

In [21]:

```
import pandas as pd
```

In [22]:

```
df = pd.read_csv('diabetes.csv')
```

In [23]:

```
print(df.head())
```

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

	DiabetesPedigreeFunction	Age	Outcome
0	0.627	50	1
1	0.351	31	0
2	0.672	32	1
3	0.167	21	0
4	2.288	33	1

In [24]:

```
#1 Finding the range of values  
print(df.describe())
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin
\					
count	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479
std	3.369578	31.972618	19.355807	15.952218	115.244002
min	0.000000	0.000000	0.000000	0.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000
75%	6.000000	140.250000	80.000000	32.000000	127.250000
max	17.000000	199.000000	122.000000	99.000000	846.000000

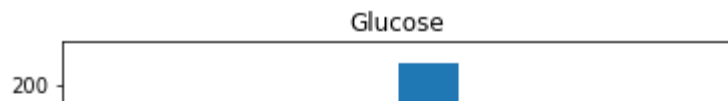
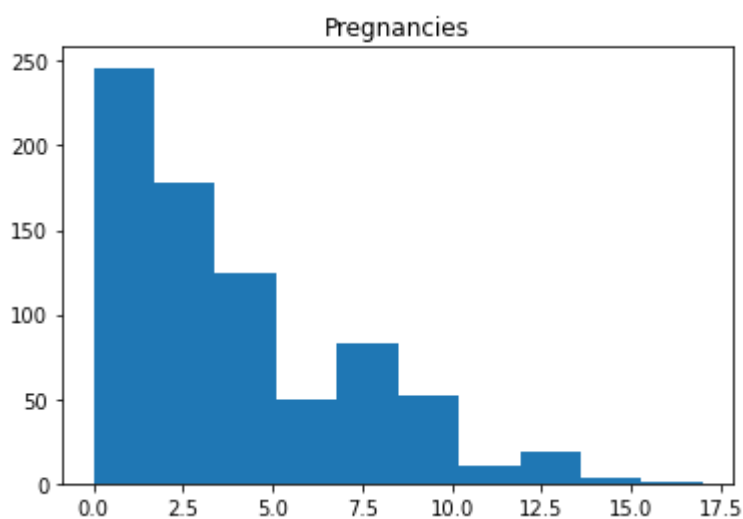
	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000
mean	31.992578	0.471876	33.240885	0.348958
std	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.078000	21.000000	0.000000
25%	27.300000	0.243750	24.000000	0.000000
50%	32.000000	0.372500	29.000000	0.000000
75%	36.600000	0.626250	41.000000	1.000000
max	67.100000	2.420000	81.000000	1.000000

In [7]:

```
import matplotlib.pyplot as plt
```

In [10]:

```
#plot histogram  
for col in df.columns:  
    if df[col].dtype == 'float64' or df[col].dtype == 'int64':  
        plt.hist(df[col], bins=10)  
        plt.title(col)  
        plt.show()
```



In [17]:

```

from sklearn.preprocessing import MinMaxScaler
# Load the diabetes dataset
diabetes = load_diabetes()
X, y = diabetes.data, diabetes.target
feature_names = diabetes.feature_names
dataset = pd.DataFrame(X, columns=feature_names)

# Normalize the features using min-max scaling
scaler = MinMaxScaler()
X_scaled = scaler.fit_transform(X)

# Print the first 5 rows of the normalized features
print(X_scaled[:5, :])

```

```

-----
--
NameError                                Traceback (most recent call las
t)
Input In [17], in <cell line: 3>()
      1 from sklearn.preprocessing import MinMaxScaler
      2 # Load the diabetes dataset
----> 3 diabetes = load_diabetes()
      4 X, y = diabetes.data, diabetes.target
      5 feature_names = diabetes.feature_names

NameError: name 'load_diabetes' is not defined

```

In [18]:

```

from sklearn.model_selection import train_test_split

# Split the normalized data into training and testing subsets
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.2, random_s

# Print the shapes of the training and testing subsets
print("Training subset shape:", X_train.shape, y_train.shape)
print("Testing subset shape:", X_test.shape, y_test.shape)

```

```

-----
--
NameError                                Traceback (most recent call las
t)
Input In [18], in <cell line: 4>()
      1 from sklearn.model_selection import train_test_split
      3 # Split the normalized data into training and testing subsets
----> 4 X_train, X_test, y_train, y_test = train_test_split(X_scaled, y,
test_size=0.2, random_state=42)
      6 # Print the shapes of the training and testing subsets
      7 print("Training subset shape:", X_train.shape, y_train.shape)

NameError: name 'X_scaled' is not defined

```

In [26]:

```
# 2 Normalizing the dataset
url = "https://raw.githubusercontent.com/jbrownlee/Datasets/master/pima-indians-diabetes
names = ['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', '
df = pd.read_csv(url, names=names)

# Split the dataset into features and label
X = df.drop('Outcome', axis=1)
y = df['Outcome']

# Normalize the features using MinMaxScaler
scaler = MinMaxScaler()
X_norm = scaler.fit_transform(X)

# Print the first 5 rows of normalized features
print(X_norm[:5])
```

```
[[0.35294118 0.74371859 0.59016393 0.35353535 0.          0.50074516
  0.23441503 0.48333333]
 [0.05882353 0.42713568 0.54098361 0.29292929 0.          0.39642325
  0.11656704 0.16666667]
 [0.47058824 0.91959799 0.52459016 0.          0.          0.34724292
  0.25362938 0.18333333]
 [0.05882353 0.44723618 0.54098361 0.23232323 0.11111111 0.41877794
  0.03800171 0.          ]
 [0.          0.68844221 0.32786885 0.35353535 0.19858156 0.64232489
  0.94363792 0.2          ]]
```

In [27]:

```
# Splitting the data into training and testing subsets
X_train, X_test, y_train, y_test = train_test_split(X,y, test_size=0.2, random_state=42)
print("X_train shape: ", X_train.shape)
print("y_train shape: ", y_train.shape)
print("X_test shape: ", X_test.shape)
print("y_test shape: ", y_test.shape)
```

```
X_train shape: (614, 8)
y_train shape: (614,)
X_test shape: (154, 8)
y_test shape: (154,)
```

In [36]:

```
from sklearn.decomposition import PCA
# Apply PCA to reduce the dimensionality
pca = PCA(n_components=2)
X_pca = pca.fit_transform(X)

# Print the explained variance ratio of the first two principal components
print("Explained variance ratio:", pca.explained_variance_ratio_)

# Print the first 5 rows of the reduced dataset
print(X_pca[:5])
```

```
Explained variance ratio: [0.88854663 0.06159078]
[[-75.71465491 -35.95078264]
 [-82.3582676   28.90821322]
 [-74.63064344 -67.90649647]
 [ 11.07742273  34.89848586]
 [ 89.74378806 -2.74693708]]
```

In [45]:

```

from keras.models import Sequential
from keras.layers import Dense

# Define the model architecture
# This model contains 16 neurons with 1 hidden layer
# The output layer has 1 neuron
model = Sequential()
model.add(Dense(16, activation='relu', input_dim=X_train.shape[1]))
model.add(Dense(1, activation='sigmoid'))

# Compile the model
model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['accuracy'])
X_train_pca = X_train.iloc[:, :2]

# Train the model
# Training the model using fit method
# validation set to monitor the performance of the model
model.fit(X_train, y_train, epochs=100, batch_size=32, validation_data=(X_test, y_test))

```

```

Epoch 1/100
20/20 [=====] - 0s 8ms/step - loss: 7.4521 -
accuracy: 0.4202 - val_loss: 6.0188 - val_accuracy: 0.4351
Epoch 2/100
20/20 [=====] - 0s 3ms/step - loss: 4.2080 -
accuracy: 0.5423 - val_loss: 3.2250 - val_accuracy: 0.4610
Epoch 3/100
20/20 [=====] - 0s 2ms/step - loss: 2.7712 -
accuracy: 0.5456 - val_loss: 2.5086 - val_accuracy: 0.5325
Epoch 4/100
20/20 [=====] - 0s 3ms/step - loss: 2.3498 -
accuracy: 0.5586 - val_loss: 2.1931 - val_accuracy: 0.5455
Epoch 5/100
20/20 [=====] - 0s 2ms/step - loss: 2.0341 -
accuracy: 0.5570 - val_loss: 1.9826 - val_accuracy: 0.5584
Epoch 6/100
20/20 [=====] - 0s 3ms/step - loss: 1.7961 -
accuracy: 0.5814 - val_loss: 1.7918 - val_accuracy: 0.5714
Epoch 7/100
20/20 [=====] - 0s 2ms/step - loss: 1.5510 -
accuracy: 0.6000 - val_loss: 1.5510 - val_accuracy: 0.5818

```

IMPLEMENTING THE SAME CODE WITH DIFFERENT NO OF NEURONS

In [46]:

```

# By increasing the no of neurons the model will be able to identify complex patterns.

from keras.models import Sequential
from keras.layers import Dense

# Define the model architecture
# This model contains 16 neurons with 1 hidden layer
# The output layer has 1 neuron
model = Sequential()
model.add(Dense(32, activation='relu', input_dim=X_train.shape[1]))
model.add(Dense(1, activation='sigmoid'))

