# In [1]:

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
data=pd.read_csv('diabetes.csv')
data
```

## Out[1]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	DiabetesPedigre	İ
0	2	138	62	35	0	33.6		
1	0	84	82	31	125	38.2		
2	0	145	0	0	0	44.2		
3	0	135	68	42	250	42.3		
4	1	139	62	41	480	40.7		
1995	2	75	64	24	55	29.7		
1996	8	179	72	42	130	32.7		
1997	6	85	78	0	0	31.2		
1998	0	129	110	46	130	67.1		
1999	2	81	72	15	76	30.1		
2000 r	ows × 9 colur	nne						
20001	ows ~ a colui	11113						
4							<b>&gt;</b>	

# In [2]:

data.shape

# Out[2]:

(2000, 9)

# In [3]:

data.head(10)

# Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	DiabetesPedigreeFunc
0	2	138	62	35	0	33.6	0.
1	0	84	82	31	125	38.2	0.
2	0	145	0	0	0	44.2	0.
3	0	135	68	42	250	42.3	0.
4	1	139	62	41	480	40.7	0.
5	0	173	78	32	265	46.5	1.
6	4	99	72	17	0	25.6	0.
7	8	194	80	0	0	26.1	0.
8	2	83	65	28	66	36.8	0.
9	2	89	90	30	0	33.5	0.
4							<b></b>

# In [4]:

data.tail(10)

# Out[4]:

								_
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	DiabetesPedigro	l -
1990	3	111	90	12	78	28.4		
1991	6	102	82	0	0	30.8		
1992	6	134	70	23	130	35.4		
1993	2	87	0	23	0	28.9		
1994	1	79	60	42	48	43.5		
1995	2	75	64	24	55	29.7		
1996	8	179	72	42	130	32.7		
1997	6	85	78	0	0	31.2		
1998	0	129	110	46	130	67.1		
1999	2	81	72	15	76	30.1		~
4							<b>&gt;</b>	

```
In [5]:
```

```
data.describe()
```

#### Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	ı
count	2000.000000	2000.000000	2000.000000	2000.000000	2000.000000	2000.000000	
mean	3.703500	121.182500	69.145500	20.935000	80.254000	32.193000	
std	3.306063	32.068636	19.188315	16.103243	111.180534	8.149901	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	63.500000	0.000000	0.000000	27.375000	
50%	3.000000	117.000000	72.000000	23.000000	40.000000	32.300000	
75%	6.000000	141.000000	80.000000	32.000000	130.000000	36.800000	
max	17.000000	199.000000	122.000000	110.000000	744.000000	80.600000	
4						•	

# In [6]:

```
data.info()
```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2000 entries, 0 to 1999
Data columns (total 9 columns):

Column	Non-Null Count	Dtype
Pregnancies	2000 non-null	int64
Glucose	2000 non-null	int64
BloodPressure	2000 non-null	int64
SkinThickness	2000 non-null	int64
Insulin	2000 non-null	int64
BMI	2000 non-null	float64
DiabetesPedigreeFunction	2000 non-null	float64
Age	2000 non-null	int64
Outcome	2000 non-null	int64
	Glucose BloodPressure SkinThickness Insulin BMI DiabetesPedigreeFunction Age	Pregnancies 2000 non-null Glucose 2000 non-null BloodPressure 2000 non-null SkinThickness 2000 non-null Insulin 2000 non-null BMI 2000 non-null DiabetesPedigreeFunction 2000 non-null Age 2000 non-null

dtypes: float64(2), int64(7)
memory usage: 140.7 KB

# In [7]:

```
print("no of pregencies in original dataset:" +str(len(data.index)))
```

no of pregencies in original dataset:2000

# In [8]:

```
data.isnull().values.any()
```

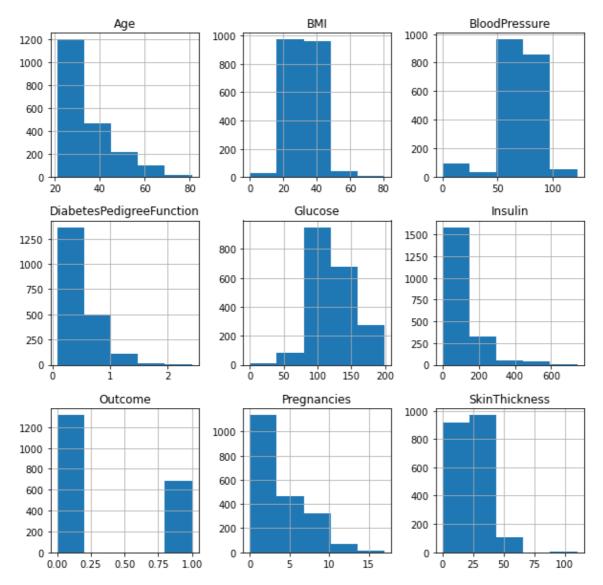
## Out[8]:

False

#### In [9]:

```
#histogram
data.hist(bins=5,figsize=(10,10))
```

#### Out[9]:



# In [10]:

#correlation
data.corr()

# Out[10]:

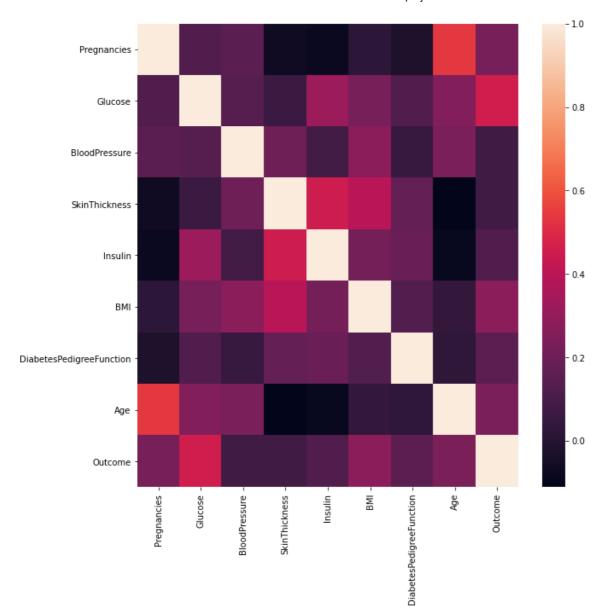
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	
Pregnancies	1.000000	0.120405	0.149672	-0.063375	-0.076600	(
Glucose	0.120405	1.000000	0.138044	0.062368	0.320371	(
BloodPressure	0.149672	0.138044	1.000000	0.198800	0.087384	(
SkinThickness	-0.063375	0.062368	0.198800	1.000000	0.448859	(
Insulin	-0.076600	0.320371	0.087384	0.448859	1.000000	(
ВМІ	0.019475	0.226864	0.281545	0.393760	0.223012	
DiabetesPedigreeFunction	-0.025453	0.123243	0.051331	0.178299	0.192719	(
Age	0.539457	0.254496	0.238375	-0.111034	-0.085879	(
Outcome	0.224437	0.458421	0.075958	0.076040	0.120924	(
4					<b>&gt;</b>	

## In [11]:

```
#correlation using heat maps
plt.figure(figsize=(10,10))
sns.heatmap(data.corr())
# we can see skin thickness,insulin,pregnencies and age are full independent to each ot
her
#age and pregencies has negative correlation
```

# Out[11]:

<matplotlib.axes.\_subplots.AxesSubplot at 0xa59ad00>

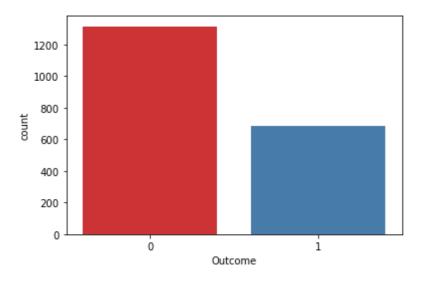


## In [12]:

```
sns.countplot(x=data['Outcome'],palette='Set1')
#0 means no diabeted
#1 means patient with diabtes
```

## Out[12]:

<matplotlib.axes.\_subplots.AxesSubplot at 0xb043d90>

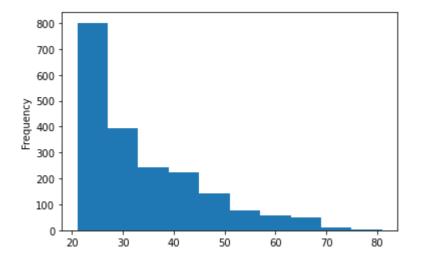


## In [13]:

```
data["Age"].plot.hist()
```

## Out[13]:

<matplotlib.axes.\_subplots.AxesSubplot at 0xb0786e8>



## In [14]:

```
data.isnull().sum()
```

## Out[14]:

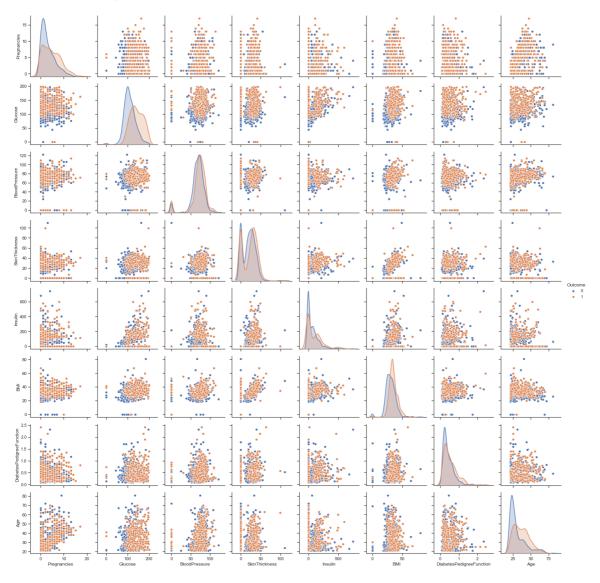
Pregnancies 0 Glucose 0 BloodPressure 0 SkinThickness 0 Insulin 0 BMI 0 DiabetesPedigreeFunction 0 Age 0 Outcome 0 dtype: int64

# In [15]:

```
sns.set(style="ticks")
sns.pairplot(data, hue="Outcome")
```

# Out[15]:

## <seaborn.axisgrid.PairGrid at 0x688f8b0>

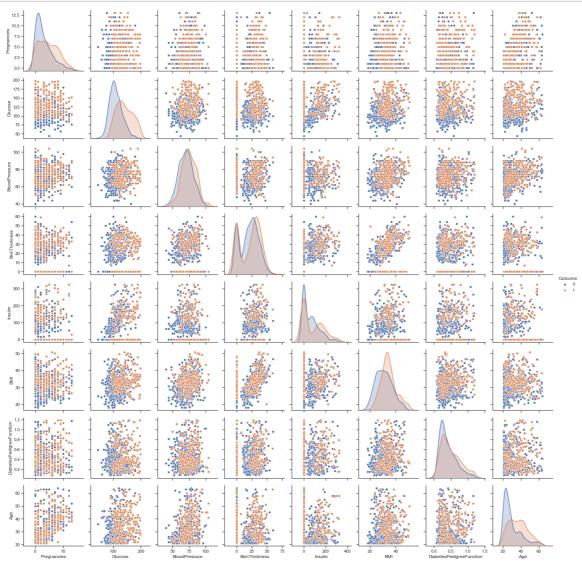


```
In [16]:
```

```
#outlier remove
Q1=data.quantile(0.25)
Q3=data.quantile(0.75)
IQR=Q3-Q1
print("****Q1**** \n",Q1)
print("\n****Q3**** \n",Q3)
print("\n****IQR****\n",IQR)
\#print((df < (Q1 - 1.5 * IQR)))/(df > (Q3 + 1.5 * IQR)))
****01****
 Pregnancies
                               1.000
Glucose
                             99,000
                             63.500
BloodPressure
SkinThickness
                              0.000
Insulin
                              0.000
BMI
                             27.375
DiabetesPedigreeFunction
                              0.244
                             24.000
Age
Outcome
                              0.000
Name: 0.25, dtype: float64
****03****
                                6.000
 Pregnancies
                             141.000
Glucose
BloodPressure
                              80.000
SkinThickness
                              32.000
Insulin
                             130.000
BMI
                              36.800
DiabetesPedigreeFunction
                               0.624
                              40.000
Age
Outcome
                               1.000
Name: 0.75, dtype: float64
****IQR****
                                5.000
 Pregnancies
                              42.000
Glucose
BloodPressure
                              16.500
                              32.000
SkinThickness
Insulin
                             130.000
BMI
                               9.425
DiabetesPedigreeFunction
                               0.380
                              16.000
Age
Outcome
                               1.000
dtype: float64
In [17]:
data_out = data[\sim((data < (Q1 - 1.5 * IQR)) | (data > (Q3 + 1.5 * IQR))).any(axis=1)]
data.shape,data_out.shape
Out[17]:
((2000, 9), (1652, 9))
```

## In [19]:

```
#Scatter matrix after removing outlier
sns.set(style="ticks")
sns.pairplot(data_out, hue="Outcome")
plt.show()
```



## In [20]:

```
#lets extract features and targets
X=data_out.drop(columns=['Outcome'])
y=data_out['Outcome']
```

## In [21]:

```
#Splitting train test data 80 20 ratio
from sklearn.model_selection import train_test_split
train_X,test_X,train_y,test_y=train_test_split(X,y,test_size=0.2)
```

## In [22]:

```
len(train_X)
```

## Out[22]:

1321

```
In [23]:
len(train y)
Out[23]:
1321
In [24]:
len(test_X)
Out[24]:
331
In [25]:
len(test_y)
Out[25]:
331
In [26]:
train_X.shape,test_X.shape,train_y.shape,test_y.shape
Out[26]:
((1321, 8), (331, 8), (1321,), (331,))
In [27]:
from sklearn.metrics import confusion_matrix,accuracy_score,make_scorer
from sklearn.model selection import cross validate
def tn(y_true, y_pred): return confusion_matrix(y_true, y_pred)[0, 0]
def fp(y_true, y_pred): return confusion_matrix(y_true, y_pred)[0, 1]
def fn(y_true, y_pred): return confusion_matrix(y_true, y_pred)[1, 0]
def tp(y true, y pred): return confusion matrix(y true, y pred)[1, 1]
#cross validation purpose
scoring = {'accuracy': make_scorer(accuracy_score), 'prec': 'precision'}
scoring = {'tp': make_scorer(tp), 'tn': make_scorer(tn),
           'fp': make_scorer(fp), 'fn': make_scorer(fn)}
def display_result(result):
    print("TP: ",result['test_tp'])
    print("TN: ",result['test_tn'])
    print("FN: ",result['test_fn'])
    print("FP: ",result['test_fp'])
```

#### In [28]:

```
#Lets build the model
#Logistic Regression
\#s(z)=1/(1+e^{-z}) z=input
import warnings
warnings.filterwarnings("ignore")
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import roc_auc_score
acc=[]
roc=[]
clf=LogisticRegression()
clf.fit(train_X,train_y)
y_pred=clf.predict(test_X)
#find accuracy
ac=accuracy_score(test_y,y_pred)
acc.append(ac)
#find the ROC AOC curve
rc=roc_auc_score(test_y,y_pred)
roc.append(rc)
print("\nAccuracy {0} ROC {1}".format(ac,rc))
#cross val score
result=cross_validate(clf,train_X,train_y,scoring=scoring,cv=10)
display result(result)
#display predicted values uncomment below line
pd.DataFrame(data={'Actual':test_y,'Predicted':y_pred}).head()
```

Accuracy 0.797583081570997 ROC 0.7342032967032968

TP: [25 19 22 26 24 26 21 25 25 23]
TN: [80 83 82 78 77 85 78 85 83 80]
FN: [18 24 21 17 19 16 21 17 17 19]
FP: [10 6 7 11 12 5 12 5 7 10]

#### Out[28]:

	Actual	Predicted
62	0	0
1850	0	0
851	0	0
969	0	1
1280	0	0

#### In [29]:

9/1/2020

```
#KNN
from sklearn.neighbors import KNeighborsClassifier
clf=KNeighborsClassifier(n_neighbors=3)
clf.fit(train_X,train_y)
y_pred=clf.predict(test_X)
#find accuracy
ac=accuracy_score(test_y,y_pred)
acc.append(ac)
#find the ROC AOC curve
rc=roc_auc_score(test_y,y_pred)
roc.append(rc)
print("\nAccuracy {0} ROC {1}".format(ac,rc))
#cross val score
result=cross_validate(clf,train_X,train_y,scoring=scoring,cv=10)
display_result(result)
#display predicted values uncomment below line
pd.DataFrame(data={'Actual':test_y,'Predicted':y_pred}).head()
```

#### Accuracy 0.8670694864048338 ROC 0.8435210622710622

TP: [38 32 36 31 32 33 31 33 35 34]
TN: [75 77 82 83 79 85 77 81 81 77]
FN: [5 11 7 12 11 9 11 9 7 8]
FP: [15 12 7 6 10 5 13 9 9 13]

#### Out[29]:

	Actual	Predicted
62	0	0
1850	0	0
851	0	0
969	0	0
1280	0	0

## In [30]:

9/1/2020

