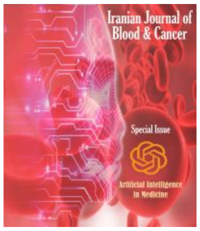
IJBC 2023; 15 (3): 112-124

Iranian Journal of Blood & Cancer



Original Article

AI-driven malaria diagnosis: developing a robust model for accurate detection and classification of malaria parasites

Zohre Fasihfar[1], Hamidreza Rokhsati[2*], Hamidreza Sadeghsalehi[3], Mustafa Ghaderzadeh[4*], Mehdi Gheisari[5]

[1] Faculty Member, Electrical and Computer Engineering Department, Hakim Sabzevari University, Iran

[2] Department of Computer, Control and Management Engineering, Sapienza University of Rome, Italy

[3] Department of Neuroscience, Faculty of Advanced Technologies in Medicine, Iran University of Medical Sciences, Tehran, Iran

[4] Department of Artificial Intelligence, Smart University of Medical Science, Tehran, Iran

[5] Department of Cognitive Computing, Institute of Computer Science and Engineering, Saveetha School of Engineering Saveetha Institute of Medical and Technical Sciences, Chennai, India.

ARTICLE INFO

Article History:
Received: 09/06/2023
Accepted: 18/08/2023

Keywords:
Malaria Parasites,
Image Processing
Artificial Neural Network
Deep Learning
Convolutional Neural Network

***Corresponding authors:**
Hamidreza Rokhsati
Email:
rokhsati.1960699@studenti.uniroma1.it

Mustafa Ghaderzadeh
Email: Mustaf.ghaderzadeh@sbmu.ac.ir

Abstract

Background: Malaria remains a significant global health problem, with a high incidence of cases and a substantial number of deaths yearly. Early identification and accurate diagnosis play a crucial role in effective malaria treatment. However, underdiagnosis presents a significant challenge in reducing mortality rates, and traditional laboratory diagnosis methods have limitations in terms of time consumption and error susceptibility. To overcome these challenges, researchers have increasingly utilized Machine Learning techniques, specifically neural networks, which provide faster, cost-effective, and highly accurate diagnostic capabilities.

Methods: This study aimed to compare the performance of a traditional neural network (NN) with a convolutional neural network (CNN) in the diagnosis and classification of different types of malaria using blood smear images. We curated a comprehensive malaria dataset comprising 1,920 images obtained from 84 patients suspected of having various malaria strains. The dataset consisted of 624 images of Falciparum, 548 images of Vivax, 588 images of Ovale, and 160 images from suspected healthy individuals, obtained from local hospitals in Iran. To ensure precise analysis, we developed a unique segmentation model that effectively eliminated therapeutically beneficial cells from the image context, enabling accurate analysis using artificial intelligence algorithms.

Results: The evaluation of the traditional NN and the proposed 6-layer CNN model for image classification yielded average accuracies of 95.11% and 99.59%, respectively. These results demonstrate that the CNN, as a primary algorithm of deep neural networks (DNN), outperforms the traditional NN in analyzing different classes of malaria images. The CNN model demonstrated superior diagnostic performance, delivering enhanced accuracy and reliability in the classifying of malaria cases.

Conclusion: This research underscores the potential of ML technologies, specifically CNNs, in improving malaria diagnosis and classification. By leveraging advanced image analysis techniques, including the developed segmentation model, CNN showcased remarkable proficiency in accurately identifying and classifying various malaria parasites from blood smear images. The adoption of machine learning-based approaches holds promise for more effective management and treatment of malaria, addressing the challenges of underdiagnosis and improving patient outcomes.

Please cite this article as: Fasihfar Z, Rokhsati H, Sadeghsalehi H, Ghaderzadeh M, Gheisari M. AI-driven malaria diagnosis: developing a robust model for accurate detection and classification of malaria parasites. Iranian Journal of Blood and Cancer. 2023;15(3):112-124.

1. Introduction

Malaria is a hazardous disease commonly transmitted through the bites of infected Anopheles mosquitoes, which can lead to severe complications. The Plasmodium parasite is carried by these mosquitoes, and when they bite a person, the parasite enters their bloodstream. Researchers have identified three types of malaria parasites that can potentially infect humans, namely P. ovale, Plasmodium vivax, and P. falciparum. Studies have shown that P. falciparum can cause a more severe form of the disease, increasing the risk of mortality risk for individuals exposed to this type of malaria. It is important to note that infected mothers can transmit the disease to their newborns, resulting in congenital malaria. Additionally, malaria can give rise to various dangerous side effects (1–4).

Studies indicate that the malaria parasite has a complicated, multi-stage life cycle in two living beings: vertebrate hosts and vector mosquitoes. The parasites survive and develop in the intracellular and extracellular environments of both hosts, aided by a toolkit of >5,000 genes and their respective particular proteins, which assist in the invasion and development of several cell types and avoidance of the host immune response. Therefore, the parasite passes through different stages of progression, including sporozoites (Gr. spores = seeds: the mosquito transmits the infectious form), trophozoites (Gr. trophies = nourishment: the form that multiplies in the erythrocytes), merozoites (Gr. meros = piece: the phase of erythrocyte invasion), and gametocytes (sexual phases). It should be noted that each stage has a specific structure, shape, and protein complement. However, the proteins on the surface and metabolic pathways continue to change during these phases, which can cause issues in developing vaccines and drugs by involving parasites in evading immune clearance (5–7). Investigations indicate that three common malaria parasites can be found in Iran, including in the south of Kerman province, the central and southern areas of Sistan and Baluchistan provinces, and the eastern areas of Hormozgan province. **Table 1** shows these three common parasites in Iran and their differential characteristics. Studies indicate three major malaria areas in Iran, including southern Kerman province, the central and southern areas of Sistan and Baluchistan provinces, and the eastern areas of Hormozgan province. **Table 1** shows the differentiating characteristics of the Malaria Parasites.

