Metaheuristic Optimization Review (MOR) *Vol. 01, No. 01, PP. 55-65, 2024*

Machine Learning Approaches for Malaria Risk Prediction and Detection: Trends and Insights

Ahmed Mohamed Zaki[1,*], Khaled Sh. Gaber[1], Faris H. Rizk[1], Mahmoud Elshabrawy Mohamed[1]

[1]Computer Science and Intelligent Systems Research Center, Blacksburg 24060, Virginia, USA

Email: Azaki@jcsis.org; khsherif@jcsis.org; faris.rizk@jcsis.org; mshabrawy@jcsis.org

Abstract

The current review summarizes the latest trends in malaria literature, emphasizing transmission ecology, new diagnostics and treatment. It stresses the additional focus on the transmission, according to the spatiotemporal models and predictive analytics, which help identify periods and the locations with the most significant risk, noting that these processes should consider the environmental factors. The change in the diagnostic approach, especially the introduction of artificial intelligence techniques such as deep learning, has improved the rate and precision at which malaria parasites are diagnosed in resource-limited countries where time is of the essence. Furthermore, there have been significant advances in drug discovery due to machine learning applications that have made it quicker to find new antimalarial drugs in the face of drug resistance. Despite these developments, there are still problems such as drug resistance, socio-economic disparities, and the environment that are being altered and still require an integrated and transdisciplinary approach. Combining these determinants is indispensable for eliminating these challenges and further promoting global efforts to control malaria.

Keywords: Malaria; Transmission ecology; Machine learning; Drug resistance and diagnostics

1. Introduction

Malaria ranks high in the list of health problems that people face both around the globe and especially more so in the regions within the tropics and subtropics, as it dramatically taxes health systems and the economies around those regions in general. It is estimated that nearly 240 million people are infected, and over 600,000 deaths result from the infection annually; the condition continues to be one of the top debilitating and fatal diseases, especially among the risk groups, children, and expectant women. For the past years, many researchers have devoted their efforts to better understanding and intervention; the problem with malaria also persists owing to issues like drug resistance, climate change, and poverty, among others, that make it hard to put control measures in place of the disease [1]; This literature review aims to expand on the current malaria research availabilities, particularly on the ecology of transmission, new tools for diagnosis, and treatment aspects. Understanding these areas will enable us to appreciate why malaria control remains a challenge and how new interventions may further malaria control [2].

Malaria has complex transmission dynamics associated with various ecological factors such as the weather, land distribution, or even the level of mosquito population. For example, several recent articles have underscored the role of spatio-temporal models for the risk assessment of malaria transmission. In the southeast x region of Iran, Minab district, researchers combined geographic data with their assessment of

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

environmental conditions suitable for malaria vector reproduction. The investigations have also shown that most effective transmission seasons differ from each other, as the first and last quarters years are higher than the rest, driving seasonal variability. Moreover, they researched four Anopheles species and reported that Anopheles stephensi was the dominant species, indicating the impact of vector dynamics on malaria transmission [3].

It should be noted that ecological studies are critical in malaria management methods. Knowing the influence of environmental factors on vector populations and transmission risks, health authorities can take appropriate measures directed at particular areas. For instance, early warning systems estimated to be predictive billions can enable the planning of proactive vector control in at-risk communities to decrease the malaria burden [4].

An early diagnosis and identification of the disease is paramount for prompt treatment of malaria. Unfortunately, the conventional blood smear microscopy methods, among other techniques that are employed to diagnose this endemic, have some sensitivity and specificity thresholds where a delay in the administration of treatment can arise. However, recent developments in diagnostic methods, especially that of artificial intelligence such as machine and deep learning, have proved to help in the swift and precise diagnosis of malaria [5].

For instance, in one research, the specialists made a convolutional neural network (CNN) for the automated image analysis for malaria detection in blood smears. As a result, the model demonstrated an astounding accuracy of 97.74%, considerably better than traditional diagnostic techniques. The new day diagnostic tools enable real-time data and machine learning algorithms to increase the accuracy of the tools and warn of possible occurrence cases of malaria outbreaks. This is advantageous in a place with limited geographical spread and no trained lab personnel or diagnostic machines [6].

Again, the continued creation of internet-based systems leads to more cases of new methods being used in malaria diagnosis. These systems offer a solution to the problem of climate change by using machine learning algorithms on climate data to imply the threat EST of an impending malaria outbreak, which is an effective way of controlling the disease. This integration of technology in the public health system, especially in the diagnosis process, makes it possible to make a quicker diagnosis and improve the effectiveness of the response system, resulting in better health outcomes in areas dominated by malaria [7].