```
#Random forest
from sklearn.ensemble import RandomForestClassifier
clf=RandomForestClassifier()
clf.fit(train_X,train_y)
y_pred=clf.predict(test_X)
#find accuracy
ac=accuracy_score(test_y,y_pred)
acc.append(ac)
#find the ROC AOC curve
rc=roc_auc_score(test_y,y_pred)
roc.append(rc)
print("\nAccuracy {0} ROC {1}".format(ac,rc))
#cross val score
result=cross_validate(clf,train_X,train_y,scoring=scoring,cv=10)
display_result(result)
#display predicted values uncomment below line
pd.DataFrame(data={'Actual':test_y,'Predicted':y_pred}).head()
```

#### Accuracy 0.9758308157099698 ROC 0.9696886446886447

TP: [41 40 41 39 40 41 41 41 41 39]
TN: [85 88 86 87 87 89 89 89 87 88]

FN: [2 3 2 4 3 1 1 1 1 3] FP: [5 1 3 2 2 1 1 1 3 2]

#### Out[30]:

	Actual	Predicted
62	0	0
1850	0	0
851	0	0
969	0	0
1280	0	0

#### In [31]:

```
#Naive Bayes Theorem
#import library
from sklearn.naive_bayes import GaussianNB
clf=GaussianNB()
clf.fit(train_X,train_y)
y_pred=clf.predict(test_X)
#find accuracy
ac=accuracy_score(test_y,y_pred)
acc.append(ac)
#find the ROC AOC curve
rc=roc_auc_score(test_y,y_pred)
roc.append(rc)
print("\nAccuracy {0} ROC {1}".format(ac,rc))
#cross val score
result=cross_validate(clf,train_X,train_y,scoring=scoring,cv=10)
display_result(result)
#display predicted values uncomment below line
pd.DataFrame(data={'Actual':test_y,'Predicted':y_pred}).head()
```

Accuracy 0.7492447129909365 ROC 0.7179258241758241

TP: [27 22 27 29 24 28 24 29 27 25]
TN: [79 77 75 71 72 74 80 73 79 75]
FN: [16 21 16 14 19 14 18 13 15 17]
FP: [11 12 14 18 17 16 10 17 11 15]

#### Out[31]:

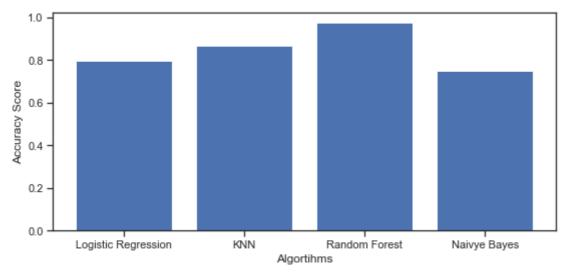
	Actual	Predicted
62	0	0
1850	0	0
851	0	0
969	0	1
1280	0	0

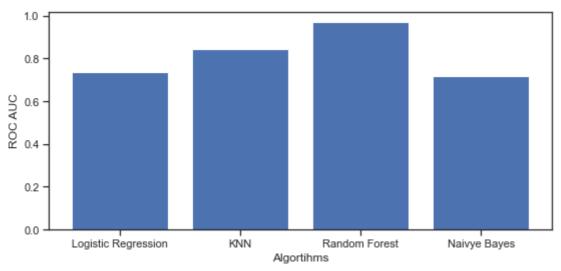
#### In [32]:

```
#Lets plot the bar graph

ax=plt.figure(figsize=(9,4))
plt.bar(['Logistic Regression','KNN','Random Forest','Naivye Bayes'],acc,label='Accurac
y')
plt.ylabel('Accuracy Score')
plt.xlabel('Algortihms')
plt.show()

ax=plt.figure(figsize=(9,4))
plt.bar(['Logistic Regression','KNN','Random Forest','Naivye Bayes'],roc,label='ROC AU
C')
plt.ylabel('ROC AUC')
plt.xlabel('Algortihms')
plt.show()
```





#### In [ ]:

```
#Random forest has highest accuracy 98% and ROC_AUC curve 97%
#model can be improve more if we take same count of labels
#in our model 30% is diabetic and 70% no diabetic patient
#model can be improve with fine tunning
```