Artificial Intelligence System for Malaria Diagnosis

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Abstract—**Malaria threats have remained one of the major global health issues over the past decades specifically in low-middle income countries. 70% of the Kenya population lives in malaria endemic zones and the majority have barriers to access health services due to factors including lack of income, distance, and social culture. Despite various research efforts using blood smears under a microscope to combat malaria with advantages, this method is time consuming and needs skillful personnel. To effectively solve this issue, this study introduces a new method integrating InfoGainAttributeEval feature selection techniques and parameter tuning method based on Artificial Intelligence and Machine Learning (AIML) classifiers with features to diagnose types of malaria more accurately. The proposed method uses 100 features extracted from 4000 samples. Sets of experiments were conducted using Artificial Neural Network (ANNs), Naïve Bayes (NB), Random Forest (RF) classifiers and Ensemble methods (Meta Bagging, Random Committee Meta, and Voting). Naïve Bayes has the best result. It achieved 100% accuracy and built the model in 0.01 second. The results demonstrate that the proposed method can classify malaria types accurately and has the best result compared to the reported results in the field.**

Keywords—Malaria diagnosis; malaria symptoms; artificial intelligence and machine learning classifier; malaria classifier

I. INTRODUCTION

Malaria has been endemic in the developing society and the most devastating illness in the African region which has 95% malaria cases and death burden and estimated 241 million has been [20] spent on malaria prevention and treatment strategies by the Ministry of Health and international partners in Kenya. This includes distribution of long-lasting Insecticide-treated Nets, indoor residual spraying (IRS) in selected areas, intermittent preventive treatment during pregnancy and effective malaria case management [11]. However, mortality has not decreased. According to the World Health Organization [19], malaria cases registered in Kenya were 6 million in 2021 and 228 million cases reported globally that led to 627,000 diseases worldwide in 2020. This problem is severe in sub-Saharan Africa where 94% deaths are registered annually. This condition is predicted to become worse especially in the Coastal and Western regions that are the pandemic that has compromised malaria treatment and intervention measures [15]. Moreover, 70% of the population of Kenya who live in

rural areas lives below poverty level [20]. Malignant tertian malaria caused by plasmodium falciparum species accounts for over 99% of malaria cases in Kenya [9].

We conducted a study and discovered high rates of individuals who undertakes self-treatment when attacked by malaria in rural areas in Kenya. The study found that 98% of participants had symptoms of malaria within six months of the study. 85% of participants did not visit healthcare services due to various reasons. For example, lack of money, transport, consultation fee, treatment fee etc. 58% bought non-prescribed anti-malaria drugs for malaria treatment. These are issues that require intervention.

Machine learning (ML) gives powers to develop more accurate malaria diagnosis approaches, whereas ML-based-methods performance depends on the quality of input features (Symptoms). Various solutions including Artificial intelligence (AI) and ML with feature-set have been used to classify malaria into four types. Devi et al. [7], performed analysis of a feature set on malaria-infected erythrocyte classification, using the Artificial Neural Network–Genetic (ANN-GA) Algorithm. This process included illumination correction, erythrocyte segmentation, feature extraction and classification. Six features were identified and evaluated using different classifiers such as Support Vector machine (SVM), K-nearest neighbours (KNN) and Naïve Bayes (NB) algorithms with a dataset to detect malaria. The experimental results demonstrated that the dataset (combined morphological, texture and intensity data) outperformed other datasets. However, six features is not enough to detect malaria accurately.

A study was carried out by Oladele et al. [12] to develop Neuro-Fuzzy expert system diagnostic software implemented with Microsoft Visual C# (C Sharp) programming language and Microsoft SQL Server 2012 to manage the database. The authors conducted oral interviews with the medical practitioners whose knowledge was captured into the knowledge based on Fuzzy Expert System. Questionnaires were administered to the patients and filled in by the medical practitioners on behalf of the patients to capture the main symptoms. The strength noted is that DIAGMAL gave accurate diagnostic predictions. However, there is no indication of effective performance compared to other existing malaria diagnosis systems in the field.

Recent academic research focused on ML techniques with data to predict malaria (Wang et al., [18]; Ramdzan et al., [13]; Shimizu et al., [16]. However, mortality is still increasing. A new annual World Malaria report from the World Health Organization has shown a dramatic rise in malaria deaths [19]. Besides, there is a lack of malaria diagnosis Apps stated by Marita et al.[9].

The proposed approach is based on Multiple algorithms applying parameter tuning to optimize model performance and to classify malaria symptoms accurately. Using InfoGainAttributeEval selected the most significant 100 features. The classifiers utilized Artificial Neural Networks (ANNs), Naïve Bayes (NB), Random Forest (RF) and Ensemble methods (Meta Bagging, Random Committee Meta, and Voting). To the best of our knowledge, existing researches have not considered this integrated method.

Our contributions involve a new method; (1.) combining InfoGainAttributeEval feature selection technique, selecting 100 most significant features extracted from 4000 samples. (2.) Parameter tuning approach that optimizes model's performance (3) Identified knowledge about local community needs, barriers of access to healthcare services in Western Kenya in remote community settings.

The main aim of the proposed study is to introduce a new method for malaria diagnosis integrating InfoGainAttributeEval feature selection techniques and parameter tuning methods based on Artificial Intelligence and Machine Learning (AI & ML) classifiers with features to accurately distinguish types of malaria, including Malignant, Tertian, Quartan and Suspected malaria.

Specifically, this study has the following objectives:

- Identify different sources to enable extraction of features and non-symptom related factors.

- Build state-of-the-art models based on ANN, NB, RF and Ensemble methods (Bagging, Random Committee & Voting) with features.

- Train the models using multiclass classifiers with features to measure model performances.

- Evaluate the methods and compare the results with the best results in the field to demonstrate the merit of the proposed method.

The proposed study is significant because the outcome is expected to alleviate diagnosis of malaria in the remote communities within which limited supply of doctors' struggle to provide adequate diagnosis. Overall, the local communities' healthcare needs will be met.

The remaining section of this paper is structured as follows: Section II reviews related work. Section III describes the methods, including samples (sources), data collection, feature extraction, feature selection, algorithms, patient's future inputs, participants responses including Ethical statement/participant consent. Section IV presents Evaluation metrics and it describes experimental procedures. Section V presents experimental results. Section VI provides discussion including comparisons, limitation, and strength of the proposed method. Section VII presents conclusion and future work.

II. RELATED WORK

A. Artifical Intelligence and Machine Learning

First Conventional methods rely on the expert's skill for diagnosing malaria and are time consuming. As such various researchers have attempted to tackle malaria using Artificial Intelligence and machine learning techniques as a tool to predict risk factors.

Based on AI, Madhu et al., [23] predicted malaria using Artificial Neural Network with patient's history and symptoms. By applying back propagation learning rules, the results achieved 85% accuracy. However, this approach used limited dataset which can be improved by extending more dataset.

The study by Kim et al. [24] proposed a sensing method using digital in-line holographic microscopy (DIHM) combined with machine learning algorithms to sensitively detect unstained malaria-infected red blood cells. The DIHM-based AI does not require blood smear and the test results achieved 97.5% accuracy. However, this study only used 13 features which does not cover all essential symptoms.