The increasing occurrence of drug resistance constitutes a major hurdle in managing malaria. Given that the malaria-causing organism can adjust to standard antimalarial drugs, there is a significant urgency in developing alternative treatment regimes. Recent studies have started employing machine learning techniques to provide faster development of antimalarial agents [8], [9].

Using data points in one attempt, researchers could apply the antimalarial activity prediction against Plasmodium falciparum to several machine learning models. The results showed that Support Vector Machine (SVM) and XGBoost models provided a high level of prediction, exceeding 85% accuracy on completely independent test sets. This approach helps find new drugs for the particular disease and helps screen large compound libraries effectively, thereby saving time and cost of drug development [10].

In addition, some new approaches, like the use of Bayesian models, have been suggested to allow different groups of people and institutions to come together to find new medicines against malaria. Thus, these models allow diffusing Innovations through sharing Resources without infringing any values or Rights; these models encourage members from the publicly orientated sector to make healthy contributions, thus quickening the search for incredible drugs [11].

To sum up, malaria is still a very complicated and troubling health issue facing the world that requires immediate and multi-pronged action. The articles reviewed highlight the need to control malaria through synergistic ecological, advanced diagnostics and treatment interventions.

However, I observe drug-resistant organisms, climate change, and poverty still posing a threat. These problems cannot be tackled in isolation but rather through coordinated local, national, and international activities involving researchers, healthcare workers, and policymakers. We can enhance our control efforts and eliminate malaria by leveraging technology and creative research. Sustaining investment in research and evidence-based implementation strategies is crucial. It is important to remember that malaria is preventable, and our work is vital in its global containment.

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

With this literature review, we aim to drive future explorations, interventions or interest in malaria research, leading to better health outcomes and more efforts to eradicate malaria in these regions.

2. Literature Review

Progress on malaria control needs to be improved in most tropical and subtropical regions. In this literature review, I present the novel findings from malaria research conducted in the past few years, touching on many issues such as the ecology of transmission, new diagnostic tools, and the effective treatment of malaria. Based on these studies, we hope to appreciate the multifaceted problem of malaria and suggest possibilities for further research and interventions.

Malaria continues to be the leading parasitic illness in tropical and sub-tropical areas, affecting over 240 million people each year. Therefore, the study mentioned in [12] has been conducted to evaluate the environmental factors for malaria transmission in Iran's southeastern region, particularly the Minab district of Hormoz, a province, using a geographical spatiotemporal model. Techniques used were GDD forecasts, larval breeding sites, and spatial Maxent maps to identify vulnerable locations. The highest risk period for students was found to be during the first and fourth quarters, in line with the Gradient Model Risk Index. The study also evaluated the ecological status of water bodies that harbored four vectors, Anopheles culicifacis, A thali, A fluviatilis, and ASephensti; according to the vector survey, ASephensti was the most abundant and widespread. The present data analysis relied on Maxent predictive models to determine risky villages in the Minab district. It acknowledged that studies of this kind that consider spatial and temporal evaluations could play an essential role in integrating malaria control programs in specific regions and in deploying early warnings. Furthermore, they also find that the contending transmission risk model for malaria may be transported to other endemic regions in the tropics and subtropics.

According to the research cited in [13], malaria was defined as the most severe parasitic disease in the tropic and subtopic zones, with an incidence of more than 240 million per year. This comprehensive study aims to examine the hazards of malaria transmission within the specified environment using a spatiotemporal model of the Minab district in the Hormozgan province, the southeastern region of Iran. The work used techniques like GDD for predictive studies, larval habitat ecology, and MaxEnt mapping of risky environments. It was further revealed that the Gradient Model Risk index pointed to January to April and October to December as the periods of high transmission period. Additionally, the study evaluated the ecological conditions of water bodies hosting four vector species: The following species of anopheles were identified – anopheles culicifacies, anopheles thali, anopheles fluviatilis, and anopheles stephensi, where anopheles stephensi is most dominant and highly distributed. The integration of MaxEnt predictive models we availed helped in furthering the development of a higher risk acknowledgment of villages at risk and, therefore, highlighted the significance of these spatio-temporal assessments in local malaria control strategies and the early warning systems based on these risk factors. In addition, the factors considered in the proposed risk model may be extended to other malaria-prone areas within the tropical and subtropical world.

In the presented research [14], a dataset of 195143 compounds crawled from the database containing known and experimentally verified compounds was selected to construct several classification models intended for predicting the antimalarial activity against *Plasmodium falciparum*. In this study, four machine learning methods, including support vector machine (SVM), random forest (RF), K-nearest neighbor (KNN), and XG Boost, were applied to a heterogenous antimalarial data. The optimal feature selection approach was employed to select the relevant descriptors for the analysis from a pool of possible descriptors by eliminating features likely to contribute less than the majority of the variation in the data when fitted to the model function. The models were well assessed for domains important for model applications, Y-scrambling, and AUC-ROC curves. In addition, probability calibration and predictiveness curves were employed to measure the predictiveness of the models. H3 Based on the results, SVM and XGBoost have displayed higher performances, approximately above 85 % accuracy of an independent test set. For the probability prediction, total gain (TG) values of 0.67 and 0.75 for SVM and XGBoost, respectively, from the predictiveness curve, showed that the models were reliable and well calibrated. These models also prove the stability by correctly identifying high-affinity compounds from validation using PubChem antimalarial bioassay data. The results show that all the chosen models are stable and can be helpful for the fast identification of new malarial agents.

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

This is particularly important given what has been said in [15]. New antimalarial therapies must be generated to allow participating organizations without a substantial library of compounds or resources for high-throughput screening. This remains particularly true within machine learning models where additional volumes of training data are also beneficial in improving the model's robustness and expanding the practical implementation area. The work looked at predicting the formation of Bayesian models derived from screening several datasets for compounds that can exhibit activity at the blood stage of malaria. One of the main techniques described is disseminating the Bayesian QSAR models for thousands to millions of proprietary compound data among researchers from both commercial and nonprofit organizations. This model-sharing approach enables the construction of consensus models that perform better than the single, individual models while keeping the individual training sets of compounds anonymous. The structure enhances cooperation and speeds up the identification of novel lead compound candidates without revealing an organization’s expertise, thus decreasing the hurdles to drug creation in an effort against malaria.

This paper analyzed [16] and found malaria to be an epidemic disease communicated through the bites of infected Anopheles mosquitoes. Malaria cases and deaths can be minimized and averted if they are diagnosed early and treated promptly; nevertheless, methods such as blood smear microscopy that laboratory technologists use are slow and inaccurate. To resolve this problem, the study postulated a web-based system to enhance the efficiency of malaria testing in laboratories. In diagnosing malaria parasites in blood cells, performance was compared between the CNN model, explicitly designed for diagnosing malaria parasites, and the Transfer Learning Model, VGG19. The proposed custom CNN model achieved an accuracy of 97.74%, and since the model is tailored for the specific parameters involved, it is realistic for real-world implementation. Besides the diagnostic functions, the study provided a sensitization tool, the malaria outbreak warning system that warns communities about the threats of climatic conditions. The system utilizes an ML model – A Logistic Regression using a Gradient Descent Optimizer wherein actual-time data from the Open Weather API can predict a malaria epidemic and present a single-click probability overview to the user.

As described in [17], the study used data from 2016 to 2021 obtained from the DHIMS2, a detailed, representative system used by the Ghana Health Service. The study also uses an interactive web-based spatial disease mapping system and Bayesian geospatial modeling to evaluate the quantitative differences and aggregations of malaria-risky areas in 260 districts in Ghana. For the observed malaria case data at each district level, the study displayed the malaria cases, district name, and sIR accompanied by the RR and the corresponding standard errors using web-based graphical techniques. This approach offered a straightforward way of achieving and describing the spatial distribution and conditions of malaria incidence, affecting tactical activities in malaria control.

In the publication cited as [18], the study addressed the problem of the malaria burden within subtropical climates where access to health monitoring centers is scarce. To reduce the effects of the disease, a new large-scale architecture was suggested to predict malaria incidences in particular regions. The approach synchronized satellite data and clinical records with an LSTM classifier to forecast malaria occurrences in Telangana. The model accurately determined a 12-month cycle based on seasonal differences across several regions while demonstrating varying effects depending on the environment. The findings highlighted the importance of considering both host and vector environmental and clinical factors in transmission. This study established that running an Apache Spark-based LSTM model is a highly effective means of identifying malaria hotspots and establishing a solid health surveillance strategy for timely disease intervention.

The routine procedure for assessing disease [19] prevalence involves microscopy of blood smears for parasite-positive packed red blood cells, and technicians handle this exercise. The shortcoming of this conventional method is then complemented by sophisticated computer vision and deep learning solutions for the automated differentiation of the malarial parasite from the blood smear image captured by the microscope as either infected or uninfected. The first problem is identifying malarial parasites from blood smear data, which determines accuracy. In the proposed work, the malarial parasites of the smear blood cell images are detected using a deep convolutional neural network (DCNN) model. The main goal of the work is to (i) compare the validation loss and accuracy after adjusting the hyperparameters to categorize the images and (ii) calculate the Kappa Coefficient as well as Matthew’s correlation coefficient. The generalizations of the proposed model are made by evaluating the two optimizers, Adam and Adagrad, at different epochs. The

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

proposed DCNN model achieved an overall accuracy of 98.9% compared to the current best models while solely working on hyperparameters optimization.