# Compile the model
model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['accuracy'])
X_train_pca = X_train.iloc[:, :2]

# Train the model
# Training the model using fit method
# validation set to monitor the performance of the model
model.fit(X_train, y_train, epochs=100, batch_size=32, validation_data=(X_test, y_test))

```

```

Epoch 1/100
20/20 [=====] - 1s 10ms/step - loss: 8.4687 -
accuracy: 0.3730 - val_loss: 6.3064 - val_accuracy: 0.3506
Epoch 2/100
20/20 [=====] - 0s 3ms/step - loss: 3.6688 -
accuracy: 0.4609 - val_loss: 2.2537 - val_accuracy: 0.4545
Epoch 3/100
20/20 [=====] - 0s 3ms/step - loss: 1.6702 -
accuracy: 0.5049 - val_loss: 1.2872 - val_accuracy: 0.6429
Epoch 4/100
20/20 [=====] - 0s 3ms/step - loss: 1.3683 -
accuracy: 0.5603 - val_loss: 1.2114 - val_accuracy: 0.6299
Epoch 5/100
20/20 [=====] - 0s 3ms/step - loss: 1.2386 -
accuracy: 0.5407 - val_loss: 1.1242 - val_accuracy: 0.6104
Epoch 6/100
20/20 [=====] - 0s 3ms/step - loss: 1.1236 -
accuracy: 0.5440 - val_loss: 1.0364 - val_accuracy: 0.6039
Epoch 7/100
20/20 [=====] - 0s 3ms/step - loss: 1.0525 -
accuracy: 0.5440 - val_loss: 1.0364 - val_accuracy: 0.6039

```

ACCURACY WITH DIFFERENT NUMBER OF NEURONS

In [49]:

```

neurons = [4, 8, 16, 32, 64]
accuracies = []

for n in neurons:
    # create model with n neurons in hidden layer
    model = Sequential()
    model.add(Dense(n, activation='relu', input_dim=X_train.shape[1]))
    model.add(Dense(1, activation='sigmoid'))

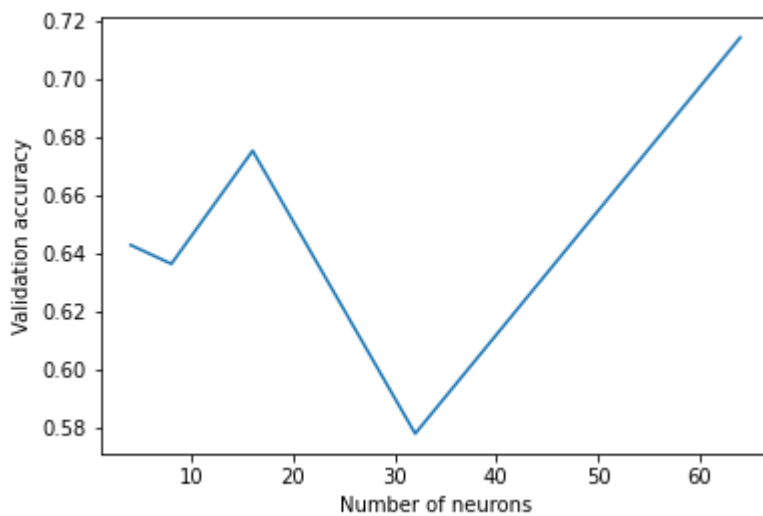
    # compile and fit model
    model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
    history = model.fit(X_train, y_train, validation_data=(X_test, y_test), epochs=50, b

    # record validation accuracy
    accuracies.append(history.history['val_accuracy'][-1])

# plot accuracy vs number of neurons
import matplotlib.pyplot as plt

plt.plot(neurons, accuracies)
plt.xlabel('Number of neurons')
plt.ylabel('Validation accuracy')
plt.show()

```



CONFUSION MATRIX AND CLASSIFICATION REPORT

In [54]:

```

from sklearn.metrics import confusion_matrix
y_pred = model.predict(X_test)
y_pred_binary = [1 if p >= 0.5 else 0 for p in y_pred]
cm = confusion_matrix(y_test, y_pred)
cr = classification_report(y_test, y_pred)

print('Confusion matrix:\n', cm)
print('Classification report:\n', cr)

```

5/5 [=====] - 0s 1ms/step

--

ValueError Traceback (most recent call last)

Input In [54], in <cell line: 4>()

