Problem Statement

The purpose is to predict whether the Pima Indian women shows signs of diabetes or not. We are using a dataset collected by "National Institute of Diabetes and Digestive and Kidney Diseases" which consists of a number of attributes which would help us to perform this prediction.

Constraints on data collection

All patients whose data has been collected are females at least 21 years old of Pima Indian heritage

```
#Import all the necessary modules
import numpy as np
import sklearn
from sklearn import metrics
import pandas as pd
#import pylab as plb
import matplotlib.pyplot as plt
%matplotlib inline
plt.style.use('ggplot')
import pickle
from sklearn.preprocessing import LabelEncoder
from sklearn import preprocessing
from sklearn import model_selection
from sklearn.linear_model import LogisticRegression
```

Q1. Load the PIMA Indian Diabetes file into Python DataFrame.

The file can be accessed directly from the URL (https://archive.ics.uci.edu/ml/machine-learning-databases/pima-indians-diabetes/pima-indians-diabetes.data or you may first download it to a local folder and then load it into Python dataframe. Let us assume the data frame is named pima_df

It is always a good practice to eye-ball raw data to get a feel of the data in terms of number of structure of the file, number of attributes, types of attributes and a general idea of likely challenges in the dataset. You would notice that it is a comma separated file. There are no column names!. Check the associated folders and find out about each attribute the name. What information is available about the data.

Q2. Print 10 samples from the dataset

pima_df.head(10)

₽		Preg	Plas	Pres	skin	test	mass	pedi	age	class
	0	6	148	72	35	0	33.6	0.627	50	1
	1	1	85	66	29	0	26.6	0.351	31	0
	2	8	183	64	0	0	23.3	0.672	32	1
	3	1	89	66	23	94	28.1	0.167	21	0
	4	0	137	40	35	168	43.1	2.288	33	1
	5	5	116	74	0	0	25.6	0.201	30	0
	6	3	78	50	32	88	31.0	0.248	26	1
	7	10	115	0	0	0	35.3	0.134	29	0
	8	2	197	70	45	543	30.5	0.158	53	1
	9	Я	125	96	Λ	Λ	0 0	ი 232	54	1

Q3 Print the datatypes of each column and the shape of the dataset

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
         768 non-null int64
Plas
         768 non-null int64
Pres
         768 non-null int64
skin
         768 non-null int64
         768 non-null int64
test
mass
         768 non-null float64
         768 non-null float64
pedi
age
         768 non-null int64
```

pima_df.iloc[:,0:8].describe().transpose()

₽		count	mean	std	min	25%	50%	75%	max
	Preg	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
	Plas	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
	Pres	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
	skin	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
	test	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
	mass	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10
	pedi	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
	age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00

```
pima_df.columns
```

```
□→ Index(['Preg', 'Plas', 'Pres', 'skin', 'test', 'mass', 'pedi', 'age', 'class'], dty
```

There are '0's in the data. Are they really valid '0's or they are missing values? Plasma, BP, skin thickness etc. these values cannot be 0. look at column by column logically to understand this.

Q4 Replace all the 0s in the column with the median of the same column value accordingly.

```
pima_df1 = pima_df
pima_df1.describe().transpose()
```

	count	mean	std	min	25%	50%	75%	max
Preg	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Plas	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
Pres	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
skin	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
test	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
mass	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10
pedi	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42

pima_df1[(pima_df1['Plas'].values==0)==True]

₽		Preg	Plas	Pres	skin	test	mass	pedi	age	class
	75	1	0	48	20	0	24.7	0.140	22	0
	182	1	0	74	20	23	27.7	0.299	21	0
	342	1	0	68	35	0	32.0	0.389	22	0
	349	5	0	80	32	0	41.0	0.346	37	1
	502	6	0	68	41	0	39.0	0.727	41	1