The research in [20] adopted the conventional approach to diagnosing malaria: assessing Giemsa-stained blood smears under a microscope to identify parasites containing erythrocytes. They improved it using computer vision and deep learning. The study further showed that a deep convolutional neural network (DCNN) could be used to flag malaria parasites automatically from the images of blood cells. A few essential features include the detailed focus on parametric value adjustment for proper validation and enhanced accuracy for correctly categorizing images as parasitized or uninfected cells. The given method improves the system accuracy by almost fivefold as it offers an integrated feature extraction and classification solution instead of technicians and smear quality. The study's total sample images were 26,188, of which 13,105 were parasitized and 13,083 were uninfected. Using the kappa coefficient (KC) and the Matthews correlation coefficient (MCC) to analyze the model's performance, the researchers proved that the deep learning approach is more reliable than the conventional malaria diagnostic method.

In the article [21], the study addressed acute severe malaria anemia, a severe life-threatening condition most common among children in sub-Saharan Africa. SMA thus requires fresh whole blood transfusion and then antimalarials. The World Health Organization (WHO) operationally defines severe malaria anemia or SMA as a packed cell volume of <16 % or Hb < 0.5 g/dL in addition to any level of parasite density among children under five. SMA necessitates immediate blood transfusion followed by antimalarial treatment. The World Health Organization (WHO) defines SMA as a hemoglobin (Hb) concentration below 0.5 g/dL or a hematocrit under 16%, accompanied by any level of parasite density. The condition is characterized by a sharp drop in hematocrit, probably due to increased phagocytosis in the spleen, which causes changes in the shape of RBCs. SMQ used to be diagnosed clinically. History, examination, hematocrit and peripheral blood film examination were used to diagnose SMA, and it was often tricky when parasitemia was very low. Besides improving current diagnostic techniques, this study established and validated the Multiple Instance Learning framework to Identify SMA (MILISMA). This deep learning tool was established to diagnose SMA using evaluation criteria of the current WHO criteria based on early morphological changes in RBCs before the clinical manifestation of SMA occurs. This makes this model suitable for large-scale systematic identification of early RBC morphological signals, complementing further monitoring of at-risk SMA patients. The capacity for the Bendigrams to identify unusual RBCs in low parasitemia is a clinical checkpoint, which gives a measure of efficacy, which includes the ability to react earlier by detecting possible progression to severe anemia, thereby possibly lowering the mortality rate of affected patients.

Malaria is a deadly disease in the world, and it can be diagnosed using antigen tests and microscopy, though these two methods are imprecise and sometimes lengthy. Therefore, a dependable and fast early prognosis of malaria timely is wanted. The study outlined in [22] considers this problem by examining different machine learning (ML) methods. The research provides a new technique for applying an extreme learning machine (ELM) algorithm in malaria diagnosis. The study employs CNNs as feature extractors and classifiers to obtain improved and comparable models. The research utilizes two versions of a malaria image dataset: the original and a modified survey, with samples with ambiguous characteristics removed. Notably, the study also begins with a parasite inflator to improve the contrast of the smaller, darker parasite forms in blood smear images of red blood cells. The proposed CNN-Deep ELM (DELM) model evaluation shows a higher accuracy of 97.79% for the initial dataset and 99.66% for the modified one. It is a more effective technique than others described in the literature, which is why this model is so helpful and influential in diagnosing malaria.

Immunogenic cell death (ICD) is a highly controlled cell death process primarily designed to enhance immunity when the body is exposed to various aggressors, notably tumors and infectious agents. Still, it remains unclear how it is targeted in human malaria. The analysis done in [23] aimed to look at cohorts with *Plasmodium falciparum* infections cross-sectionally, studying at a particular point in time to identify different types of ICD and the level of parasitemia and immunity. The research with consensus clustering was used to divide into subtypes ICD and ssGSEA to evaluate the immune landscape. Incorporating high parasitemia, the researchers identified hub genes associated with ICD and performed DEG analysis, functional enrichment, PPI networks, and predictive modeling using LASSO regression and random forest. They constructed a nomogram to depict the relationship between these hub genes and the level of parasitemia, which was assessed using a receiver operating characteristic (ROC) curve. The findings presented two

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

subtypes associated with ICD. Falciparum* infected population. For Subtype 1, the adaptive immune responses were better, and parasitemia was lower than for Subtype 2. For instance, in the DEG analysis, subtype 1 displayed active biological pathways involving proliferation, T-cell receptor signaling, and activation. In contrast, subtype 2 was associated with high levels of cytokine signaling and inflammation. They also used the machine to identify two hub genes of CATCD3E and FCGR1A from PPI network analysis.

During the COVID-19 pandemic, the authorities are more interested in the number of people hospitalized while attempting to predict the situation's outcome, particularly at the hospital level. In the investigation presented in [24], a model was suggested to fit empirical hospitalization data due to COVID-19, which the authors considered a modification of the classical SIR model of infectious diseases. It was proven that with the fitted parameters and initial conditions, this time-fixed model of 2 parameters provided the root relative square error of less than 10 percent for Belgium from March 15, 2020, until July 15, 2020. The analysis addressed a tri-fold approach: stochastic uncertainty kappa, parameter uncertainty beta, and model uncertainty delta to derive the SIR model confidence intervals. Most impressively, the model correctly predicted the next two months with a mean absolute percentage error (MAPE) of less than 4% when trained on data within a target window of three weeks centered on the peak of hospitalization in Belgium. Each of the French department's territories was subjected to the same experiment, with 14 departments exhibiting a MAPE of less than 20%.

Nonetheless, when applied to data training that lasted through the peak of hospitalizations, the model's performance considerably declined. The research also covers diseases such as malaria, which is endemic to Senegal and accounts for numerous hospital visits, especially in the rainy seasons. Generalized linear models (GLMs) applied to predictive modeling of malaria incidence incorporated climatic factors like rainfall, average temperature, relative humidity, and previous malaria cases recorded in Dakar, using distributions like Poisson, negative binomial, and Gaussian. The forecasting algorithms followed the procedures for measuring the meteorological explanatory variables at a certain lag.

Malaria is an illness resulting from the bite of a parasite called Plasmodium, which is transmitted by the Anopheles mosquito, and it is still among the most challenging health issues in the world in many sub-Saharan African nations. Therefore, developing a proper digital approach for detecting and identifying different types of Plasmodium and their respective life cycles is critical. In the article referenced as [25], a detailed case study is provided on the subject of the performance of various methods of feature extraction from blood smear images to detect and classify malaria parasites within Faster R-CNN backbone models. The blood smear images utilized in this study were obtained from Rwanda, making it relevant to the sub-Saharan region. The research presents a detailed analysis of several feature extraction methods and their applications in the developing world.

It is envisaged that specific machine learning techniques will enhance scientific discovery efforts in some healthcare-related fields. However, the practical application of these methods depends on adequately structured high-quality datasets. A study needs to be conducted in the existing literature on the protein antigen candidates of the malaria parasite Plasmodium falciparum [26], which this paper accentuates since it causes diseases such as malaria. Possible antigens must be found to pave the way for the active development of antimalarial drugs and vaccines. Since experimental work is quite expensive and lengthy, based on machine learning techniques to assist in that work, as is the case in this research, it is likely to cut down the period of developing drugs and vaccines that are requisite for fighting malaria. Therefore, the authors defined the PlasmoFAB dataset as a well-structured and organized machine-learning model applicable to *P. falciparum* protein antigen candidate identification process. This dataset was developed with an exhaustive literature survey and expertise in the field that sought to apply accurate labels distinguishing potential antigen candidates from cytoplasmic elements. The study also assessed the benchmark by evaluating different well-known prediction algorithms with protein localization prediction tools in terms of their success in identifying protein antigen candidates. The findings indicate that the services available for general purposes are inadequate for the task, whereas the trained models using the specific PlasmoFAB dataset performed much better, proving the usefulness of the dataset in the search for putative protein antigens.

Table 1 presents a compilation of current research on using artificial neural networks and other affiliated technologies in malaria prediction, diagnosis, and treatment. These studies, which are the result of

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

collaborative efforts, encompass various methodologies inclusive of geographic information systems and space-time analysis for enumerating high malaria transmission risk zones and creating novel machine learning algorithms like Support Vector Machines, Convolutional Neural Networks, and Long Short Term Memory for precise disease diagnosis. Further, several works also highlight the importance of deep learning for improving the diagnostic information for automated detection of malaria parasites in blood smears and morphological changes in red blood cells that indicate severe malaria anemia. In addition, machine learning was applied as a tool to enhance the speed of drug discovery to determine the antimalarial activity and identify protein antigen candidates. The developments illustrated here show how combining a machine learning approach with conventional methods can enhance malaria administrative activities, enhance resource utilization, and help identify early that enable early intervention, particularly in areas with scarce health infrastructures.

