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A Modified Approach to Malaria Diagnosis Using Artificial Bee Colony Algorithm

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Abstract:- Malaria is a life-threatening disease in Nigeria and it is caused by the bite of a female anopheles mosquito. Malaria is increasing in an uncontrolled way but its diagnosis is still at a very poor state in Nigeria. The World Health Organization (W.H.O) reported that an estimate of fifty million children in Africa died of malaria from the years 2015 to 2019. In this study, we developed an Enhanced Malaria Diagnostic Model using Artificial Bee Colony (ABC) algorithm. Structured Analysis and Design Technique (SADT) was adopted as methodology, and we further implemented with Hypertext Pre-processor (PHP), and MySQL. In addition, the Enhanced Malaria Diagnostic Model will be beneficial to doctors and specialists in life-threatening disease such as malaria, and the Nigerian Centre for Disease Control (NCDC).

Keywords:- *Artificial Bee Colony (ABC); Diagnosis; Malaria; SADT.*

I. INTRODUCTION

Malaria is a life-threatening disease in Nigeria and the infection is known as plasmodium with symptoms such as headache, body aches, chills, sweating, fever, nausea and vomiting. Malaria is defined as an intermittent and remittent fever that is perpetuated by a protozoan parasite, which attacks the red blood cells. Malaria is caused by female anopheles mosquitoes.

Over the years, there have been gains in the diagnosis of malaria especially in terms of symptoms processing and corresponding result. However, inconsistencies and latencies associated with the present malaria diagnosis model have continued to be a serious life-threatening malady. Furthermore, prompt and correct diagnosis is important for effective management of malaria cases in order to reduce morbidity and mortality caused by delayed or poor management of patients particularly under-five years and pregnant women.

Malaria diagnosis has depended on clinical diagnosis (based on patients' history and symptoms), which has low specificity leading to over-diagnosis and over-treatment. Meanwhile, the diagnosis of malaria in Nigeria is still at a very poor state and it poses a great threat to the populace. In addition, Statistical research from the United Nations (UN) suggested that three hundred annual deaths and fifty-one (51) million sicknesses occur in Nigeria because of malaria.

The mentioned malady is due to the absence of an improved machine-learning oriented concept such as Artificial Bee Colony (ABC) algorithm. Hence, the need of an Enhanced Malaria Diagnostic Model is highly indispensable.

Furthermore, Malaria has also claimed several lives in the world due to negligence and poor treatment. For instance, the World Health Organization (W.H.O) reported that an estimate of fifty million children in Africa died from malaria from the years 2015 to 2019. The poor state of malaria diagnosis in Nigeria has continued to increase the mortality rate of patients with the disease.

The application of Information Communication Technology (ICT) could reduce the mortality rate and time taken to consult a specialist. In other words, the need for an Enhanced Malaria Diagnostic Model is highly indispensable.

This study intends to address the problem of poor malaria diagnosis process in Nigeria’s Health Care Sector. The mentioned problem is caused by several factors which encompass latencies in the diagnosis process, errors in symptom checks, and obsolete diagnosis systems in health-care institutions. The emergence of ICT applications to Nigeria’s Health Sector has contributed to good decision-making processes by doctors and specialists which has also positively influenced the health sector through the reduction of uncertainties and imprecision in the diagnosis of health related issues.

The aim of this study is to develop an Enhanced Malaria Diagnostic Model using Artificial Bee Colony Algorithm. The specific objectives of the study include designing a web-based system for accepting and processing malaria symptoms, to train the proposed web-based system with Deep Neural Network, to test the proposed web-based system with medical-related datasets, implement the proposed web-based system with Hypertext Pre-processor (PHP) and MySQL and to evaluate the performance accuracy of the proposed web-based system using appropriate performance metrics.

II. LITERATURE REVIEW

A. Artificial Bee Colony Algorithm as a Tool for Malaria Diagnosis

The Artificial Bee Colony Algorithm (ABC) models real-world problems in order to design an effective diagnosis system. It was introduced by Dervis Karaboga in 2005. Furthermore, the ABC algorithm is an optimization algorithm that deals with the foraging behavior of honeybee swarm. The algorithm is also a branch of Swarm Intelligence (SI) which is rapidly convergent, highly flexible, strong and less robust. Swarm Intelligence (SI) can be characterized as the collective behavior of decentralized and self-organized systems that are natural or artificial [1].

The algorithm of ABC consists of Scouts bees, Employed bees, and Onlooker bees. It is the duty of the employed bees to locate the available sources of food and to present them to the Onlookers. The Scout bees are abandoned food sources; they are Employed bees with abandoned food sources.

The Onlookers collects food sources shown by the Employed bee according to the food sources available. ABC algorithm assumes that for every food source it exists only one artificial bee which implies that the number of employed bees is the same as the number of food sources in the colony [2].