Semakula et al. [25] used household information data and Bayesian belief network with defined probabilities methods to predict malaria. Their work achieved 91.11% accuracy. However, other factors such as environmental change was not considered in the study which has an impact of mosquitoes.

Equally, the study by Morang'a et al.[10] explored haematological data extracted from 2,207 participants in Ghana and used Machine learning approaches such as ANN to find the techniques that can accurately evaluate uncomplicated malaria (UM) from non-malarial infections (nMI) and severe malaria (SM), utilizing haematological parameters. ANN with three hidden layers was used to classify UM, nMI and SM. The multi-classification models scored in the range of 94% to 98% accuracy.

Similarly, Kumar et al, [26]. proposed malaria detection using deep convolution neural network. Their studies achieved 97% accuracy. However, the downside of this study was that the dataset used is not clear how they were selected and feature size. The accuracy from this data is questionable.

The latest trend in Machine learning has also been applied. The study by Sherrad et al., [15] was the first to explore convolutional neural networks to distinguish between infected and uninfected cells in thin blood smears. They used Convolutional Neural Network (CNN) since deep learning does not need hand crafted features, which is the biggest advantage.

There are other researchers who have applied deep learning with images. Fuhad et al., [27] proposed an entirely automated Convolutional Neural Network (CNN) based model for the diagnosis of malaria from the microscopic blood smear images. Using image data and CNN, they achieved 98.2% and 72.1% respectively for white blood cells. However, the accuracy needs improving for effective diagnosis.

Other researchers took a different approach to combat malaria. Santosh and Ramesh [14] conducted research to determine malaria abundances using ANN with clinical and environmental variables with Big Data on the geographical location of Khammam district, Telanagana, India. Their method utilized large data across different seasons to improve accuracy in real practice. The highest accuracy they achieved was 81.7%. However, this accuracy requires more exploration to improve malaria models. 12% of the environmental data and 7% of clinical data were missing and yet these variables are necessary to attain accurate predictive power. Therefore, correct predictive data are required to improve the accuracy.

The study by Shambhu et al. [28] provided a review of techniques and discusses (i) acquisition of image dataset, (ii) preprocessing, (iii) segmentation of RBC, and (iv) feature extraction. They also discussed selection, and (v) classification for the detection of malaria parasites using blood smear images.

Shimizu at el., [16] conducted a cross-sectional survey and recognized Plasmodium falciparum infections, Plasmodium vivax and Plasmodium knowlesi in the southern province of Thailand. Equally, Indonesia marked a key milestone in reducing 50% of dual plasmodium falciparum and Plasmodium vivax parasites which corresponds to 66% reduction in death rates from malaria.

The study by Arowolo et al., [1] proposed a combined a novel analysis of variance (ANOVA) with ant colony optimisation (ACO) approach as a hybrid feature selection to select relevant genes to minimise the redundancy between genes, using SVM for classification. The experimental outcomes based on the high-dimensional of gene expression data demonstrate that ANOVA-ACO can make relevant decisions for clinicians in the designs of drugs and approaches to eradicate malaria infections in humans. Although the strength seems promising, to be competent amongst the existing relevant work, the speed of the performance should be provided.

A study by Awotunde, et al. [2] developed a model to diagnose Malaria and Typhoid Fever using a Genetic Algorithm (GA), a Neuro-Fuzzy Inference System (GENFIS). They identified that GA module determines the best set of network parameters and distributes them to the appropriate hidden layer nodes. Their model achieved an accuracy of 97.2%."

To improve malaria diagnosis models, Awotunde, [3] utilised Support Vector Machine (SVM) algorithms and Adaboost, together with ensemble methods. Redundant or extraneous features were extracted using Chi-square to assess the model. The classification accuracy with six features obtained achieved 97%.

The studies above have considered uses of AI and ML approaches, NF rules based on symptoms to develop models for malaria diagnosis. But the existing approaches have not considered a combined method based on ANN and features to classify malaria into one of possible types more accurately. Moreover, the microscopic testing techniques cause delay at the start of treatment.

The proposed study uses a new method that has not been consider with the reported method to address this problem robustly.

B. Long-short Term Memory Network (LSTM)

Another work by Awotunde et al., [4] proposed a framework to predict malaria-endemic in selected geographical locations such as Nigeria. In their work, long short-term memory (LSTM) classifier was employed with Satellite and clinical data. The results indicate that the LSTM algorithm provides an efficient method for detecting situations of widespread malaria. The results demonstrate higher accuracy. However, there was no indication of the size of data used and the data is used in the validation strategy.

III. METHODOLOGY

The proposed approach is based on a combined method, using Artificial Intelligence (AI) and Machine Learning (ML) classifiers with features. The proposed method was chosen because while ML algorithms handles vast dataset and performs well in various domains, AI technique identifies correlations within data, thus making them good techniques to classify malaria in different types more accurately. The types are Malignant, Benign Tertian, Benign Quartan or Suspected malaria. Our methodology consists of five functional components as shown in Fig. 1 and are detailed below:

A. Sample (Sources)

Samples consist of 4000 questionnaires and individual participants. A questionnaire was designed to gather resident's information about malaria issues. Initially, a pilot study was carried out using questionnaires with 100 students at Maseno University to assist in preparation and test the questionnaire's effectiveness (comprehension, logic, acceptability, length & technical quality) before the main data collection, in which the instrument was deemed suitable after the pre-testing.

B. Data Collection

Data collected consisted of demographics, barriers of healthcare factors and malaria history (non-symptoms), symptoms (also known as features or data set) signs. After gaining consent from participants, out of 4000 participants, questionnaires were used to collect data from 3490 participants. The questionnaires were randomly handed to individual participating in the villages with the permission from the sub-chief of the area and administrator. The study covered a cluster of 125 in 6 villages in Ugenya, Alego and Gem in Siaya county in Western Kenya which are mosquito endemic regions. Also questionnaire were administered to 510 patients during clinical procedure (checking blood pressure, temperature, heartbeat, breath and colour of the eye to diagnosis malaria), and filled by nurse on behalf of patients through the assistance of medical officers in Siaya County Clinic Centres within the same clusters in Ugenya, Alego and Gem in Siaya County. We collected qualitative and quantitative data integrating symptom related factors including Malaria History, Malaria symptoms, signs and non-symptom related factors including demographics data e.g. Age, gender, location] and barriers of healthcare information. The data are important since it enables malaria diagnosis, indicates whether

a patient suffered from malaria or not and enables the understanding of the patient's needs.

The sample size is adequate with the assumption that every member of the population had equal opportunity of being selected with 95% confidence level and confidence interval of 5%.

The data collection was conducted in the period of July/August 2019. This date was extended to December 2021 to January 2022 due to covid-19 restrictions. During the same period of data collection within the same clusters and county, symptoms were also extracted and the summary is presented in Table I.

C. Feature Extraction

Symptoms are features used to diagnose (classify) malaria into one of the possible types. Types of malaria include Malignant, Benign Tertian, Benign Quartan and Suspected malaria. Each form of malaria is caused by distinct parasites. Malignant malaria is a fatal form of malaria caused by Plasmodium falciparum, a deadliest malaria parasite. The presentation of falciparum is very variable, and it imitates typhoidal symptoms – patients with falciparum may pass into a typhoidal condition without prompt treatment. Tertian malaria is caused by Plasmodium Vivax and Oval parasites. This parasite causes a fever every 2nd day. Quartan malaria is caused by a parasite known as Plasmodium Malariae. This parasite causes a fever every 3rd day.

