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Malaria cell identification using improved machine learning and modified deep learning architecture

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ABSTRACT

Malaria continues to be a serious problem for public health because of its occurrence in tropical and subtropical areas with inadequate healthcare systems and few resources. For prompt intervention and treatment of malaria, effective and precise diagnosis is essential. Professional pathologists examine blood smear films by hand to get a microscopic diagnosis and another way they will do a rapid antigen malaria test which produces the result of 50% accuracy. Convolutional neural network (CNN) is a type of deep learning (DL) model that has been effectively used for a variety of image recognition applications. Our suggested approach uses, improved machine learning (IML) methods like support vector machine (SVM)+principal component analysis (PCA) fit, SVM+t-distributed stochastic neighbor embedding (t-SNE) fit, and CNN architecture with an accuracy of 86.23%, 88.27%, and 97.16% accuracy respectively, to combine feature extraction, data augmentation, and modify the layers by including the SVM algorithm in the final layer of the CNN architecture. The proposed method will significantly reduce pathologists' burden by automating the identification of malaria and improving diagnosis accuracy in resource-constrained contexts.

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1. INTRODUCTION

An infectious disease called malaria is spread by mosquitoes and affects both humans and other species. Symptoms of human malaria usually include headaches, vomiting, fever, and exhaustion. Seizures, coma, jaundice, and even death may result in extreme situations [1]. After being bitten by an infected Anopheles mosquito, symptoms often appear 10 to 15 days later. People may experience recurrences of the condition months later if they are not appropriately managed [2]. Reinfection often results in milder symptoms in those who have recently recovered from an infection [3]. Table 1 shows the malaria-infected cases and deaths caused due to malaria in the recent years from 2019 to 2023 as illustrated in the world Malaria report [1]. Figure 1 shows the rise in Malaria cases worldwide year-wise from 2019 to 2023 and Figure 2 shows the rise in Malaria deaths worldwide year-wise details from 2019 to 2023.

Conventional techniques [4] for automating the malaria detection procedure include intricate image-processing methods using manually designed elements, such as size, texture, color, shape, and intensity [5]. These techniques identify red blood cells via microscopic photos [6] by applying several segmentation

methods. Following the selection of relevant features for red blood cells [7], segmented images are classified that are infected and uninfected using a calculated set of features. For instance, morphologically based techniques are utilized to segment [8] cell pictures with structural elements to highlight red blood cell features [9], including roundness, which increases the accuracy of categorization. Different approaches are used in the literature to classify, extract features [10], and segment [9] malaria diagnoses. There is a trade-off between model accuracy and computational complexity, meaning that as a model's accuracy rises, so does its computational complexity, according to an analysis of both modern and traditional malaria detection techniques. The problem with classification algorithms is achieving high accuracy [11] increases the time constraint, developing a model that provides good accuracy with minimal time is the scope of this research work. For instance, a deep neural network [12], [13] is discovered to have a higher accuracy than a support vector machine (SVM) [13], [14], despite the SVM's faster computation time for classification tasks [15].

Table 1. Malaria cases and deaths year wise details

Sl.no	Year	Malaria cases (millions)	Malaria deaths (*1,000)
1	2022	249	608
2	2021	244	615
3	2020	244	630
4	2019	232	576

