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Performance Evaluation of Artificial Neural Network and Decision Tree Machine Learning Models in Malaria Prediction

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I. INTRODUCTION

Malaria disease continues to be one of the endemic diseases in Nigeria, Africa, and some parts of the world. Millions of people suffer from the disease annually which results in high death statistics. Malaria is lethal and is at the top of the charts when compared to other diseases, in terms of mortality rate. This situation has made research in malaria disease infections, control, prediction, and treatment a topical concern to researchers both nationally and internationally - even by organizations such as the World Health Organization (WHO).

This research implores the use of two Machine Learning algorithms which are Artificial Neural Network (ANN) and Decision Tree Classifier, on a locally collected Malaria dataset, to evaluate their performance accuracies. The artificial Neural Network Model optimizes for a high prediction accuracy of 95.50% at two hidden layers with 55 and 65 neurons respectively. The activation functions used were Relu and Sigmoid as well as Adam optimizer. Similarly, the Decision Tree classifier's optimum prediction accuracy was 94.17% when pruned at the maximum depth of 4 and cost complexity value of 0.001. Therefore, Artificial Neural Network was adjudged as an algorithm with the highest prediction accuracy based on the Malaria dataset.

However, in the context of the study and the application of the model in real-life disease prediction in the healthcare sector, the Decision Tree classifier did a better feature engineering which revealed the patterns of the Malaria symptoms. This white-box model of decision tree would be more beneficial to health professionals who may need to isolate and treat symptoms in the case of patients with drug resistance. The study concludes that the two algorithms could be used complementarily in disease prediction because of their relative strengths.

1.1 Objectives of the Study

i. Identify the major clinical signs and symptoms from local clinical data that are necessary for accurate predictions of malaria disease using machine learning.
ii. Identify the hyper parameter values at which the algorithms perform best and at what stage the models were able to predict Malaria correctly.
iii. Compare the prediction accuracy of each algorithm (Artificial Neural Network and Decision Tree Algorithms).

II. LITERATURE REVIEW

2.1 Conceptual Understanding of Machine Learning and Data Mining

Machine Learning is among the many approaches available within the field of artificial intelligence research which uses several probabilistic, statistical, and optimization techniques in training large data sets, to examine and "learn" challenging patterns in complicated, big, and noisy data. It's all about figuring out how to perform better in future forecasts based on what you have learnt from prior data (Cruz & Wishart, 2007). For example, learns to respond intelligently or accurately forecast sickness based on a set of observations. Machine learning's goal is to create learning systems that can learn on their own, without the need for human involvement. While humans are prone to making errors during analysis or while trying to create correlations between several features, machine learning may be utilized. It is utilized to improve a system's efficiency and also machine design (Archana & Elangovan, 2014). Machine learning is a sort of artificial intelligence that uses grouping and classifying algorithms to predict current sickness using real-world data. Many researchers who are attempting to forecast illness using medical data, find this technique to be exciting (Durairaj & Ranjani, 2013).

Unsupervised and supervised learning are the two major kinds of machine learning (de Ridder, de Ridder, & Reinders, 2013). Without any instruction or user intervention, unsupervised learning identifies an underlying structure in the data. In contrast, supervised learning uses a labeled dataset to construct a prediction model. In the absence of rigid programming restrictions, supervised machine learning infers a prediction model from a dataset. This means that the machine learning algorithm can handle data with many variables because programming rules for every combination of variables is unnecessary. The number of variables is also referred to as the dimensionality. During supervised learning, the algorithm feeds each example to the model in the form of an input vector of

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features, and the model returns a prediction in the form of an output vector. The algorithm then compares the output with the example's label. The label is also known as the ground truth. If the prediction is off from the ground truth, the algorithm tunes the model's parameters to make better predictions. The representation, evaluation, and optimization components of supervised machine learning algorithms are based on these principles. In Classification problems, supervised machine learning algorithms are widely adopted for solving such problems (Domingos, 2012). Examples of these algorithms are the Artificial Neural Network, Support Vector Machines, K-nearest Neighbor and Decision Tree, etc.

2.2 Artificial Neural Network Layers

In an Artificial Neural Network, there might be several layers. Each layer receives many inputs to its nodes, depending on the complexity of the information to be processed, and transmits the information to the next layer after performing certain mathematical computations. As a result, each layer feeds information to the next. Unlike the input and output layers, the number and size of each training hidden layer for any particular issue are unknown at the outset (Basheer & Hajmeer, 2000). In an artificial neural network, there are three types of layers; input, hidden, and output layers.

i. Input Layer: This is the layer responsible for grouping the network's input data group upon introduction. Before any form of analysis, the input layer parameters have to be selected. Each of the input neurons gets sent to the next layer; the hidden layer. The quantity of input data is the same as the number of neurons in an input layer.
ii. Hidden Layer: This is the fundamental function of the network. Data received from the input layer gets processed within the hidden layers, before being transferred to the output layer.
iii. Output Layer: This is where the learning occurs. The output (consisting of hidden layers) is put together into linear units. The output layer is the last layer within the network where processing and outputting the received data from the hidden layer happens. The number of neurons within the network equals the number of outputs received.

III. METHODOLOGY

3.1 Data Collection

As the research must be conducted using real-life data, malaria data gotten from the Primary Healthcare Center (PHC) in the Mile Six area within Jalingo, Taraba State, Nigeria, forms bulk of the dataset. With each patient record pulled out and reviewed for signs and symptoms of malaria and and then, a check for laboratory confirmation of results from the diagnosis. Moreso, the data is rearranged to meet the expected format of Data Mining and Machine Learning.

3.2 Required Dataset Size

This study used a purposive sampling method since the dataset was personally collated directly from the field by the researcher, and based on the dataset available in the study area. The study used 400 instances of datasets to ensure a more robust model, in tandem with the number used in a study like Okagbue *et al.* (2021), to build a similar malaria model.

3.3 Data Preparation and Normalization

Data preparation is important for every data mining tool. Before the collection of data, the researcher was guided within the ethical guidelines involved with data collection. Therefore, names and file numbers of patients contained in the data source file are eliminated in the pre-proceesing of the data - to ensure anonymity. Since more data with informative features usually result in better performance, effort is spent on labelling and normalizing data.

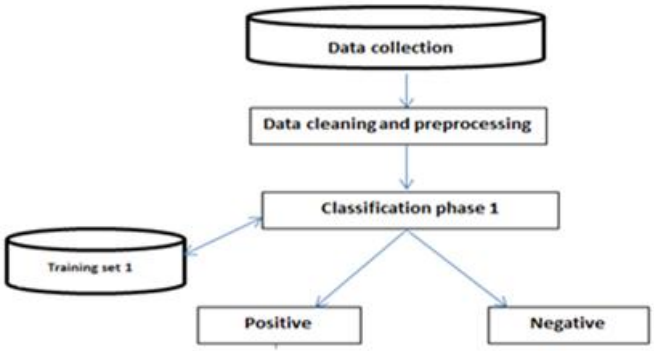

Figure 3.1: Prediction Framework

3.4 Modelling Approach

Graphical representation of process model of the artificial neural network and decision tree classifier will be used to illustrate the working structure of the model with the aid of Unified Modeling Language (UML).

To model the malaria diagnosis prediction symptoms such as (*fever, vomiting, coma, respiratory distress, convulsion, headache and nausea*) would be used as input parameters.

The graphical modelling process of the malaria dataset is as shown below:

3.5 Model Training and Training Algorithm

The objective of model training is to minimize an objective function which will be used in finding the class of the predicted malaria (i.e., whether positive or negative). To train the Neural Network by adjusting the weight, this would adopt back propagation algorithm, an iterative procedure. This procedure has three steps:

i. Forward propagation: To compute the best weights of the input criteria, the feed forward method will be employed. The feed forward algorithm's mathematical models
ii. Backward Propagation: The partial derivatives of the performance regarding the weights and biases determined in each layer are propagated backwards toward the input layer, with the mistakes at the output layer transmitted backwards toward the input layer.
iii. Weight adjustment: Based on the gradient, a nonlinear numeric optimization technique identifies the weights that minimizes the error.

Additionally, the decision tree classifier model training involves the following steps:

1. Designing the preliminary decision tree model

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2. Evaluating the performance of the model

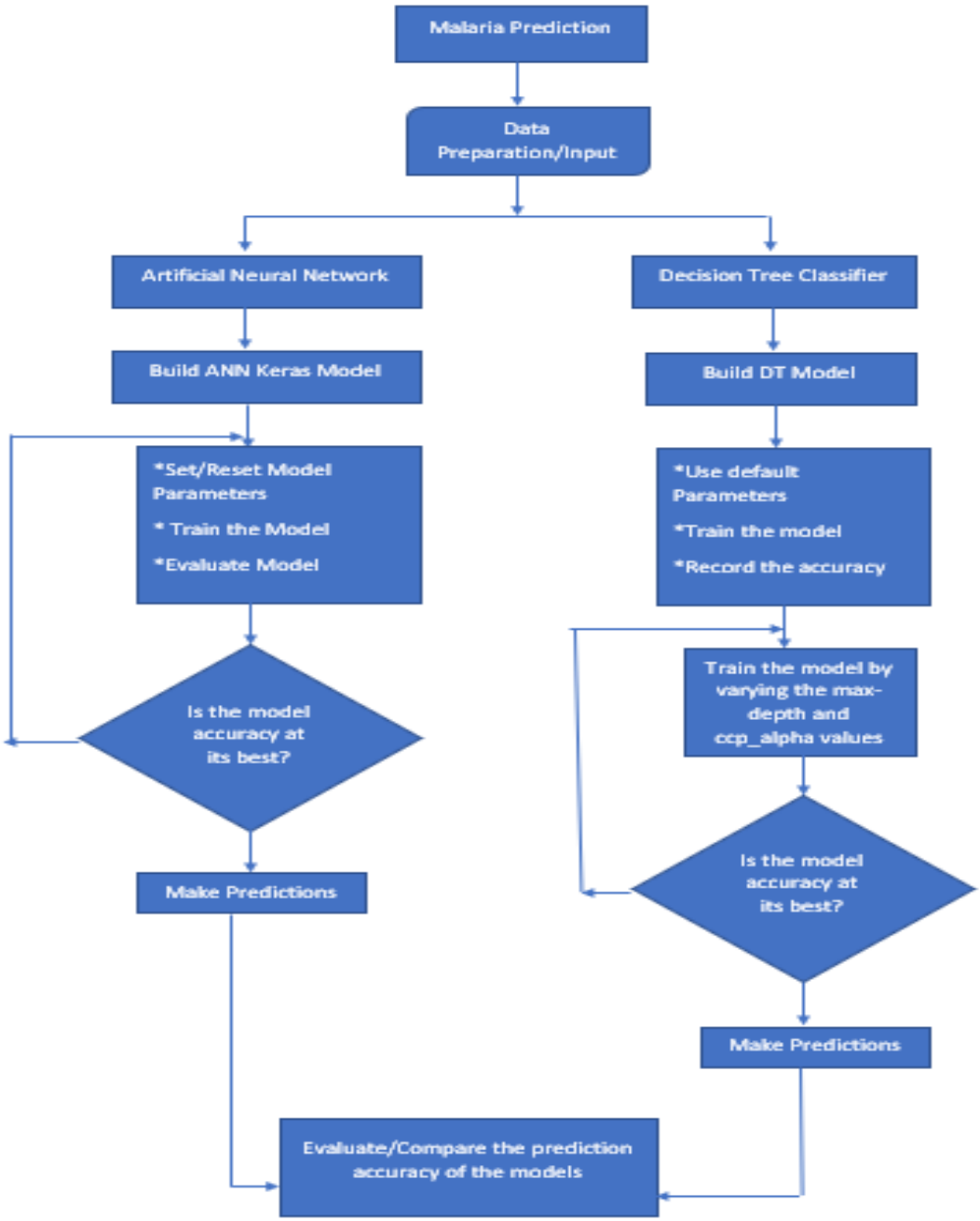

Figure 3.2: The Graphical Representation of the Malaria Prediction Approach

IV. Result and Analysis

4.1 Data Presentations for Artificial Neural Network and Decision Tree Models

To build an Artificial Neural Network model and Decision Tree model for malaria prediction, parameters that would form the model inputs must be identified and collected. Raw data on Malaria was collected from a primary healthcare center in Jalingo, Taraba State. A total of 400 manual samples were obtained and the data was extracted from the patients file to make the dataset. The data was coded into a Microsoft Excel sheet and converted into a comma separated values (csv) file. This was done in order to make it easy for the python data frame to read it from the jupyter file folder already installed from the anaconda packages.

In addition, the patient ID numbers which were originally collected with the data were later removed by the researcher. This was to ensure anonymity of the datasets and satisfies one of the ethical procedures for using healthcare data in research. The different data items used in predicting Malaria are as shown below in the table below. The independent symptoms/variables

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for Malaria prediction as gathered from the medical health facility are: *Fever, Vomiting, Nausea, Loss of appetite, Headache, Cough, Fatigue, Catarrh, Body pains, stomach pain, Back pain, Dizziness, Diarrhea, Heart burn*. The dependent variable is the class or the diagnosis status of the patients.

TABLE 4.1: Malaria Dataset Sample

```
In [30]: import pandas as pd
         dataframe = pd.read_csv("MalariaFieldData1.csv")
         #dataframe[dataframe.Class==0]
         dataframe
```

Out[30]:

	Fever	Vomiting	Nausea	Loss of Appetite	Headache	Cough	Fatigue	Catarrh	Body Pains	Stomach Pain	Back Pain	Dizziness	Diarrhea	Heart Burn	Class
0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1
1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	1
2	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
3	1	0	0	0	0	1	0	1	0	0	0	0	0	0	1
4	1	1	0	0	1	1	0	1	0	0	0	0	0	0	1
5	1	0	0	0	0	0	0	0	1	1	1	0	0	1	1
6	1	0	0	0	1	0	0	1	0	1	0	0	0	0	1
7	1	0	0	0	1	0	0	1	0	0	0	0	0	0	1
8	1	0	0	0	1	1	0	1	1	0	0	0	0	0	1
9	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
390	1	1	0	0	1	0	0	0	1	0	0	0	0	1	1
391	1	1	0	0	0	0	0	0	0	1	0	0	0	1	1
392	0	0	0	0	1	0	0	0	1	1	0	0	1	1	1
393	1	1	0	0	1	0	0	0	0	1	0	0	0	0	1
394	0	1	0	0	1	0	0	0	0	1	0	1	0	0	1
395	1	1	0	0	1	0	0	0	0	0	0	0	0	0	1
396	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
397	1	1	0	0	1	0	0	0	0	1	0	0	0	0	1
398	1	0	0	0	1	0	1	0	0	0	0	0	0	0	1
399	1	0	0	0	1	0	0	0	0	1	0	0	0	0	1

400 rows × 15 columns

==========Displaying the Classes of the Datasets==========

```
In [3]: dataframe.groupby('Class').size()
Out[3]: Class
        0     48
        1    352
        dtype: int64
```

Figure 4.1: Showing the Classes of the Dataset

Also, the malaria dataset has two classes. These are the positive, represented as 1, and Negative, represented as 0. The positive class shows that a patient has Malaria while the negative is the reverse. This makes this prediction-based classification a binary classification task. Therefore, the 0s and 1s represent the two classes of the malaria prediction problem. The classes of the datasets as identified by python data frame is as indicated below. The 0s has 48 data items, while the 1s has 352 data items.

4.2 Performance of Artificial Neural Network Model for Malaria

Artificial Neural Network performance on new dataset is stochastic or probabilistic. Therefore, the model building process goes through a series of experiments, in order to ascertain the optimal number of layers and neurons at which the algorithm performs at its highest. The neural network library known as Keras is used – with its model in Sequential stacks of layers inbuilt in python programming language that supports multi-layer network, used. After the dataset was partitioned and initial parameters set, the model was trained at 50 epochs in order to obtain the performance of the model and accuracy metrics as shown below:

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```
Epoch 1/50
400/400 [==============================] - 0s - loss: 0.3962 - acc: 0.8800
Epoch 2/50
400/400 [==============================] - 0s - loss: 0.3326 - acc: 0.8800
Epoch 3/50
400/400 [==============================] - 0s - loss: 0.2945 - acc: 0.8800
Epoch 4/50
400/400 [==============================] - 0s - loss: 0.2391 - acc: 0.8800
Epoch 5/50
400/400 [==============================] - 0s - loss: 0.1783 - acc: 0.9050
Epoch 6/50
400/400 [==============================] - 0s - loss: 0.1359 - acc: 0.9500
Epoch 42/50
400/400 [==============================] - 0s - loss: 0.0771 - acc: 0.9725
Epoch 43/50
400/400 [==============================] - 0s - loss: 0.0730 - acc: 0.9775
Epoch 44/50
400/400 [==============================] - 0s - loss: 0.0737 - acc: 0.9675
Epoch 45/50
400/400 [==============================] - 0s - loss: 0.0724 - acc: 0.9725
Epoch 46/50
400/400 [==============================] - 0s - loss: 0.0715 - acc: 0.9775
Epoch 47/50
400/400 [==============================] - 0s - loss: 0.0756 - acc: 0.9675
Epoch 48/50
400/400 [==============================] - 0s - loss: 0.0743 - acc: 0.9700
Epoch 49/50
400/400 [==============================] - 0s - loss: 0.0690 - acc: 0.9775
Epoch 50/50
400/400 [==============================] - 0s - loss: 0.0708 - acc: 0.9700

: <keras.callbacks.History at 0xe110ad0>
```

Figure 4.2: Showing Performance of the Model and Accuracy Metrics

TABLE 4.2: Showing the ANN Experiment Data

Hidden Layer	Layer (s)/Neurons	Activation Functions	Optimizer	Accuracy
1	20	relu, Softmax	adam	88%
1	25	relu, softmax	adam	88%
1	25	relu, softmax	adagrad	88%
1	20	Relu, sigmoid	adam	91.50%
1	25	relu, sigmoid	adam	93.25%
1	30	relu, sigmoid	adam	93.25
1	40	relu,sigmoid	adam	94.25%
1	50	relu, sigmoid	adam	94.00%
1	55	relu, sigmoid	adam	94.00%
2	55, 15	relu, Sigmoid, sigmoid	adam	94.50%
2	55,20	relu, sigmoid, sigmoid	adam	94.50%
2	55,30	relu, Sigmoid, sigmoid	adam	94.75%
2	55,40	relu, sigmoid, sigmoid	adam	94.75%
2	55,50	relu, sigmoid, sigmoid	adam	94.75%
2	55,55	relu, sigmoid	adam	94.75%
2	55,60	relu, sigmoid, sigmoid	adam	94.50%
2	***55,65***	***relu, Sigmoid, sigmoid***	***adam***	***95.50% Done***
2	55,70	relu, Sigmoid, sigmoid	adam	94.50%

The prediction model architecture defines the number of layers, neurons in each layer and the activation function of the model. The artificial neural network model for this Malaria prediction started experimentally with an architecture that has one hidden layer and progresses to a satisfactory level of three layers: an input, a hidden, and an output layer consisting of four (14) inputs and twenty (20) neurons and an output layer.

The number of layers and neurons at the input and hidden layer were varied for different performance of the network until the model performance was optimized with fifty (55) at the first layer and sixty (65) neurons in the middle layer. Two activation functions and an optimizer were used, these are Relu activation function at the input layer and sigmoid activation function at the output layer as well as Adam optimizer.

Table 4.2 above shows the performance of the neural network reached optimum performance at an accuracy of 95.25%.

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From the Keras sequential model, the final model is as shown in figure 9 below:

Layer (type)	Output Shape	Param #
dense_4 (Dense)	(None, 55)	825
dropout_2 (Dropout)	(None, 55)	0
dense_5 (Dense)	(None, 65)	3640
dense_6 (Dense)	(None, 1)	66

Total params: 4,531.0
Trainable params: 4,531.0
Non-trainable params: 0.0

Figure 4.3: Showing the Keras Final Model for Malaria Prediction

4.3 Neural Network Model Evaluation Results

From Table 4.2 above, the performance of the neural network reached optimum performance at an accuracy of 95.25%. This Neural Network model was evaluated using K-Fold Cross Validation. Cross Validation methods are usually adopted as a performance measure for Neural Network models, to assess the statistical relevance of the classifier. The procedure is to create a K-Fold partition of the whole dataset, repeat *K* times to use *K*-1 folds for training and a left fold for validation, and finally average the error rates of *K* experiments. The K = 5 is statistically coherent in this study since the datasets have 400 data features. The K-Fold of 5 will give equal segmentation of the datasets before the final performance is obtained.

In addition to obtaining an optimum performance and artificial neural model structure for the Malaria prediction with the dataset, it is also important to visualize how the dataset partitions performed generally. Based on this background, the model accuracy and model loss in relation to training and test dataset partitions are important metrics that can reveal the performance of the different dataset partitions. Below is the graphical view of the model accuracy and loss - in relation to training and test partitions.

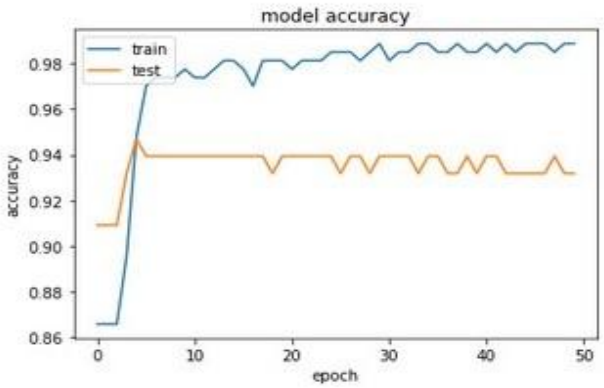

Figure 4.4: Showing the Graph for Model Accuracy

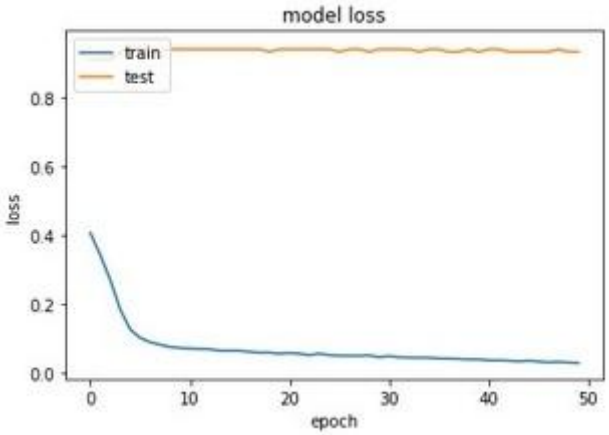

Figure 4.5: Showing the Graph for Model Loss

From the graph in figure 4.4 above, showing the model accuracy, it could be seen that both training and test split dataset model accuracy started and increased at different points. While the training dataset started at around 87 %, the test partition started at 91%. While the test dataset partition performance plateaued between 95% and 94%, the training dataset partition performed better than the test partition. At the training phase, the training partition had spiraled into almost 100% performance as seen in the graph.

Similarly, the model loss graph shown in figure 4.4 revealed that the training loss learns better with a reduction in loss values from 0.4 to almost zero, as the training epoch increased. However, the test model loss value did not reach a reasonable reduction, as epochs increased.

In the same vain, Confusion Matrix was also used to estimate the performance of the prediction accuracy based on the test datasets which was 20% (80) of the 400-total dataset. The result of the Confusion Matrix result was shown below:

The results showed that out of the class 0 (negative) of the malaria dataset within the test data, 4 out of the 7 samples were predicted correctly. While in the class 1 (positive) malaria

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dataset within the test data, 69 out of the 73 samples were predicted correctly.

```
                    precision    recall  f1-score   support

class 0(Negative)       0.50      0.57      0.53         7
class 1(Positive)       0.96      0.95      0.95        73

      avg / total       0.92      0.91      0.92        80

===== Confuision Matrix Result====
[[ 4  3]
 [ 4 69]]
```

4.4 Model Prediction of the Artificial Neural Network

The major reason for building a machine learning model is to make predictions. Therefore, the last and important part of artificial neural network model building is to make prediction on unseen data called the test dataset. The Malaria prediction based on the clinical symptoms in health data using the artificial neural network model was binary classification model that generates two output/labels based on the learning of the model through earlier training on input datasets. The two expected output samples from this study are:

i. Negative
ii. Positive

To make predictions, this work used the model designed to generate predictions on new data or the unseen dataset called the test dataset by calling the predict function such as predict() on the model.

```
========== Encoded Prediction Codes ======
[1 1 1 1 1 1 0 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 1 1 1
 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0
 1 1 1 1 1 1]
===== Corresponding Meaning of Codes======
['Positive' 'Positive' 'Positive' 'Positive' 'Positive' 'Positive'
 'Negative' 'Positive' 'Positive' 'Positive' 'Positive' 'Positive'
 'Positive' 'Negative' 'Positive' 'Positive' 'Positive' 'Positive'
 'Positive' 'Positive' 'Positive' 'Positive' 'Positive' 'Positive'
 'Positive' 'Positive' 'Positive' 'Positive' 'Positive' 'Positive'
 'Positive' 'Negative' 'Positive' 'Positive' 'Positive' 'Positive'
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 'Positive' 'Positive' 'Positive' 'Positive' 'Positive' 'Positive'
 'Negative' 'Positive' 'Positive' 'Negative' 'Positive' 'Positive'
 'Negative' 'Positive' 'Positive' 'Positive' 'Positive' 'Positive'
 'Positive' 'Positive' 'Positive' 'Positive' 'Positive' 'Positive'
 'Positive' 'Negative' 'Positive' 'Positive' 'Positive' 'Positive'
 'Positive' 'Positive']
```

Figure 4.6: Showing the Prediction in Binary and the Encoded Meaning

The prediction result was based on the prediction accuracy of 95.50% of the neural network model and dataset performance of 80% for training and 20% for testing. The summary of the dataset partition is as shown below, from the simulation results.

```
-------- Summary of Datasets uded ------------
('Training dataset used out of 75,4:', (320, 11))
('Labels used corresponding to the trained sets', (320, 2))
('Test datasets used out of 75,4:', (80, 11))
('Labels used for testing', (80, 2))
```

4.5 Performance of Decision Tree Classifier Model for Malaria

The performance of the Decision Tree classifier was experimented in two stages in this study. First, the default parameters of the Decision Tree classifier were used and the performance of the model recorded. Secondly, the model was enhanced by tinkering with some of the parameters of the Decision Tree algorithm.

4.5.1 Default Performance of the Decision Tree Classifier on the Malaria Dataset

The performance of a Decision Tree classifier for predicting the class of the given class of Malaria from the dataset starts from the root node of the tree. The Decision Tree classifier compares the values of the root node with the other parts of the divided dataset using the attribute selection measure and the decision tree parameters. These parameters are:

```
In [10]: clf.get_params()

Out[10]: {'ccp_alpha': 0.0,
          'class_weight': None,
          'criterion': 'gini',
          'max_depth': None,
          'max_features': None,
          'max_leaf_nodes': None,
          'min_impurity_decrease': 0.0,
          'min_impurity_split': None,
          'min_samples_leaf': 1,
          'min_samples_split': 2,
          'min_weight_fraction_leaf': 0.0,
          'random_state': None,
          'splitter': 'best'}
```

Figure 4.7: Showing Selected Decision Tree Parameters

To improve the performance of the tree, reduce memory consumption, the complexity and size of the trees, the parameters should be controlled by setting the values of the classifier. However, the initial decision tree performance without regulating the parameters and using the default values give the following performances:

The Decision Tree classifier model was build based on the Malaria datasets and was fit to the training datasets; this gave the predictions as shown in Figure 15 below:

```
In [9]: # to build classification tree
        from sklearn.tree import DecisionTreeClassifier
        clf = DecisionTreeClassifier()
        clf = clf.fit(x_train, y_train)

In [11]: predictions = clf.predict(x_test)
         predictions

Out[11]: array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 0, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 0], dtype=int64)
```

Figure 4.8: Showing the Decision Tree Model and Predictions

Moreover, the prediction accuracy of the test dataset was calculated. The accuracy on the unseen datasets on the test dataset earlier partitioned was 96.67% as shown below:

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```
In [20]: from sklearn.metrics import accuracy_score
         accuracy_score(y_test, predictions)*100

Out[20]: 96.66666666666667
```

Figure 4.9: Showing Accuracy of Test Dataset

The classification report metrics inbuilt into the Classifier was outputted as shown below. The report showed the test partitions, the precision, the recall and the f1 score. The weighted average of the accuracy was the same as the accuracy score shown above.

```
In [21]: from sklearn.metrics import classification_report
         print(classification_report(y_test, predictions, target_names=['Negative','Positive']))

                      precision    recall  f1-score   support

            Negative       0.75      0.90      0.82        10
            Positive       0.99      0.97      0.98       110

            accuracy                           0.97       120
           macro avg       0.87      0.94      0.90       120
        weighted avg       0.97      0.97      0.97       120
```

Figure 4.10: Showing Classification Report Metrics

V. CONCLUSION

Artificial Neural Network and Decision Tree classifier algorithms were experimented on the same Malaria datasets in this research with a view of evaluating their performances. Both algorithms performed well on the dataset. However, after a series of experiments with the Artificial Neural Network parameters and Decision Tree classifier, the performance accuracy of the Artificial Neural Network was higher. The Artificial Neural Network performance accuracy peaked at 95.50% while that of the Decision Tree was 94.17%. While the Artificial Neural Network model took much time to build in a series of varying parameters such as network layers, neurons, activation functions and optimizers, to arrive at an optimum performance, the Decision Tree classifier was much easier to build.

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