100 malaria symptoms were captured using different sources from the 4000 samples. i.) using questionnaire with 3490 individuals out of the clinical setting. ii.) Also questionnaire were administered to 510 patients during clinical procedure (checking blood pressure, temperature, heartbeat, breath and colour of the eye to diagnosis malaria), and filled by nurse on behalf of patients through the help of medical officers in Siaya County Clinic Centres within the same clusters in Ugenya, Alego and Gem in Siaya County. Virtue's family physician (VFP) book was used to identify the symptoms that were collected outside the clinical environment and some in the clinical settings (VFP book, 1971). Symptoms of malaria can be fever, chills, headache, sweats, fatigue and others.

D. Feature Selection

InfoGainAttributeEval feature selection techniques were used to select the most significant 100 features extracted from 4000 samples. InfoGainAttributeEval method ranks all the features in the dataset. While InfoGainAttributeEval technique is important because it omits the features that have lower ranks and produce the predictive accuracy of classification algorithms. One limitation of the method is that weights put by the rankers algorithms are different than those by the classification algorithms so there is a possibility of overfitting. A summary of the symptoms are presented in Table I.

E. Algorithms

Various classification algorithms exist that have been used for malaria symptom classification to solve malaria cases.

These include K-Nearest Neighbours (KNN), Support vector machine (SVM), Logistic regression (LR) that achieved 85% accuracy [6]. These errors are far above the standard level of confidence.

The proposed study utilizes AI and ML techniques, supervised learners and Ensemble methods to classify malaria accurately. Extensive experiments were conducted based on ANN, NB and RF algorithms. The chosen algorithms can handle qualitative and quantitative values and are robust to outliers. Further, ensemble methods were utilized to improve the accuracy of results of the models. These include Meta Bagging, Random Committee Meta and Voting. The reason for selecting the proposed method is that it can classify malaria accurately (within seconds). The algorithms use Waikato Environment for Knowledge Analysis (WEKA), a popular suite of ML software written in Java. It has four integrated editors which are useful for training and testing processes.

1) Artificial neural network: is simply called neural networks (NNs). ANN has been found to satisfactorily address complex nonlinear function, as such facilitate image recognition, natural language processing and classification of behaviour patterns.

2) Naïve Bayes: Although it is a simple technique, NB is a powerful classifier for developing models that assign labels to the features where labels are drawn from training datasets. It is used in our study since it has the benefit of not requiring a very large amount of training data to estimate parameters required for classification. NB also has a limitation which is over simplicity.

3) Random forest: is a supervised ML classifier that combines the output of diverse decision tree algorithms to reach a single result. It uses ensemble learning which is a technique that can handle both classification and regression problems, enabling it to be used in Healthcare to diagnose patients and to predict complex problems. It is chosen in our study since it offers a more accurate classification in comparison to decision tree algorithms and can handle missing data [21].

4) Ensemble method: Ensemble method is a machine learning technique which combines various base models in order to generate optimal predictive models. The ensemble method has been driven by the perception that an appropriate integration of different classification algorithms might improve prediction performance. In multiple classifiers, the scores generated by contributing classifiers on component feature sets are taken as inputs to the combined function.

Supposing we combine D component models for a classification task, the ensemble model can be formulated as:

$$0_j(X) = F \begin{pmatrix} 0_{11}(X_1),\dots & 0_{1j}(X_1),\dots & 0_{1C}(X_1) \\ . & \dots & . \\ 0_{Dj}(X_D),\dots & 0_{Dj}(X_D),\dots, & 0_{DC}(X_D) \end{pmatrix},$$

(1)

TABLE I.   SYMPTOMS (FEATURES) SUMMARY

Malignant Malaria	Quartan Malaria
• **Fever:** malignant contains irregular fever	• **Ague fits:** in quartan, ague begins in the afternoon
• **More ill:** presentation of patients become more ill with irregular fever	• **Cold stage:** the cold stage has longer intervals in quartan
• **Develop Typhoid:** Patients may pass into a typhoid condition without promptly treatment.	• **Attack repeats:** double quartan, attacks repeat themselves on the same day and on alternative days
Tertain Malaria	**Suspected malaria**
• **Headache and malaise:** The disease begins with headache and malaise	• **Headache and Thirst:** are some of the characteristics of symptoms that cause suspicion of malaria in a patient.
• **Ague:** patients experience ague after headache and malaise has three stages	• **High body Temperature:** patients' temperature rises to 105° degrees Fahrenheit at this stage, after a short time, the body temperature drops down.
• **Cold, Hot and Sweating:** these are stages of ague. The cold stage lasted 2 hours, feeling debility with nausea. hot stage follows which last 6 hours. After the hot fever passes off, a sweating stage follows that causes perspiration to break out.	• **Vomiting:** a condition when a patient has a feeling of debility with nausea and vomit.

Where $O_{Kj}(X_K)$ is the output score of the classification model, for class j and F(.) shows the combining function of the ensemble components can be produced by different classification algorithms on different data sets.

F. Patients Future Inputs

For medical facility operation, a system to diagnose malaria will be developed using fuzzy If – Then rules which will assist to input more patient's details during clinical visit. The system will check individual patient's inputs which consist of demographic (Age, sex, place of residence) signs and indications of patient's complaint and symptoms such as headache, vomiting against know features. If quartan malaria,

malignant or tertian malaria is detected, the patient's treatment/prescription is generated in real-time (within seconds). If suspected malaria is detected, recommendation of further tests is generated. If no symptoms are detected, then the patient is informed, and no action as presented in Fig. 1.