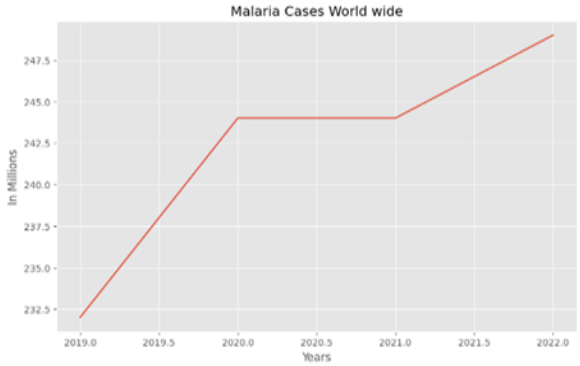

Figure 1. Malaria cases worldwide

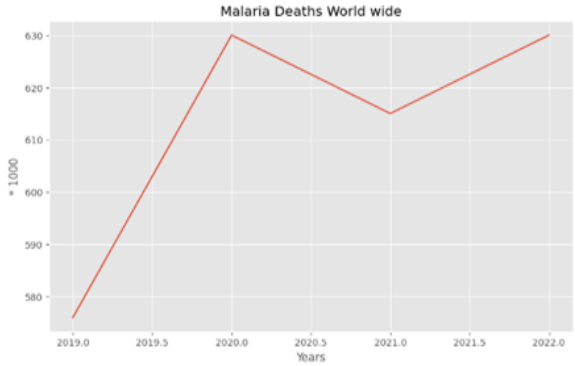

Figure 2. Malaria deaths worldwide

Deep learning (DL) methods [3] have been used in recent years to automatically diagnose malaria with respectable detection rates. Because DL models' hidden layers automatically extract features, they do not require the calculation of hand-crafted features, through data analysis. Large datasets are needed for DL models [11] to train neural networks and increase model accuracy [16]. Nonetheless, comparatively modest datasets are accessible for medical applications such as malaria detection. This is because assembling an annotated dataset necessitates pathologists' input, which is not easily accessible. Recently discovered picture augmentation approaches in DL models [2] allow higher generalization and prevent overfitting to overcome the lack of available datasets. By taking the original image and converting it into several images using transformation techniques like rotation, shear, and translation, augmentation expands the dataset and helps the model perform more accurately. Convolutional neural networks (CNNs) [17] are popular and computationally efficient for classification tasks [6], [13].

In this work, we assess the performance of several deep-learning models currently in use for the identification of malaria from microscopic [18] blood pictures. We also suggest an effective deep-learning [19] approach for the differentiation between malaria cells that are infected and those that are not. The suggested personalized, CNN-based algorithm [20] beats every DL model that has been tested. Bilateral filtering is used in the suggested method to enhance image quality, and image augmentation [21] techniques are employed to improve model generalization. Our model features five convolutional and pooling layers in a sequential CNN architecture. The suggested approach's effectiveness is assessed using a benchmark malaria dataset, and the outcomes are contrasted with those of other, comparable methods that are currently in use. The outcomes demonstrate that our approach outperforms the strategies that were compared and delivers outstanding performance. The primary objective of this research work is to develop a model that produces good accuracy with minimal time by combining an IML algorithm in DL architecture. The proposed work consists of:

- The malaria dataset's parasite and healthy cell photos are transformed into data labels that are employed in SVM to classify cells as having either an infection or not between 0 and 1.
- To improve picture categorization, and visualization and lessen the number of dimensions in the data, t-distributed stochastic neighbor embedding (t-SNE) and principal component analysis (PCA)–2D are used along with SVM.
- The CNN model is developed and refined with key parameters to increase classification accuracy.
- Finally, PCA implemented SVM [22] is used in the final layer of CNN technique, which can improve the level of accuracy of classification.

This is how the remainder of the paper is structured. Section 2 reviews the literature on automated malaria detection. Section 3 provides information on the train and test dataset, data preprocessing, and performance assessment of the suggested improved machine learning (ML) approach, and also, we see the modified DL model architecture. In section 4, the results are discussed. And finally, in section 5 the research work is concluded.

2. RELATED WORK

Masud *et al*. [23] shows how CNNs, a type of DL architecture, can effectively identify malaria in real-time with a high degree of sensitivity and precision. In the research work, a CNN model with two fully linked dense layers and four convolutional blocks was developed by this work. At a resolution of 224×224×3, 27,558 segmented cell pictures were classified using this model. Their suggested model's trainable parameters are less (409 K) than those of other, more complicated models; addressing this model's simplicity will be the first step in solving the overfitting issue. But it is time-consuming and some models require more than a day to train. There may be a need for ensemble methods to improve prediction.