```

2 y_pred = model.predict(X_test)
3 y_pred_binary = [1 if p >= 0.5 else 0 for p in y_pred]
----> 4 cm = confusion_matrix(y_test, y_pred)
5 cr = classification_report(y_test, y_pred)
7 print('Confusion matrix:\n', cm)

```

File ~\anaconda3\lib\site-packages\sklearn\metrics_classification.py:30

7, in confusion_matrix(y_true, y_pred, labels, sample_weight, normalize)

```

222 def confusion_matrix(
223     y_true, y_pred, *, labels=None, sample_weight=None, normalize
= None

```

```

224 ):
225     """Compute confusion matrix to evaluate the accuracy of a cla
ssification.

```

```

226
227     By definition a confusion matrix :math:`C` is such that :mat
h:`C_{i,j}`

```

```

(...)
305     (0, 2, 1, 1)
306     """
--> 307     y_type, y_true, y_pred = _check_targets(y_true, y_pred)
308     if y_type not in ("binary", "multiclass"):
309         raise ValueError("%s is not supported" % y_type)

```

File ~\anaconda3\lib\site-packages\sklearn\metrics_classification.py:93,

in _check_targets(y_true, y_pred)

```

90     y_type = {"multiclass"}
92     if len(y_type) > 1:
--> 93         raise ValueError(
94             "Classification metrics can't handle a mix of {0} and {1}
targets".format(

```

```

95             type_true, type_pred
96         )
97     )
99     # We can't have more than one value on y_type => The set is no mo
re needed
100     y_type = y_type.pop()

```

ValueError: Classification metrics can't handle a mix of binary and continuous targets

MLP WITH 2 HIDDEN LAYERS

In [55]:

```
from sklearn.neural_network import MLPClassifier

# create MLP model with two hidden layers
model = MLPClassifier(hidden_layer_sizes=(64, 32))

# fit the model to the training data
model.fit(X_train, y_train)
```

Out[55]:

```
MLPClassifier(hidden_layer_sizes=(64, 32))
```

In [56]:

```
y_pred = model.predict(X_test)
```

In [57]:

```
print(y_pred)
```

```
[1 0 0 0 0 1 0 0 1 0 0 0 0 0 0 1 0 0 1 0 0 0 1 0 0 1 0 0 0 0 0 0 1 1 0 1
0
0 0 1 0 0 0 0 0 0 1 0 0 0 0 1 1 0 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0 1 1 0 0
0
0 0 0 1 0 0 1 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 1 0 1 1 0 0
0
0 0 1 0 1 1 0 0 1 0 0 0 0 1 1 0 1 1 0 1 1 0 1 0 0 0 0 1 0 0 0 0 1 0 0 0
0
0 0 0 0 1 0]
```

MLP WITH 3 HIDDEN LAYERS

In [61]:

```
from sklearn.neural_network import MLPClassifier

# define the model with three hidden layers
model = MLPClassifier(hidden_layer_sizes=(20, 10, 5))

# train the model on the training data
model.fit(X_train, y_train)
```

Out[61]:

```
MLPClassifier(hidden_layer_sizes=(20, 10, 5))
```

In [62]:

```
y_pred = model.predict(X_test)
```

In [63]:

```
print(y_pred)
```

```
[1 0 0 0 1 1 0 0 1 1 1 1 1 0 0 1 0 0 1 0 0 0 0 0 1 0 0 0 0 0 1 1 1 0 1
1
0 1 1 0 0 0 1 0 1 1 0 0 1 0 1 1 1 0 0 0 0 0 1 0 0 0 1 0 1 0 0 0 1 1 0 0
0
0 0 0 1 0 0 1 0 0 0 0 1 1 1 0 0 0 0 0 0 1 0 1 0 1 0 0 0 1 1 1 0 1 1 0 0
0
1 0 1 0 0 1 0 0 1 0 0 0 0 1 0 0 1 1 0 1 1 0 1 1 0 1 1 1 0 0 0 1 1 0 0 0
0
0 1 0 0 1 0]
```

USING LOGISTIC REGRESSION FOR THIS MODEL

In [68]:

```
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()

# train the model on the training data
model.fit(X_train, y_train)

# make predictions on the test data
y_pred = model.predict(X_test)
```

```
C:\Users\pavan\anaconda3\lib\site-packages\sklearn\linear_model\_logisti
c.py:814: 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 i
n:

<https://scikit-learn.org/stable/modules/preprocessing.html> (<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 (https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression)

```
n_iter_i = _check_optimize_result(
```

In [1]:

```
print(y_pred = model.predict(X_test))
```

```
-----  
--  
NameError                                Traceback (most recent call las  
t)  
Input In [1], in <cell line: 1>()  
----> 1 print(y_pred = model.predict(X_test))  
  
NameError: name 'model' is not defined
```

In []: