Technological Institute of the Philippines	**Quezon City - Computer Engineering**
Course Code:	CPE 019
Code Title:	Emerging Technologies in CpE 2 - Fundamentals of Computer Vision
2nd Semester	AY 2023-2024

ACTIVITY NO.	**Assignment 5.2: Build and Apply Multilayer Perceptron**
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Section	CPE32S3
Date Performed:	03/20/2024
Date Submitted:	03/26/2024
Instructor:	Engr. Roman M. Richard

OBJECTIVES

In this assignment, you are task to build a multilayer perceptron model. The following are the requirements:

- Choose any dataset
- Explain the problem you are trying to solve
- Create your own model
- Evaluate the accuracy of your model

Note: Submit a PDF, the dataset and the notebook you used for this assignment.

REQUIRED RESOURCES

- PC / Laptop with Internet Access
- **Python libraries:** pandas, numpy, matplotlib.pyplot, and seaborn.
- **Datafiles:** heart.csv
- Link of dataset: https://www.kaggle.com/code/mragpavank/heart-disease-uci

SCENARIO / BACKGROUND

The Heart Disease UCI dataset contains the following variables such as age, sex, chest pain (cp), resting blood pressure (trestbps), serum cholesterol levels (chol), fasting blood sugar level (fbs), resting electrocardiogram (restecg), max. heart rate(thalac), exercise-induced angina (exang), ST depression induced by exercise (oldpeak), peak exercise ST segment (slope), No. of major vessels colored by fluoroscopy (ca), thallium stress test(thal), & presence of heart disease(pred_attribute).

The target variable will be "the pred_attribute" since my goal here is to create a model that predict whether the patient has a heart disease or not by labeling it as 0 - absence and 1.

Data Exploration

- Importing the libraries and dataset
- Head(), Tail(), Info()
- Visualization using Histogram

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
```

```
dataset = pd.read_csv("/content/heart.csv", na_values="?")
dataset.rename(columns={"target": "pred_attribute"}, inplace=True)
```

```
# Replacing the value 1,2,3,4 to 1 to distinguish betweem presence (1) and absence (0) of heart disease
dataset["pred_attribute"].replace(inplace=True, value=[1, 1, 1, 1], to_replace=[1, 2, 3, 4])

np_dataset = dataset.to_numpy()

feature_names = ['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs',
                 'restecg','thalach', 'exang', 'oldpeak', 'slope', 'ca', 'thal']
```

```
dataset.head(20)
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	pred_attrib
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	
5	57	1	0	140	192	0	1	148	0	0.4	1	0	1	
6	56	0	1	140	294	0	0	153	0	1.3	1	0	2	
7	44	1	1	120	263	0	1	173	0	0.0	2	0	3	
8	52	1	2	172	199	1	1	162	0	0.5	2	0	3	
9	57	1	2	150	168	0	1	174	0	1.6	2	0	2	
10	54	1	0	140	239	0	1	160	0	1.2	2	0	2	
11	48	0	2	130	275	0	1	139	0	0.2	2	0	2	
12	49	1	1	130	266	0	1	171	0	0.6	2	0	2	
13	64	1	3	110	211	0	0	144	1	1.8	1	0	2	
14	58	0	3	150	283	1	0	162	0	1.0	2	0	2	
15	50	0	2	120	219	0	1	158	0	1.6	1	0	2	
16	58	0	2	120	340	0	1	172	0	0.0	2	0	2	
17	66	0	3	150	226	0	1	114	0	2.6	0	0	2	
18	43	1	0	150	247	0	1	171	0	1.5	2	0	2	
19	69	0	3	140	239	0	1	151	0	1.8	2	2	2	

```
dataset.tail(20)
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	pred_attri
283	40	1	0	152	223	0	1	181	0	0.0	2	0	3	
284	61	1	0	140	207	0	0	138	1	1.9	2	1	3	
285	46	1	0	140	311	0	1	120	1	1.8	1	2	3	
286	59	1	3	134	204	0	1	162	0	0.8	2	2	2	
287	57	1	1	154	232	0	0	164	0	0.0	2	1	2	
288	57	1	0	110	335	0	1	143	1	3.0	1	1	3	
289	55	0	0	128	205	0	2	130	1	2.0	1	1	3	
290	61	1	0	148	203	0	1	161	0	0.0	2	1	3	
291	58	1	0	114	318	0	2	140	0	4.4	0	3	1	
292	58	0	0	170	225	1	0	146	1	2.8	1	2	1	
293	67	1	2	152	212	0	0	150	0	0.8	1	0	3	
294	44	1	0	120	169	0	1	144	1	2.8	0	0	1	
295	63	1	0	140	187	0	0	144	1	4.0	2	2	3	
296	63	0	0	124	197	0	1	136	1	0.0	1	0	2	
297	59	1	0	164	176	1	0	90	0	1.0	1	2	1	
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3	
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3	
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3	
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3	
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2	

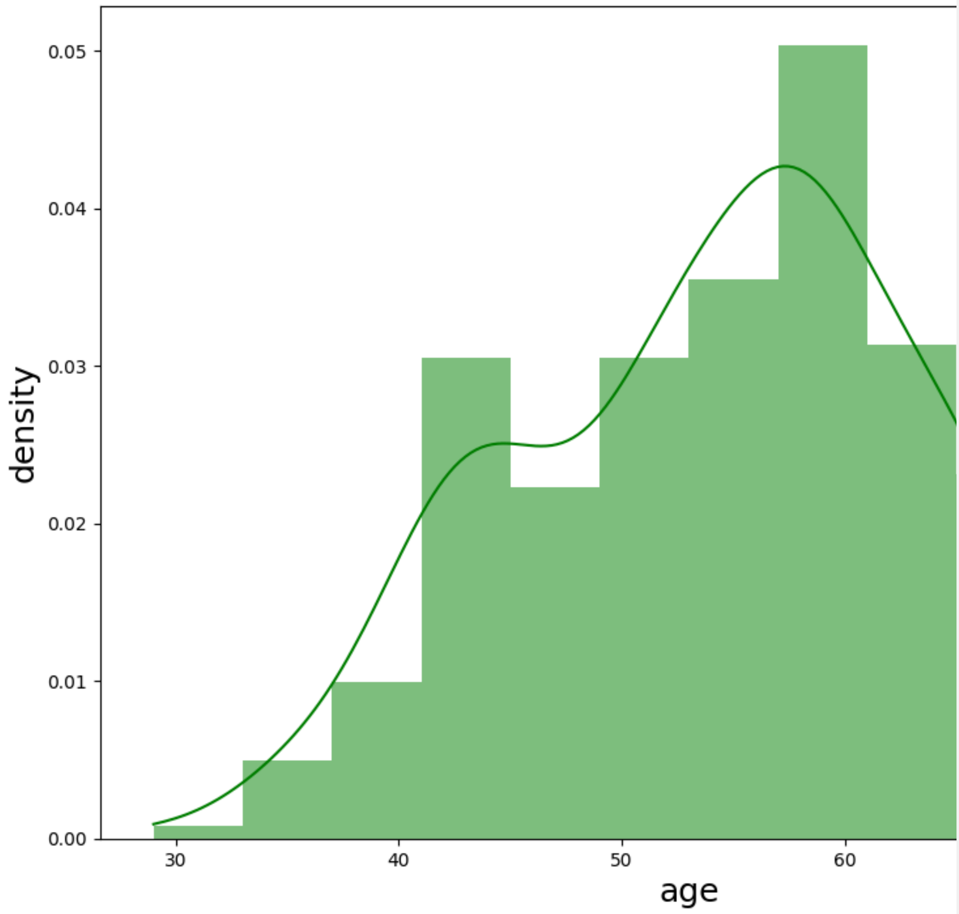
```
dataset.info()
```

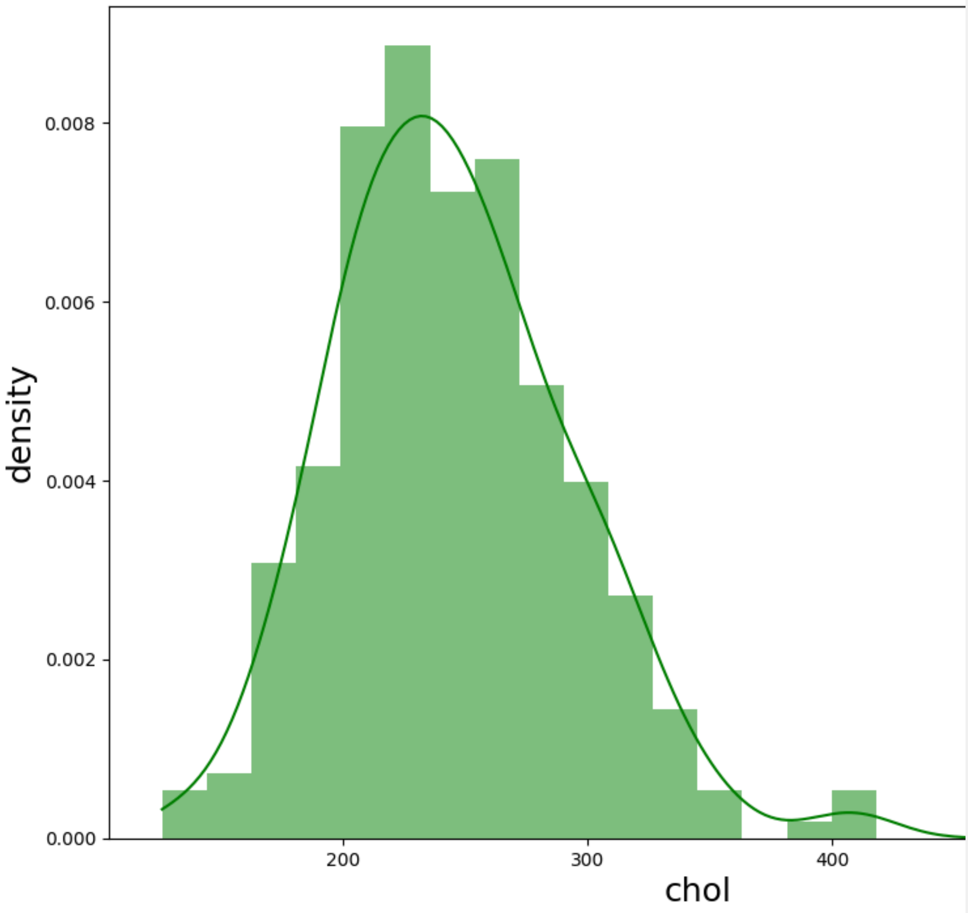
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   age             303 non-null    int64  
 1   sex             303 non-null    int64  
 2   cp              303 non-null    int64  
 3   trestbps        303 non-null    int64  
 4   chol            303 non-null    int64  
 5   fbs             303 non-null    int64  
 6   restecg         303 non-null    int64  
 7   thalach         303 non-null    int64  
 8   exang           303 non-null    int64  
 9   oldpeak         303 non-null    float64
 10  slope           303 non-null    int64  
 11  ca              303 non-null    int64  
 12  thal            303 non-null    int64  
 13  pred_attribute  303 non-null    int64  
dtypes: float64(1), int64(13)
memory usage: 33.3 KB
```

