```
In [1]:
#importing libraries
import numpy as np #2 perform mathematical operations on arrays
import pandas as pd #for data analysis
import seaborn as sns #statistical graphics
from sklearn.preprocessing import StandardScaler #resize the distribution of values
from sklearn.model selection import train test split #measure the accuracy of the model
from sklearn import svm #fit the data u provide, returning a "best fit" hyperplane that
devides/categorizes ur data
from sklearn.metrics import accuracy score #measure model performance
from sklearn.model selection import cross val score
#load the dataset 2 pandas data frame for manupulating the data
raw diabetes data =
pd.read csv(r"C:\Users\mouni\OneDrive\Desktop\diabetesdetection.csv")
#now v hv 2 replace null values with null string otherwise it will show errors
#v will store this in variable claaed "mail data"
diabetes dataset = raw diabetes data.where((pd.notnull(raw diabetes data)), '')
#lets check the shape of the dataset
diabetes_dataset.shape
Out[2]:
(768, 9)
In [3]:
```

Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	Diabete
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.00000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500
75%	6.000000	140.250000	80.00000	32.000000	127.250000	36.600000	0.626250
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000

In [4]:

#counts no of observations per category
sns.countplot(diabetes_dataset['Outcome'])

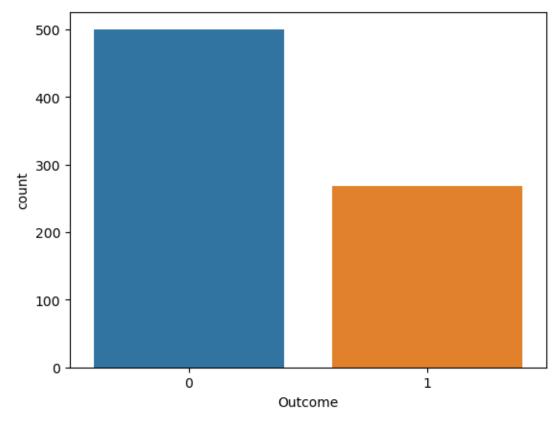
diabetes dataset.describe(include = "all")

C:\Users\mouni\anaconda3\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variable as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

warnings.warn(

Out[4]:

<AxesSubplot:xlabel='Outcome', ylabel='count'>



In [5]:

#checking no.of diabetes & non-diabetes

#v can c how many examples r there for class 1 & 0
print(diabetes dataset['Outcome'].value counts())

0 500

1 268

Name: Outcome, dtype: int64

In [6]:

#v r just finding the mean values of diabetic & non diabetic

#the mean value of non diabetic is less thn compared 2 diabetic

#this difference is very imp for us & this is how our ML Algo can find the difference b/w / it can predict b/w diabetic & non diabetic

diabetes_dataset.groupby('Outcome').mean()

Out[6]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	Diab
Outcome							
0	3.298000	109.980000	68.184000	19.664000	68.792000	30.304200	0.42973

	Pregnancies	Glucose	Blood	Pressure Skir	Thickness	Insulin	ВМІ	Diab
Outcome								
1	4.865672	141.25746	70.8246	22.16	4179	100.335821	35.142537	0.5505
In [7]:		_						
=	g the variab			7 \				
				, Age) as X				
=	a drop the o roping the c			on axis $= 1$				
				come', axis =	1 \			
x - drape	tes_dataset.	arop (corum	iis – Touto	come, axis -	⊥)			
#assignin	g labels(0 &	1) as V						
=	g labels(0 & tes dataset[
	ccs_dataset[Juccome]						
In [8]:	#nrinting th	e data (Pre	anancies	Glucose,	Age)			
					., Age) 			
	#printing th	e lahels(O	٤ 1)					
				SkinThicknes	s Insulin	n BMI \		
0	6	148	72	3		33.6		
1	1	85	66	2		26.6		
2	8	183	64	_		23.3		
3	1	89	66	2				
4	0	137	40	3				
	• • •							
763	10	101	76	4		32.9		
764	2	122	70	2		36.8		
765	5	121	72	2		26.2		
766	1	126	60		0 0			
767	1	93	70	3				
•	_		. •	J	, and the second	-		
Diab	etesPedigree	Function	Age					
0	. 5	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					
760		0.015						

[768 rows x 8 columns]