These are core of our combined framework from which data were collected and enabled feature extraction and selection, leading to features split into training-set and test-sets. The training set is used to generate models and to train the model. The unseen test set is used to test the validity of the models. The test set demonstrates how well the model generalizes on the unseen data.
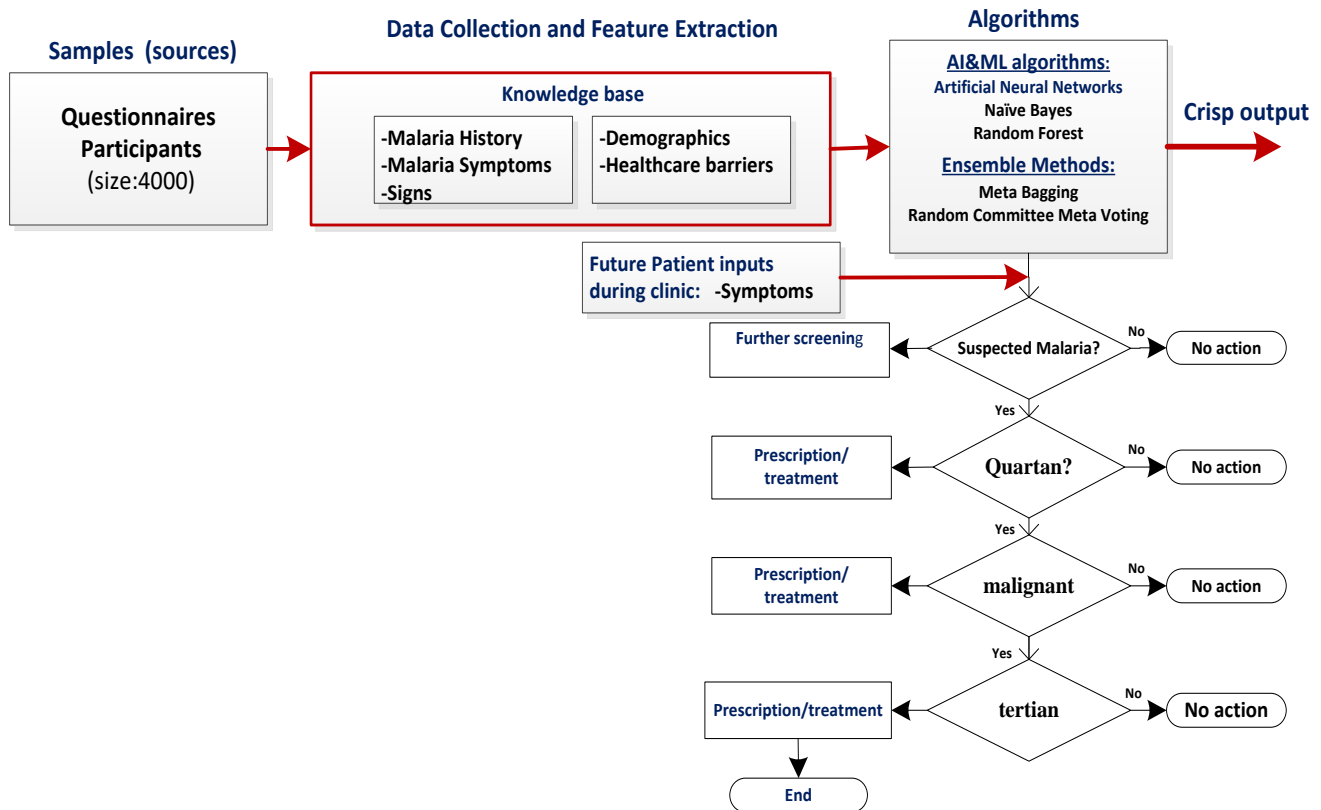

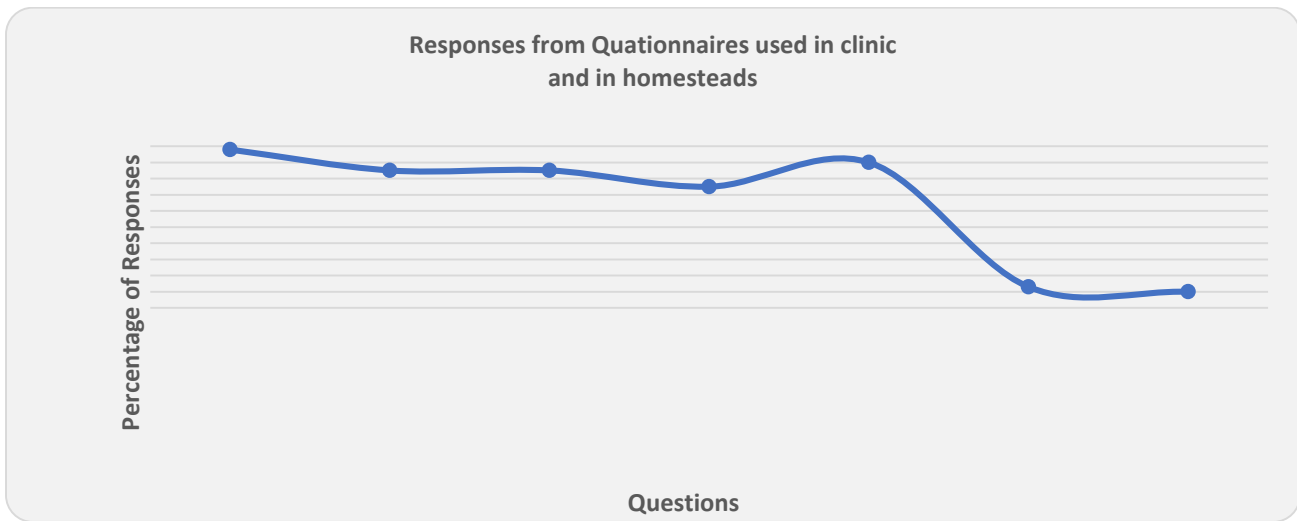Fig. 1.   Methodology structure flow.

Fig. 2.   Participant's responses from questionnaires.

G. Participants Responses

A total number of 4000 questionnaires were administered to respondents. Fig. 2 shows that 87.3% individuals who participated reported contracting malaria symptoms within six months of the study. Out of 87.3% (3490) who contracted malaria, 12.7% (510) cases were confirmed malaria through clinical procedures of checking blood pressure, temperature, heartbeat, breath and colour of the eye. These are some of the procedures. While 85% (2966.5) out of 87.3% did not visit healthcare service due to lack of finance or being a distant away from quality health service or due to lack of transport. These participants described the symptoms at the time of illness that was confirmed at the time of the study using virtue's family physician book [17]. Out of these, 58% were self-medicated by buying non-prescribed anti-malaria drugs through Chemistry counters or used herbal treatment. 10% felt healthcare services within their communities were very costly, while others lack quality health facilities. Dispensary level is the most common health service used by these community members. The head of the homestead (male or female) makes decisions during illness for all family members living in their homestead. This helps in understanding the existing barriers so that AI intervention can be considered appropriately. No incentive was given to participants.

H. Ethics Statement and Participant Consent

Ethical approval for this study was obtained from the ethics committee, Computer and Information Science, University of Northumbria (7/2019). All the participants in our study had given written informed consents before participating in the study. To comply with the privacy of individuals, the questionnaires were filled anonymously without any name disclosure. Participants were aware that they had the right to withdraw from the study at any time should they decide to do so. All methods were carried out in accordance with the related guidelines and regulations.

IV.   EXPERIMENTAL PROCEDURES

Machine Learning models can be utilized to classify malaria proposed in literature. In order to classify malaria types

and vigorously evaluate our new method. Most significant 100 features selected were used based on ANN, NB, RF algorithms, Ensemble methods (Bagging, Random Committee & Voting) to evaluate the new method.

A. Evaluation Metrics

The A model evaluation is an important part of building the AIML model. The most popular evaluation metrics employed for classification is Accuracy. But with imbalanced data relying on Accuracy alone for measurement can be misleading. Based on the proposed approach the appropriate evaluation metric used are Accuracy (ACC), True Positive (TP), False Positive (FP), Precision, Recall, F-Measure, Receiver Operator under the Curve (ROC), speed taken to build models and Confusion Matrix. As can be seen, these are demonstrated in experiment in the next sections.

Four extensive experiments are conducted in detail in Sections IVA(1) to IVA(4) The whole dataset (Symptoms) have been used for evaluation as well as the data set from each malaria types. This was performed to test the effectiveness of the data set. The first experiment applied all the selected features to classify malaria, The second experiment used Malignant features, Quartan and suspected cases excluding Tertian. The third used features from Tertian, Quartan and suspect cases, excluding Malignant. The fourth experiment used Malignant, Tertian and Quartan features to train and test the model. The reason for using the different sizes of features is to rigorously assess our method from different angles for best performance.