ABC Algorithm can be implemented in the diagnosis system with the format of the algorithm given below.

```
Step1: Initialize food source to employed bees Supply Symptoms to get the major disease
Step2: Repeat Until each employed bee gets its food source, and dances in its hive Find any exact matching for the entered symptoms and display
Step 3: Onlookers identify the Employed Bee positions and takes the nearest positions which are empty IF matching disease is not there, go with the neighbor disease and display
Step 4: Scouts are the bees where they don't match with the symptoms in the knowledge base then it displays knowledge is insufficient
Step 5: Display the best food source which shows the place in the hive
Step 6: Until the requirement is satisfied, loop is to be run.
```

B. Related Work

Kemi & Olutomilayo [3], developed an Expert System for Diagnosis of Malaria and Typhoid Fever. The study considered developing an Expert System that could assist in diagnosing malaria. Furthermore, their developed Expert System was rule-based and contained in its knowledge-base, some important rules on malaria causative agents, environmental and climatic factors which can favor the multiplicity of malaria transmission. The authors did a good job. However, the following identified limitations in their work include:

Latency, inconsistency, few symptoms input and errors in symptom checks and diagnosis due to upgrade failure and absence of ABC algorithm, which would have made the system more intelligent through integration of new ideas with the learner's existing schemata.

Dereje et al, [4], carried out a research on a web-based Expert System for the prevention, diagnosis and treatment of malaria using two Ethiopian local languages (Amharic and Afan Oromo). The study aimed at developing and using Malaria expert system to provide support in the Prevention, prediction and diagnosis of malaria using the two widely spoken languages in Ethiopia (Amharic and Afan Oromo). According to the authors, "there are still some problems in creating such systems as most people in rural areas of Ethiopia are illiterate and computer literacy cannot be expected from them". The authors did a good job. However, the datasets used for training and designing their model was not trained with machine learning algorithms which further resulted to latencies in their model performance.

Kenneth et al, [5], looked at Medical Diagnosis Expert System for Malaria Related Diseases for Developing Countries. The study focused at how appropriate an application of Medical Diagnosis Expert System (MDES) is to manage diseases in developing countries. This is as a result of poor query plans and non-user-friendly interfaces that are supported by these existing data mining algorithms. Their system can also be considered as a difficult task due to application of complex algorithms. Secondly, the mined datasets are not stable at a location. The reports of intelligence and security agencies are the result of collecting, processing, and analysing information.

Olugbenga et al, [6], carried out a study on building a Computer-based Expert System for Malaria Environmental Diagnosis: This is as a result of poor query plans and non-user-friendly interfaces that are supported by these existing data mining algorithms. Diagnosis can also be considered as a difficult task due to application of complex algorithms. Secondly, the mined datasets are not stable at a location. The reports of intelligence and security agencies are the result of collecting, processing, and analysing information. Hence to solve these problems stated we need to develop a hybridized models for improved intelligence gathering in Rivers state which combines human intelligence HUMINT), and open source intelligence (OSINT). However, a major limitation of their study is that the developed model was deficient in benchmarking and cost benefits analysis.

Indra & Sangeeta, [7], carried out an Analytical Study of Data Mining Applications in Malaria Prediction and Diagnosis. The authors analysed a variety of techniques, approaches and different tools and its impact on the healthcare sector especially for vector borne disease malaria. This is as a result of poor query plans and non-user-friendly interfaces that are supported by these existing data mining algorithms. Their system can also be considered as a difficult task due to application of complex algorithms. Secondly, the mined datasets are not stable at a location. The reports of intelligence and security agencies are the result of collecting, processing, and analyzing information. The authors did a good job. However, the discussed issue on the application of data mining techniques to malaria diagnosis was not implemented to a machine-learning model, which would have provided more clarification and understanding.

III. METHODOLOGY

The Methodology for the Proposed System Design is Structured Analysis and Design Technique (SADT). SADT is a structured analysis modeling language, which uses two types of diagrams: activity models and data models. It was developed in the late 1960s by Douglas T. Ross, and was formalized and published as IDEF0 in 1981.