0.315 23

0

767

0 1

1 0

```
2
      1
3
4
      1
763
     0
764
     0
765
766
      1
767
Name: Outcome, Length: 768, dtype: int64
In [9]:
#DATA STANDARDIZATION
#if there is a difference in the range of all these values
#it will b difficult for our ml model 2 make sm predictions
#in ost cases v try 2 standardize the data in a particular range & that helps our ml 2
make better predictions
#v r loading the StandardScaler & fitting the data 2 the variable "x"
#v r fitting all these inconsistent data wyt out StandardScaler function
#now v need transform this data
#based on that Standardization v r transforming all the data 2 the common range
scaler = StandardScaler()
scaler.fit(X)
standardized data = scaler.transform(X)
X = standardized data
In [10]:
print(X) #print this data in the standardized data
print("-----
----")
print(Y) #printing the labels(0 & 1)
\#as v can c here all these values here r in the range of 0 & 1
#so this will help our model 2 make better predictions
#coz all the values r almost in the similar range
[[\ 0.63994726\ \ 0.84832379\ \ 0.14964075\ \dots\ \ 0.20401277\ \ 0.46849198
   1.4259954 ]
 [-0.84488505 \ -1.12339636 \ -0.16054575 \ \dots \ -0.68442195 \ -0.36506078
  -0.190671911
 -0.105584151
 [0.3429808 \quad 0.00330087 \quad 0.14964075 \quad ... \quad -0.73518964 \quad -0.68519336
  -0.275759661
 [-0.84488505 \quad 0.1597866 \quad -0.47073225 \quad \dots \quad -0.24020459 \quad -0.37110101
  1.17073215]
 [-0.84488505 - 0.8730192 \quad 0.04624525 \dots -0.20212881 -0.47378505
  -0.87137393]]
1
      0
2
```

1

```
3
       0
       1
763
       0
764
       0
765
       Λ
766
       1
767
Name: Outcome, Length: 768, dtype: int64
#spliting the dataset in2 Training & Testing
#test size --> 2 specify the percentage of test data needed ==> 0.2 ==> 20%
#random state --> specific split of data each value of random state splits the data
differently, v can put any state v want
#v need 2 specify the same random state everytym if v want 2 split the data the same
way everytym
#stratifying it based on the y, so that the data is split in the crt way
#stratify --> for crt distribution of data as of the original data(2 split the data
correctly as of the original data)
#if i dont mention stratify = y, the distribution of 0 & 1 can b very different in the
training data & testing data
X_train, X_test, Y_train, Y_test = train test split(X, Y, test size = 0.2, stratify =
Y, random state = 2)
In [12]:
#lets c how many examples r there for each cases
#checking dimensions of data
print(X.shape, X_train.shape, X_test.shape)
(768, 8) (614, 8) (154, 8)
In [13]:
#lets c how many examples r there for each cases
#checking dimensions of labels
print(Y.shape, Y train.shape, Y test.shape)
(768,) (614,) (154,)
In [14]:
#SKLEARN APPLYING MACHINE LEARNING ALGORITHM
#training the support vector Machine Classifier
#loading the SVM 2 the variable "classifier"
#training the SVM Model with Training Data
#v r fitting the data x train, y train 2 the model which is the svm model, so the model
is trained with the data
#linear kernel SVM is used whn the data is Linearly separable(separated using single
#it is used whn there r large no of features in particular dataset
#train a linear SVM classifier on the training data
classifier = svm.SVC(kernel = 'linear').fit(X train, Y train)
```

In [15]:

```
#prediction on train data(PRDECTING SEEN DATA)
X train prediction = classifier.predict(X train)
X train prediction
Out[15]:
0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0,
      0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
      0, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1,
      0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 1, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0,
      1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 0, 1,
      1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 1, 0,
      1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0,
      1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 0, 0,
      1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1,
      0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 1, 1, 0, 1,
      0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 1, 1, 1, 0, 0, 0, 0, 0,
      0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0,
      0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0,
      0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0,
      0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 1, 0, 1, 0,
      0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0, 1, 1, 1,
      0, 0, 1, 1, 1, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 0, 0, 1, 1, 0,
      0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
      0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1,
      0, 0, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0,
      0, 0, 0, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0,
      0, 1, 0, 1, 0, 0, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 0, 0, 0, 0, 1,
      0, 0, 1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 1, 0, 1, 1, 1, 1, 0, 0, 0,
      0, 0, 0, 1, 0, 1, 1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 1, 0,
      0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0,
      0, 0, 0, 0, 1, 0, 1, 1, 0, 1, 1, 0, 0, 0, 0, 1, 1, 1, 0, 0, 0, 0,
      0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0],
     dtype=int64)
In [16]:
#prediction on test data(PREDECTING UNSEEN DATA)
X test prediction = classifier.predict(X test)
X test prediction
Out[16]:
array([0, 0, 1, 1, 0, 0, 0, 1, 0, 1, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0,
      1, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1,
      0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0,
      0, 1, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0,
      1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
      1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1,
      1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0],
     dtype=int64)
```

In [17]:

#v r finding the accuracy_score on the training data 2 check how the model performs on traing data

training data accuracy = accuracy score(X train prediction, Y train)

```
#v r finding the accuracy score on the testing data 2 check how the model performs on
testing data
test data accuracy = accuracy score(X test prediction, Y test)
#print the accuracy score on training data
print('Accuracy score of the training data : ', training data accuracy)
#print the accuracy score on testing data
print('Accuracy score of the test data : ', test data accuracy)
Accuracy score of the training data: 0.7866449511400652
Accuracy score of the test data: 0.7727272727272727
In [19]:
#mean accuracy (accuracy score)
#measuring the accuracy of the model against the training data
classifier.score(X train, Y train)
Out[19]:
0.7866449511400652
In [20]:
#mean accuracy (accuracy score)
#measuring the accuracy of the model against the test data
classifier.score(X test, Y test)
Out[20]:
0.7727272727272727
In [21]:
#cross validation
#it is used to protect against overfitting in a predictive model,
#particularly in a case where the amount of data may be limited. In cross-validation,
#you make a fixed number of folds (or partitions) of the data, run the analysis on each
fold, and then average the overall error estimate.
#cv = 5 ==> partition the data in2 4 Training & 1 Testing Data parts
print(cross val score(classifier, X, Y, cv = 5))
[0.76623377 0.75974026 0.75974026 0.81699346 0.76470588]
In [27]:
input data = (5,166,72,19,175,25.8,0.0,51)
# changing the input data to numpy array
input data as numpy array = np.asarray(input data)
# reshape the array as we are predicting for one instance
input data reshaped = input data as numpy array.reshape(1,-1)
# standardize the input data
std data = scaler.transform(input data reshaped)
print(std data)
prediction = classifier.predict(std data)
print(prediction)
if (prediction[0] == 0):
```

```
print('The person is not diabetic')
else:
  print('The person is diabetic')
[ [ \ 0.3429808 \quad \  1.41167241 \quad \  0.14964075 \quad -0.09637905 \quad \  0.82661621 \quad -0.78595734 ]
  -1.42512243 1.51108316]]
[0]
The person is not diabetic
C:\Users\mouni\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not
have valid feature names, but StandardScaler was fitted with feature names
  warnings.warn(
In [23]:
import pickle #keeps track of the objects it has already serialized ==> allows saving
model in very little tym
In [24]:
#save the model trained in the file "trained model.sav" to a new file called
"diabetes trained model.pkl"
filename = 'diabetes trained.sav'
pickle.dump(classifier, open(filename, 'wb'))
In [25]:
#loading the saved model
loaded model = pickle.load(open('diabetes trained model.sav', 'rb'))
In [26]:
input data = (5,166,72,19,175,25.8,0.587,51)
# changing the input data to numpy array
input data as numpy array = np.asarray(input data)
# reshape the array as we are predicting for one instance
input data reshaped = input data as numpy array.reshape(1,-1)
# standardize the input data
std data = scaler.transform(input data reshaped)
print(std data)
prediction = classifier.predict(std data)
print(prediction)
if (prediction[0] == 0):
  print('The person is not diabetic')
  print('The person is diabetic')
[[\ 0.3429808 \quad \  1.41167241 \quad 0.14964075 \quad -0.09637905 \quad 0.82661621 \quad -0.78595734]
   0.34768723 1.51108316]]
[1]
The person is diabetic
C:\Users\mouni\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not
have valid feature names, but StandardScaler was fitted with feature names
  warnings.warn(
In [ ]:
```