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A Predictive Symptoms-based System using Support Vector Machines to enhanced Classification Accuracy of Malaria and Typhoid Coinfection

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Abstract

High costs of medical equipment and insufficient number of medical specialists have immensely contributed to the increment of death rate especially in rural areas of most developing countries. According to Roll Back Malaria there are 300 million acute cases of malaria per year worldwide, causing more than one million deaths. About 90% of these deaths happen in Africa, majorly in young children. Besides malaria when tested; a large number is coinfecting with typhoid. Most often, symptoms of malaria and typhoid fevers do have common characteristics and clinicians do have difficulties in distinguishing them. For instance in Nigeria the existing diagnostic systems for malaria and typhoid in rural settlements are inefficient thereby making the result to be inaccurate and resulting to treatment of wrong ailments. Therefore in this paper, a predictive symptoms-based system for malaria and typhoid coinfection using Support Vector Machines (SVMs) is proposed for an improved classification results and the system is implemented using Microsoft Visual Basic 2013. Relatively high performance accuracy was achieved when tested on a reserved data set collected from a hospital. Hence the system will be of a great significant use in terms of affordable and quality health care services especially in rural settlement as an alternative and a reliable diagnostic system for the ailments.

Index Terms: Malaria, Typhoid, Support Vector Machines, Coinfection, Microsoft Visual Basic.

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1. Introduction

According to Roll Back Malaria there are 300 million acute cases of malaria per year world wide, causing more than one million deaths. About 90% of these deaths happen in Africa, majorly in young children, Edicha et al., 2014. Malaria in Nigeria, according to the Nigerian Ministry of Health (MoH), cases roughly 60% of

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outpatient visits to health facilities; 30% of childhood deaths; 25% of deaths in children less than one year; and 11% of maternal deaths. Interestingly, Panchbhai et al., 2012 asserted in their work that malaria perhaps originated in Africa and came along with human voyage to the Mediterranean shores, India and South East Asia. Furthermore, the Federal MoH estimates roughly 132 billion Naira spent on malaria per year in the form of treatment costs, prevention, loss of man-hours, etc. With these statistics, it is obvious that health is essential for economic prosperity.

Indeed, rural areas of developing nations in Africa are major victims of limited and few accessible medical facilities and medical personnel because they are concentrated in the urban areas. These and many other challenges in the health sector necessitated computer based diagnosis systems, Oguntimilehin et al., 2014. The fundamental reason for visiting a hospital is to get proper treatment and attention without delay from the best hands. No patient wants to be a specimen for a doctor especially one that has not improved on the knowledge gained since graduation from the medical school and at the same time, patients do not like to be delayed in receiving treatment for whatever reasons. But all these aforementioned have become the order of the day in most hospitals; especially in developing countries. Patients cannot get to see the doctor at the right time and there are some patients that find it difficult communicating their health issues and the doctor in turn has no time to keep asking the probable questions Fatumo et al., 2013. Another issue that has posed a problem in medicine in the developing world is the inadequate infusion of technology to aid the activities involved in the practice. Fatumo et al., 2013.

Typhoid fever is a worldwide health problem. Its impact is difficult to measure because the clinical picture is confused with those of many other febrile infections. Furthermore, the disease is undervalued because there are no bacteriology laboratories in most areas of developing countries; Scribd, 2015. These factors are believed to make many cases going undiagnosed. On the basis of the literature and the incidence of typhoid fever recorded in control groups in large vaccine field trials with good laboratory support it has been estimated that roughly 17 million cases of typhoid fever and 600,000 associated deaths occur annually according to Scribd, 2015.

According to the work of Onyido et al., 2012, a study of co-infection of typhoid and malaria fevers was carried out in Ekwulumili Community, Nnewi South, L.G.A., Anambra State, Nigeria, between May and July, 2012. Venous blood samples were collected from apparently healthy individuals who did not show any signs and symptoms of malaria and typhoid fevers. A total of 200 subjects comprising 52 (25%) males and 148(74%) females were examined. Of the 200 participants sampled, 40(20%) tested positive for malaria, 11 (5.5%) tested positive for typhoid fever and 10(5.0%) were coinfecting with malaria and typhoid fevers. More females (5.41%) than the males (3.85%) were coinfecting with typhoid and malaria fevers. Although Pradhan, 2011 asserted that the signs and symptoms (nausea, vomiting, abdominal pain, diarrhea etc) of malaria and typhoid fevers do have common characteristics and clinicians do have difficulties in distinguishing them. The researcher equally affirmed that an incorrect elucidation of rapid diagnostic tests holdup the treatment of definite infection and concluded that further research is indispensable to enhance diagnoses of coinfection and eradicate phony interpretation of malaria rapid diagnostic tests.

The cost of advanced medical equipment and services has created a gap between those who can and can't afford it. This gap has been a major challenge in the world's healthcare program. Some part of Nigeria has suffered so much from this gap created by the cost of providing advanced medical equipment and services. In almost all our rural areas there has been an increase in death rate due to absence of specialists and most of the advanced medical equipment and facilities needed. Thus there is a pressing need for an alternative means of providing medical services especially in our rural area. To this end, the research work aimed at providing alternative system by applying SVM using the Math Lab application in malaria and typhoid support diagnosis.

i. Support Vector Machines (SVMs)

According to Ali et al., 2011, amongst other machine learning models; SVM which was invented by Vapnik is the most popular model that executes classification more accurate and faster than most other models in many

application domains such as bioinformatics. The SVM is a supervised learning method that produces input-output mapping functions from a set of labeled training data. The mapping function is either a classification function or a regression function. In case of classification, kernel functions are usually used to map training data to a high-dimensional input space in which the input data become more separable than to the original input space. Maximum-margin hyperplanes are then found on the space. The model produced depends only on some data points of the training data near the class boundaries. Wang, 2005. SVMs regarding its high accuracy and flexibility in modeling various sources of data in the area of computational biology, an aspect of bioinformatic were further stated in the work of Dash et al., 2012. The importance of SVM classifier and its applications cannot be over emphasized. This was further affirmed in the work of Jiang et al., 2011 for classification of biological data. That is; in the problem of protein classification. The experimental results of their research work show that the string-based kernel in combination with SVM classifier presents appreciably better than the traditional spectrum kernel method.

2. Related Works

The research work of Oguntimilehin et al., 2015 identified malaria fever as a great threat to economic growth and killer of millions of people annually especially in Africa and Asia nations. Insufficient medical experts and equipment were identified as well known factors for this ugly development in curbing the menace. Hence, the sole aim of the work was reviewing some Predictive Models that are computer-driven developed to manage malaria. And examine the future needs to present computer based feasible classifiers in diagnosis and treatment of malaria cases. This justifies the importance of our research work; which is applying SVM to classifier and diagnoses malaria and typhoid fevers.

In the article publication of Yang, 2004, the researcher stated that classification and prediction of biological data forms the primary task of bioinformatics. And considering the fast increase in the repository of biological data, it is imperative to adopt computer based approaches in classification process. He further restated that among these approaches, SVM offer the best prediction performance, in that SVMs are modeled to make the best use of the margin that separate two classes so that hidden data will adequately enhanced by the trained model. As a result, protease functional site recognition, protein function prediction, protein and DNA sequence to mentioned but few are some of the areas of bioinformatics where SVMs have been broadly applied. Thus, it is also justify applying it in diagnoses of malaria and typhoid fevers which also form an aspect of bioinformatics.

Considering the work of Chayadevi and Raju, 2014; they present an approach for automatic malaria detection with fuzzy based color segmentation, fractal feature extraction and Adaptive Resonance Theory (ART) neural network classification. Based on these features, malaria parasites in an image can be identified. Identification is done using four classifiers- ART based neural network, Support Vector Machine (SVM), Neural Network based Back propagation Feed Forward (NN-BPFF) and k-Nearest Neighbour (k-NN). These classifiers automatically classify the images as malaria and non-malaria. Thus, typhoid was not considered and it is co-infection with that of malaria.

According to the work of Widodo and Wijiyanto, 2014; they proposed a system that automatically detects tropical malaria on blood smears image using SVM that involved two main steps. Support Vector Machines method used in this study are based on binary SVM one against all. Features used are statistics, Gray Level Co-occurrence Matrix (GLCM) and Gray Level Run Length Matrix (GLRLM).

In the work of Suryawanshi and Dixit, 2013; they designed a system which is capable to detect the presence of malaria parasite within the blood cell images by comparing the test image features with the training dataset and classification is done to check whether the human host is suffering from Malaria by using Euclidean Distance Classifier & SVM. However, results show that SVM gives better accuracy of 93.33% than that of Euclidean Distance Classifier which is 80%.

3. The Design of Predictive Symptoms-based (Classifier) System

The scope of data collected is within one health centre which is called Mount Moriah medical and Diagnostics Centre Nnewi/Nnobi, Anambra state, Nigeria. A total of 184 data was collected which contains a patient’s symptoms and the associated lab test results which were used to developed the system via SVM. These data collected are categorized as follow.

i. Data Variable (Input and Target)

The input variables are those symptoms that a patient observed before coming to hospital, the test results and some biodata of the patient. They include high temperature, headache, doziness/weakness, body/abdominal pain, vomiting, age, gender, widal count and MP. Table 1 summarizes the data variable transformation. It shows input set and the range of their possible values called domains. High Temperature, body/abdominal pain, headache and doziness /weakness has two possible values which can be either yes or no i.e. 0 or 1. Age takes an integer value while gender takes one for female and zero for male. Widal count and MP are the target which can take 0, 1, or 2 depending on the level of malaria or typhoid a patient has.

Table 1. Data Variable Transformation

S/N	INPUT SET	DOMAIN 1	DOMAIN 2	DOMAIN 3
1	High Temperature	Yes = 1	No = 0	
2	Body/ Abdominal pain	Yes = 1	No = 0	
3	Headache	Yes = 1	No = 0	
4	Doziness/ Weakness	Yes = 1	No = 0	
5	Vomiting	Yes = 1	No = 0	
6	Age	Integer		
7	Gender	Female = 1	Male=0	
8	Widal count (Target)	Not significant=0	Medium=1	High=2
9	MP	Not seen=0	Medium =1	High=2

ii. Input-Output Data Transformation

The output data are classified based on the level of typhoid and malaria of each patient. A patient with level zero (represented as 0) is classified to be a victim of no typhoid or malaria, a patient with level one (represented as 1) is classified to be a victim of medium typhoid or malaria and a patient with level three (represented as 2) is classified to be a victim of high typhoid or malaria. Tables 2 and 3 summarize typhoid and malaria input-output transformation respectively.

Table 2. Target Data Transformation for Typhoid

Highest_widal count	Extent	Class
Less than 80	Not significant	0
Equals 80 or 160	Medium	1
Greater than 160	High	2

Table 3. Target Data Transformation for Malaria

MP	Extent	Class
No +	Not seen	0
+ or ++	Medium	1
+++ and above	High	2

Tables 2 and 3 show the transformation of the widal count and MP respectively into the various classes. In Table 2 when the highest widal is less than 80 it means that the patient have no typhoid and belong to class zero(0), when patient's widal count highest is 80 or 60 then it means that the patient belong to class one(1). Finally, when a patient's highest widal count is more than 160 then the patient belong to class two (2). The same applied to Table 3 just that instead of widal count we used MP.

iii. SVM Model and its Tools.

SVM uses the concept of maximum margin hyperplane in identifying the Support Vectors (SV) which it uses to make classification decisions as shown in figure 1. The following optimization equations show how SVM is implemented in most packages like MATLAB used in this paper. The weight W (vector) with the largest margin can be deduced by obtaining the solution of the following optimization problem as in the work of Yaser et al., 2012.

$$\text{Minimize } \frac{1}{2} W^T W \quad (1)$$

$$\text{Subject to } y_n (W^T x_n + b) \geq 1; n=1,2,\dots,N \quad (2)$$

Again, the optimization problem in equations 1 and 2 can be transformed in Lagrange model as in equations 3 and 4.

$$\text{Maximize } L(\alpha) = \sum_n \alpha_n - \frac{1}{2} \sum_{n=1}^N \sum_{m=1}^N \alpha_n \alpha_m y_n y_m x_n^T x_m \quad (3)$$

$$\text{Subject to } \alpha_n \geq 0 \text{ for } n=1,2,\dots,N \text{ and } \sum_{n=1}^N y_n = 0 \quad (4)$$

The above optimisation problem in equation 3 and 4 is a quadratic programming problem and it fits convex optimization which can be solved using any quadratic programming package like MATLAB etc, Yaser et al., 2012.

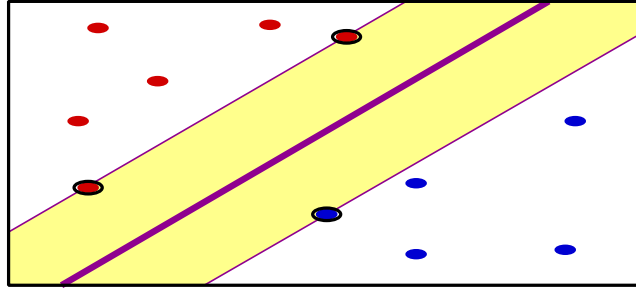


Fig.1. Support vectors; Source: cs1156x lecture slide, Yaser et al., 2012

The support vectors are all we need to solve the classification problem, Yaser, 2012. Thus the weight W and the bias b can be computed as follows:

$$W = \sum_{n=sv} \alpha_n y_n x_n \quad (5)$$

$$b = y - W^T x \quad (6)$$

Where $\Sigma_{n=sv}$ are those points that are support vectors (that is, those points that are on the margin); x_n corresponds to the inputs (symptoms); y_n is the resultant class of x_n (either not seen, medium or high as in Table 3.3 for malaria. Same applicable to typhoid); α_n is langrage multiplier. In the case of equation 6, x and y is the input-output of any support vector. In order to predict new input data (symptoms) of a patient, the prediction model for the proposed system (final hypothesis $g(x)$) is given as:

$$g(x) = \text{sign}(W^T x + b) \begin{cases} \text{class 1 if } g(x) = -1 \\ \text{class 2 if } g(x) = 1 \end{cases} \quad (7)$$

The system is described to be class 1 if the model is equal to negative one, else class 2 if the model is equal to positive one. However, most of the real life data set are not linearly separable, thus a kernel K is used to map the data set into a higher feature dimension space where the data set is linearly separable. When using kernel the final hypothesis is given as in equation 8.

$$g(x) = \text{sign} \left(\sum_{\alpha_n > 0} \alpha_n y_n K(x_n, x) + b \right) \begin{cases} \text{class 1 if } g(x) = -1 \\ \text{class 2 if } g(x) = 1 \end{cases} \quad (8)$$

Depending on the kernel been used, when a new input(x) is to be predicted, the kernel is used to computed unique value using x_n and x which is the value used for the prediction. Hence, equation 8 is SVM typically used for binary class. However, we implored equation 9 to implement the proposed predictive symptom-based

system for malaria and typhoid coinfection, which estimates the class likelihood of a data (\mathbf{x}). In this research work the data point is gotten when a user fills the questions on the symptom's interface of the application.

$$p(\mathbf{x}) = \left(\sum_{\alpha_n > 0} \alpha_n y_n K(\mathbf{x}_n, \mathbf{x}) + b \right) \quad (9)$$

When a user fills the questions on the symptom's interface all the various classifier computes their own class likelihood. The classifiers among malaria which has the highest class likelihood estimate is selected as the predicted class, the same is also applied to typhoid classifier.

The SVM tool used in this research work is MATLAB which is one of most acknowledged tool for data analysis in science and engineering community. MATLAB being a bundle of several packages used in computation, we make use of one of the package that is designed to training SVM (`fitsvm(X,Y,Name,Value)`)

`SVMModel = fitsvm(X, Y, Name, Value)` returns a support vector machine classifier with additional options specified by one or more Name, Value pair arguments. For example you can specify the type of cross validation, the cost for misclassification, or the type of score.

4. The System Architecture

The system architecture as shown in Fig. 2 depicts the structural view of the system and various actions that user can take in order to utilize the system. First, when a user launched the application, questions are presented on the symptom's interface for answers and then click submit button. The system will then compute class likelihood measure for all classifiers and select the classifier that has the highest value of class likelihood measure and finally the selected class is display back to the user.



Fig.2. System Architecture

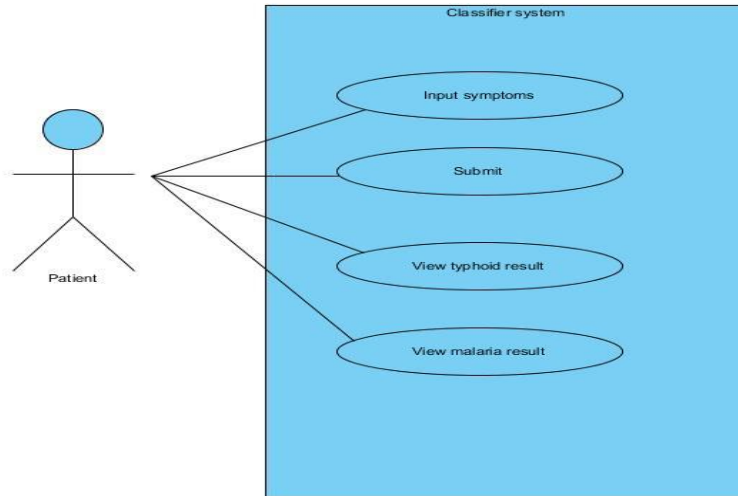


Fig.3. Use Case Diagram for the Proposed System

Table 4. Use Case Documentation

USE CASENAME	DESCRIPTION	ACTOR INVOLVE
Input symptoms	The user enters his or her symptoms by answering the question on the symptoms interface	Patient
Submit	A button on the symptoms interface where the user submits the answered question	Patient
View typhoid result	The user view the displayed typhoid result	Patient
View malaria result	The user view the displayed malaria result	Patient

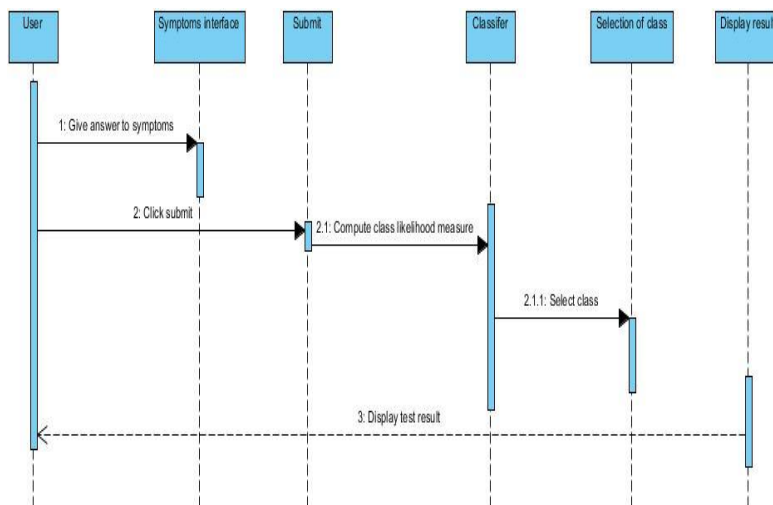


Fig.4. Sequence Diagram for the Proposed System

Fig. 4 presents the sequence which operation follows in the system. When user launches the application, questions on the symptom's interface appeared for answer and then click submit button. The system will then compute the class likelihood measure for all the classifier and select the class with highest value of class likelihood measure. Finally, the selected class is displayed back to the user.

5. Implementation

The implementation of the proposed system was carried out using Microsoft excel for holding the data, Matlab for training the classifier and finally Microsoft Visual Basic 2013 for the development of the Graphical User Interface (GUI). The choice of visual basic 2013 to design the graphic user interface and code the classifiers is influenced because it is relatively simple to use and also since most of our computers runs on windows operating system, this will increase the acceptability of the proposed system since user will not find it difficult to install. This system is targeted to run on both 32 and 64bits windows operating system. The screenshots of the proposed system are shown in Figures 5 and 6a and b at design and run time respectively.

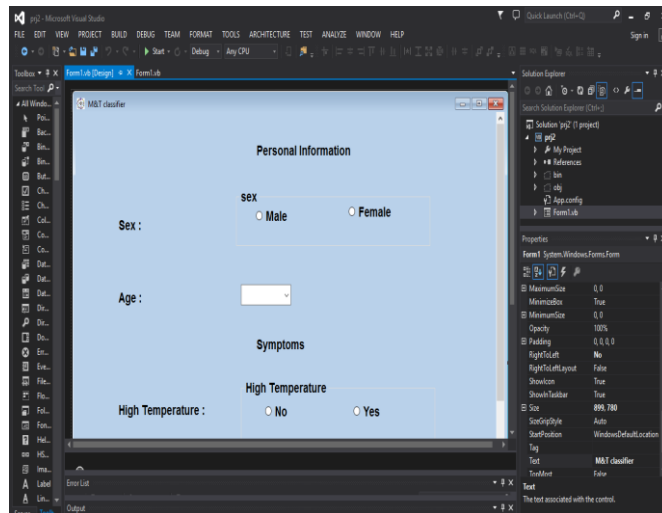


Fig.5. GUI of M & T Predictive System at design time

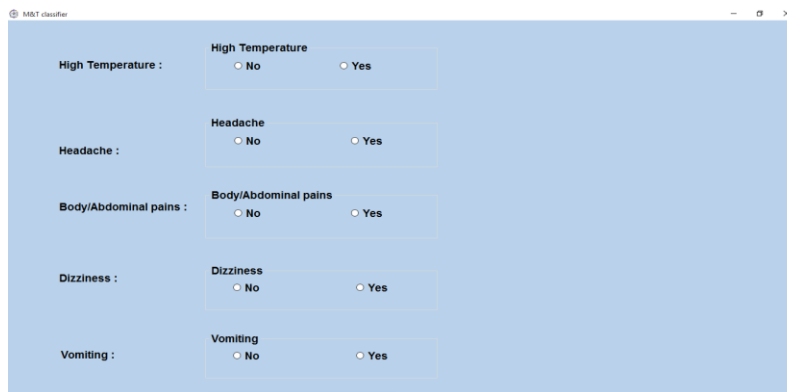


Fig.6a. M & T Predictive System at run time

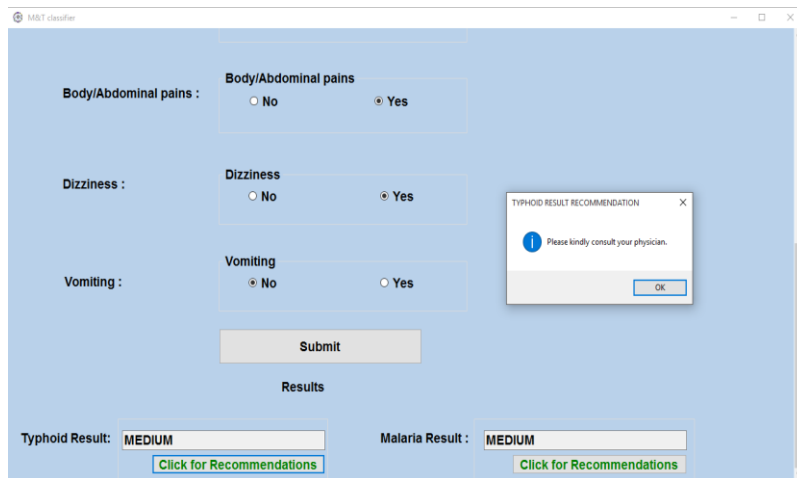


Fig.6b. M & T Predictive System at run time

At run time, the user provides answer to the questions been displayed on the symptom’s interface and click the submit button. If all the fields are properly filled, the system responds with the respective results of malaria and typhoid as shown in fig 6b. The user can click the recommendation button for further recommendation for advice or treatment by medical specialist. When the recommendation is clicked a message-box is displayed which shows “consult your physician with no further delay” if the result of the coinfection is high, but if the result of the coinfection is medium or not seen; the system displays “ please kindly consult your physician” or “you have no problem”.

6. Results and Discussion

Table 5 shows the result of various malaria classifiers gotten from a data set of 184 data point using One-Against-All. 164 data points was used for training and 20 were reserved for testing whole system. The ‘Age’ feature is normalized using its mean (36) and linear kernel was used in the training. The three classes that is; classes 0, 1 and 2 shows 90%, 70% and 80% as their respective cross validation accuracy which were considered to be fair enough.

Table 5. Malaria Classifiers

S/N	Class	Classifier Name	Cross validation accuracy
1	0	SVM_M_0	90%
2	1	SVM_M_1	70%
3	2	SVM_M_2	80%

Table 6 equally presents the result of various typhoid classifier gotten from a data set of 184 data point, where 164 was used for training and 20 was reserved for testing. The ‘Age’ feature is normalised using its mean (36) and also linear kernel was used in the training.

Table 6. Typhoid Classifiers

N/S	Class	Classifier Name	Cross validation accuracy
1	0	SVM_T_0	91%
2	1	SVM_T_1	57%
3	2	SVM_T_2	65%

Thus, we used linear kernel during training on a set of 164 data point and an accuracy of 90%, 70%, and 80% were reached for classifier of various class of malaria that is class 0, class 1, and class 2 respectively as shown in Table 5. Also Table 6 summarises the performance of typhoid classifiers that is 91%, 57% and 65% were reached.

7. Summary and Conclusion

This paper presents a predictive symptom-based system for malaria and typhoid coinfection using support vector machines to improved the classification accuracy and results of the coinfection; which is aimed at providing a computer based alternative quality healthcare solution that is effective, relatively accurate and affordable especially for developing nations like Nigeria that are challenged with shortages of medical specialists and facilities. More also, the available few medical resources are situated at urban areas which is liable to make life difficult for rural dwellers. Having using MATH lab for the SVMs, the data set was held using Microsoft Excel and the proposed system was finally implemented using MS VB 2013 so as to have a working application that will assist medical personnel as well as any trained individual.

Performance evaluation was carried out using reserved 20 data point (patients). Out of the 20 data point, 16 malaria cases were classified correctly and 4 malaria was misclassified thereby making the system 80% accuracy for classifying malaria. On the other hand, 12 typhoid cases were classified correctly and 8 were misclassified thereby the system has 60% accuracy for classifying typhoid.

8. Further Study

In any field of studies especially in software development, it is not unusual to develop a system without expected deficiencies or limitations. These could be associated with many factors which include the proficiency level of the researcher(s) on the subject matter or time factor. Below are the deficiencies of this system.

- Inability to train with more data points and using data set that has more features as symptoms for both ailments
- The model is solely based on data set obtained from a hospital, thus having potential of streamlining the model to a particular region of the country. To avoid this, a further research can be done using data set from various regions of the country and beyond

Therefore, further work can be carried out on this proposed system based on these limitations.

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