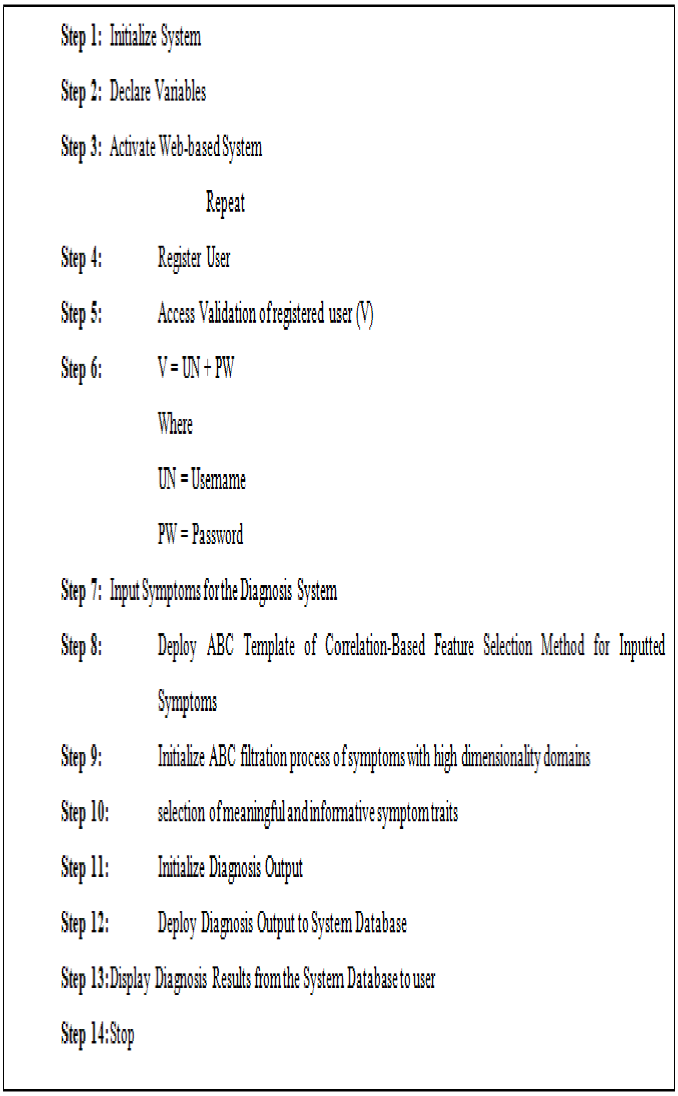
A. Justification of the Adopted Methodology

SADT has proven to be successful in the development of software systems, specifically in the requirements gathering phase. SADT notations consist of box-arrow diagrams (blocks), with four arrows, one on each side defined as: input, output, control and mechanism and one activity in the middle. Their definitions consist of the following:

i) Activity: An activity is any function or process that serves to transform inputs into outputs
ii) Input: The data/information required by an activity to start the transformation process
iii) Output: the data/information produced by the activity as a result of this transformation
iv) Control: Any constraint that affects the behavior of activity in some way
v) Mechanism: Persons, resources, or any means that are required to run the activity

B. Algorithm of the Proposed Model

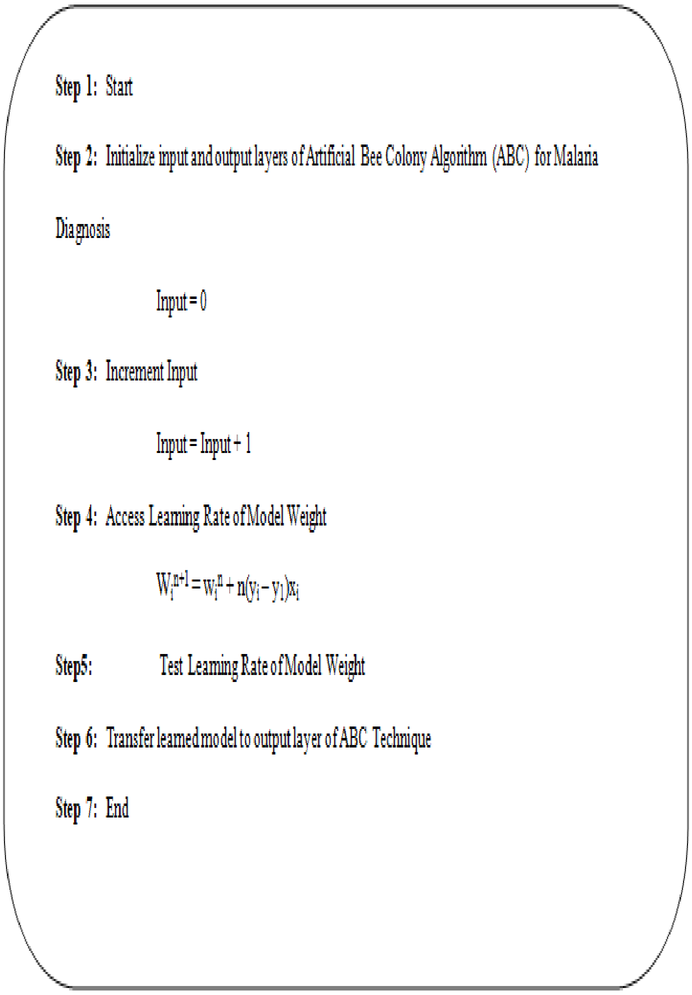
Fig. 3.1 shows the proposed model algorithm



```
Step 1: Initialize System
Step 2: Declare Variables
Step 3: Activate Web-based System
            Repeat
Step 4:     Register User
Step 5:     Access Validation of registered user (V)
Step 6:     V = UN + PW
            Where
            UN = Username
            PW = Password
Step 7: Input Symptoms for the Diagnosis System
Step 8:     Deploy ABC Template of Correlation-Based Feature Selection Method for Inputted
            Symptoms
Step 9:     Initialize ABC filtration process of symptoms with high dimensionality domains
Step 10:    selection of meaningful and informative symptom traits
Step 11:    Initialize Diagnosis Output
Step 12:    Deploy Diagnosis Output to System Database
Step 13: Display Diagnosis Results from the System Database to user
Step 14: Stop
```

