follows: Black – 0

White - 1

We can assign predicted values for both the categories such as Y> 0.5 goes to class white and vice versa. Although, there will be some predictions for which the value can be greater than 1 or less than 0 making them hard to classify in any class. Nevertheless, linear regression can work decently for binary classification but not that well for multi-class classification. Hence, we use classification methods for dealing with such problems.

Logistic Regression

- Logistic regression is one such regression algorithm which can be used for performing classification problems.
- It calculates the probability that a given value belongs to a specific class.
- If the probability is more than 50%, it assigns the value in that particular class else if the probability is less than 50%, the value is assigned to the other class.
- Therefore, we can say that logistic regression acts as a binary classifier.

Working of a Logistic Model

For linear regression, the model is defined by: y = B0 + B1x and for logistic regression, we calculate probability, i.e. y is the probability of a given variable x belonging to a certain class. Thus, it is obvious that the value of y should lie between 0 and 1.

But, when we use equation(i) to calculate probability, we would get values less than 0 as well as greater than 1. That doesn't make any sense . So, we need to use such an equation which always gives values between 0 and 1, as we desire while calculating the probability.

Sigmoid function

We use the sigmoid function as the underlying function in Logistic regression.

Why do we use the Sigmoid Function?

- The sigmoid function's range is bounded between 0 and 1. Thus it's useful in calculating the probability for the Logistic function.
- It's derivative is easy to calculate than other functions which is useful during gradient descent calculation.
- It is a simple way of introducing non-linearity to the model.
- Although there are other functions as well, which can be used, but sigmoid is the most common function used for logistic regression.

Evaluation of a Classification Model

- In machine learning, once we have a result of the classification problem, how do we measure how accurate our classification is? For a regression problem, we have different metrics like R Squared score, Mean Squared Error etc. what are the metrics to measure the credibility of a classification model?

- Metrics In a regression problem, the accuracy is generally measured in terms of the difference in the actual values and the predicted values. In a classification problem, the credibility of the model is measured using the confusion matrix generated, i.e., how accurately the true positives and true negatives were predicted. The different metrics used for this purpose are:

    - Accuracy
    - Recall
    - Precision
    - F1 Score
    - Specifity
    - AUC(Area Under the Curve)
    - ROC(Receiver Operator Characteristic)
    - Classification Report

Confusion Matrix

- True Positive(TP): A result that was predicted as positive by the classification model and also is positive
- True Negative(TN): A result that was predicted as negative by the classification model and also is negative
- False Positive(FP): A result that was predicted as positive by the classification model but actually is negative
- False Negative(FN): A result that was predicted as negative by the classification model but actually is positive. ***The Credibility of the model is based on how many correct predictions did the model do.**

ROC(Receiver Operator Characteristic)

We know that the classification algorithms work on the concept of probability of occurrence of the possible outcomes. A probability value lies between 0 and 1. Zero means that there is no probability of occurrence and one means that the occurrence is certain.

But while working with real-time data, it has been observed that we seldom get a perfect 0 or 1 value. Instead of that, we get different decimal values lying between 0 and 1. Now the question is if we are not getting binary probability values how are we actually determining the class in our classification problem?

There comes the concept of Threshold. A threshold is set, any probability value below the threshold is a negative outcome, and anything more than the threshold is a favourable or the positive outcome. For Example, if the threshold is 0.5, any probability value below 0.5 means a negative or an unfavourable outcome and any value above 0.5 indicates a positive or favourable outcome.

Now, the question is, what should be an ideal threshold?

AUC(Area Under Curve)

It helps us to choose the best model amongst the models for which we have plotted the ROC curves The best model is the one which encompasses the maximum area under it. In the adjacent diagram, amongst the two curves, the model that resulted in the red one should be chosen as it clearly covers more area than the blue one.

When to use recall and when to you precision

We have thousands of free customers registering in our website every week. The call center team wants to call them all, but it is imposible, so they ask me to select those with good chances to be a buyer (with high temperature is how we refer to them). We don't care to call a guy that is not going to buy (so precision is not important) but for us is very important that all of them with high temperature are always in my selection, so they don't go without buying. That means that my model needs to have a high recall, no matter what is the precision

Advantages of Logisitic Regression

- It is very simple and easy to implement.
- The output is more informative than other classification algorithms.
- It expresses the relationship between independent and dependent variables Very effective with linearly seperable data.