```
pima_df1['Plas'].median()
```

[→ 117.0

med = pima_df1.median()
med

```
3.0000
С→
    Preg
              117.0000
    Plas
    Pres
              72.0000
               23.0000
    skin
               30.5000
    test
               32.0000
    mass
               0.3725
    pedi
               29.0000
    age
                0.0000
    class
    dtype: float64
```

```
pima_df1['Plas'] = pima_df1['Plas'].replace(0,np.median(pima_df1['Plas']))
pima_df1['Pres'] = pima_df1['Pres'].replace(0,np.median(pima_df1['Pres']))
pima_df1['skin'] = pima_df1['skin'].replace(0,np.median(pima_df1['skin']))
pima_df1['test'] = pima_df1['test'].replace(0,np.median(pima_df1['test']))
pima_df1['mass'] = pima_df1['mass'].replace(0,np.median(pima_df1['mass']))
```

pima_df1.describe().transpose()

[→		count	mean	std	min	25%	50%	75%	max
	Preg	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
	Plas	768.0	121.656250	30.438286	44.000	99.75000	117.0000	140.25000	199.00
	Pres	768.0	72.386719	12.096642	24.000	64.00000	72.0000	80.00000	122.00
	skin	768.0	27.334635	9.229014	7.000	23.00000	23.0000	32.00000	99.00
	test	768.0	94.652344	105.547598	14.000	30.50000	31.2500	127.25000	846.00
	mass	768.0	32.450911	6.875366	18.200	27.50000	32.0000	36.60000	67.10
	pedi	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
	age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
	class	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

Q5 Print the descriptive statistics of each & every column using describe() function

pima_df1.describe().transpose()

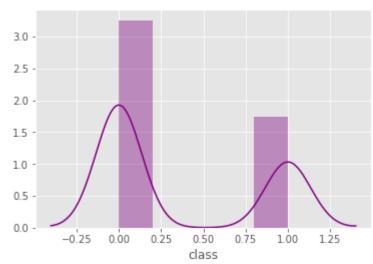
₽		count	mean	std	min	25%	50%	75%	max
	Preg	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
	Plas	768.0	121.656250	30.438286	44.000	99.75000	117.0000	140.25000	199.00
	Pres	768.0	72.386719	12.096642	24.000	64.00000	72.0000	80.00000	122.00
	skin	768.0	27.334635	9.229014	7.000	23.00000	23.0000	32.00000	99.00