1) Experiment 1# evaluation of Artificial Neural Network (ANN): In experiment 1, the goal is to assess the overall performance for the proposed method, using a supervised Multi-Layer ANN algorithm with the most significant 100 selected features. Assessing the performance of the proposed model is important because it increases user's confidence. To assess how well the proposed model performs, evaluation metrics for multiclass classification were used that are ACC, TP, FP, Precision, Recall, F-Measure, ROC Curve, speed taken to build models and Confusion Matrix. Parameters are

tuned to find the best fit and applied optimization method. 3 units (10, 20, 40) are set at the hidden layer. The units are initialized randomly before training begins.

The standard level of confidence error is 5% for all classifiers since an average error above 5% is considered unsuccessful, while below 5% is deemed successful. The validation threshold used is 2-fold cross-validation because it can handle the conventional data well and helps to avoid over-fitting. Features are randomly split into training sets and test-set. The training of Multi-Layer ANN is conducted with the back-propagation learning algorithm to learn instances on a full training set and evaluate performance on independent unseen test-set. This process is repeated twice. Roles are reversed and train on a test-set and test on training-set. We use Multi-Layer ANN since it is a general-purpose tool, which has been applied successfully in classification problems in medical diagnosis for heart attacks. Results are described in Section V.

a) ANN model: based on ANN, the model was generated within 3.01 seconds from the training set. As shown in Fig. 3, ANN is a Multi-layer artificial neural network with 3 layers which are input layer, hidden layers and output layer has specific steps in the process of training and testing the model. The layers used a sigmoid activation function. These layers are elucidated below.

b) Input Layer: Features for ANN are put through the input layer and are directly transferred to the second layer by each neuron. This mathematical function is presented as:

$$y_i^{(1)} = x_i^{(1)}, \qquad (2)$$

where $x_i^{(1)}$ is the input and $y_i^{(1)}$ is the output neuron i in layer 1.

c) Hidden Layers: These layers are between the input and output. Neurons in the hidden layers detect the features, weights of the neurons and display the features hidden in the inputs. The features are then utilized by the output layer in determining the output pattern. The output of neurons 3 and 4 in the hidden layers are calculated as:

$$Y_3 = \text{sigmoid } (X_1W_{13} + X_2W_{23}-\theta_3) = 1/[1+e^{-(1x0.5+1x0.4-1x0.8)}]$$
$$= 0.5250 \qquad (3)$$

$$Y_4 = \text{sigmoid } (X_1W_{14} + X_2W_{24}-\theta_4) = 1/[1+e^{-(1x0.9+1x1.0+1x0.1)}]$$
$$= 0.8808 \qquad (4)$$

d) Output Layer: the output layer receives the inputs transmitted from layer 3 and 4, then performs the calculations through the neurons.

As can be seen in Fig. 3, the networks with 3 layers learn relatively fast. They converge in less than 500 epochs. Once the training is performed, the network is tested with a set of unseen test samples to test how well the model performs. The test result is shown in Section V.

2) Experiment #2 evaluation of naïve bayes: The purpose of Experiment 2 is to examine the performance of the model using instances of classes Malignant, Quartan and suspected cases excluding Tertian. Naïve Bayes supervised algorithm is utilized to classify the instances accurately. As described in Section V and shown in Fig. 3, we employ evaluation metrics to examine how well the proposed feature model performs. We could use a percentage split, with some percentage of the dataset used to train and the rest used for testing to get reliable evaluation results. The Supplied Test set was utilized to test the proposed model on a user-specified dataset. 75 instances of features from Malignant, Quartan and suspect of malaria excluding tertian are utilised to generate and learn data model, and another set of data to test the model. Parameters are assigned based on accuracy and speed of learning to ensure high-quality performance. The training is done on a training set and testing done on a test set. The roles are swapped, trained on a test set and tested on a training set. It is important to evaluate a classifier on an independent unseen set, which means the model is tested with an unseen independent test set. A standard confidence level of error is 5% since an average error above 5% is considered unsuccessful and below 5% is considered successful. Experiment 2 results are provided in Section VB.

3) Experiment #3: evaluation based on random forest: The aim of experiment 3 is to measure the model performance for validity and accuracy, utilizing Random Forest, base classifier with a total of 75 instances of classes Tertian, Quartan and suspect cases, excluding Malignant. Similarly, as described in Section IV, we measure how well the proposed feature model performs. The evaluation threshold used is 2-fold cross-validation because it can handle the conventional data well (Sivarao and El-Tayeb, 2009) and helps to avoid overfitting .Features are randomly split. Training is performed on a training set and testing on a testing set. This process is repeated twice while roles are reversed, training on a test-set and testing on a training-set. This is done such that training set is used only once for training and testing is performed on unseen independent sample test sets to achieve the most accurate model performance. Parameters are tuned, 100 number of iterations with 1 seed and 500 epochs are assigned. Similarly, evaluation methods utilized to evaluate the model performance are Accuracy, TP, FP, Precision, Recall, F-Measures, ROC, Time taken to build model and confusion Matrix. The result is provided in Section V.

4) Experiment #4 evaluation of ensemble methods: The goal of Experiment 4 is to evaluate and demonstrate the rigour of our models, classifying malaria into one of possible types: Malignant, Tertian, Quartan or Suspected malaria. The Bagging, Random Committee and Voting were used to evaluate the models. The techniques create multiple models and combine them to produce robust results.

Bagging also known as bootstrap aggregation is a technique that is best used with models that have a low bias and a high variance, meaning that the predictions they are highly dependent on the specific features from which they are trained. The most used algorithm for bagging that fits this requirement of high variance is decision trees.

With bagging, we produce many different decision structures. We do that by having several different training sets of the same size. We sample the original training set and build a model for each one. Therefore, Meta Bagging is deployed. We choose a bag size of 100% that samples the training set to get another set of the same size, but this will sample with replacement. That means we get different sets of the same size each time we sample. However, each set might contain repeats of the original training-sets (instances). We choose the classifier we want to bag and the number of bagging iterations and random-number seed.

The Random Committee is chosen for being capable of handling different perspectives of the problem. It is also. capable of encouraging new models to become an expert for instances misclassified by earlier models. The intuitive justification for this is that in real life, committee members should complement each other's expertise by focusing on different aspect of the problem. To combine all built models, we use vote, which weighs models according to their performance.

Voting is the simplest ensemble algorithm, yet very effective in classification and regression problems. It creates two or more sub-models. Each sub-model makes predictions that are combined in some way, by taking the mean or the mode of the predictions, enabling each sub-model to vote on what the result should be.

The evaluation of the feature model using the three ensemble methods, 75 instances of classes Malignant, Tertian and Quartan excluding suspected cases were deployed. Each feature is randomly split into a training-set and test-set. They are fed to each classifier, which produces different predictions. All the base model outputs are combined in a final model and the decision is made based on the majority vote or by looking at the predictions or weights (output of all base model) - one learner/Classifier, which produces better outputs than any single classifier. We used a two-fold cross-validation method

to ensure that the positive and negative cases in the training-set and test-set are proportionate to the cases in the dataset.

One disadvantage is that it produces output that is difficult to analyse, but the advantage is that the method often achieves very good performance.

V. RESULTS

A. *Experiment 1: Results Based on Artificial Neural Network*

Experiment 1 assessed the overall performance of the proposed method based on Multi-Layer ANN with metric evaluation to demonstrate the model accuracy performance which addresses objective 1 to 3. Table II shows detailed accuracy by class. The experiment achieved a higher accuracy. Column 2 shows the results achieved accuracy of 100% in all four classes. This indicates that 100 instances are classified correctly and 0% are incorrectly classified instances. Speed to build the model was 3.01 seconds. As we can see in Table II, all the evaluation metrics including True Positive, True Negative, Precision, Recall, Receiver Operator Characteristic curve together with Weighted Average for all classes obtained 1.000 (100%). In which case, the weighted Average value for the proposed model is as high as possible. This means the model is doing better than randomly guessing.

Table II shows how well the model performed. Using the Confusion Matrix, the matrix has four values in the Y-Axis that are: a, b, c and d. Values on the diagonal of the matrix demonstrate how many classifications for each class. are correct. In the test data set, 25 instances belong to class a. Therefore, true classes have 25 items. By looking at all the values in row a, it can be inferred that, out of 25 instances, the model indicates that 25 instances belong to class a (correctly classified), 25 instances belong to class b, 25 instances belong to class c and 25 instances belong to class d. Values in class a depict that model classified 25 instances as class a, b, c and d (sum of all the values in class a, b, c and d).
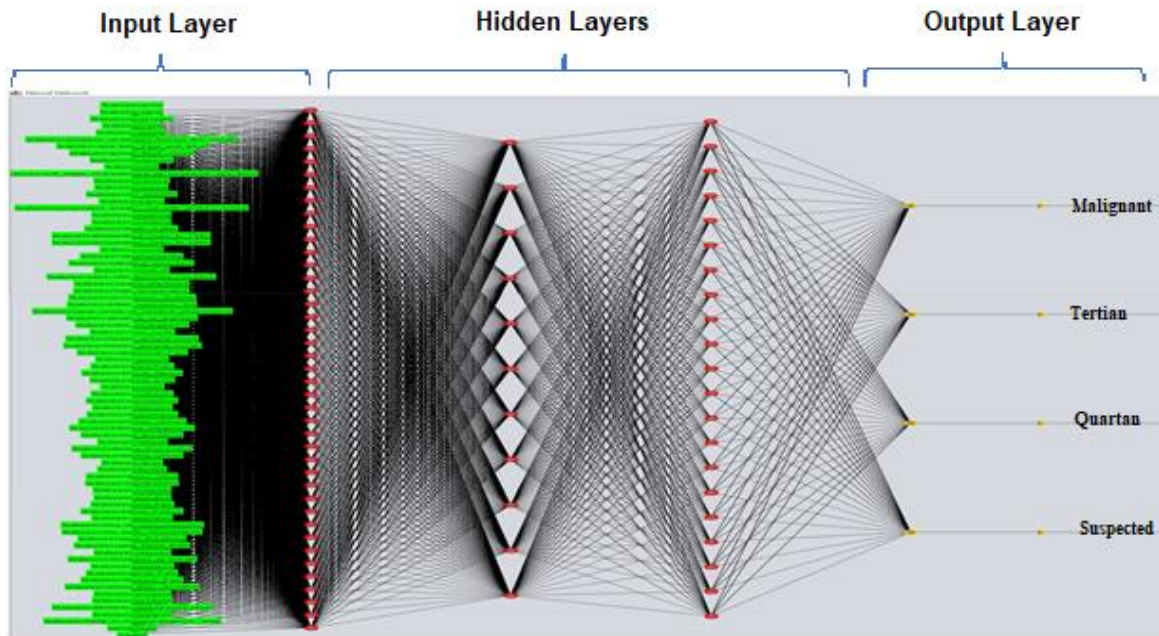

Fig. 3. Multi-Layer ANN for Artificial Intelligent diagnosis system.

TABLE II. EXPERIMENT 1 RESULTS - EVALUATION BASED ON MULTI-LAYER ANN

Class	Accuracy	TP	FP	Precision	Recall	F-Measure	ROC Curve Avg	Time to build model
Malignant	100**%**	1.000	1.000	1.000	1.000	1.000	1.000	0.01 Secs
Tertian	100**%**	1.000	1.000	1.000	1.000	1.000	1.000	0.006 Secs
Quartan	100**%**	1.000	1.000	1.000	1.000	1.000	1.000	0.006 Secs
Suspect cases	100**%**	1.000	1.000	1.000	1.000	1.000	1.000	0.006 Secs
Weighted Avg.	**100%**	**1.000**	**1.000**	**1.000**	**1.000**	**1.000**	**1.000**	

= = = Confusion Matrix = = =						
a **b** c d			← - classified as			
25 **0** 0 0	|	a	=	MALIGNANT_FEVER		
0 **25** 0 0	|	b	=	TERTIAN_FEVER		
0 **0** 25 0	|	c	=	QUARTAN_FEVER		
0 **0** 0 25	|	d	=	SUSPECTED_FEVER		

The results in Table II demonstrate that the combined method using multi-Layer ANN algorithms with features (symptoms) and non-symptom factors can classify malaria accurately within seconds and has the best performance compared to the reported results in the field.

It has been found that features and non-symptom factors as well as parameters have played a crucial role in the classification of possible classes correctly.

B. Experiment 2: Results Based on Naïve Bayes

The proposed feature model performance was examined utilizing Naïve Bayes algorithm with instances fromMalignant, Quartan and suspect cases of malaria and applying user supplied test set. We utilized the same evaluation metric as was used in Experiment 1 to examine how well the proposed feature model performs. Equally, Table III shows detailed accuracy by class, column 2 shows the accuracy results achieved 100% in all the classes. Time taken to test the model was 0.01 seconds. This indicates that 75 instances are classified correctly, while incorrectly classified instances are 0%. Similarly, as Table III demonstrates, all the evaluation metrics including True Positive, True Negative, Precision, Recall, Receiver Operator Characteristic curve together with Weighted Avg. for all classes obtained 1.000 (100%). Accuracy measures

types of malaria and discriminates correctly as Malignant, Quartan and suspected malaria among the total number of features tested. This means the result is quite accurate and resembles experiment 1 results.

Similar to experiment 1 results, we evaluated our model performance using Confusion Matrix to see how well the model performed. The matrix has three values in the Y-Axis that are: a, b and c. Values on the diagonal of the matrix show how many classifications for each class are correct. It shows 25 instances belonging to class a. Thus, true classes have 25 instances. In view of all the values in row a, it can be implied that, out of 25 instances, the model calculates 25 instances belonging to class a (correctly classified), 25 instances belonging to class b and 25 instances belong to class c. Values in class a depict that model.

The results in Table III indicate that our combined method using NB algorithms with features (symptoms) from all the four classes can classify malaria symptoms accurately has the best performance compared to the reported results in the field.

Like experiment 1, we found that features and non-symptom factors as well as parameters have played a crucial role in classifying four possible classes accurately.

TABLE III. EXPERIMENT 2 RESULTS - EVALUATION BASED ON NAÏVE BAYES

Class	Accuracy	TP	FP	Precision	Recall	F-Measure	ROC Curve Avg	Time to build model
Malignant	100**%**	1.000	1.000	1.000	1.000	1.000	1.000	0.01 Secs
Quartan	100**%**	1.000	1.000	1.000	1.000	1.000	1.000	0.006 Secs
Suspected Fever	100**%**	1.000	1.000	1.000	1.000	1.000	1.000	0.006 Secs
Weighted Avg.	**100%**	**1.000**	**1.000**	**1.000**	**1.000**	**1.000**	**1.000**	

= = = Confusion Matrix = = =					
a **b** c			← - classified as		
25 **0** 0	|	a	=	MALIGNANT_FEVER	
0 **25** 0	|	b	=	QUARTAN_FEVER	
0 **0** 25	|	c	=	SUSPECTED_FEVER	

C. Experiment 3: Results Based on Random Forest

The goal of experiment 3 was to evaluate the merit of the features of the Tertian, Quartan and suspected cases of malaria, except Malignant malaria, usingRandom Forest algorithm. Table IV, column 1 shows that the results achieved are 100% accuracy. This means correctly classified instances are 75 (100%) and incorrectly classified instances are 0 (0%). Time taken to build the model was 0.03secs and 0.01sec time to test the model. This is a high performance. In this experiment results, the confusion matrix represents 3 rows showing true classes and 3 columns representing models' correct prediction. This has also addressed objectives 1 to 3.

As seen in experiment 3 results, the matrix in experiment 3 results has three values in the Y-Axis, which are: a, b and c. Values on the diagonal of the matrix show how many classifications for each class are correct. It shows that 25 instances belong to class a. Thus, true classes have 25.instances. In view of all the values in row a, it can be implied that, out of 25 instances, the model calculates 25 instances belonging to class a (correctly classified), 25 instances belonging to class b and 25 instances belonging to class c. Values in class a depict that model classified 25

instances as class a, b and c (sum of all the values in class a, b and c). We can see that matrix in Table IV, all classes performed well.

D. Experiment 4: Results Based on Ensemble Methods

This section presents the performance of Ensemble classification methods. To demonstrate how well features (symptoms) perform in diagnosing malaria into either Malignant, Tertian, Quartan or Suspected malaria, the Ensemble of classification algorithms (Meta Bagging, Random Committee Meta, and Voting) with different features were used. Ensemble learners integrated the perspectives of several learners to improve performance. This also rigorously scrutinised the features to demonstrate how well they generalise to unseen data. The average accuracies of the three ensemble methods are provided in Table V. It can be noted that the performance of the ensemble classification algorithms is consistently high across the feature sets. The performance based on Bagging, Random committee and Vote algorithms achieved 100% accuracy across the chosen algorithms. Also, precision, recall, ROC curve average attaining 1.000 (100%) performance and Time to build the model is 0.006 Secs. The results have demonstrated the best performance.

TABLE IV. EXPERIMENT 3 RESULTS EVALUATION BASED ON RANDOM FOREST

Class	Accuracy	TP	FP	Precision	Recall	F-Measure	ROC Curve Avg	Time to build model
Malignant	100%	1.000	1.000	1.000	1.000	1.000	1.000	0.006 Secs
Quartan	100%	1.000	1.000	1.000	1.000	1.000	1.000	0.006 Secs
Suspected Fever	100%	1.000	1.000	1.000	1.000	1.000	1.000	0.006 Secs
Weighted Avg.	**100%**	**1.000**	**1.000**	**1.000**	**1.000**	**1.000**	**1.000**	

a	b	c				< - - classified as		
25	0	0	|	a	=	TERTIAN_FEVER		
0	25	0	|	b	=	**QUARTAN_FEVERS**		
0	0	25	|	c	=	SUSPECTED_FEVER		

TABLE V. EVALUATION OF ENSEMBLE METHODS RESULTS

Classifiers	Features	Accuracy	Precision	Recall	F-Measure	ROC Curve Avg	Time to build model
Meta Bagging	Malignant	100%	1.000	1.000	1.000	1.000	0.006 Secs
Meta Random Committee	Tertian	100%	1.000	1.000	1.000	1.000	0.006 Secs
Meta Vote	Quartan	100%	1.000	1.000	1.000	1.000	0.006 Secs
Weighted Avg.		100%	1.000	1.000	1.000	1.000	

E. Performance Evaluation

We evaluated the quality of the three multiclass classifiers (ANN, NB, RF), using all features with all classes including (Malignant, Benign Tertian, Benign Quartan symptoms and suspected malaria) types of malaria to test the overall performance of our method. Without performing appropriate evaluation with different metrics, using only ACCURACY (TP +TN)/(TP + TN + FN + FP) is not always reliable. It causes issues when models are employed on unseen data, leading to

poor diagnosis [6]. We integrate the area under the ROC Curve to evaluate our multiclass classifiers and malaria diagnostic model performance since it is a useful method for rigorous evaluation [22]. Plotting the sensitivity (TPR) versus specificity (FPR) on a ROC Curve was performed and calculated the recall and the FPR. ROC curve combines these measures and generates evaluation standards. This curve allows to visualize the increase or decrease between True Positive Rate (or sensitivity) and False Positive Rate (or specificity). The dashed line would be random guessing (no

predictive value). When the curve is closer to the 45-degree diagonal of the ROC space, the less accurate the experiment is. Anything below the dashed line is considered worse than guessing. Classifiers providing curves closer to the Top-Left corner demonstrate a better performance. We can view a ROC curve for a multiclass model in Fig. 4. Each curve presents a class. It shows a diagonal line on the horizontal-axis and x-axis presenting original and standard values, which suggests that features seem to follow a normal distribution without deviation from a straight diagonal line.

It can be noticed that the ROC is not dependable on the class distribution which renders it useful for measuring classifiers for cases such as malaria.

The results in Table IV demonstrate that the combined method using RF algorithms with symptoms and non-symptom factors can classify malaria accurately within seconds and has the best performance compared to the reported results in the field.

We found that features (symptoms) and non-symptom factors as well as parameters have played a crucial role in classifying three possible classes correctly.
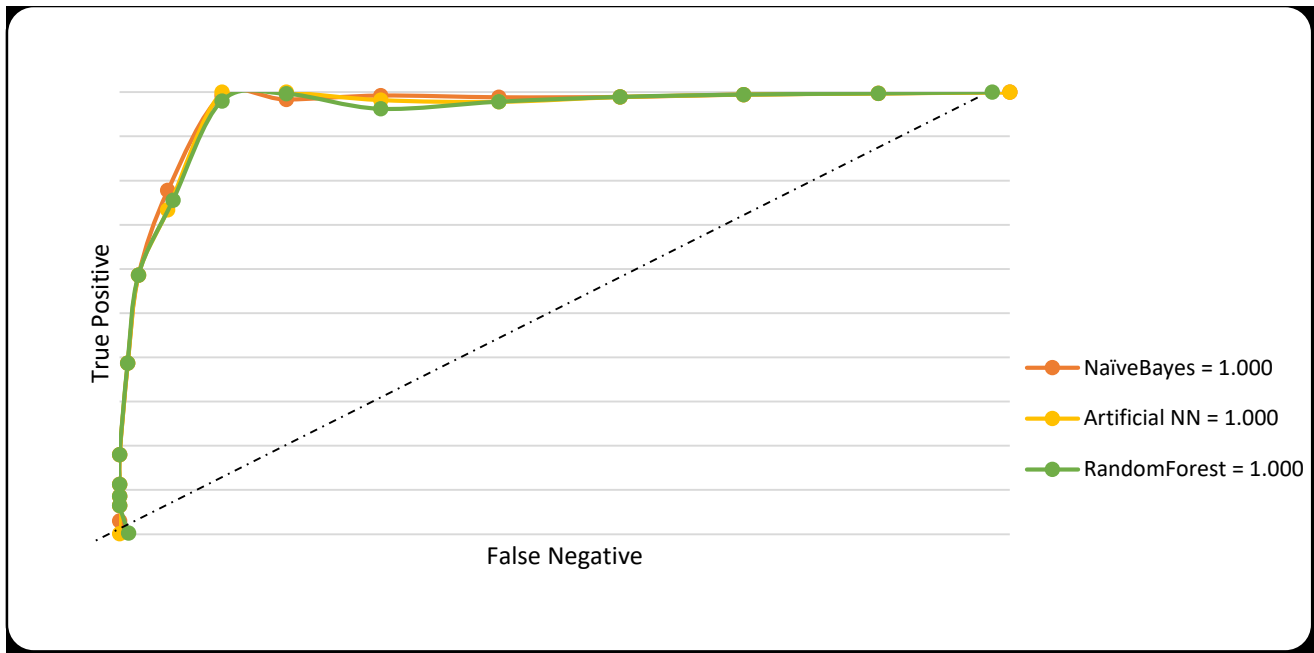

Fig. 4. ROC Curve developed using ANN, NB and RF with features.

VI. DISCUSSION

The main aim of our study is to introduce a novel method for malaria diagnosis combining InfoGainAttributeEval feature selection techniques and parameter tuning methods, using Artificial Intelligence and Machine Learning (AIML) classifiers with features/non-symptom factors to diagnose malaria into Malignant, Tertian, Quartan and Suspected malaria more accurately.

The proposed study contributed by introducing a novel method, combining (1) InfoGainAttributeEvalas, a feature selection method selected 100 most significant features from the initial 100 that were extracted from 4000 samples. We used ANNs, NB, RF classifiers and Ensemble methods. (2) Parameter tuning approach was used to optimize the model's performance. (3) Identified knowledge about local community needs in remote community settings. This combined method is novel, and other studies have not considered this method in the field. The performance in all experiments with supervised algorithms, ensemble methods with features have consistently produced higher results. AIML classifiers – ANN, NB, RF Ensemble methods with features have achieved 100% accuracy. If we compare our results across conducted

experiments with the work of Bria et al [5] which is the closest work to our work. The proposed work achieving 100% accuracy has outperformed the existing work in the field with a difference of 14% which is high performance. Overall, the results indicate that the proposed method with features offers higher accuracy and has the best performance.

The next section presents some relevant works that investigated malaria using ML techniques that has been compared with the proposed study. These include the study by Santosh and Ramesh [14], Morang'a et al. [10] as shown in Table VI.

TABLE VI. COMPARISON OF THE PROPOSED STUDY WITH THE EXISTING RELATED WORK

	Algorithms	Features	%
Barraclough et al.	ANNs, NB, RF	100	100%
Morang'a et al. (2020)	ANNs	-	94%-98%
Bria et al. (2021)	LR, SVM, KNN	-	84% - 86%
Santosh and Ramesh (2019)	ANNs	-	82%
Modu et al (2017)	SVM	33	80.6%-99%

A. Comparison of the Proposed Study with the Existing Related Work

Santosh and Ramesh [14] deployed clinical and environmental variables with Big Data using ANNs for mosquito abundance prediction in the geographical location of Khammam district, Telanagana in India. The average accuracy ranges from 82% to 17% accuracy.

Morang'a et al. [10] employed haematological data extracted from 2,207 participants in Ghana, using multi-layer classification. ANN scored a range of 94% to 98.3% accuracy.

In relation to relevant research all studies used ML classifiers to automatically learn features with a common goal to diagnose malaria into different classes. However, our evaluation method has exceeded all techniques reviewed in the relevant work.

Our finding indicates that the proposed method can classify malaria accurately within seconds and has the best result compared to the reported related results.

1) Limitation: During the process of experimenting with different numbers of hidden neurons, the experiment indicates that the number of neurons in the hidden layers affects the speed of training the network in the method achieving time to build the model in the range of 0.01 to 0.006 seconds (Zurada, 1992 [13]. Complex patterns cannot be distinguished by a small number of hidden neurons, but a large number of them can dramatically add burden to the computational field. When the number of hidden neurons is greater, the greater the ability of the network to distinguish existing patterns. However, if the number of hidden neurons is very large, the network might simply memorise all training samples. This may block it from generalising or producing correct outputs when presented with unseen data. Also using InfoGainAttributeEval has some limitations that weights put by the ranker algorithms are different than those by the classification algorithms so there is a possibility of overfitting. Having a larg number of neurons in the hidden layers could affects the speed of training the network hence it could cause a lack of generalisation to unseen data. This problem can be solved by deploying the right number of neurons and the right number of epochs.

2) Strength: On the other hand, we deployed three algorithm powers instead of using one algorithm power. The models built by combining the multiple classifiers are more reliable and more sophisticated to classify instances from the training and testing sets correctly, using two-cross-fold-validation.

VII. CONCLUSION

Over $810 Million have been spent in some parts of Trans-Saharan Africa to reduce malaria burden (Ministry of Health, 2015). The study by [6] investigated significant malaria symptoms and non-symptom-related factors for malaria diagnosis in endemic regions of Indonesia. Our work contributes a novel method, combining InfoGainAttributeEval, Parameter tuning approach to optimise best performance, identified knowledge about barriers of access to healthcare services in remote communities and needs of the community in remote settings in Western Kenya.

The experimental results demonstrated that the proposed method can diagnose malaria symptoms more accurately and reduce malaria burden. Deploying two-fold cross-validation, the proposed method was evaluated based on ANN, NB and RF, using 100 most significant features from the initial 100 that were extracted from 4000 samples. Further ensemble learning classifiers were employed to demonstrate the merit of the proposed method. The results of the experiments showed that the proposed method achieved 100% accuracy across all experiments. Measurement of Precision, Recall, ACC, F-Measure, Confusion Matrix and ROC Curve also presented higher accuracy rates of 100% accuracy score. High score can be because of using small data, meaning that the dataset consists of just 1–10 samples. A relatively small dataset can negatively affect the performance of a model due to over-fitting, which is when a model performs well with the training data but poorly on new independent data. Promising solution to this problem is to use cross-validation. In all our experiments 2-fold cross-validation was applied.

In all the 5 experiments in the proposed study, the results achieved are 100% accuracy. The results demonstrate that our combined method using multiclass algorithms with features and non-symptom factors can classify malaria symptoms accurately within seconds and has the best performance compared to the reported results in the field.

We found that features and non-symptom factors are important and have played a crucial role in the diagnosis of malaria in four possible types of classes.

A. Future Work

The next step will be to implement a fully working and tested diagnosis Application for remote settings. This was impacted with challenges such funds cut and travel restrictions due to Covid-19 in terms of co-developing the application and travelling in remote areas to perform testing.

CONFLICT OF INTERESTS

There is no conflict of interest to declare.

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