Rajaraman *et al.* [24] authors have detailed about, to classify parasitized and uninfected blood cells and enable the diagnosis of illnesses, feature extractors employ pre-trained CNN-based DL models. The three convolutional layers in the suggested model each have three×three filters with two-pixel steps; the first two convolutional layers have 32 filters each, while the final convolutional layer has 64 filters. Two layers that are completely joined. The segmented cells that make up the model input have a resolution of 100×100×3 pixels. They assessed the ability of pre-trained CNNs AlexNet, visual geometry group (VGG)-16, Xception, ResNet-50, and DenseNet-121 in particular to extract traits from infected and parasitized cells. A random grid search method was used to optimize these models' hyperparameters.

Maqssod *et al.* [6] find the following aspects: a model including five convolutional layers, five max-pooling layers, and two fully-connected layers receive the 125×125×3 input images. The five convolutional layers of the model are equipped with 32, 64, 128, 256, and 300 filters, as well as a 3×3 kernel size and rectified linear unit (ReLU) activation function. By displaying the CNN model's tailored convolutional layers. A 96.82% classification accuracy is obtained in the experiment. The efficacy of the suggested customized CNN model in identifying malaria from microscopic blood smears, as well as the effectiveness of several DL models currently in use for effective malaria detection. Limited availability of datasets. Transferred learning models' limitations. Lack of formal approval consent for publicly available national institutes of health (NIH) malaria dataset. The aim of the research work [25] is that the information was gathered to lessen the workload of microscopists in areas with limited resources and enhance diagnostic precision by employing an artificial intelligent (AI)-driven algorithm to identify and divide up red blood cells. The objective of this work is to establish a new benchmark for AI-based malaria detection efforts and demonstrate that even with a two-layer convolution network, state-of-the-art accuracy can be attained. Although the approach is advertised as having state-of-the-art level accuracy without requiring costly preprocessing, any potential drawbacks or difficulties with practical use are not thoroughly covered. The training error is computed on the learned model after the training phase, which ends when validation accuracy reaches 95%. About 95.4% of the tests were completed with accuracy, which is satisfactory.

In both thick and thin smear microscopic [26] images, typical techniques for image processing have been employed on these images, such as morphological operations and adaptive threshold techniques, to isolate the parasite candidates from the background. When the quality diversity of their input data increases, classical ML algorithms which rely on hand-engineered features find it more difficult to generalize [13], [19], [20], [26]. Lately, there have been noteworthy advancements in the utilization of DL algorithms for many possibilities for medical imaging, namely object recognition [27], picture segmentation and reconstruction [28], and classification tasks. Furthermore, from microscopic pictures of thin and thick blood smears, DL-based CNN algorithms [29] prove to have a greater impact than conventional image processing and improved machine learning (IML) techniques in the detection and recognition of malaria parasites [7], [24].

3. PROPOSED METHOD IML AND MODIFIED DL ARCHITECTURE

Figure 3. demonstrates the procedure of applying train and test data to SVM: with the radial basis function (RBF) kernel, the algorithm can effectively handle non-linearity and is particularly well-suited for dichotomous classification. In addition, resistant to overfitting, even while working with a lot of features. Prepare data-create target variable, and divide the dataset into training and testing data with a split ratio of 0.8, For C and gamma, grid-search on a 10×10 paramgrid produced optimal values of 0.000977 for gamma and 70782 for C, evaluation, print the accuracy and plot of confusion matrix and classification report of F1 score, precision and accuracy. The same procedure is repeated for the t-SNE+SVM classifier and the same parameters are extracted as a result. Both PCA-implemented class object feature visualization and t-SNE-implemented class object visualization is shown and discussed in the section 6.