Disadvantages of Logisitic Regression

- Not effective with data which are not linearly seperable.
- Not as powerful as other classification models.
- Multiclass classifications are much easier to do with other algorithms than logisitic regression.
- It can only predict categorical outcomes.

Python Implementation

In [3]:
```
# Importing necessary libraries
import pandas as pd  # For reading the file and other necessary operations
import numpy as np  # For calculating mean, median, and other operations
from sklearn.preprocessing import StandardScaler  # For scaling the data
from sklearn.linear_model import LogisticRegression  # Importing logistic regressi
from sklearn.model_selection import train_test_split  # For splitting the data int
from sklearn.metrics import accuracy_score, confusion_matrix, roc_curve, roc_auc_s
import matplotlib.pyplot as plt  # Visualization library for data analysis
import seaborn as sns  # Visualization library for data analysis
%matplotlib inline
```

Businesscase: To predict whether a patient will have diabetes or not??

Binary classification

In [4]:
```
# Import the data
data = pd.read_csv("diabetes.csv") # Reading the Data
```

In [5]:
```
data.head()#it will give you first  5 rows
```

Out[5]:

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

In [6]:
```
data.tail()#it will give you last 5 rows
```

Out[6]:

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

In [7]:
```
data.info()# To check  data type and  non null value of all columns
```

```
<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 [8]:
```
data.describe()#used to view some basic statistical details like percentile, mean,
```

Out[8]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPe
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	
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	
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	

Exploratory Data Analysis

Univariate Analysis

In [9]:
```
!pip install sweetviz
```

```
Collecting sweetviz
  Downloading sweetviz-2.1.4-py3-none-any.whl (15.1 MB)
Requirement already satisfied: tqdm>=4.43.0 in c:\users\admin\anaconda3\lib\site-packages (from sweetviz) (4.64.0)
Requirement already satisfied: numpy>=1.16.0 in c:\users\admin\anaconda3\lib\site-packages (from sweetviz) (1.21.5)
Requirement already satisfied: importlib-resources>=1.2.0 in c:\users\admin\anaconda3\lib\site-packages (from sweetviz) (5.12.0)
Requirement already satisfied: pandas!=1.0.0,!=1.0.1,!=1.0.2,>=0.25.3 in c:\users\admin\anaconda3\lib\site-packages (from sweetviz) (1.5.3)
Requirement already satisfied: jinja2>=2.11.1 in c:\users\admin\anaconda3\lib\site-packages (from sweetviz) (2.11.3)
Requirement already satisfied: matplotlib>=3.1.3 in c:\users\admin\anaconda3\lib\site-packages (from sweetviz) (3.7.1)
Requirement already satisfied: scipy>=1.3.2 in c:\users\admin\anaconda3\lib\site-packages (from sweetviz) (1.7.3)
Requirement already satisfied: zipp>=3.1.0 in c:\users\admin\anaconda3\lib\site-packages (from importlib-resources>=1.2.0->sweetviz) (3.7.0)
Requirement already satisfied: MarkupSafe>=0.23 in c:\users\admin\anaconda3\lib\site-packages (from jinja2>=2.11.1->sweetviz) (2.0.1)
Requirement already satisfied: fonttools>=4.22.0 in c:\users\admin\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetviz) (4.25.0)
Requirement already satisfied: pyparsing>=2.3.1 in c:\users\admin\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetviz) (3.0.4)
Requirement already satisfied: python-dateutil>=2.7 in c:\users\admin\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetviz) (2.8.2)
Requirement already satisfied: kiwisolver>=1.0.1 in c:\users\admin\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetviz) (1.3.2)
Requirement already satisfied: packaging>=20.0 in c:\users\admin\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetviz) (21.3)
Requirement already satisfied: contourpy>=1.0.1 in c:\users\admin\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetviz) (1.1.0)
Requirement already satisfied: cycler>=0.10 in c:\users\admin\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetviz) (0.11.0)
Requirement already satisfied: pillow>=6.2.0 in c:\users\admin\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetviz) (9.0.1)
Requirement already satisfied: pytz>=2020.1 in c:\users\admin\anaconda3\lib\site-packages (from pandas!=1.0.0,!=1.0.1,!=1.0.2,>=0.25.3->sweetviz) (2021.3)
Requirement already satisfied: six>=1.5 in c:\users\admin\anaconda3\lib\site-packages (from python-dateutil>=2.7->matplotlib>=3.1.3->sweetviz) (1.16.0)
Requirement already satisfied: colorama in c:\users\admin\anaconda3\lib\site-packages (from tqdm>=4.43.0->sweetviz) (0.4.6)
Installing collected packages: sweetviz
Successfully installed sweetviz-2.1.4
```

In [10]:

```python
import sweetviz as sv #  library for univariant analysis

my_report = sv.analyze(data)## pass the original dataframe

my_report.show_html() # Default arguments will generate to "SWEETVIZ_REPORT.html"
```

```
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\dataframe_report.py:74: FutureWarning: iteritems is deprecated and will be removed in a future version. Use .items instead.
  all_source_names = [cur_name for cur_name, cur_series in source_df.iteritems()]
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\dataframe_report.py:109: FutureWarning: iteritems is deprecated and will be removed in a future version. Use .items instead.
  filtered_series_names_in_source = [cur_name for cur_name, cur_series in source_df.iteritems()
```

```
| [  0%]   00:00 ->…
```

```
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_numeric.py:25: FutureWarning: The 'mad' method is deprecated and will be removed in a future version. To compute the same result, you may do `(df - df.mean()).abs().mean()`.
  stats["mad"] = series.mad()
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_numeric.py:25: FutureWarning: The 'mad' method is deprecated and will be removed in a future version. To compute the same result, you may do `(df - df.mean()).abs().mean()`.
  stats["mad"] = series.mad()
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_numeric.py:25: FutureWarning: The 'mad' method is deprecated and will be removed in a future version. To compute the same result, you may do `(df - df.mean()).abs().mean()`.
  stats["mad"] = series.mad()
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_numeric.py:25: FutureWarning: The 'mad' method is deprecated and will be removed in a future version. To compute the same result, you may do `(df - df.mean()).abs().mean()`.
  stats["mad"] = series.mad()
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_numeric.py:25: FutureWarning: The 'mad' method is deprecated and will be removed in a future version. To compute the same result, you may do `(df - df.mean()).abs().mean()`.
  stats["mad"] = series.mad()
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_numeric.py:25: FutureWarning: The 'mad' method is deprecated and will be removed in a future version. To compute the same result, you may do `(df - df.mean()).abs().mean()`.
  stats["mad"] = series.mad()
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_numeric.py:25: FutureWarning: The 'mad' method is deprecated and will be removed in a future version. To compute the same result, you may do `(df - df.mean()).abs().mean()`.
  stats["mad"] = series.mad()
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_numeric.py:25: FutureWarning: The 'mad' method is deprecated and will be removed in a future version. To compute the same result, you may do `(df - df.mean()).abs().mean()`.
  stats["mad"] = series.mad()
C:\Users\Admin\anaconda3\lib\site-packages\sweetviz\series_analyzer_cat.py:28: FutureWarning: iteritems is deprecated and will be removed in a future version. Use .items instead.
  for item in category_counts.iteritems():
Report SWEETVIZ_REPORT.html was generated! NOTEBOOK/COLAB USERS: the web browser MAY not pop up, regardless, the report IS saved in your notebook/colab files.
```

Bivariate Analysis

In [11]:

```python
data.head()
```

Out[11]:

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

In [12]:

```python
data.columns
```

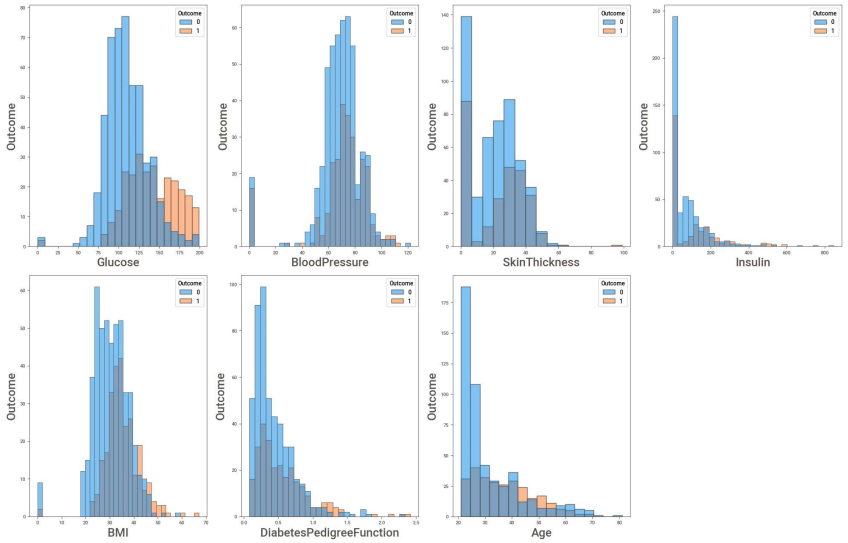
Out[12]:

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

In [13]:
```
data1=data[['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age']]
```

In [14]:
```
plt.figure(figsize=(20,25), facecolor='white')#To set canvas
plotnumber = 1#counter

for column in data1:#accessing the columns
    if plotnumber<=16 :
        ax = plt.subplot(4,4,plotnumber)
        sns.histplot(x=data1[column],hue=data.Outcome)
        plt.xlabel(column,fontsize=20)#assign name to x-axis and set font-20
        plt.ylabel('Outcome',fontsize=20)
    plotnumber+=1#counter increment
plt.tight_layout()
```



Data preprocessing

In [15]:
```
data
```

Out[15]:

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

768 rows × 9 columns

Steps to perform in Feature engineering/data preprocessing

1)Check missing values.Check for corrupted values if any. 2)Convert categorical variable into numerical 3)Handle outlier. 4)Scale the data 5)Transformation of data 6)Balance the data.

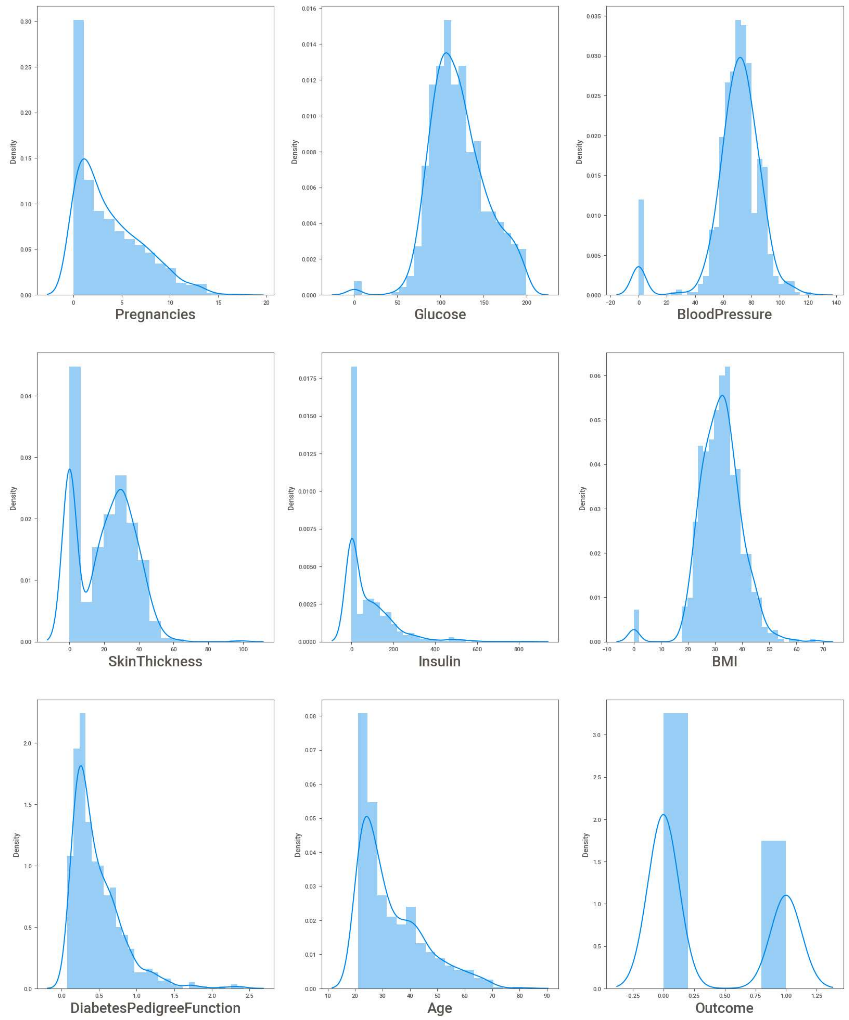
- It seems that there are no missing values in our data. Great, let's see the distribution of data:

In [16]:
```
# let's see how data is distributed for every column
plt.figure(figsize=(20,25), facecolor='white')#defining  canvas size
plotnumber = 1 #maintian count for graph

for column in data:
    if plotnumber<=9 :# as there are 9 columns in the data
        ax = plt.subplot(3,3,plotnumber)# plotting 9 graphs (3-rows,3-columns) ,plo
        sns.distplot(data[column])#plotting dist plot to know distribution
        plt.xlabel(column,fontsize=20)

    plotnumber+=1
plt.show()
```

```
C:\Users\Admin\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWa
rning: `distplot` is a deprecated function and will be removed in a future versio
n. Please adapt your code to use either `displot` (a figure-level function with si
milar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
C:\Users\Admin\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWa
rning: `distplot` is a deprecated function and will be removed in a future versio
n. Please adapt your code to use either `displot` (a figure-level function with si
milar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
C:\Users\Admin\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWa
rning: `distplot` is a deprecated function and will be removed in a future versio
n. Please adapt your code to use either `displot` (a figure-level function with si
milar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
C:\Users\Admin\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWa
rning: `distplot` is a deprecated function and will be removed in a future versio
n. Please adapt your code to use either `displot` (a figure-level function with si
milar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
C:\Users\Admin\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWa
rning: `distplot` is a deprecated function and will be removed in a future versio
n. Please adapt your code to use either `displot` (a figure-level function with si
milar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
C:\Users\Admin\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWa
rning: `distplot` is a deprecated function and will be removed in a future versio
n. Please adapt your code to use either `displot` (a figure-level function with si
milar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
C:\Users\Admin\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWa
rning: `distplot` is a deprecated function and will be removed in a future versio
n. Please adapt your code to use either `displot` (a figure-level function with si
milar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
C:\Users\Admin\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWa
rning: `distplot` is a deprecated function and will be removed in a future versio
n. Please adapt your code to use either `displot` (a figure-level function with si
milar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



In [17]:

```
data
```

Out[17]:

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

768 rows × 9 columns

In [18]:
```
data.loc[data['BMI']==0].head() # How many rows have BMI=0
```

Out[18]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction
9	8	125	96	0	0	0.0	0.232
49	7	105	0	0	0	0.0	0.305
60	2	84	0	0	0	0.0	0.304
81	2	74	0	0	0	0.0	0.102
145	0	102	75	23	0	0.0	0.572

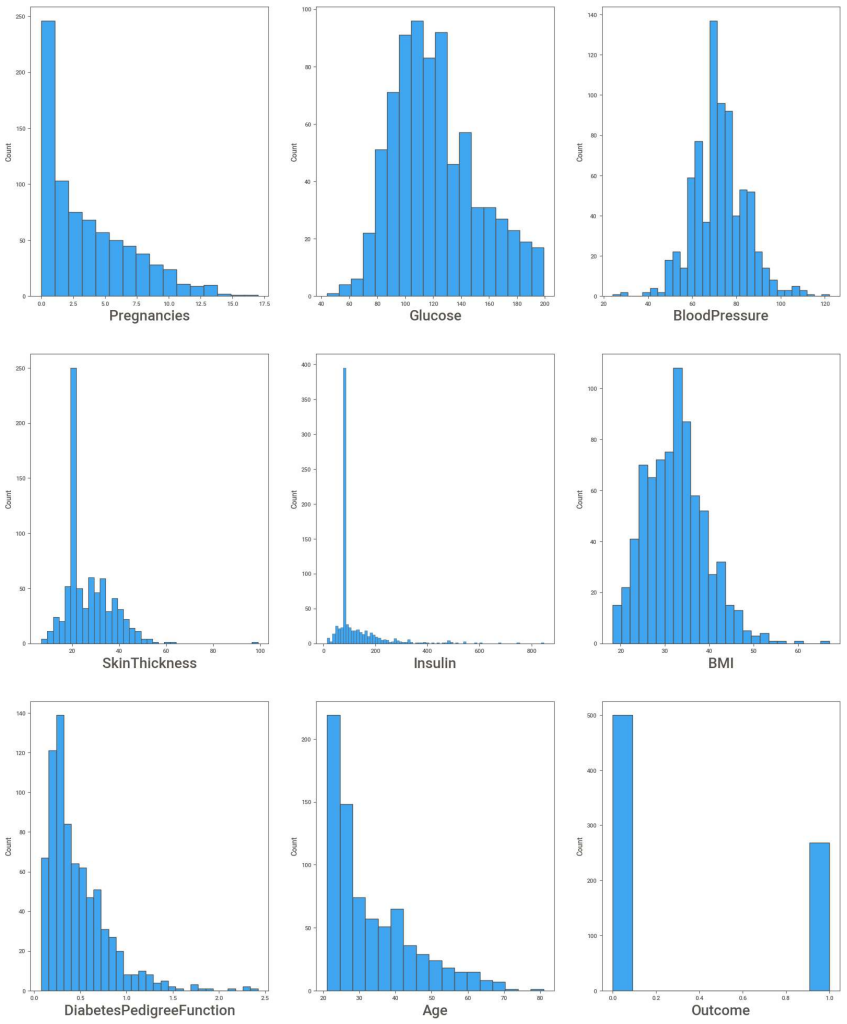
In [19]:
```
data['BMI'].mean()#bmi column mean
```

Out[19]:
```
31.992578124999998
```

In [20]:
```
# Replacing zero values with the mean of the column
data['BMI'] = data['BMI'].replace(0, data['BMI'].mean())  # Replacing 0 with the me
data['BloodPressure'] = data['BloodPressure'].replace(0, data['BloodPressure'].mean
data['Glucose'] = data['Glucose'].replace(0, data['Glucose'].mean())  # Replacing 
data['Insulin'] = data['Insulin'].replace(0, data['Insulin'].mean())  # Replacing 
data['SkinThickness'] = data['SkinThickness'].replace(0, data['SkinThickness'].mean
```

In [21]:
```
# let's see how data is distributed for every column
plt.figure(figsize=(20,25), facecolor='white')
plotnumber = 1

for column in data:
    if plotnumber<=9 :
        ax = plt.subplot(3,3,plotnumber)
        sns.histplot(data[column])
        plt.xlabel(column,fontsize=20)
    plotnumber+=1
plt.show()
```



The data looks much better now than before. We will start our analysis with this data now as we don't want to lose important information. If our model doesn't work with accuracy, we will come back for more preprocessing.

Feature Selection

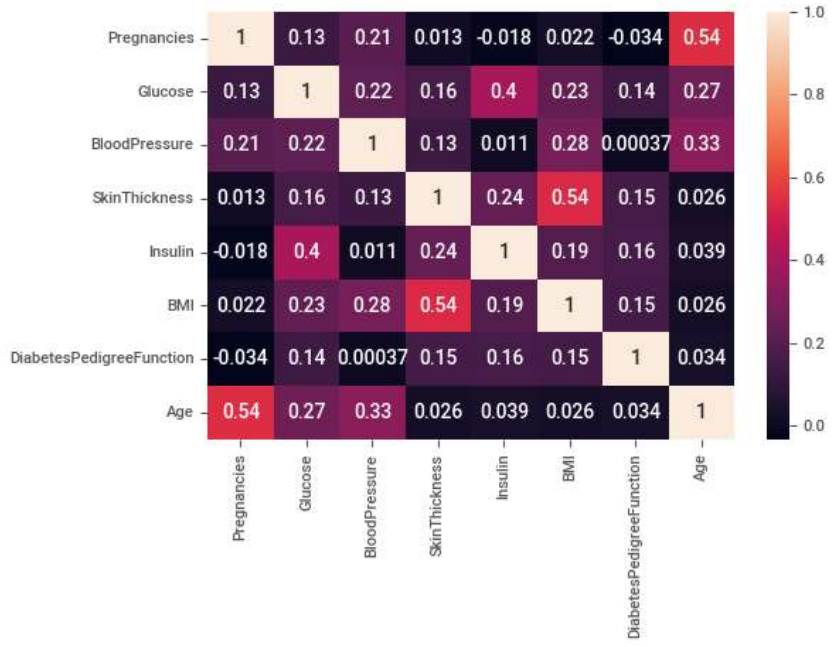
Steps to follow in feature selection

1)Removing redundant columns-->one unique value columns,ids columns,serial no.

2)Check for highly correlated features.If correlation between 2 numerical feature is more than 0.9,remove one of them.

In [22]:
```
sns.heatmap(data.drop('Outcome',axis=1).corr(),annot=True)  # checking for correla
```

Out[22]:
```
<Axes: >
```



In [23]:
```
#checking the duplicate rows
data.duplicated().sum()
```

Out[23]:
```
0
```

Model Creation

In [24]:
```
# Step:1 Define Dependant and indenpendant veriable
X = data.iloc[:,:8]
y = data.Outcome

# Step:2 Create Taring and testing data
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.20,random_state=4

# Step:4 Model creation
from sklearn.linear_model import LogisticRegression
LR = LogisticRegression() # Object Creation

# Step:5 Fit the data
LR.fit(X_train,y_train)

# Step:6 Prdiction on test data
y_predict = LR.predict(X_test)
y_predict
```

```
C:\Users\Admin\anaconda3\lib\site-packages\sklearn\linear_model\_logistic.py:458:
ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
```

Out[24]:
```
array([0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0, 1, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0,
       0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 1, 1, 0,
       0, 1, 1, 0, 0, 1, 0, 1, 1, 0, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 0, 0,
       0, 1, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0,
       0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1,
       0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1,
       0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0],
      dtype=int64)
```

MODEL EVALUATION

In [25]:
```
from sklearn.metrics import accuracy_score, recall_score, precision_score, f1_scor

# confusion matrix
print(confusion_matrix(y_test, y_predict))

# accuracy_score
AC = accuracy_score(y_test, y_predict)
print('accuracy score', AC)

# recall
recall = recall_score(y_test, y_predict)
print('recall', recall)

# precision
precision = precision_score(y_test, y_predict)
print("precision", precision)

# f1 score
f1 = f1_score(y_test, y_predict)
print('f1 score', f1)

# roc curve
print(roc_auc_score(y_test, y_predict))

# classification report
print(classification_report(y_test, y_predict))

# cross-tab
print(pd.crosstab(y_test, y_predict))
```

```
[[84 15]
 [19 36]]
accuracy score 0.7792207792207793
recall 0.6545454545454545
precision 0.7058823529411765
f1 score 0.679245283018868
0.7515151515151515
              precision    recall  f1-score   support

           0       0.82      0.85      0.83        99
           1       0.71      0.65      0.68        55

    accuracy                           0.78       154
   macro avg       0.76      0.75      0.76       154
weighted avg       0.78      0.78      0.78       154

col_0     0   1
Outcome
0        84  15
1        19  36
```

MULTICLASS CLASSIFICATION

In [26]:
```
data=pd.read_csv('iris.csv')# loading another dataset for multiclass classificatio
```

In [27]:
```
data.head()# first 5 rows
```

Out[27]:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
0	5.1	3.5	1.4	0.2	setosa
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa

In [28]:
```
data.Species.value_counts()
```

Out[28]:
```
setosa        50
versicolor    50
virginica     50
Name: Species, dtype: int64
```

MODEL CREATION

In [29]:
```
X=data.loc[:,['Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width']] #indep
y=data.Species #dependent variable
```

In [30]:
```
X_train,X_test,y_train,y_test=train_test_split(X,y,random_state=42)# training and
```

In [31]:
```
from sklearn.linear_model import LogisticRegression
LR=LogisticRegression(multi_class='ovr')# logistic regression for multiclass class
```

In [32]:
```
LR.fit(X_train,y_train)#  training model
```

Out[32]:
```
LogisticRegression(multi_class='ovr')
```

In [33]:
```
y_hat=LR.predict(X_test)# predicting the results
```

MODEL EVALUATION

In [34]:
```
pd.crosstab(y_test,y_hat) # confusion matrix
```

Out[34]:

col_0	setosa	versicolor	virginica
Species			
setosa	15	0	0
versicolor	0	10	1
virginica	0	0	12

In [35]:
```
recall=recall_score(y_test,y_hat,average='weighted') #checking recall
recall
```

Out[35]:
```
0.9736842105263158
```

In [36]:
```
precision=precision_score(y_test,y_hat,average='weighted')# checking precision
precision
```

Out[36]:
```
0.9757085020242916
```

In [37]:
```
print(classification_report(y_test,y_hat))#recall,precision,f1 scores and accuracy
```

```
              precision    recall  f1-score   support

      setosa       1.00      1.00      1.00        15
  versicolor       1.00      0.91      0.95        11
   virginica       0.92      1.00      0.96        12

    accuracy                           0.97        38
   macro avg       0.97      0.97      0.97        38
weighted avg       0.98      0.97      0.97        38
```

Model Saving : Pickle File

In [40]:
```
import pickle

# open file where you want to store a data
file = open('logistic_regression_model.pkl','wb')

# dump information to that file
pickle.dump(LR,file)
```

The pickle.dump() function is used to save the trained logistic regression model 'LR' to the file in binary format.

You can now load this model later from the pickle file and use it for making predictions without the need to retrain the model.