Table 1: Summary of Literature Review

Study	**Objective**	**Methods**	**Key Findings**	**Implications**
[12]	Assess environmental factors for malaria transmission in southeastern Iran	Used GDD forecasts, larval breeding sites, and Maxent mapping	Identified high-risk periods for malaria and specific villages most at risk. Anopheles stephensi was the most widespread vector.	Spatial-temporal evaluations are crucial for malaria control and early warnings, potentially transferable to other endemic regions.
[13]	Examine malaria transmission risks in Minab district, Iran	Utilized spatiotemporal modeling, MaxEnt mapping, and environmental data	Highlighted critical transmission periods and identified Anopheles stephensi as dominant vector; MaxEnt model marked high-risk villages.	Validated the importance of integrating environmental data for malaria control strategies.
[14]	Predict antimalarial activity of compounds against *P. falciparum*	Used SVM, RF, KNN, and XGBoost on a dataset of 195,143 compounds	SVM and XGBoost achieved high accuracy (85%+), identifying effective compounds from PubChem data.	Machine learning can speed up the identification of potential antimalarial drugs.
[15]	Develop collaborative ML models to identify antimalarial compounds	Bayesian QSAR models on proprietary datasets	Consensus models outperformed single models without revealing proprietary data.	Model-sharing promotes cooperation in drug discovery while protecting intellectual property.
[16]	Enhance malaria diagnosis efficiency in labs	Custom CNN and VGG19 models for blood cell analysis	Custom CNN achieved 97.74% accuracy; Logistic Regression model used for outbreak prediction based on weather data.	Highlights the potential of CNNs in diagnostics and the use of ML in real-time outbreak prediction.
[17]	Map malaria-risk areas in Ghana	Bayesian geospatial modeling and web-based disease mapping	Showed malaria distribution across 260 districts, highlighting high-risk regions	Geospatial analysis can improve malaria control strategies by identifying vulnerable districts.

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

[18]	Forecast malaria incidence in Telangana using satellite data	LSTM classifier, satellite data, and clinical records	LSTM identified seasonal malaria patterns with high accuracy.	Emphasizes the importance of environmental and clinical factors for predicting malaria hotspots.
[19]	Detect malaria parasites in blood smear images	Deep Convolutional Neural Network (DCNN)	Achieved 98.9% accuracy with optimized hyperparameters and demonstrated reliable automated malaria diagnostics.	DCNNs provide a fast, accurate diagnostic alternative to traditional microscopy.
[20]	Improve malaria diagnosis via deep learning	Deep Convolutional Neural Network (DCNN)	Significant accuracy improvement in detecting infected cells compared to technicians.	DCNN-based systems improve diagnostic accuracy and reduce reliance on human analysis.
[21]	Identify Severe Malaria Anemia (SMA) early	Multiple Instance Learning framework (MILISMA) and WHO diagnostic criteria	Early SMA indicators from morphological changes in RBCs allow early diagnosis and intervention.	Useful in regions with limited lab facilities, preventing complications from delayed SMA diagnosis.
[22]	Diagnose malaria via machine learning	Extreme Learning Machine (ELM) and CNN as feature extractors	DELM model achieved 99.66% accuracy on modified dataset	Improved accuracy of malaria diagnostics, proving effective for rapid diagnostics.
[23]	Study immunogenic cell death (ICD) in malaria	LASSO regression, random forest, DEG analysis, and PPI networks	Identified two ICD subtypes and hub genes associated with different immune responses to *P. falciparum*.	Provides insight into malaria's immune impact, informing future research and treatment approaches.
[24]	Forecast COVID-19 hospitalizations and apply model to malaria prediction	Modified SIR model with stochastic and parametric uncertainty	Accurately predicted peak hospitalizations; model adapted for malaria with weather and case data	Flexible SIR model can be adapted for both COVID-19 and malaria forecasting.
[25]	Enhance malaria detection in Rwanda using deep learning	Faster R-CNN for feature extraction on blood smears	Demonstrated improved feature extraction specific to malaria detection in sub-Saharan Africa	Effective feature extraction improves malaria diagnostic accuracy in resource-limited settings.
[26]	Identify potential malaria antigen	Created the PlasmoFAB dataset; used ML	Trained models using PlasmoFAB dataset outperformed general-	Specific datasets like PlasmoFAB aid in drug discovery and

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

	candidates for drug development	models for protein localization	purpose tools in identifying antigens	vaccine research for malaria.

The review summarized above emphasizes the complexity of malaria and the current trends in addressing this disease. Efforts range from assessing the habitats conducive to malaria parasites' reproduction to inventing state-of-the-art diagnostic devices and treatment regimes. Nevertheless, issues on drug resistance and the emergence of new infections remain a big challenge. Adopting an interdisciplinary approach to malaria, including teaching machine learning, working with genomicists and immunologists, etc., aims to provide better, longer-lasting solutions to controlling and eradicating malaria. More research and global reaction to these requests are required to realize this aspiration.