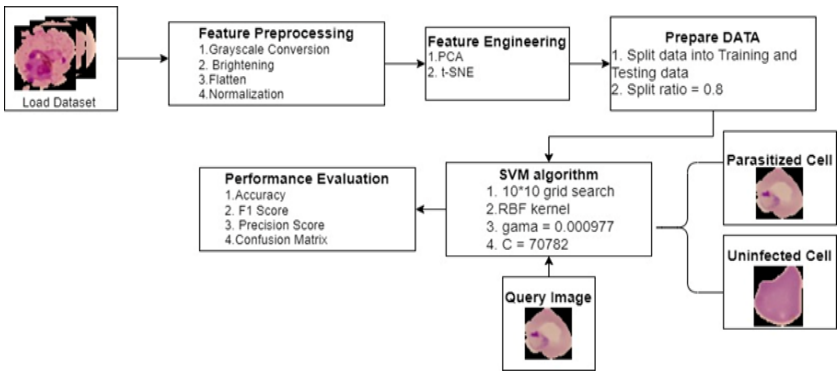

Figure 3. Block diagram for implementing SVM (PCA+t-SNE)

3.1. Data acquisition

We have used a malaria dataset that is publically accessible from the NIH website. This dataset was initially utilized by Rajaraman *et al.* [24], Yu *et al.* [30] and other researchers to detect malaria parasites in blood smear images. The dataset is open access and is made publicly available by US Health Medical Sciences and also modification to the dataset is allowed as per the license agreement. Chittagong Medical College Hospital in Bangladesh gathered the data by taking pictures of slides showing thin blood smears stained with Giemsa from 200 patients, of whom 34% had P. Falciparum infection. Dataset availability-"NIH Malaria dataset", which is accessible to the public on the NIH [31] Figure 4. shows the samples of parasitized and uninfected cells in the dataset used for conducting project.

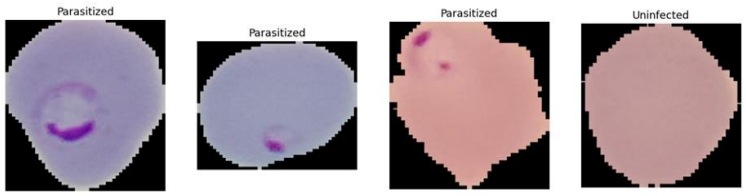

Figure 4. Sample of uninfected and parasitized cells

3.2. Feature preprocessing

The dataset's photos are not all the same size. With three color channels (RGB). For a faster model convergence, we want to resize the photos to 64×64×3, which is the input image size of m CNN model being developed. A few representative photos from the normal and parasitized groups are displayed in Figure 4. To accurately detect malaria parasites in a patient, these patterns in cell pictures will be recognized by the suggested DL model. Figure 5, shows the grayscale version of sample image and Figure 6, indicates brightness adaptation for the grayscale converted image. The darkest sections of the picture are the stains of the affected cells, which could be useful in the algorithm to distinguish between infected and uninfected samples preprocessing steps include converting to a grayscale image, brightening the image background, flattening, and normalization.

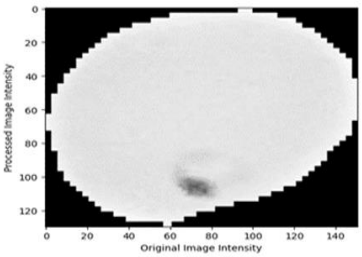

Figure 5. Grayscale image

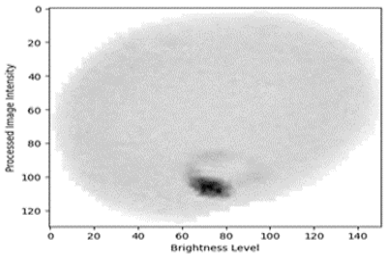

Figure 6. Brightening image background

3.3. Feature engineering

As indicated in the block diagram Figure 6, PCA for feature engineering ought to be applied to the following reasons. This technique can reduce the features by identifying the components that account for a significant portion of the variance. This makes it easier to train the model for the SVM, which is the preferred model class in any instance where PCA is suggested. 95% of the variance is already explained by 96 components. These PCA visual results appear quite promising: when examining the first two main components, the first one displays a light color within the sample area, signifying it is healthy, and the second one displays a black color, signifying it is parasitized.