Early diagnosis plays a crucial role in the treatment of malaria. Therefore, many researchers have studied intelligent diagnostic methods for malaria diagnosis. There have been various proposals for improving current diagnostic tests, including reducing costs, increasing specificity, and improving ease of use through hardware and software advancements (8–10). In recent years, there has been a significant increase in the use of artificial intelligence-based methods, particularly ML, in the timely diagnosis of malaria through image analysis. ML methods are problem-solving methods for complex problems that have been shown to achieve tremendous results in decision-making and the prediction of health data. These methods learn from experience and identify valuable patterns from large, unstructured, and complex data sets to predict future events (9–12). Due to the high volume of health data production, one of the biggest challenges facing the healthcare industry today is diagnosing diseases with accuracy and at affordable costs. Accurate prediction of clinical results is necessary for clinical, managerial, and financial decisions. it can lead to better patient care and disease management, which is one of the methods of accurate disease prediction using ML methods (10,12,13). Apart from that, a lack of a correct diagnosis may lead to mismanagement of

Table 1. Types of malaria parasites and their differential diagnosis methods

	P. falciparum	*P. vivax*	*P. ovale*
RBC Size	Not enlarged	Enlarged	Enlarged
RBC Shape	Round, sometimes crenate	Round or oval, frequently bizarre	Round or oval, often fimbriae
RBC Color	Normal, but it possibly gets darker and	Normal to pale	Normal
Initial trophozoite (ring)	Smallest, delicate, and sometimes 2 chromatin dots	Relatively large; one chromatin dot	Compact; one chromatin
Schizont	Middle-sized, compressed, several chromatin masses, rough pigments, infrequently observed in the peripheral blood	Big, amoeboid, multiple chromatin masses, very small pigments	Middle-sized, compressed, little chromatin masses, rough pigments
Gametocyte	Crescent-shaped, larger, and slender; central chromatin	Spherical; compressed.	Like *P. vivax*, but smaller

other diseases that have symptoms associated with malaria. Considering the expected behavior of self-medication with malaria drugs and the existing challenges in the health system in most low-income countries, such as Iran, there is a need for a learning-based machine diagnosis model. Therefore, in this research, an attempt will be made to present a malaria diagnosis model using ML concepts. This model will be obtained by comparing the efficiency of two standard algorithms and introducing the most efficient algorithm.

2. Methods

Over the past decade, researchers have worked on malaria image processing and proposed many ML techniques. In the past few years, there have been several studies on the automatic diagnosis of malaria, all of which can be categorized from two perspectives. The first perspective is to use traditional ML methods, where feature extraction and engineering are done manually. Due to the feature selection by the user, many of these methods suffer from problems such as feature selection bias and ignoring important features. The second perspective is using Deep Learning (DL) algorithms in malaria image analysis (12,13). In this view, feature extraction is fully automatic and free from arbitrary selection or feature bias. Due to the importance of classifying malaria parasites in determining treatment protocols, no comprehensive study has been done in this field yet.

In this section, the model design and methodology of malaria image processing will be discussed. In this part, for better feature extraction, the images are pre-processed in the first step, then segmented to get the essential parts of the images and remove the unnecessary parts.

2.1. Overview of the Study Methodology

In the first step, dataset images are used to extract features and classify them using the proposed models. **Figure 1** shows the general schematic of the proposed methodology for this study in the diagnosis and classification of malaria images.

Reviewing the studies conducted on artificial intelligence-based methods for diagnosing malaria, it was discovered that among traditional ML methods, the use of an artificial neural network was most effective in classifying malaria images. Among DL

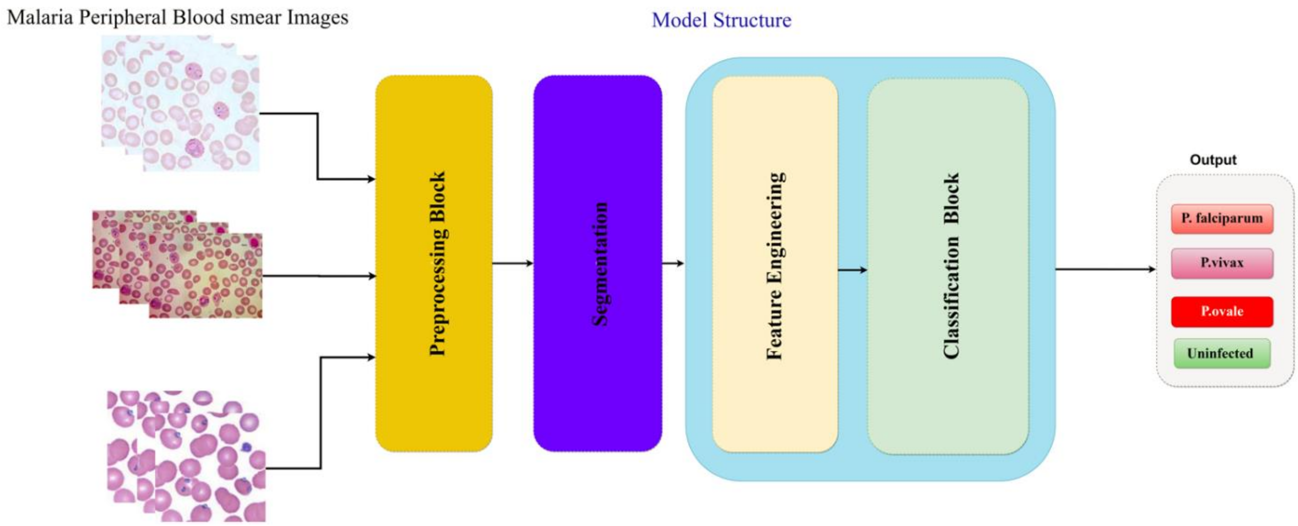


Figure 1. An overview of the malaria diagnosis process model.

