Computer Models For Malaria Infections, Diagnosis And Transmission Analysis

Haroon ur Rashid Kayani, Fatma Hussain, Saba Zulfiqar, Hafiz Burhan Ul Haq, Aftab Ahmad Malik

Abstract: The main objective of healthcare stakeholders is to control vector-borne infections such as Malaria. For this purpose, the utmost possible resources are continually being utilized, including computer-aided models to identify infection and its spread. These models offer precise, quantifiable estimates of epidemiological results of different control measures. The complicated life cycle of the causative agent, parasite density, vector infectiousness, and environmental factors often limit computer-based malarial models’ efficacies to predict transmission, morbidity, and mortality. Sophisticated algorithms translate the effects of numerous conventional therapeutic interventions and cohesive management plans. This review highlights the application of computer simulation models, data mining, artificial intelligence, and other algorithms in malaria monitoring, prediction, and treatment that are adopted in the epidemic scenario. These predictive and stimulatory models with variable characteristics have performed a crucial role in malaria eradication.

Index Terms: Malaria, Plasmodium falciparum, Vector, Computer Models, Disease Forecast, Machine Learning, data mining, artificial intelligence.

1 INTRODUCTION

Malaria is transmitted to humans and other animals by the Anopheles mosquito, and the microorganism responsible for this disease in Plasmodium falciparum, a unicellular protozoon. The human malaria infection cycle consists of three stages (Fig.1); the hepatic, erythrocytic, and mosquito stages. Anopheles bite infects the human liver with plasmodium that enters the red blood cells to form gametes. These gametocytes are transmitted to another mosquito gut to form sporozoites. Sporozoites are transmitted to second human host to spread the infection [1]. Malaria is responsible for the largest share of deaths in world history as every year about 200 million people are affected by the malarial infection, and about 400,000 die of this disease. It is a burden on the healthcare sector as more than 3.2 billion population worldwide is at risk of this malicious disease [2]. Crucial steps have been taken within the last ten years to eradicate malarial spread. Along with medicinal investigations, advanced computational biological techniques are accelerating the antimalarial campaign. As accurate disease diagnosis, progression, and spread forecasting is not possible by available resources, image analysis and machine learning approaches are employed in clinical and laboratory practices [1].

With the dawn of the 21st century, healthcare records collection has amplified due to computer technology advancements. It is plausible that various data administration platforms assist physicians, hospitals, and government organizations in disease surveillance. This paper highlights the application of computer simulation models, data mining, artificial intelligence, and other algorithms in malaria monitoring, prediction, and treatment [3]. An in-depth literature appraisal was done to summarize the role of various computer simulation models used in diagnosis, progression tendency, and malaria treatment predictions. Google Scholar, PubMed, Search engines were used along with data repositories such as Web of Science, IEEE Xplore, and Science Direct to collect comprehensive latest scientific records from different academia.

Haroon Ur Rashid Kayani, Consultant and Data Scientist, Lahore Pakistan. E-mail: hurkayani@gmail.com
Fatma Hussain, Department of Biochemistry, University of Agriculture, Faisalabad, Pakistan, 75500, Pakistan. E-mail: fatmauaf@yahoo.com
Saba Zulfiqar, Department of Biochemistry, Faculty of Sciences, University Medical and Dental College, Faisalabad, 38000, Pakistan. E-mail: sababasra86@gmail.com
Hafiz Burhan Ul Haq, Department of Computer Sciences, Lahore Garrison University, Lahore, 75500, Pakistan. E-mail: burhanhashmi64@lgu.edu.pk
Aftab Ahmad Malik, Department of Software Engineering, Lahore Garrison University, Lahore, 75500, Pakistan. E-mail: dr_aftab_malik@lgu.edu.pk
2 COMPUTER MODELS FOR MALARIA

Physicians diagnose diseases based on history, symptoms, and laboratory tests. Computerized models affect these decisions due to their information processing abilities. Computer software organizes patient data, classifies it, facilitates analysis in specified clinical setup, and provides simulation models or logical concepts. Computers are given case studies, pathological variables, signs & symptoms, and predicted outcomes based on prevalent symptoms. Artificial Intelligence (AI) has made computers intelligent. The dependency diagram (Fig. 2) represents the strategy adopted to develop computerized algorithms, machine learning, and data mining tools to simulate disease [3].

Boni et al. [4] developed an evolutionary-epidemiological model framework to assess single first-line treatment effectiveness for Malaria. Implementing SIS (system installation suite) type model and modified Hastings model shows that multiple first-line therapies (MFT) are better than a single treatment, and rotation of drugs or cycling is beneficial. MFT interrupts reinfection and can have a significant role in malaria eradication and management. Santosh et al. [5] suggested that an Apache-based extended short-term memory classifier computer model can forecast malaria incidence in different geographical sites. Different responses for each seasonal month were observed. It was studied that environmental and clinical parameters contribute to malarial transmission. Wang et al. [6] applied ARIMA, STL+ARIMA, BP-ANN, and LSTM network models in simulations with data on malaria along with environmental records to predict cases. Each model was used separately as well as in combination. Results indicated that stacking architecture had substantial consequences in infection prediction. Genetic studies on malarial parasite facilitate malarial control and treatment interventions. One important aspect in such studies is to monitor the structure of parasites for all possible mutations. Structural characterization involves machine learning algorithms, principal coordinate analysis (PCoA), and hierarchical agglomerative clustering (HAC). Watson et al. [7] used Plasmodium falciparum samples to assess PCoA and HAC’s role in parasites genetic epidemiology. It was suggested that clear, productive experimentations should be conducted by learning algorithms, and in the absence of these models, any results should be declared as discussions only. Manescu et al. [8] used a deep neural network for malaria diagnosis by clinical microscope images of blood films in the Sub-Saharan region. The purpose was to accomplish Deep Malaria Convolutional Neural Network classifier (DeepMCNN) for automatic diagnosis (Fig.3). The model successfully delivered results, providing an alternate method to screen malaria in large populations. It is very critical to control malaria. Numerous machine learning (ML) models developed for malarial diagnosis have their limitations. Lee et al. [9] compared six ML models. Random forest was best for parasite datasets and gradient boosting for total parasite data management. Ethnicity and clinical signs were important features while analyzing unbalanced and stable data records. Microscopic examination routinely is employed for malaria diagnosis. It is an unreliable, time-consuming conventional technique that relies upon the expertise of a microscopist. Yu et al. [10] designed a screener for microscopic analysis of malaria patient blood samples, an android mobile application, as a substitute for light microscopy using smartphones (Fig.4). It is affordable, fast, and reliable, with database potential for efficient image processing by ML algorithms.

![Fig. 2. Development of Computer Models for Diseases [3]](image)

Fig. 2. Development of Computer Models for Diseases [3]

![Fig. 3. Deep Malaria Convolutional Neural Network classifier [8]](image)

Fig. 3. Deep Malaria Convolutional Neural Network classifier [8]
All types of blood may be screened for plasmodium parasites. It acquires an image, analyses it, and then display results. Computational simulations facilitate understanding the mechanism of infections. These algorithms also highlight behavioral changes in populations and shift in government policies [11].

Similarly, Morang’a et al. [13] applied six machine learning approaches on records of malaria volunteers to differentiate between severe malaria, uncomplicated malaria, and infections other than malaria by artificial neural networks and binary classifiers. It was concluded that ML provides support in the clinical decision. Effectual malarial control demands targeted therapy, and computer prediction models assist in decision making. Bayesian networks present uncertainty, nonlinear associations, and detailed knowledge. Haddawy et al. [14] used these networks in Thailand to design a town-level malaria prediction model. Comparison of the forecast by these networks with traditional models indicated that Bayes nets are relatively better. It was concluded that spatiotemporal Bayesian nets are an excellent modelling substitute for predicting infections like malaria. Different computer models relevant to malarial pathophysiology are presented in table 1.

**TABLE 1**

<table>
<thead>
<tr>
<th>Reference</th>
<th>Contribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Janssen and Martens, [15]</td>
<td>It simulated the adaptive behaviour of mosquitoes and other parasites to contemporary pesticides</td>
</tr>
<tr>
<td>Craig et al., [16]</td>
<td>It provided a numerical idea of more refinements and predicted the effect of climate alteration on the spread of disease</td>
</tr>
<tr>
<td>Hay et al., [17]</td>
<td>It analyzed the potential effects of climate alterations on malaria in hilly areas</td>
</tr>
<tr>
<td>Kileen et al.,[18]</td>
<td>The model described previous responses in terms of environmental changes from malaria transmission, mechanism of vector involvement, and possible remedies</td>
</tr>
<tr>
<td>Hoshen and Morse,[19]</td>
<td>It was a weather-driven dynamic malaria model that predicted recurring infections of malaria</td>
</tr>
<tr>
<td>Menach et al.,[20]</td>
<td>The model asserted that oviposition of anopheles was an important factor in malaria transmission</td>
</tr>
<tr>
<td>Chitnis et al., [21]</td>
<td>This model studied the interchanging nature of malaria in a mosquito population interacting with a human population</td>
</tr>
<tr>
<td>Yakob and Yan, [22]</td>
<td>This model analyzed the effects of the larval source reduction process and bed nets treated with insecticide to reduce the malarial spread</td>
</tr>
<tr>
<td>Ngonghala et al., [23]</td>
<td>Periodic oscillations and backward bifurcation model for malaria transmission was proposed</td>
</tr>
<tr>
<td>Beignon et al., [24]</td>
<td>NHP (non-human prime) models of malaria were designed</td>
</tr>
<tr>
<td>Darkoh et al., [25]</td>
<td>A weather-based prediction model of malaria</td>
</tr>
<tr>
<td>Bent et al., [26]</td>
<td>Novel exploration techniques (NETs) for malaria policy interventions</td>
</tr>
<tr>
<td>Njim and Tanyitiku, [27]</td>
<td>Prognostic models for the clinical management of malaria and its complications</td>
</tr>
<tr>
<td>Jena et al., [28]</td>
<td>A model of malaria parasites detection using a deep neural network</td>
</tr>
</tbody>
</table>

Cao et al. [29] studied the dynamics of plasmodium gametes by a novel gametocyte dynamics model. Samples of malaria patients having Plasmodium falciparum-infected red blood cells were used. They also experimented with a more modern, robust model for checking the hypotheses formulated and came out with more accurate and trustworthy results. Bayesian hierarchical inferences were incorporated for calibration of the model and parameters validation. It was suggested model could predict the precautionary measures for the prevention of malaria. Okuneye et al. [30] described a Weather driven model for malarial transmission. All stages of the mosquito and parasite during malaria cycle were considered along with all the epidemiological parameters of malaria and their asymptomatic transmission to humans.
Accurate and authentic results were obtained depicting a significant influence of temperature on the transmission of malaria. Researchers also experimented with two different parameters in which one model included the gonotrophic cycle and the other included the sporogonic cycle. In the sporogonic cycle, under regular and constant weather conditions, no humans are affected. Simultaneously, the gonotrophic cycle affected the transmission rate and is a crucial factor to consider when devising any model for malaria transmission. It is advisable for the future models to explicitly omit the sporogonic cycle for the simplicity of the model and the efficiency improvement because addition or omission did not affect any result. Xing et al. [31] described a model to assess malarial infection dynamics in mosquitoes and humans by following the principle used earlier [32]. The human population was divided into three categories, i.e., susceptible humans who are likely to be infected by malaria, infected humans who have encountered the disease and are showing symptoms of infection and recovered humans who have successfully recovered from malaria infection. Simultaneously, the mosquito population was divided into two classes: susceptible mosquito and infectious mosquito. Recovered mosquitoes were not included because mosquitoes never recover from infection due to short life span and before the infection period ends, mosquitoes are already dead. Conditions in which infection-free condition and global equilibrium of endemic are stable were assessed. Silal et al. [33] used a model to forecast the elimination and eradication of malaria from the world by 2030. This model was also designed to include the costs of elimination of malaria from the Asia-Pacific region. Data were collected from 22 countries located in the Asia-Pacific region. This prediction model suggested that all countries considered in this model will successfully eliminate malaria by 2030. However, the model considered only two malaria-causing species of Plasmodium, i.e., Plasmodium falciparum and Plasmodium vivax. According to the suggestive results, China, Sri Lanka, and the Republic of North Korea do not need to change the parameters imposed already for the effective control of malaria, and to continue all the current interventions. Whereas Bhutan, Vietnam, Bangladesh, Philippine, and Nepal can eradicate this infection if they will use mosquito nets, indoor insecticides and will strengthen prevailing healthcare systems. Other countries could achieve malaria elimination by employing some innovative methods in drug synthesis and mass drug administration. Gharakhanlou et al. [34] presented ABM (agent-based model) to study the dynamic transmission of malaria caused by Plasmodium vivax. In this study, environmental factors are temperature, humidity, vegetation, the altitude of the area under consideration, the proximity of rivers nearby and population density in the said area. The first three factors, temperature, humidity and vegetation were considered variable parameters. In comparison, other factors were considered constant. This was a case study from Sarbaz, a city of Iran. Various scenarios were created and checked by this model. In each situation, one parameter was taken dynamic, and other parameters were constant and, in this way, the performance of the model was checked (Fig.6).

Healthcare stakeholders are supported by advanced computer-aided technologies to identify malarial infections and to predict transmission. Numerous computational approaches adopted in this context are highlighted in the current review. These predictive and stimulatory models with variable characteristics have performed a crucial role in malaria eradication.

REFERENCES