3.4. Prepare data

Dataset contains 27,558 images in which 13,779 are parasitized images and 13,779 are uninfected images. Table 2, shows the split of data into train and test data. We use the train size of 0.8 and test size of 0.2 that divides the data as Table 2.

Table 2. Dataset preparation

Train data		Test data	
Parasitized	11,023	Parasitized	2,756
Uninfected	11,023	Uninfected	2,756

3.5. SVM algorithm

A technique for binary classification called SVM determines the optimal boundary between several classes and it is mathematically given by (1).

$$Y = w * x + C \quad (1)$$

Where: W, X, C–weight vector, input feature vector, bias term or intercept.
Classes are usually denoted as +1 or -1.
The following is the equation for the PCA transformation of the original data set X to get the reduced data set Z (with k principal components), is mathematically given by (2).

$$Z = X * W \quad (2)$$

Where: X, W – original data matrix, the projection matrix formed by stacking the top k eigen vectors.
The original data matrix is represented by the symbol X, where a feature is symbolized by a column and a sample by a row.

3.6. Modified DL architecture

To improve classification accuracy, the CNN model is created and improved using important parameters. To further improve classification accuracy, the final layer of the CNN model uses PCA-implemented SVM. Figure 7 shows the modified DL architecture to classify the uninfected and parasitized cells.
Input size: (64, 64, 3)
Convolution model – has the following layers:
– Initialising the CNN – sequential.

- Convolution layer – (filters=32, Kernel size=(3,3), stride=(2,2), input shape=64×64×3, activation function=ReLU).
- Maxpooling layer - (Kernel size=(2,2), stride=(2,2)).
- Convolution layer – (filters=32, Kernel size=(3,3), stride=(2,2), input shape=64×64×3, activation function=ReLU).
- Maxpooling layer - (Kernel size=(2,2), stride=(2,2)).
- Flatten layer.
- Dense layer – (units=128, activation function=ReLU).
- Output layer including SVM+PCA fit for classification.

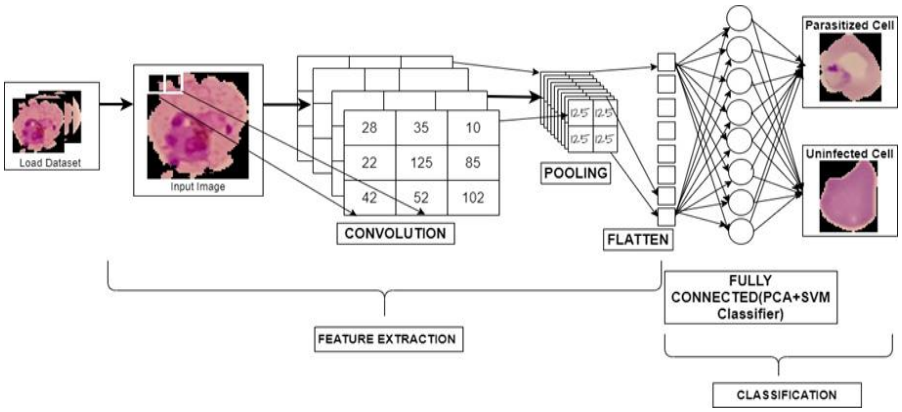

Figure 7. Block diagram of Modified CNN (SVM in the final layer)

4. RESULTS AND DISCUSSION

4.1. t-SNE+SVM classifier

Figure 8 explains the component PCA distribution of uninfected and parasitized cells with accuracy in classification of 86.23%. t-SNE ("t-distributed stochastic neighbor embedding") The figure accounts for a non-linear dimensionality reduction technique that prioritizes preserving pairwise similarities across data points. It models the resemblance between points in the low-dimensional and high-dimensional spaces using a probability distribution. The density of dots in the various t-SNE plot regions is used to infer the the concentration of data points.