methods, the use of a convolutional neural network has the most applications and performs the best in the field of malaria diagnosis from blood smear images. As a result, two models based on ANN and CNN will be used in this study to detect and classify different kinds of malaria images. The best model will then be chosen after comparing the two models' results.

2.1.1. Artificial Neural Network (ANN)

A practical method for processing data, particularly medical images, is the artificial neural network (ANN), which falls under the umbrella of soft computing. Inspired by biological nerve systems, the ANN represents weighted directed networks where nodes act as artificial neurons and edges between neurons carry assigned weights. Two types of ANN are commonly used: feedforward and recurrent networks. Recurrent networks are dynamic and produce a single set of output values, while feedforward networks are stateless and independent of prior network states. These models have been successfully employed in various studies involving malaria classification, including our investigation (**Figure 2**). Artificial neurons possess weights that are adjusted during the learning process, influencing the strength of signals transmitted through connections. Additionally, artificial neurons may have thresholds that determine signal transmission based on aggregated signals. Combinations of layers in the ANN perform different transformations on inputs, with signals traversing from the input layer to the output layer (14–16). In our study, we applied a 2-layer ANN feed-forward network with sigmoid and soft maximum transfer functions in the hidden and output layers, respectively. This network was employed for classifying cells into four categories: P. falciparum, P. vivax, P. ovale, and normal.

2.1.2 Conventional Neural Network (CNN)

Deep Learning (DL), a critical subset of Machine Learning (ML) algorithms, has emerged in the past decade as a robust technique for analyzing medical imaging. With its ability to overcome the limitations inherent in traditional ML methodologies, DL has demonstrated strong performance in the diagnostics and categorizing a broad range of medical imaging

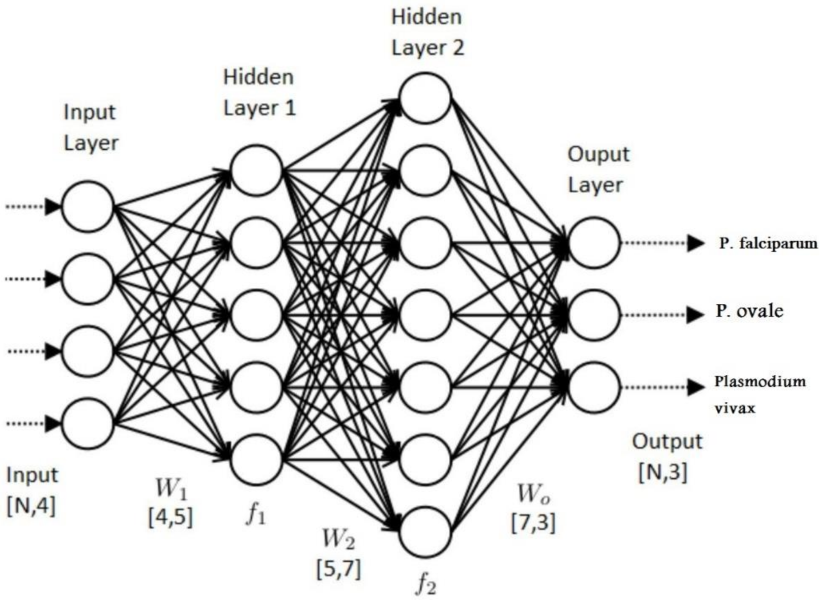


Figure 2. Structure of feedforward Neural Network.

types. Among the various DL models, the Convolutional Neural Network (CNN) has gained considerable traction in medical image classification. Its popularity stems from its ability to autonomously extract features, a capacity that makes it particularly suitable for image prediction tasks. CNNs typically comprise tens or even hundreds of layers, each layer learning to detect diverse features within images. The training process involves the application of filters to each image at different resolutions, with the output from each convolution serving as the input to the subsequent layer. As a result, the initial filters learn basic features such as edges and brightness levels, gradually escalating in complexity to identify features that uniquely characterize an object. The CNN topology (**Figure 3**) use three popular layers with different mechanisms (17–19).

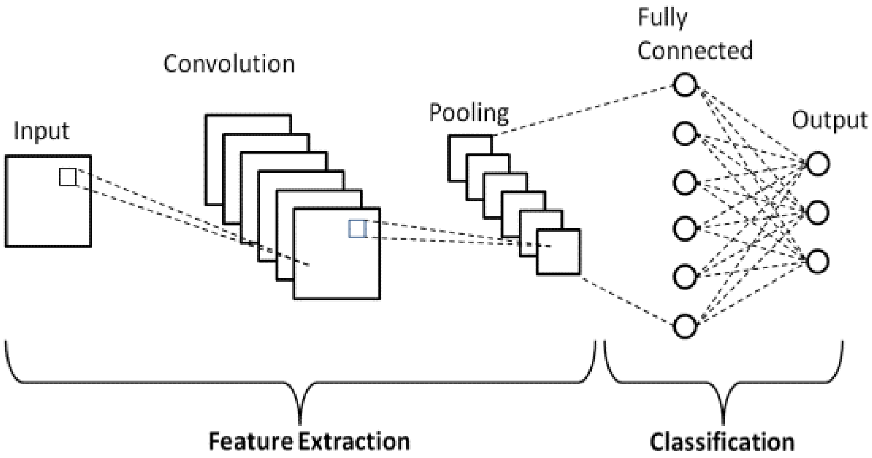


Figure 3. The overall structure of CNN.

Convolution, would put the input images through a collection of convolutional filters, all of which activate specific features in the images (18).

Rectified linear units (ReLU), cause more rapid and efficient training by plotting the negative values to 0 and preserving the positive values. Such a condition is occasionally called activation, as the actuated features would have just proceeded into the next layer (18).

Pooling, makes the output easy by doing the non-linear down-sampling and declining the numbers of the factors, which a network should learn (18).

2.2 Dataset

The data for this study were collected from the three most prevalent parasites in Iran. Following the camera's collection of the slides, these data were obtained using a lab microscope. The number of slides and photos taken of each malaria parasite is listed in the **Table 2.**

All of the dataset's photos were shuffled in the current study before being given to the networks to make sure that the network does not always encounter data from a certain class throughout each iteration. In actuality, each category includes pictures from three groups of infected and non-infected patients, all with different tags on them. The datasets utilized in this study were split up into groups for model training and testing, as indicated in **Table 3**.

2.3. Proposed Method

The primary objective of this study was to create a classification model for malaria disease. This was achieved through a meticulous selection of specific blood components, guided by their morphology and clinical expertise. The methodology for accomplishing this goal comprised a series of sequential steps, which included image segmentation as the initial phase. Following segmentation, the images were subjected to normalization and standardization processes. Finally, the preprocessed and segmented images were fed to the developed models, which were deployed to carry out the classification task.

2.4. Data Preprocessing and Feature Extraction

Machine vision applications typically necessitate preprocessing, which directly influences the performance of ML-based models. Preprocessing methods aid in preparing input data to accomplish tasks such as noise reduction, diagnostic enhancement, highlighting relevant image features, and expediting the training of DL models. The suggested technique for data preprocessing involved three stages: segmentation, decoding and resizing, and normalization. In this study, following the resizing process, microscopic images were captured using a microscope. Subsequently, the image contrast was enhanced, resulting in sharper edges for different parts of the image. Afterward, the images were converted to the HSV format, and a Double filter was applied for analysis. It is important to note that HSV comprises three key attributes Hue, Saturation, and Value (20–23). Images were transferred from RGB space to HSV space. This transfer was done using formulas (EQ. s 1 to 3).

Finally, if the value obtained in this method is more significant than 0.98, then the cell is considered a complete circle, and its center is shown in purple. However, the non-noise and sharp images have been converted into black and white. Then, the feature vector extraction was performed. Thus, the cell shape is measured, and the environment is obtained. In addition, the form factor has been used to measure the image standards. Notably, for those shapes, with a completely circular shape, the value is equal to 1 and

Table 2. The local dataset of Malaria and its subclasses

Type of Malaria parasites	Num of Infected patient	Num of Infected Images
P. FALCIPARUM	24	624
P. VIVAX	25	548
P. OVALE	27	588
NORMAL	8	160
SUM	**84**	**1920**

Table 3. The datasets were categorized according to the table to be used for training and testing for models.

Dataset	Train rate	Validation rate	Test rate
Malaria infected cases	75%	5%	20%
Sum	1440	96	384

for any other shapes, which is not suitably circular, is less than 1. completely circular shape, the value is equal to 1 and for any other shapes, which is not suitably circular, is less than 1.

Moreover, cell roundness would be important. Then, also in this research the Gabor filter was applied to the images. In general, a Gabor filter is a linear filter that would be employed to analyze the texture According to some researchers, this implies that it fundamentally examines if any particular frequency contents are found in the images in certain directions in a localized area surrounding the point or area of analysis or not. It has been demonstrated that they are specifically suitable to represent and discriminate the texture. However, according to the spatial domain, a two-dimensional Gabor filter is a Gaussian kernel function regulated via a sinusoidal plane wave. In addition, because of the multiplication-convolution property (Convolution theorem), the Fourier transform of the impulse response of a Gabor filter is to convolute the Fourier transform of the harmonic function (sinusoidal function) and Fourier transform of the Gaussian function. Furthermore, the filter has a real and an imaginary component that indicates the orthogonal directions (20,24,25). The two components may be formed into a complex number or used individually (EQ. s 4 to 8).

Where λ represents the wavelength of the sinusoidal component, Ɵ stands for orienting the regular stripes to parallel stripes of the Gabor function. Ψ refers to the stage offset of the sinusoidal function. In addition, σ is the sigma or standard deviation of the Gaussian envelope. Finally, ɣ represents the spatial aspect ratio and determines the support elasticity of the Gabor function.

Therefore, consideration of a set of Gabor filters containing diverse frequencies and orientations can be beneficial in extracting the advantageous features of the images. Thus, in the discrete domain, 2D Gabor filters are expressed as (Eq. 9 and 10):

Where B and C refer to the normalizing factors that should be estimated, notably, two-dimensional Gabor filters are highly used to process the images, particularly in extracting the features to analyze and segment the texture, as Fig 4 illustrates.

After segmenting the images and obtaining the segmented image that includes essential blood components for malaria diagnosis and classification. These images need a classifier to classify the features in the next step. In this research, we used two standard classifiers in classifying features of malaria parasite images. The reason for using these two classifiers was their acceptable performance in previous studies. Based on the research design, each image has been read into MATLAB. Then, the images

formulas (EQ. s 1 to 12)	
$H = \tan(\frac{3(G-B)}{(R-G)+(R-B)})$	1
$S = 1 - \frac{\min(R,G,B)}{V}$	2
$V = \frac{R+G+B}{3}$	3
$g(x,y;\ \lambda,\theta,\psi,\sigma,\gamma) = \exp\left(-\frac{x'^2+\gamma^2 y'^2}{2\sigma^2}\right)\exp\left(i\left(2\pi\frac{x'}{\lambda}+\psi\right)\right)$	4
$g(x,y;\ \lambda,\theta,\psi,\sigma,\gamma) = \exp\left(-\frac{x'^2+\gamma^2 y'^2}{2\sigma^2}\right)\cos\left(i\left(2\pi\frac{x'}{\lambda}+\psi\right)\right)$	5
$g(x,y;\ \lambda,\theta,\psi,\sigma,\gamma) = \exp\left(-\frac{x'^2+\gamma^2 y'^2}{2\sigma^2}\right)\sin\left(i\left(2\pi\frac{x'}{\lambda}+\psi\right)\right)$	6
$x' = x\cos\theta + ysin\theta \quad , \quad y' = -xsin\theta + ycos\theta$	7,8
$G_c[i,j] = Be^{-\frac{(i^2+j^2)}{2\sigma^2}}\cos\left(2\pi f(i\, cos\theta + j\, sin\theta)\right)$	9
$G_s[i,j] = Ce^{-\frac{(i^2+j^2)}{2\sigma^2}}\sin\left(2\pi f(i\, cos\theta + j\, sin\theta)\right)$	10
$Sensitivity = Recall = \frac{True\ Positive}{True\ Positive + False\ Negative}$	11
$Accuracy = \frac{True\ Negative + True\ Posetive}{Totall\ Cases}$	12

have been resized and serialized for generating the input to the MatConvnet toolbox. It should be mentioned that before running data to the CNN network for training, normalization has been used for improving the local contrast and brightness and whitening the whole dataset through an eigenvalue decomposition (EVD) operation on the covariance matrix.

3. Result

Two models were used in the present study. Both models were tuned after the initial design, and their hyperparameters were adjusted to optimize them to reach an optimal model.

3.1. Performance Metrics

The sensitivity, specificity, and accuracy evaluation criteria were established based on the model's performance using a confusion matrix to objectively assess the efficacy of the chosen method. Sensitivity in this context was outlined as the proportion of infected cases that the model accurately identified to all actual malaria cases. The ratio of accurately identified non-infected cases as all real non-infected cases define specificity. Accuracy was further defined as the percentage of all malaria-infected and non-infected cases that were correctly identified from the blood pictures. The formulas of the evaluation criteria are given in equations (Eq. 11 and 12) (26,27).

3.2. Models Structure

The first model was an ANN, whose optimal structure was obtained by adjusting the number of layers and the weights of these networks. Also, the second model, which was a CNN model, obtained a changing the hyperparameters of that model. The

Table 4. Parameters of both phases of the model after tuning.

Optimizer	Learning rate	Initial learning rate	Decay rate	Decay steps	Loss	Epoch	Batch size
Adam	Exponentially decay	0.0005	0.94	66	Cross entropy	80	30

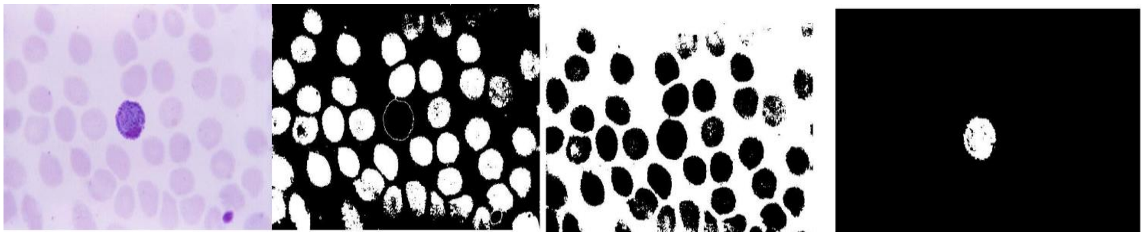


Figure 4. Image Segmentation pipeline including (HSV transformation and Gabor filter

hyperparameters of this model are shown in the **Table 4**.

The suggested CNN model is thoroughly explained in **Figure 5**. The feature extraction block and transition layers have the same exact specifications as the original references. The classifier layers of the suggested model classified the characteristics in both stages using the best possible layer combination. Batch Normalization, a dropout layer to prevent over-fitting, and finally a final layer with an activation function termed a ReLU (rectified linear unit) were used to establish the architecture of these layers.

The results of the model evaluation on the test dataset are provided first in this section. We used the cross-validation approach to assess the suggested model, which establishes how generalizable and independent of the training data the findings of statistical analysis on a dataset are. This approach is primarily employed in prediction applications to evaluate the model's practical utility. A cross-validation period typically entails two complementary subsets of data being divided, learning and fitting on one subset (training data), then testing/validating using the data from the other set (validation/test data). Validation is carried out multiple times with various subsets to reduce dispersion, and the validation results are averaged. The data are divided into K subsets for K-fold cross-validation, one of which is always utilized for validation and the other K-1 for training. Every data fold is utilized exactly once for training and once for validation during this process, which is repeated K times. As a final estimation, the mean outcomes of these K validation times are chosen. The 5-fold validation method was chosen in this study because it is frequently used in classification research, and **Table 5** and **6** reports the mean of the final results for each model.

Table 5. The proposed NN model's accuracy on the test data.

Type	Num	Sensitivity
Falciparum.schizont	40	88.93%
Falciparum.trophozoite	38	90.49%
Falciparum.gametocyte	37	93.99%
Ovale.schizont	37	89.35%
Ovale.trophozoite	39	98.72%
Ovale.gametocyte	39	96.23%
Vivax. Schizont	38	99.54%
Vivax. trophozoite	38	98.9%
Vivax.gametocyte	40	94.88%
Non-infected	38	93.38%

Table 6. The proposed CNN model's accuracy on the test data.

Type	Num	Accuracy
Falciparum.schizont	40	98.98%
Falciparum.trophozoite	38	99.57%
Falciparum.gametocyte	37	98.99%
Ovale.schizont	37	99.36%
Ovale.trophozoite	39	99.78%
Ovale.gametocyte	39	99.93%
Vivax. Schizont	38	99.94%
Vivax. trophozoite	38	99.98%
Vivax.gametocyte	40	99.79%
Non-infected	38	98.59%

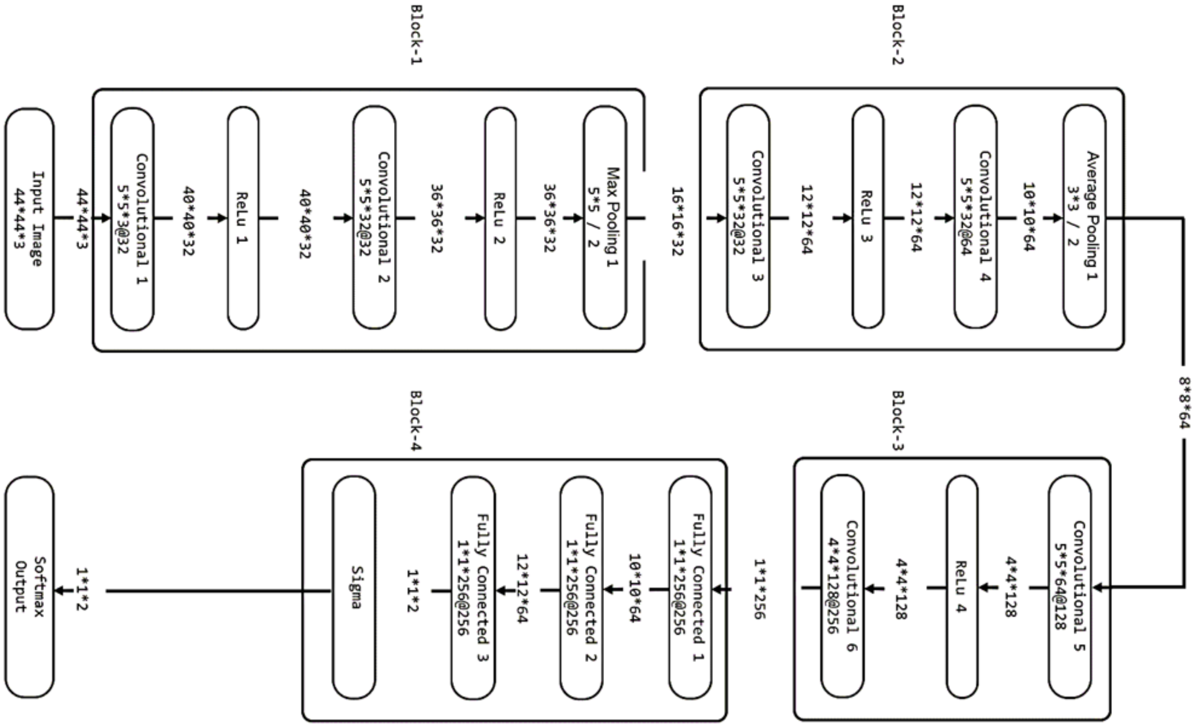


Figure 5. The proposed model for Malaria diagnosis and detection based on CNN models and peripheral blood images

On the test data of 264 sample pairs, the mean final evaluation accuracy is equivalent to 99.85%. The proposed model based on CNN was found to have an overall superior performance than the neural network model after comparing the two models' performances. **Table 7** displays this performance comparison between the two models (ANN and CNN).

Table 7. Comparing the Accuracy of the ANN and CNN models in the classification of malaria

Type	Num	ANN	CNN
Falciparum	115	91.13%	99.18%
Ovale	115	94.76 %	99.69 %
Vivax	116	99.43%	99.90%

More measurements were applied in the section that follows to look at the effectiveness of the two approaches in terms of performance. These metrics' values are displayed in the **Table 8**.

The performance metrics of the two models are compared in **Figure 6**. A quick look at the chart reveals that the CNN network outperformed in detecting various types of malaria parasites and distinguishing between these classes.

After analyzing all the evaluation criteria values, it was concluded that the method suggested by the CNN algorithm performed better in identifying and classification various types of malaria. This improved performance is thought to be the automatic extraction of image features.

4. Conclusion and Feature Work

The approaches employed in the current study include several segmentation techniques, normalization and

Table 8. The overall metric performance on the test data.

Model	*Accuracy*	*Sensitivity*	*Specificity*	*Precision*	*Recall*	*F-Score*	*MMC*
ANN	95.11%	95.10%	95.12%	91.15%	95.10%	93.08%	94.20%
CNN	99.59%	99.58%	99.59%	95.62%	99.58%	97.56%	98.68%

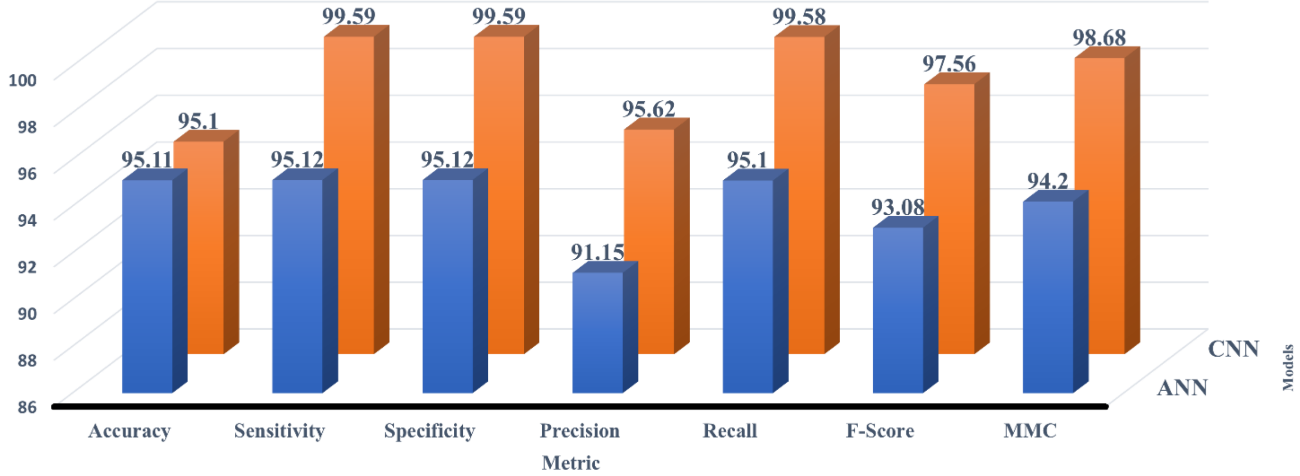


Figure 6. Performance comparison of the two proposed models based on all performance metrics.

standardization, and, lastly, ML and DL algorithmic frameworks.

The Gabor filter was employed to segment malaria peripheral blood pictures for the first time in this study. Because extraneous blood components were removed as a result of this segmentation approach, the models were able to achieve high accuracy in showing key components. On the other hand, the characteristics of the segmented pictures were accurately categorized using popular artificial intelligence techniques like ANN and DL. It is advised that researchers focus on the following technical details in their subsequent work on identifying medical pictures, particularly malaria.

4.1. Sufficient size of the used dataset

Utilizing large datasets is a crucial aspect that contributes to the effectiveness of ML techniques (4). In the context of DL methods, the size of the dataset significantly impacts the ability to recognize patterns related to cardiac diseases. Inadequate data can lead to an increased risk of overfitting and negatively impact the accuracy of ML models.

4.2. Apply methods to avoid Overfitting

The investigation of the studies on Malaria detection with various ML methods revealed that a large number of these studies had not tackled overfitting concepts and had not presented techniques for escaping this severe challenge of ML and DL methods. However, overfitting arises in some methods, and preventive approaches should be adopted for the implementation of these models. In this respect, we suggest employing more voluminous datasets and the dropout technique in the DL domain.

4.3. Try several ML methods or DL Networks

Different ML methods and DL networks display various pattern recognition and malaria detection capabilities. Therefore, it is suggested that future research use many algorithms and choose the most effective one. Similarly, for CNNs, we propose evaluating the performance of different kinds of pre-trained networks and adjusting the hyperparameters of the most efficient network. Additionally, it is recommended that more recent DL architectures and cutting-edge technologies be employed to improve outcomes in the detection and classification of all kinds of medical pictures, including photos of malaria. With the development of mobile phone processors, it is predicted that even in the far future, these artificial intelligence models will be integrated into mobile phones so that clinical professionals can take images via the microscope's eyepiece and diagnose illness at the point of care.

Declarations of interest

None.

Conflict of Interest

The authors declare that they have no conflict of interest.

Acknowledgment

The research reported in this publication was under Grant number 835-19-0-0 from the Smart University of Medical Sciences, Tehran, Iran.