Fig. 3.1: Algorithm of the Proposed System Model

IV. APPLICATION OF ABC ALGORITHM TO THE PROPOSED MODEL



```
Step 1: Start
Step 2: Initialize input and output layers of Artificial Bee Colony Algorithm (ABC) for Malaria Diagnosis
        Input = 0
Step 3: Increment Input
        Input = Input + 1
Step 4: Access Learning Rate of Model Weight
        $W_i^{n+1} = w_i^n + n(y_i - y_i)x_i$
Step5: Test Learning Rate of Model Weight
Step 6: Transfer learned model to output layer of ABC Technique
Step 7: End
```

Fig. 4.1: Application of ABC Algorithm Technique to the Proposed Model

V. RESULT AND DISCUSSION

The Present Malaria Diagnostic Model is a Web Application that is backed up by a Local Host Server. Hence, the study implemented the frontend and backend of the system with Xampp Server as illustrated in fig. 5.1 and 5.2 respectively

a) APPLICATION FRONTEND PROCEDURES:

i) Start

ii) Launch XAMPP

iii) Launch Notepad++

i) Enter source codes for Application Frontend, Run program on Mozilla Firefox or Google Chrome browser

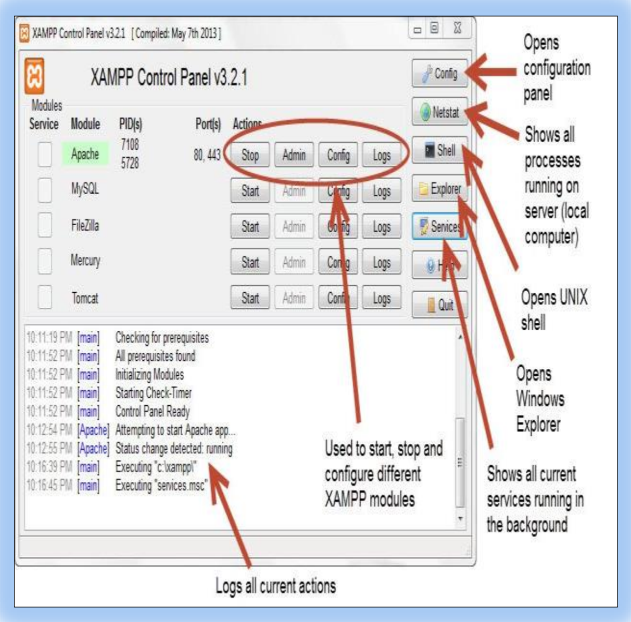
b) STEP ONE: (Setting up Xampp Server Installation):

In order to install the Xampp server, the user of the system must download the Xampp executable file, before running the installation as an administrator. Once the download is done, the user double clicks on the executable file to commence the installation. A Xampp executable file enables the installation of a local host server on the system. It ranges from 32 to 64 bits. Fig. 5.1 shows the xampp server setup page, fig. 5.2 shows the xampp server control panel.

Setup - XAMPP

Welcome to the XAMPP Setup Wizard.

Fig. 5.1: Xampp Setup Page



```
10:11:19 PM  [main]    Checking for prerequisites
10:11:52 PM  [main]    All prerequisites found
10:11:52 PM  [main]    Initializing Modules
10:11:52 PM  [main]    Starting Check-Timer
10:11:52 PM  [main]    Control Panel Ready
10:12:54 PM  [Apache]  Attempting to start Apache app...
10:12:55 PM  [Apache]  Status change detected: running
10:16:39 PM  [main]    Executing "c:\xampp\"
10:16:45 PM  [main]    Executing "services.msc"
```

Opens configuration panel

Shows all processes running on server (local computer)