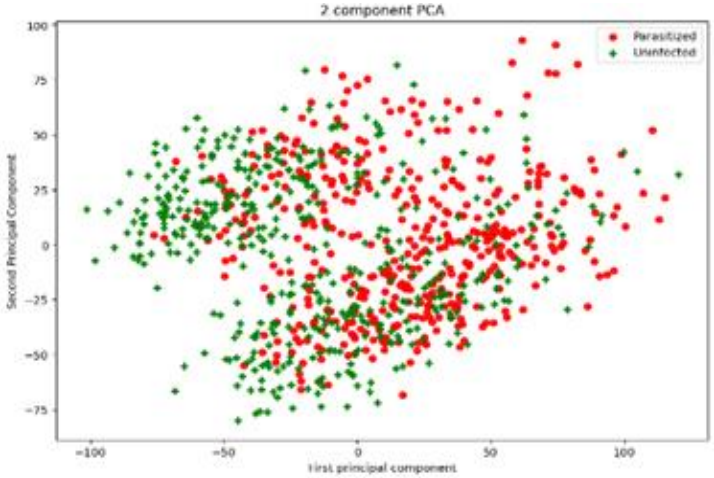

Figure 8. Component t-SNE distribution

4.2. PCA+SVM classifier

Figure 9 explains the component PCA distribution of uninfected and parasitized cells with accuracy in classification of 88.27%. From Figure 9, we can understand using a linear dimensionality reduction technique, one may identify the plot's axes, where the data varies most variably. These constituent parts have orthogonal relationships with one another. Points on the PCA plot that are close to one another are most likely comparable in the high-dimensional space.

CNN: Figure 10, shows the accuracy result of CNN is 97.16% and Figure 11, shows the loss of CNN is 0.1% which is further decreasing. CNN, is used in two distinct ways and is essential to the classification method of DL parasitized and uninfected cells. Accuracy is increased by maximizing and adjusting the receiver operating characteristic (ROC) Curve, and the final layer of CNN uses the SVM (PCA implemented) ML methodology to improve accuracy in classifying parasitized and uninfected cells. CNN by using the SVM in the final stratum of the model for better classification.