References

1. Poostchi M, Ersoy I, McMenamin K, Gordon E, Palaniappan N, Pierce S, et al. Malaria parasite detection and cell counting for human and mouse using thin blood smear microscopy. J Med Imaging [Internet]. 2018;5(4):44506. Available from: https://doi.org/10.1117/1.JMI.5.4.044506
2. Díaz G, González FA, Romero E. A semi-automatic method for quantification and classification of erythrocytes infected with malaria parasites in microscopic images. J Biomed Inform. 2009;42(2):296–307.
3. Poostchi M, Ersoy I, McMenamin K, Gordon E, Palaniappan N, Pierce S, et al. Malaria parasite detection and cell counting for human and mouse using thin blood smear microscopy. J Med Imaging. 2018;5(4):44506.
4. Litjens G, Kooi T, Bejnordi BE, Setio AAA, Ciompi F, Ghafoorian M, et al. A survey on deep learning in medical image analysis. Vol. 42, Medical Image Analysis. Elsevier B.V.; 2017. p. 60–88.
5. Razzak MI. Automatic detection and classification of malarial parasite. Int J Biometrics Bioinforma. 2015;9(1):1–12.
6. Pattanaik PA, Swarnkar T, Sheet D. Object detection technique for malaria parasite in thin blood smear images. In: 2017 IEEE International Conference on Bioinformatics and Biomedicine (BIBM). IEEE; 2017. p. 2120–3.
7. Ross NE, Pritchard CJ, Rubin DM, Duse AG. Automated image processing method for the diagnosis and classification of malaria on thin blood smears. Med Biol Eng Comput. 2006;44:427–36.
8. Landier J, Parker DM, Thu AM, Carrara VI, Lwin KM, Bonnington CA, et al. The role of early detection and treatment in malaria elimination. Malar J [Internet]. 2016;15(1):363. Available from: https://doi.org/10.1186/s12936-016-1399-y
9. Kalkan SC, Sahingoz OK. Deep Learning Based Classification of Malaria from Slide Images. In: 2019 Scientific Meeting on Electrical-Electronics & Biomedical Engineering and Computer Science (EBBT). 2019. p. 1–4.
10. Aqeel S, Haider Z, Khan W. Towards digital diagnosis of malaria: How far have we reached? J Microbiol Methods [Internet]. 2023;204:106630. Available from: https://www.sciencedirect.com/science/article/pii/S0167701222002251
11. Gourisaria MK, Das S, Sharma R, Rautaray SS, Pandey M. A deep learning model for malaria disease detection and analysis using deep convolutional neural networks. Int J Emerg Technol. 2020;11(2):699–704.
12. Mustafa WA, Alquran H, Aihsan MZ, Saifizi M, Khairunizam W, Abdul-Nasir AS, et al. Malaria parasite diagnosis using computational techniques: a comprehensive review. In: Journal of Physics: Conference Series. IOP Publishing; 2021. p. 12031.
13. Jdey I, Hcini G, Ltifi H. Deep learning and machine learning for Malaria detection: overview, challenges and future directions. arXiv Prepr arXiv220913292. 2022;
14. ghi M, Asadi F, Hosseini A, Bashash D, Abolghasemi H, Roshanpour A. Machine Learning in Detection and Classification of Leukemia Using Smear Blood Images: A Systematic Review. Wang P, editor. Sci Program. 2021;2021:9933481.
15. Sadoughi F, Ghaderzadeh M. A hybrid particle swarm and neural network approach for detection of prostate cancer from benign hyperplasia of prostate. In: e-Health–For Continuity of Care. IOS Press; 2014. p. 481–5.
16. Garavand A, Behmanesh A, Aslani N, Sadeghsalehi H, Ghaderzadeh M. Towards Diagnostic Aided Systems in Coronary

Artery Disease Detection: A Comprehensive Multiview Survey of the State of the Art. El Kafhali S, editor. Int J Intell Syst [Internet]. 2023;2023:6442756. Available from: https://doi.org/10.1155/2023/6442756

17. Hosseini A, Eshraghi MA, Taami T, Sadeghsalehi H, Hoseinzadeh Z, Ghaderzadeh M, et al. A mobile application based on efficient lightweight CNN model for classification of B-ALL cancer from non-cancerous cells: A design and implementation study. Informatics Med Unlocked [Internet]. 2023;39:101244. Available from: https://www.sciencedirect.com/science/article/pii/S2352914823000862
18. Gheisari M, Ebrahimzadeh F, Rahimi M, Moazzamigodarzi M, Liu Y, Dutta Pramanik PK, et al. Deep learning: Applications, architectures, models, tools, and frameworks: A comprehensive survey. CAAI Trans Intell Technol. 2023;
19. AI-Driven Malaria Diagnosis: Developing a Robust Model for Accurate Detection and Classification of Malaria Parasites.
20. Movellan JR. Tutorial on Gabor filters. Open source Doc. 2002;40:1–23.
21. Kermany DS, Goldbaum M, Cai W, Valentim CCS, Liang H, Baxter SL, et al. Identifying medical diagnoses and treatable diseases by image-based deep learning. Cell. 2018;172(5):1122–31.
22. Loddo A, Di Ruberto C, Kocher M. Recent advances of malaria parasites detection systems based on mathematical morphology. Sensors. 2018;18(2):513.
23. Cantrell K, Erenas MM, de Orbe-Payá I, Capitán-Vallvey LF. Use of the hue parameter of the hue, saturation, value color space as a quantitative analytical parameter for bitonal optical sensors. Anal Chem. 2010;82(2):531–42.
24. Forcado MRG, Estrada JE. Model development of marble quality identification using thresholding, sobel edge detection and gabor filter in a mobile platform. In Graduate Programs, Technological Institute of the Philippines - Manila, Quiapo, Manila, Philippines; 2019. Available from: https://www.scopus.com/inward/record.uri?eid=2-s2.0-85064128503&doi=10.1109%2FHNICEM.2018.8666359&partnerID=40&md5=40eec67b571d342da5a28a6a592ea18a
25. Kamarainen J-K, Kyrki V, Kalviainen H. Invariance properties of Gabor filter-based features-overview and applications. IEEE Trans image Process. 2006;15(5):1088–99.
26. Ghaderzadeh M, Eshraghi MA, Asadi F, Hosseini A, Jafari R, Bashash D, et al. Efficient Framework for Detection of COVID-19 Omicron and Delta Variants Based on Two Intelligent Phases of CNN Models. Corsi C, editor. Comput Math Methods Med [Internet]. 2022;2022:4838009. Available from: https://doi.org/10.1155/2022/4838009
27. Ghaderzadeh M, Asadi F, Jafari R, Bashash D, Abolghasemi H, Aria M. Deep Convolutional Neural Network–Based Computer-Aided Detection System for COVID-19 Using Multiple Lung Scans: Design and Implementation Study. J Med Internet Res. 2021;23(4):e27468.