Opens UNIX shell

Opens Windows Explorer

Shows all current services running in the background

Used to start, stop and configure different XAMPP modules

Logs all current actions

Fig. 5.2: Xampp Control Panel

Fig. 5.3 shows the landing/welcome page of the web-based program. It has a beautified graphical user interface with three navigation links. The navigation links are the homepage link, the register patient link and the patient's diagnosis request link. The register patient link enables the patient to register to book an instant appointment with the expert system. Furthermore, the details required for this process encompasses the patient's first name, last name, gender, email details, residential address, phone number, username and a corresponding password. Once the patient has successfully registered, the system navigates to the login process which requires the patient to input a username and corresponding password in order to be granted access after validation by the system. Another output shows the diagnosis request section that enables the patient to provide responses to the following malaria related symptoms such as:

i) Headache
ii) Fever
iii) Vomiting

Having given responses to the malaria related symptoms, the expert system quickly processes the inputted symptoms/corresponding responses by the patient, and automatically generates the diagnosed result as final displayed output of the process to the patient. Fig. 5.4 illustrates the diagnosis result page.

This process of the Existing System is backed up by two techniques identified as the improved case-based recommender system, which process the symptoms based on past-related cases solved by human experts, and a modified Genetic Algorithm, which solve problems such as optimization and modeling, automatic programming and machine learning.

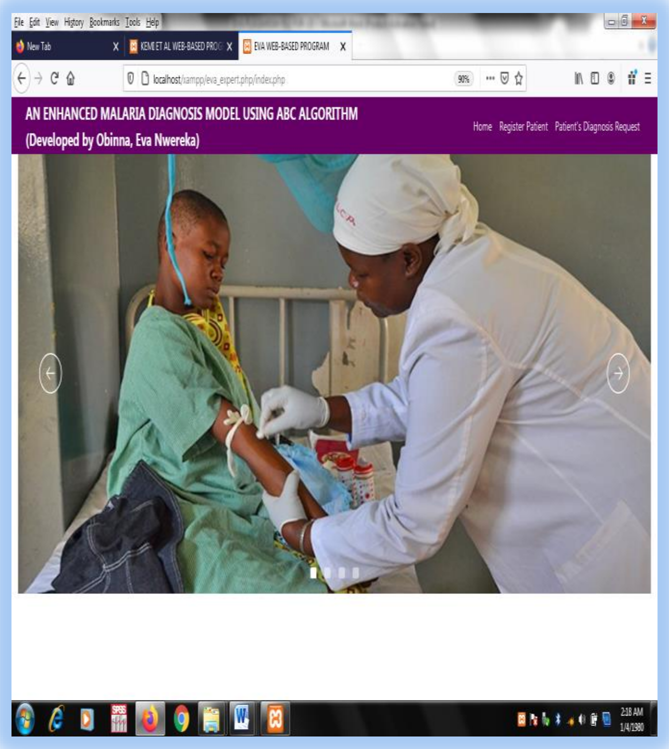
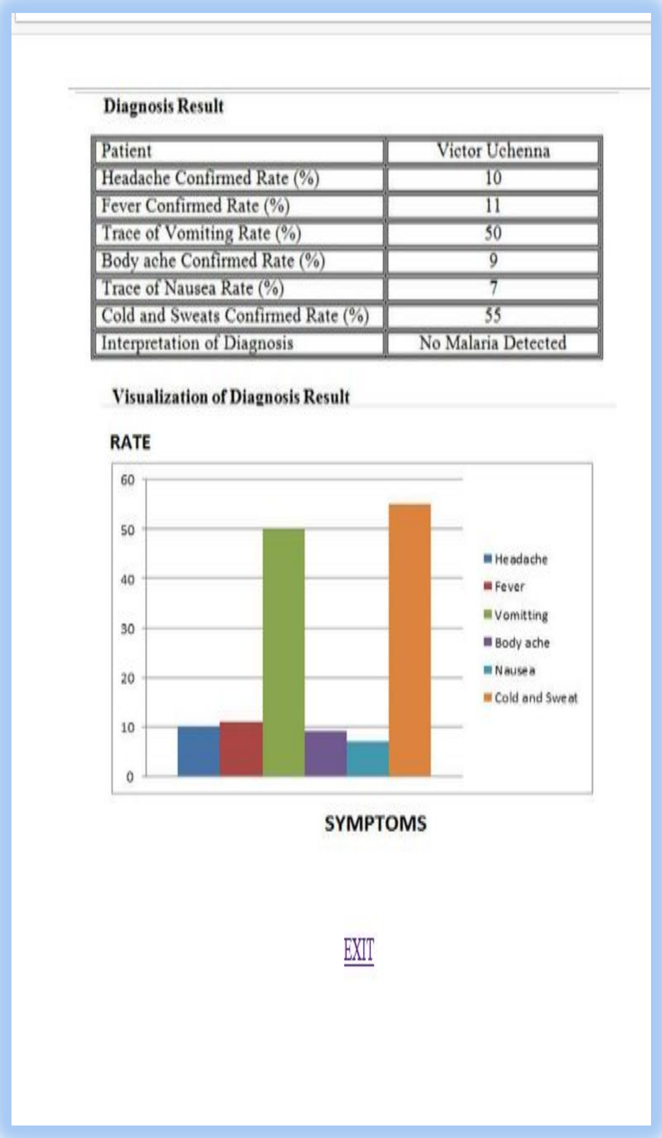