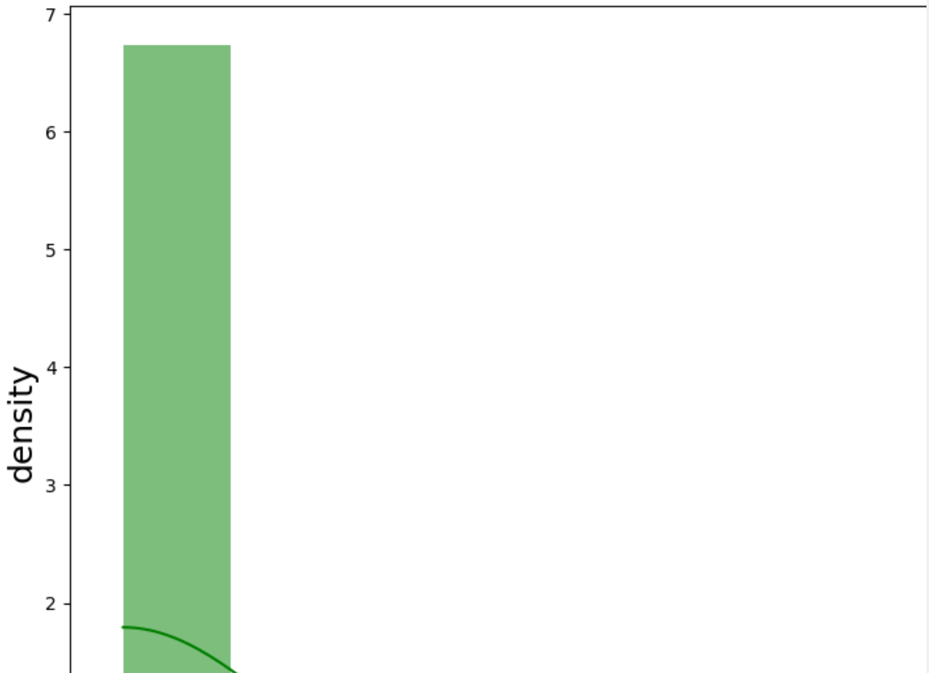
Analysis

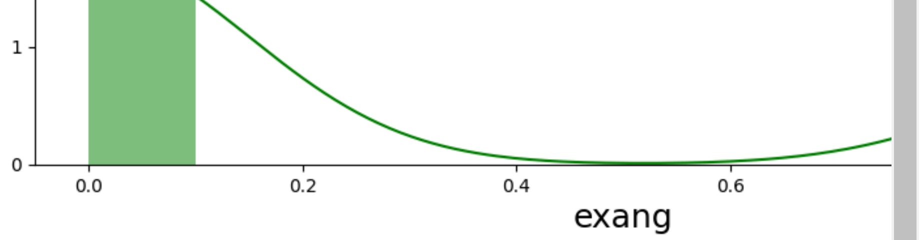
As you can see above, each column has a complete no. of entries which ensures the statistical validity. It enables more robust explonatory data analysis (EDA)

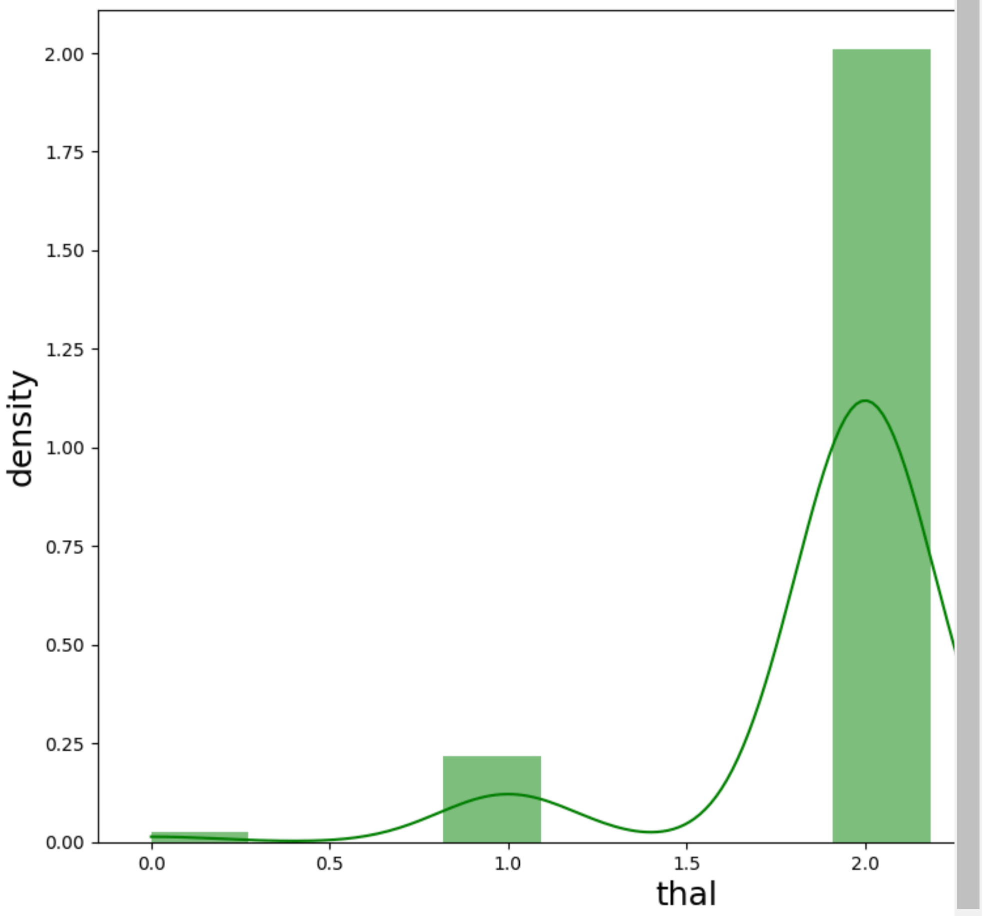
```
fig, ax = plt.subplots(ncols=4, nrows=4, figsize=(40, 30))
index = 0
ax = ax.flatten()

for col, value in dataset.items():
    col_dist = sns.histplot(value, ax=ax[index], color='green', kde=True, stat="density", linewidth=0)
    col_dist.set_xlabel(col, fontsize=18)
    col_dist.set_ylabel('density', fontsize=18)
    index += 1

plt.tight_layout(pad=0.5, w_pad=0.7, h_pad=5.0)
```


0.05
0.04
0.03
0.02
0.01
0.00
density
30
40
50
60
age


0.008
0.006
0.004
0.002
0.000
density
200
300
400
chol


7
6
5
4
3
2
density



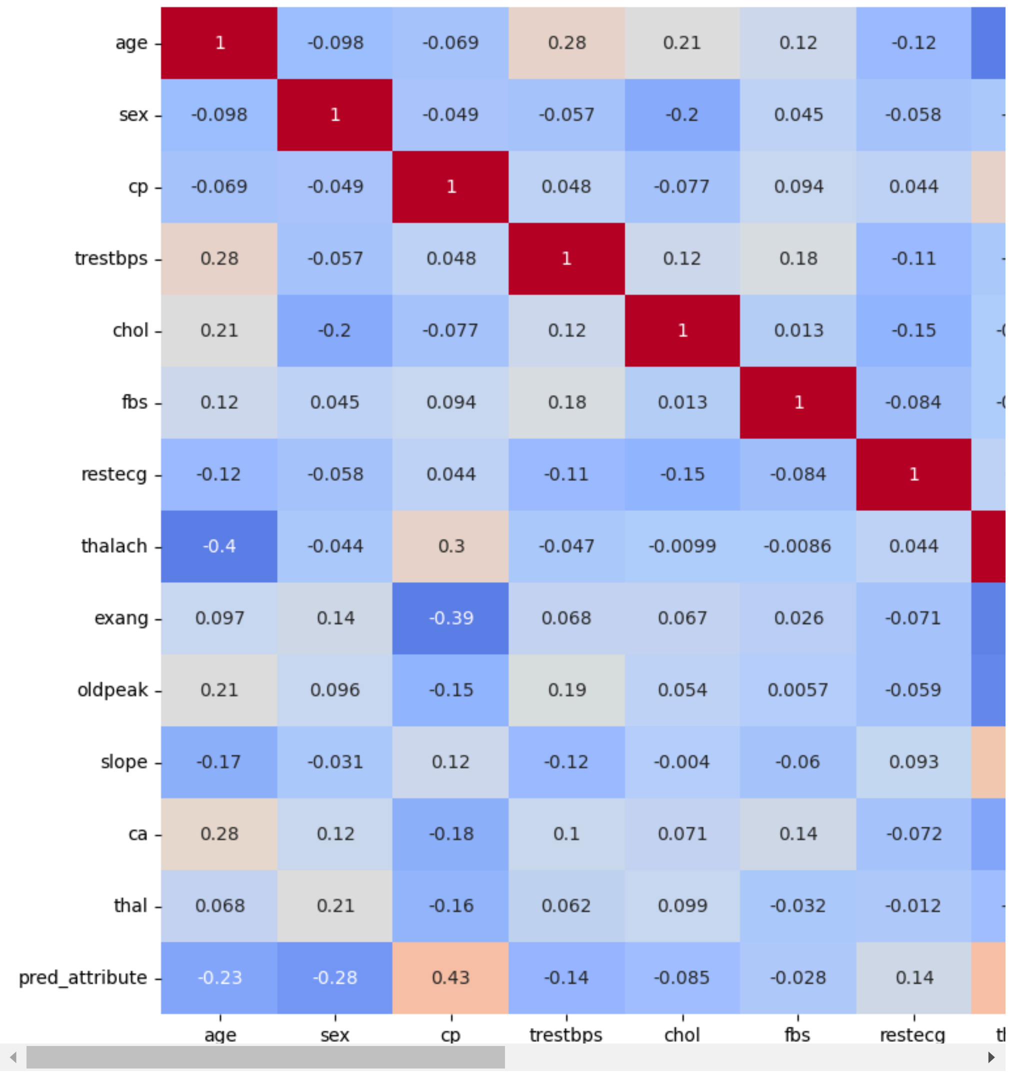


Analysis

As you can see above, that's the actual counts for each variable that presented by bar plot.

```
correlation = dataset.corr()

plt.figure(figsize = (20, 10))
sns.heatmap(correlation, cmap = 'coolwarm', annot = True)
```

```
<Axes: >
```



Analysis

The Pearson Correlation plot indicated that there's no strongly correlated features. Which means it's good from a point of view of feeding these features into learning model since there's isn't much redundant or superfluous data in training set.

Data Pre-Processing

- Deal with missing values
- Data Balancing
- Statistics
- Stratification
- Training and Testing Sets
- Prediction of Training and Testing Sets

```
dataset.isnull().sum()
```

```
age               0
sex               0
cp                0
trestbps          0
chol              0
fbs               0
restecg           0
thalach           0
exang             0
oldpeak           0
slope             0
ca                0
thal              0
pred_attribute    0
dtype: int64
```

```
#Counting the target value
dataset.dtypes
dataset['pred_attribute'].astype(int)
dataset['pred_attribute'].value_counts()
```

```
1    165
0    138
Name: pred_attribute, dtype: int64
```

```
Zero = dataset[dataset.pred_attribute == 0] # absence
One = dataset[dataset.pred_attribute == 1]  # presence
```

```
ZeroDS = Zero.sample(len(One), replace = True, random_state=100)
OneDB = pd.concat([ZeroDS, One])
```

```
count = OneDB['pred_attribute'].value_counts()
print(count)
```

```
0    165
1    165
Name: pred_attribute, dtype: int64
```

Stratification

I cplit the dataset into training and testing dataset by selecting it randomly. There's an instances that class label 1 is many than class 2, but since I stratify the data, I have now a proportionate data for both classes of training and testing data.

```
X = dataset[['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg',
             'thalach', 'exang', 'oldpeak', 'slope', 'ca', 'thal']]
y = dataset['pred_attribute']
```

```
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state= 50)

freqs = pd.DataFrame({"Training dataset": y_train.sum(),
                      "Test dataset":y_test.sum(),
                      "Total": y.sum()},
                     index=["Healthy", "Sick"])
freqs[["Training dataset", "Test dataset", "Total"]]
```

	Training dataset	Test dataset	Total
Healthy	113	52	165
Sick	113	52	165

Analysis

The dataset available from UCI repository has 303 samples;the training and test datasets are randomly selected with 30% of the original dataset corresponding to test datasets. The proportion of the classes of interest (disease/sick) in both sets are check to be similar, ensuring a fair and reliable evaluation of model's performance

```
# Checking the accuracy
from sklearn.linear_model import LogisticRegression

model = LogisticRegression(random_state = 50)
model.fit(X_train, y_train)

print("Accuracy on training set: ", model.score(X_train, y_train))
print("Accuracy on test set: ", model.score(X_test, y_test))
```

```
Accuracy on training set:  0.8632075471698113
Accuracy on test set:  0.8241758241758241
/usr/local/lib/python3.10/dist-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(
```

Analysis

The accuray for both training and testing set are approximately 86.32% and 82.42%. The Training Accuracy indicates a high training accuracy which means it learned the patterns present in training data. The Testing Accuracy indicates that the model is not overfitting excessively to the training data. There's a minor performance drop between training and testing, it demonstrate robustness and generalization capablities.

Confusion Matrix of training and test sets

Predict class labels for the training set

0 = Healthy

1 = Sick

```
pred_train = model.predict(X_train)
pd.crosstab(y_train, pred_train, rownames=['Predicted'], colnames=['Reality'], margins=True)
```

Reality	0	1	All
Predicted			
0	79	20	99
1	9	104	113
All	88	124	212

Predict class labels for the test set

0 = Healthy

1 = Sick

```
pred_test = model.predict(X_test)
pd.crosstab(y_test, pred_test, rownames=['Predicted'], colnames=['Reality'], margins=True)
```

```
Reality    0   1  All
Predicted
0         25  14   39
1          2  50   52
All       27  64   91
```

Model 1 - Multilayer Perceptron using Sequential model

The two links below was may basis to create a model for Multilayer Perceptron

Link: https://www.kaggle.com/code/rezasemyari/rice-image-classification-cnn-0-99

Link: https://colab.research.google.com/drive/1GL6gT3nJ0KFcEhY7-5k-8LMToLRceu-u?usp=sharing

```
from tensorflow import keras

features = ['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs',
                 'restecg','thalach', 'exang', 'oldpeak', 'slope', 'ca', 'thal']

input_shape = (13,)

cnn = keras.models.Sequential()
cnn.add(keras.layers.Dense(32, activation='relu', input_shape=input_shape))
cnn.add(keras.layers.Dense(64, activation='relu'))
cnn.add(keras.layers.Dropout(0.5))
cnn.add(keras.layers.Dense(1, activation='sigmoid'))

cnn.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
cnn.summary()
```

```
Model: "sequential_11"
┏━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━┳━━━━━━━━━━━━━━━━━━━━━━━━━━━━━┳━━━━━━━━━━━━━━━━━┓
┃ Layer (type)                         ┃ Output Shape                ┃         Param # ┃
┡━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━╇━━━━━━━━━━━━━━━━━━━━━━━━━━━━━╇━━━━━━━━━━━━━━━━━┩
│ dense_19 (Dense)                     │ (None, 32)                  │             448 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ dense_20 (Dense)                     │ (None, 64)                  │           2,112 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ dropout_4 (Dropout)                  │ (None, 64)                  │               0 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ dense_21 (Dense)                     │ (None, 1)                   │              65 │
└──────────────────────────────────────┴─────────────────────────────┴─────────────────┘
 Total params: 2,625 (10.25 KB)
 Trainable params: 2,625 (10.25 KB)
 Non-trainable params: 0 (0.00 B)
```

Analysis

These layers consist of dense that connected to each layer with different output shapes and parameter counts. There's a droupout layer to prevent overfitting by randomly dropping connections between neurons during training. The output layer is dense layer with single neuron, that suitable for binary classification task.

The total parameters of my model has 2,625 in total. All the parameters in my model are trainable. There are no non-trainable parameters in my model

```
cnn.compile(optimizer='adam',metrics=['accuracy'],loss='binary_crossentropy')
```

```
history = cnn.fit(X_train, y_train, epochs=100, shuffle=True,
                  batch_size=100,
                  validation_split=0.1)
```

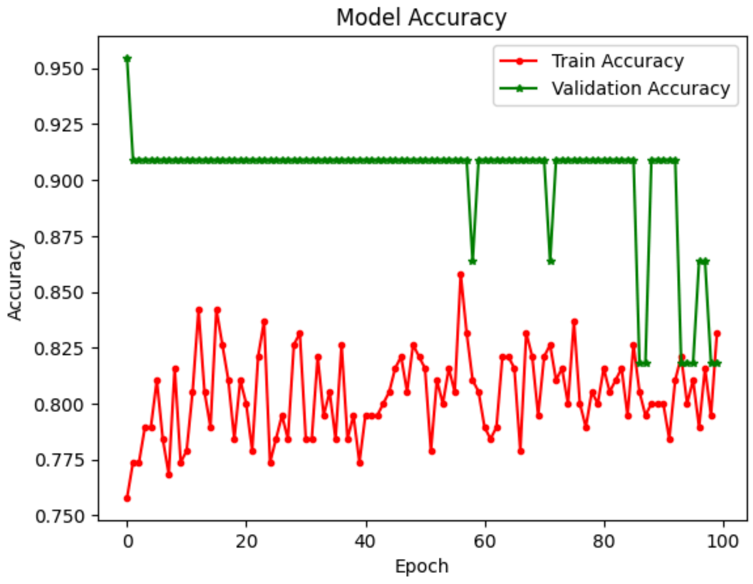
```
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 41ms/step - accuracy: 0.7865 - loss: 0.4340 - val_accuracy: 0.8182 - val_loss: 0.3937
Epoch 89/100
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 41ms/step - accuracy: 0.7967 - loss: 0.4041 - val_accuracy: 0.9091 - val_loss: 0.3939
Epoch 90/100
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 47ms/step - accuracy: 0.7767 - loss: 0.4588 - val_accuracy: 0.9091 - val_loss: 0.3963
Epoch 91/100
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 34ms/step - accuracy: 0.7900 - loss: 0.4019 - val_accuracy: 0.9091 - val_loss: 0.4020
Epoch 92/100
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 30ms/step - accuracy: 0.7961 - loss: 0.4009 - val_accuracy: 0.9091 - val_loss: 0.3968
Epoch 93/100
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 29ms/step - accuracy: 0.8004 - loss: 0.4175 - val_accuracy: 0.9091 - val_loss: 0.3964
Epoch 94/100
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 30ms/step - accuracy: 0.8207 - loss: 0.4127 - val_accuracy: 0.8182 - val_loss: 0.4009
Epoch 95/100
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 30ms/step - accuracy: 0.8033 - loss: 0.4255 - val_accuracy: 0.8182 - val_loss: 0.4064
Epoch 96/100
```

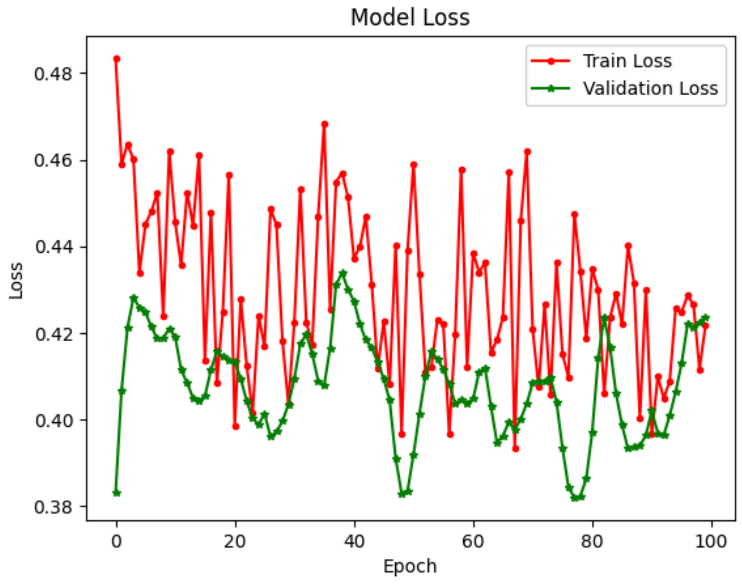
Analysis

The X and Y train here is for training data and label. I set the epoch as 100 so it passes 100 times to the entire dataset. I shuffle the training data before epoch. I also set the batch size as 100 it specifies the no. of samples that will propagated through the network before parameter update. Then 10% of training data is used for validation during training.

```
def plot(history):
    plt.plot(history.history['accuracy'], marker='o', color='red', markersize=3, label='Train Accuracy')
    plt.plot(history.history['val_accuracy'], marker='*', color='green', markersize=4, label='Validation Accuracy')
    plt.title('Model Accuracy')
    plt.ylabel('Accuracy')
    plt.xlabel('Epoch')
    plt.legend()
    plt.show()

    plt.plot(history.history['loss'], marker='o', color='red', markersize=3, label='Train Loss')
    plt.plot(history.history['val_loss'], marker='*', color='green', markersize=4, label='Validation Loss')
    plt.title('Model Loss')
    plt.ylabel('Loss')
    plt.xlabel('Epoch')
    plt.legend()
    plt.show()
```

```
plot(history)
```





Analysis