3. Conclusion

Malaria, a persistent global health threat, is most prevalent in temperate and tropical zones. This review highlights three significant trends in malaria research over the past decade: the ecology of transmission, innovative diagnostic tools, and treatment strategies. Understanding the epidemiological drivers of malaria transmission is crucial for designing effective control measures. This knowledge, coupled with spatio-temporal models and predictive analytics, can help predict high-risk areas for malaria transmission, thereby guiding vector control efforts and fostering collaboration among professionals in the field. Newer diagnostic technologies, especially machine learning and deep learning methods have been very useful in addressing the challenges associated with conventional diagnostic methods. Such innovations will facilitate faster and more precise malaria diagnosis for treatment and management of outbreaks, especially in third-world countries where infrastructural facilities may be inadequate. In addition, using machine learning techniques in drug development has also led to the discovery of antimalarial drugs at a faster pace, which is a great relief considering the prevailing resistant malaria strains. Malaria control, however, remains challenging because of the increased resistance to drugs, socio-economic factors, the environment and other reasons. To bring about these changes will take the willingness of many people from different fields, working in unison, including researchers, health care, health policy, and people living in the community. This is the best way to control malaria and wipe it out, ensuring there are funds for R&D and using proven ways and new approaches. Through the synthesis of ecology, technological advancements, and scientific cooperation, a considerable decline in malaria incidence can be envisioned. If developments in these domains address the existing challenges, they will ensure that the fight against this disease remains successful over time.

References

[1] N. J. White, "The Treatment of Malaria," New England Journal of Medicine, vol. 335, no. 11, pp. 800–806, Sep. 1996, doi: 10.1056/NEJM199609123351107.

[2] P. E. Duffy, J. P. Gorres, S. A. Healy, and M. Fried, "Malaria vaccines: a new era of prevention and control," Nature Reviews Microbiology 2024, pp. 1–17, Jul. 2024, doi: 10.1038/s41579-024-01065-7.

[3] G. Neta et al., "Advancing climate change health adaptation through implementation science," Lancet Planet Health, vol. 6, no. 11, pp. e909–e918, Nov. 2022, doi: 10.1016/S2542-5196(22)00199-1.

[4] L. Ammatawiyanon, P. Tongkumchum, A. Lim, and D. McNeil, "Modelling malaria in southernmost provinces of Thailand: a two-step process for analysis of highly right-skewed data with a large proportion of zeros," Malar J, vol. 21, no. 1, pp. 1–10, Dec. 2022, doi: 10.1186/S12936-022-04363-8/FIGURES/8.

[5] K. Hoyos and W. Hoyos, "Supporting Malaria Diagnosis Using Deep Learning and Data Augmentation," Diagnostics 2024, Vol. 14, Page 690, vol. 14, no. 7, p. 690, Mar. 2024, doi: 10.3390/DIAGNOSTICS14070690.

[6] O. Khan, J. O. Ajadi, and M. P. Hossain, "Predicting malaria outbreak in The Gambia using machine learning techniques," PLoS One, vol. 19, no. 5, p. e0299386, May 2024, doi: 10.1371/JOURNAL.PONE.0299386.

[7] N. Ghaffar Nia, E. Kaplanoglu, and A. Nasab, "Evaluation of artificial intelligence techniques in disease diagnosis and prediction," Discover Artificial Intelligence 2023 3:1, vol. 3, no. 1, pp. 1–14, Jan. 2023, doi: 10.1007/S44163-023-00049-5.

[8] A. Abdulrahman, .. Z. M., A. M. Zaki, F. H. H.Rizk, M. M. Eid, and E.-S. M. EL EL-Kenawy, "Exploring Optimization Algorithms: A Review of Methods and Applications," Journal of Artificial Intelligence and Metaheuristics, vol. 7, no. 2, pp. 08–17, 2024, doi: 10.54216/JAIM.070201.

[9] J. L. Siqueira-Neto, K. J. Wicht, K. Chibale, J. N. Burrows, D. A. Fidock, and E. A. Winzeler, "Antimalarial drug discovery: progress and approaches," Nat Rev Drug Discov, vol. 22, no. 10, p. 807, Oct. 2023, doi: 10.1038/S41573-023-00772-9.

[10] M. K. Tully, S. Dini, J. A. Flegg, J. S. McCarthy, D. J. Price, and J. A. Simpson, "Evaluation of a Bayesian hierarchical pharmacokinetic-pharmacodynamic model for predicting parasitological outcomes in Phase 2 studies of new antimalarial drugs," Antimicrob Agents Chemother, vol. 68, no. 9, p. e0086324, Sep. 2024, doi: 10.1128/AAC.00863-24.

[11] K. Farhadyar, F. Bonofiglio, M. Hackenberg, M. Behrens, D. Zöller, and H. Binder, "Combining propensity score methods with variational autoencoders for generating synthetic data in presence of latent sub-groups," BMC Med Res Methodol, vol. 24, no. 1, Dec. 2024, doi: 10.1186/S12874-024-02327-X.

[12] A. Salahi-Moghaddam, H. Turki, M. Yeryan, and M. V. Fuentes, "Spatio-temporal Prediction of the Malaria Transmission Risk in Minab District (Hormozgan Province, Southern Iran)," Acta Parasitol, vol. 67, no. 4, pp. 1500–1513, Dec. 2022, doi: 10.1007/S11686-022-00598-2/FIGURES/10.

[13] O. Bent, "Machine learning applied to prediction, control and planning from dynamic epidemiological models," 2020.

[14] Danishuddin, G. Madhukar, M. Z. Malik, and N. Subbarao, "Development and rigorous validation of antimalarial predictive models using machine learning approaches," SAR QSAR Environ Res, vol. 30, no. 8, pp. 543–560, Aug. 2019, doi: 10.1080/1062936X.2019.1635526.

[15] A. Verras et al., "Shared Consensus Machine Learning Models for Predicting Blood Stage Malaria Inhibition," J Chem Inf Model, vol. 57, no. 3, pp. 445–453, Mar. 2017, doi: 10.1021/ACS.JCIM.6B00572/SUPPL_FILE/CI6B00572_SI_004.XLSX.

[16] Areefa, S. K. Koneru, K. Pragathi, and K. Rishitha, "Malaria Parasite Detection and Outbreak Warning System Using Deep Learning," Lecture Notes in Electrical Engineering, vol. 1066 LNEE, pp. 557–572, 2023, doi: 10.1007/978-981-99-4634-1_43/FIGURES/15.

[17] J. M. K. Aheto, L. J. Menezes, W. Takramah, and L. Cui, "Modelling spatiotemporal variation in under-five malaria risk in Ghana in 2016–2021," Malar J, vol. 23, no. 1, pp. 1–12, Dec. 2024, doi: 10.1186/S12936-024-04918-X/FIGURES/6.

[18] T. Santosh, D. Ramesh, and D. Reddy, "LSTM based prediction of malaria abundances using big data," Comput Biol Med, vol. 124, p. 103859, Sep. 2020, doi: 10.1016/J.COMPBIOMED.2020.103859.

[19] M. Suriya, V. Chandran, and M. G. Sumithra, "Enhanced deep convolutional neural network for malarial parasite classification," International Journal of Computers and Applications, vol. 44, no. 12, pp. 1113–1122, 2022, doi: 10.1080/1206212X.2019.1672277.

[20] M. Suriya, V. Chandran, and M. G. Sumithra, "Design of Deep Convolutional Neural Network for Efficient Classification of Malaria Parasite," EAI/Springer Innovations in Communication and Computing, pp. 169–175, 2021, doi: 10.1007/978-3-030-47560-4_13/FIGURES/2.

[21] E. Moysis, B. J. Brown, W. Shokunbi, P. Manescu, and D. Fernandez-Reyes, "Leveraging deep learning for detecting red blood cell morphological changes in blood films from children with severe malaria anaemia," Br J Haematol, vol. 205, no. 2, pp. 699–710, Aug. 2024, doi: 10.1111/BJH.19599.

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024

[22] M. O. F. Goni et al., “Diagnosis of Malaria Using Double Hidden Layer Extreme Learning Machine Algorithm With CNN Feature Extraction and Parasite Inflator,” IEEE Access, vol. 11, pp. 4117–4130, 2023, doi: 10.1109/ACCESS.2023.3234279.

[23] Y. H. Zhang, L. H. Xie, J. Li, Y. W. Qi, and J. J. Shi, “Classification and clinical significance of immunogenic cell death-related genes in Plasmodium falciparum infection determined by integrated bioinformatics analysis and machine learning,” Malar J, vol. 23, no. 1, pp. 1–14, Dec. 2024, doi: 10.1186/S12936-024-04877-3/FIGURES/6.

[24] R. Forien and P. Lefèvre, “Mathematical Modelling of Infectious Diseases: COVID-19 and Malaria Ousmane DIAO,” 2023.

[25] Y. Bogale, C. P. Mukamakuza, and E. Tuyishimire, “Intelligent Malaria Detection and Species Classification: A Case of Rwanda,” Lecture Notes in Networks and Systems, vol. 1002 LNNS, pp. 507–520, 2024, doi: 10.1007/978-981-97-3299-9_41/FIGURES/7.

[26] J. C. Ditz, J. Wistuba-Hamprecht, T. Maier, R. Fendel, N. Pfeifer, and B. Reuter, “PlasmoFAB: a benchmark to foster machine learning for Plasmodium falciparum protein antigen candidate prediction,” Bioinformatics, vol. 39, no. Supplement_1, pp. i86–i93, Jun. 2023, doi: 10.1093/BIOINFORMATICS/BTAD206.

DOI: https://doi.org/10.54216/MOR.010105
Received: August 28, 2023 Revised: December 10, 2023 Accepted: January 11, 2024