AN ENHANCED MALARIA DIAGNOSIS MODEL USING ABC ALGORITHM
(Developed by Obinna, Eva Nwereka)

Fig. 5.3: Welcome Page of the Developed System


Diagnosis Result

Patient	Victor Uchenna
Headache Confirmed Rate (%)	10
Fever Confirmed Rate (%)	11
Trace of Vomiting Rate (%)	50
Body ache Confirmed Rate (%)	9
Trace of Nausea Rate (%)	7
Cold and Sweats Confirmed Rate (%)	55
Interpretation of Diagnosis	No Malaria Detected

Visualization of Diagnosis Result

Fig. 5.4: Diagnosis Result Page

VI. PERFORMANCE EVALUATION OF THE PROPOSED MODEL

Fig. 6.1 shows the MATLAB generated confusion matrix with results for the Present Malaria Diagnostic Model.

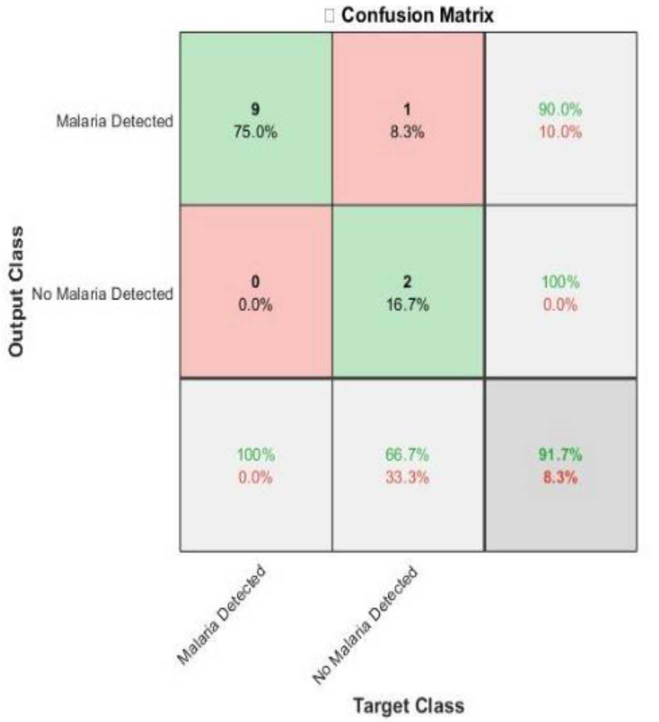


Fig. 6.1: MATLAB Generated Confusion Matrix with Results for the Present Malaria Diagnostic Model

Fig. 6.2 shows the MATLAB generated confusion matrix with results for the Enhanced Malaria Diagnostic Model.

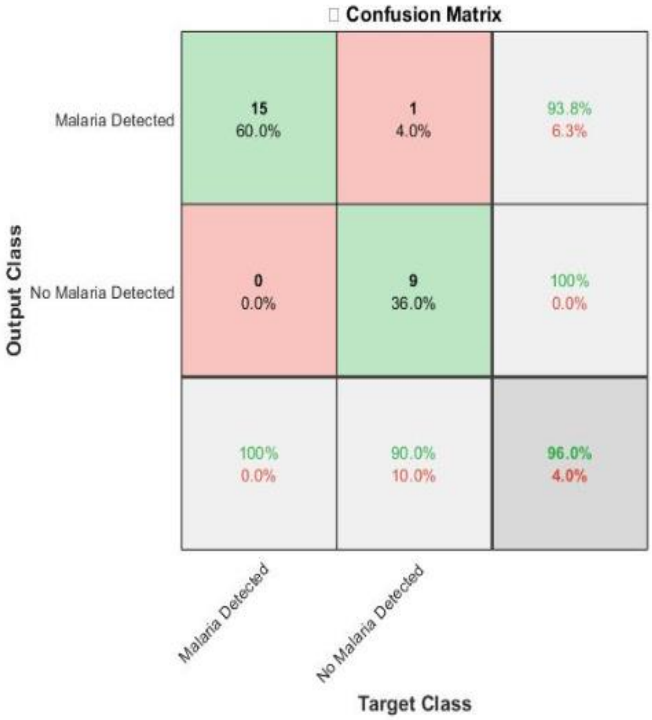


Fig. 6.2: MATLAB Generated Confusion Matrix with Results for the Enhanced Malaria Diagnostic Model.

Fig. 6.3 shows the Receiver Operating Characteristic Curve (ROC) for the Present Malaria Diagnostic Model and the Enhanced Malaria Diagnostic Model.

Fig. 6.3: ROC for both Present Malaria Diagnostic Model and the Enhanced

Malaria Diagnostic Model.

Table 6.1 shows the comparative analysis for the Present Malaria Diagnostic Model and the Enhanced Malaria Diagnostic Model.

SN.	PARAMETERS	VALUES	
		Present Malaria Diagnostic Model	Enhanced Malaria Diagnostic Model
1.	Accuracy	91.7	96.00
2.	Classification Error	8.3	4.00
3.	Number of Processed Symptoms	3	6
4.	Processing Speed	15.7s	10.22s
5.	AUC	0.95	0.97

Table 6.1: Comparative Analysis of the Present Malaria Diagnostic Model and the Enhanced Malaria Diagnostic Model.

Fig. 6.4 shows the comparative analysis chart for the Present Malaria Diagnostic Model and the Enhanced Malaria Diagnostic Model.

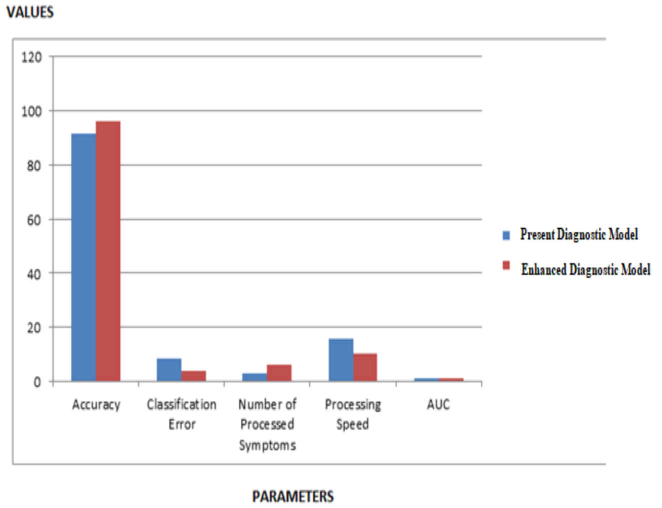


Fig. 6.4: **Comparative Analysis Chart (Source: Table 6.1)**

VII. DISCUSSION OF RESULTS

Fig. 6.1 shows the MATLAB generated confusion matrix with results for the Present Malaria Diagnostic Model. In this table, the first two diagonal cells show the number and percentage of correct classifications by the trained network. For example, in the Present Malaria Diagnostic Model, 9 cases are correctly classified as Malaria Detected. This corresponds to 75% of all 12 specimens. Similarly, 2 cases are correctly classified as No Malaria Detected. This corresponds to 16.7% of all cases. 1 of the No Malaria Identified cases is incorrectly classified as Malaria Detected and this corresponds to 8.3% of all 12 specimens in the data. Similarly, zero of the Malaria Identified cases are incorrectly classified as No Malaria Identified cases and this corresponds to 0.0% of all data. Out of 10 Malaria Detected predictions, 90.0% are correct and 10.0% are wrong. Out of two No Malaria Detected predictions, 100% are correct and 0% is wrong. Out of 9 Malaria Detected cases, 100% are correctly predicted as Malaria Detected and 0.0% are predicted as malignant. Out of 3 No Malaria Detected cases, 66.7% are correctly classified as No Malaria Detected and 33.3% are classified as Malaria Detected. Overall, 91.7% of the predictions are correct and 8.3% are wrong.

Fig. 6.2 shows the MATLAB generated confusion matrix with results for the Enhanced Malaria Diagnostic Model. In this table, 15 cases are correctly classified as Malaria Detected. This corresponds to 60% of all 25 specimens. Similarly, 9 cases are correctly classified as No Malaria Detected. This corresponds to 36.0% of all cases. One of the No Malaria Identified cases is incorrectly classified as Malaria Detected and this corresponds to 4.0% of all 25 specimens in the data. Similarly, zero of the Malaria Identified cases are incorrectly classified as No Malaria Identified cases and this corresponds to 0.0% of all data. Out of 16 Malaria Detected predictions, 93.8% are correct and 6.3% are wrong. Out of 9 No Malaria Detected predictions, 100% are correct and 0% is wrong. Out of 15 Malaria Detected cases, 100% are correctly predicted as Malaria Detected and 0.0% is predicted as malignant. Out of 10 No Malaria Detected cases, 90.0% are correctly classified as No Malaria Detected and 10.0% are classified as Malaria Detected. Overall, 96.0% of the predictions are correct and 4.0% are wrong.

Table 6.1 shows the comparative analysis of the Present Malaria Diagnostic Model and the Enhanced Malaria Diagnostic Model. Accuracy, classification error, number of processed symptoms, processing speed, and Area Under the Curve (AUC) were used as the yardstick for comparison between the Present Malaria Diagnostic Model and the Enhanced Malaria Diagnostic Model. The accuracy and classification error were obtained from fig. 6.1 and 6.2, which shows the MATLAB generated confusion matrix with results for both models respectively. The number of processed symptoms represents the symptom parameters used in the development of the Present Malaria Diagnostic Model and the Enhanced Malaria Diagnostic Model. The processing speed given in seconds was the duration it takes each model to complete a task. The AUC for both models were obtained via the use of MATLAB Data Analytic Tool. The comparative analysis of both models shows in table 6.1 that the performance of the Enhanced Malaria Diagnostic Model supersedes that of the Present Malaria Diagnostic Model.

Fig. 6.3 shows the Receiver Operating Characteristic Curve (ROC) for the Present Malaria Diagnostic Model and the Enhanced Malaria Diagnostic Model. Furthermore, accurate evaluation of both models was carried out using MATLAB Data Analytic Tool to generate the Receiver Operating Characteristic (ROC) Curve. The nature of the graphical plot is due to the volume of datasets used by the Present Malaria Diagnostic Model. In addition, the Enhanced

Malaria Diagnostic Model is an enhancement of the Present Malaria Diagnostic Model. The receiver operating characteristic curve is a graphical plot that illustrates the diagnostic ability of a binary classifier system as its discrimination threshold is varied. In addition, the Area Under the Curve (AUC) for the Present Malaria Diagnostic Model is 0.95, while Area Under the Curve for the Enhanced Malaria Diagnostic Model is 0.9688, which is approximately 0.97.

The Receiver Operating Characteristic Curve shows the performance of the models. In obtaining the accuracy, and classification error; performance evaluation was carried out via confusion matrix table, and results was generated using MATLAB. The concept of confusion matrix is to give a matrix output, and further describe the model performance.

Accuracy of the matrix was gotten by obtaining average values of the defined variables as shown in equation 1

$$\frac{(TP+TN)}{(TP+TN+FP+FN)} - (1)$$

The classification error simply determines what fractions of predictions were wrong. It is also called misclassification rate. Which has the formula:

$$1 - accuracy\ or\ \frac{(FP+FN)}{(TP+TN+FP+FN)} - -(2)$$

Where False Positive (FP) is the number of predictions where the classifier incorrectly predicts the negative class as positive. False Negative (FN) is the number of predictions where the classifier incorrectly predicts the positive class as negative. True Positive (TP) is the number of predictions where the classifier correctly predicts the positive class as positive. True Negative (TN) is the number of predictions where the classifier correctly predicts the negative class as negative.

The Enhanced Malaria Diagnostic Model was able to address limitations such as latencies and inaccurate diagnosis results of the Present Malaria Diagnostic Model. The improvement by the Enhanced Model encompassed increased processed symptoms and volume of patients' datasets.

Comparative analysis of the Present and Enhanced Malaria Diagnostic Models was carried out. Parameters for the comparative analysis encompassed Accuracy (A), Classification Error (CE), the Area under Curve (AUC), the processing speed in seconds, and the number of processed values. The obtained results of the Present Malaria Diagnostic Model based on the mentioned parameters were 91.7%, 8.3%, 0.95, 15.7, and 3 respectively. While that for the Enhanced Malaria Diagnostic Model was 96%, 4%, 0.97, 10.22 and 6 respectively. In other words, the obtained results clearly proved that the Enhanced Malaria Diagnostic Model performed better than the Present Malaria Diagnostic Model.

VIII. CONCLUSION

In this study we have developed an enhanced malaria diagnosis model using artificial bee colony algorithm. The newly developed malaria diagnostic model has the capacity to diagnose a patient base on symptoms and produce accurate result. The Artificial Bee Colony (ABC) Algorithm is an efficient algorithm proven successful in designing intelligent systems because of its simplicity and uniqueness in finding solutions to unmatched values in the knowledge base.

Deep Neural Network was also implemented to enhance the performance of the Artificial Bee Colony (ABC) Algorithm, in order to boost the performance of the enhanced malaria diagnostic model. In addition, the developed model also serves as a decision support system for the diagnosis of malaria. This is because; a decision supports system is a computer-based information system that supports business or organizational decision-making activities.

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