	test	768.0	94.652344	105.547598	14.000	30.50000	31.2500	127.25000	846.00
	mass	768.0	32.450911	6.875366	18.200	27.50000	32.0000	36.60000	67.10
	pedi	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
	age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
	class	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

Q6 See the distribution of 'Class' variable and plot it using appropriate graph.

import seaborn as sns

sns.distplot(pima_df1['class'],color='purple')

<matplotlib.axes._subplots.AxesSubplot at 0x7f22db716198>



Just for your understanding - Using univariate analysis check the individual attributes for their basic statistic such as central values, spread, tails

etc. What are your observations (any two attributes). Its an optional step and will not be graded.

Q7. Use pairplots and correlation method to observe

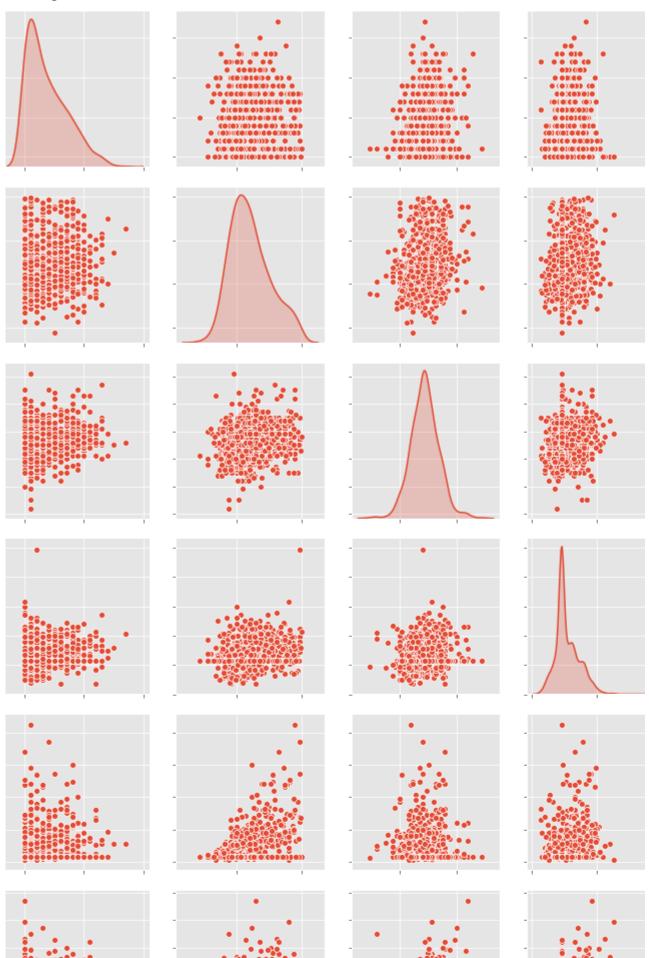
 the relationship between different variables and state your insights.

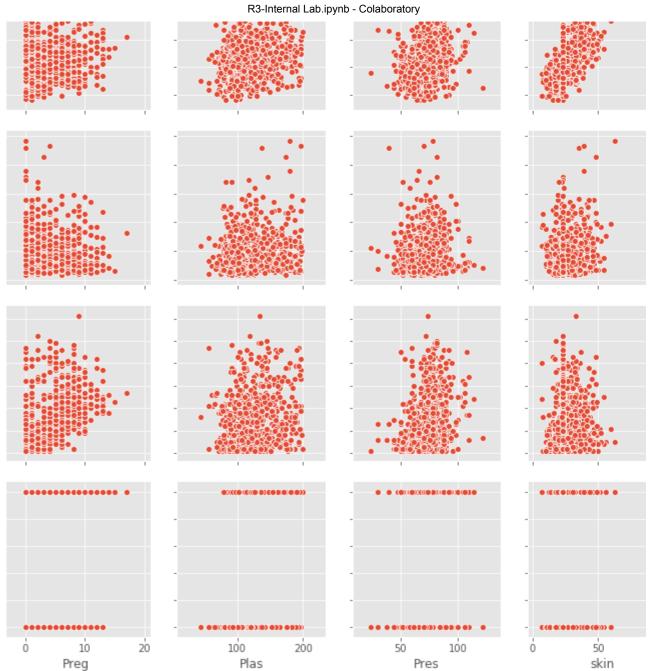
Hint: Use seaborn plot and check the relationship between different variables

sns.pairplot(pima_df1,diag_kind='kde')

 \Box

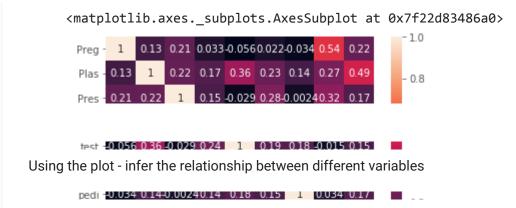
n.axisgrid.PairGrid at 0x7f22db70d7b8>





sns.heatmap(corr,annot=True)

C→



Q8 Split the pima_df into training and test set in the ratio of 70:30 (Training:Test).

```
from sklearn.model_selection import train_test_split
from scipy.stats import zscore
from sklearn.preprocessing import scale

pima_df1 = pima_df1.drop('class',axis=1)

pima_df1_z = pima_df1.apply(scale)

X = np.array(pima_df1_z)

y = np.array(pima_df['class'])

X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.30,random_state=1)
```

Q9 Create the decision tree model using "entropy"method of reducing the entropy and fit it to training data.

```
from sklearn.tree import DecisionTreeClassifier

dt_model = DecisionTreeClassifier(criterion = 'entropy' )
dt_model.fit(X_train, y_train)
```