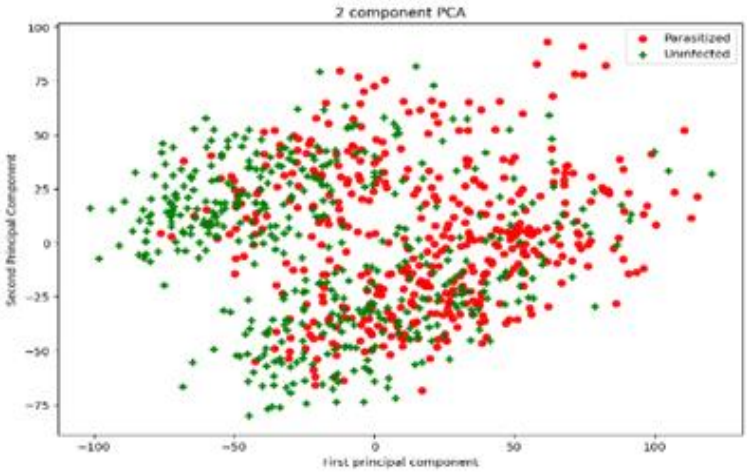

Figure 9. Component PCA distribution

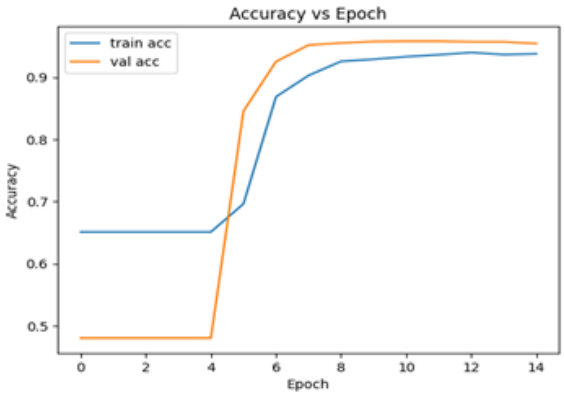

Figure 10. Accuracy plot of CNN

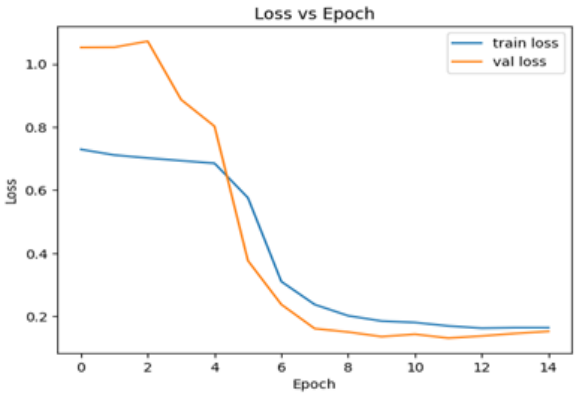

Figure 11. Loss plot of CNN

5. CONCLUSION

Our suggested method includes layer alteration, data augmentation, and feature extraction by integrating the SVM algorithm into the CNN architecture's final layer. DL approaches and sophisticated ML strategies like SVM, SVM+PCA fit, and SVM+t-SNE fit are used in achieving this. SVM yields an accuracy of 84%, SVM+t-SNE fit implementation yields an accuracy of 86.23%, SVM+PCA fit implementation yields an accuracy of 88.27%, and the CNN model yields an accuracy of 97.16% when using the SVM+PCA fit classifier. By using this study, smart hospitals can obtain malaria detection findings that are 97% accurate whereas using rapid antigen testing approaches gives 50% accuracy. The result analysis is evident in the

following graph. Further-using transfer learning techniques, conducting in-depth research on learning rate, altering CNN layers, and implementing cutting-edge DL techniques can all help increase the diagnosing accuracy of malaria. Furthermore, by employing sophisticated clustering techniques, we can eventually use the parasite's detection to ascertain the different stages of malaria depending on the quantity of parasites present in each cell.

REFERENCES

[1] World Health Organization, "World malaria report 2022", 2023. [Online]. Available: https://www.wipo.int/amc/en/mediation/. (accessed: Nov. 08, 2023).

[2] S. T. Agnandji *et al.*, "Prostration and the prognosis of death in African children with severe malaria," *International Journal of Infectious Diseases*, vol. 134, pp. 240–247, Sep. 2023, doi: 10.1016/j.ijid.2023.06.022.

[3] I. Jdey, G. Hcini, and H. Ltifi, "Deep learning and machine learning for malaria detection: overview, challenges and future directions," *International Journal of Information Technology & Decision Making*, pp. 1–32, Jul. 2023, doi: 10.1142/S0219622023300045.

[4] Y. W. Lee, J. W. Choi, and E. H. Shin, "Machine learning model for predicting malaria using clinical information," *Computers in Biology and Medicine*, vol. 129, p. 104151, Feb. 2021, doi: 10.1016/j.compbiomed.2020.104151.

[5] M. Poostchi, K. Silamut, R. J. Maude, S. Jaeger, and G. Thoma, "Image analysis and machine learning for detecting malaria," *Translational Research*, vol. 194, pp. 36–55, Apr. 2018, doi: 10.1016/j.trsl.2017.12.004.

[6] A. Maqsood, M. S. Farid, M. H. Khan, and M. Grzegorzek, "Deep malaria parasite detection in thin blood smear microscopic images," *Applied Sciences (Switzerland)*, vol. 11, no. 5, pp. 1–19, Mar. 2021, doi: 10.3390/app11052284.

[7] A. Rahman *et al.*, "Improving malaria parasite detection from red blood cell using deep convolutional neural networks," *ArXiv Preprint*, 2019, [Online]. Available: http://arxiv.org/abs/1907.10418

[8] A. Shal and R. Gupta, "A comparative study on malaria cell detection using computer vision," in *Proceedings of the Confluence 2022 - 12th International Conference on Cloud Computing, Data Science and Engineering*, IEEE, Jan. 2022, pp. 548–552. doi: 10.1109/Confluence52989.2022.9734136.

[9] S. Saleem, J. Amin, M. Sharif, G. A. Mallah, S. Kadry, and A. H. Gandomi, "Leukemia segmentation and classification: a comprehensive survey," *Computers in Biology and Medicine*, vol. 150, p. 106028, Nov. 2022, doi: 10.1016/j.compbiomed.2022.106028.

[10] S. H. Abdullah, W. M. S. Abedi, and R. M. Hadi, "Enhanced feature selection algorithm for pneumonia detection," *Periodicals of Engineering and Natural Sciences*, vol. 10, no. 6, pp. 168–180, Jan. 2022, doi: 10.21533/pen.v10i6.3397.

[11] A. H. Alharbi, C. V. Aravinda, M. Lin, B. Ashwini, M. Y. Jabarulla, and M. A. Shah, "Detection of peripheral malarial parasites in blood smears using deep learning models," *Computational Intelligence and Neuroscience*, vol. 2022, pp. 1–11, May 2022, doi: 10.1155/2022/3922763.

[12] M. A. A. Jabbar and A. M. Radhi, "Diagnosis of malaria infected blood cell digital images using deep convolutional neural networks," *Iraqi Journal of Science*, vol. 63, no. 1, pp. 380–396, Jan. 2022, doi: 10.24996/ijs.2022.63.1.35.

[13] A. Aljuaid and M. Anwar, "Survey of supervised learning for medical image processing," *SN Computer Science*, vol. 3, no. 4, p. 292, May 2022, doi: 10.1007/s42979-022-01166-1.

[14] M. Alshutbi, Z. Li, M. Alrifaey, M. Ahmadipour, and M. M. Othman, "A hybrid classifier based on support vector machine and jaya algorithm for breast cancer classification," *Neural Computing and Applications*, vol. 34, no. 19, pp. 16669–16681, Oct. 2022, doi: 10.1007/s00521-022-07290-6.

[15] N. Chinnamadha, R. Z. Ahmed, and K. Kalegowda, "Development of health monitoring system using smart intelligent device," *Indonesian Journal of Electrical Engineering and Computer Science*, vol. 28, no. 3, pp. 1381–1387, Dec. 2022, doi: 10.11591/ijeecs.v28.i3.pp1381-1387.

[16] S. Mishra, R. Kumar, S. K. Tiwari, and P. Ranjan, "Machine learning approaches in the diagnosis of infectious diseases: a review," *Bulletin of Electrical Engineering and Informatics*, vol. 11, no. 6, pp. 3509–3520, Dec. 2022, doi: 10.11591/eei.v11i6.4225.

[17] V. Magotra and M. K. Rohil, "Malaria diagnosis using a lightweight deep convolutional neural network," *International Journal of Telemedicine and Applications*, vol. 2022, pp. 1–8, Apr. 2022, doi: 10.1155/2022/4176982.

[18] P. A. Pattanaik, M. Mittal, M. Z. Khan, and S. N. Panda, "Malaria detection using deep residual networks with mobile microscopy," *Journal of King Saud University - Computer and Information Sciences*, vol. 34, no. 5, pp. 1700–1705, May 2022, doi: 10.1016/j.jksuci.2020.07.003.

[19] A. Balaram, M. Silparaj, and R. Gajula, "Detection of malaria parasite in thick blood smears using deep learning," *Materials Today: Proceedings*, vol. 64, pp. 511–516, 2022, doi: 10.1016/j.matpr.2022.04.1012.

[20] N. V. Kumari, M. Garimella, and M. Bhan, "Image labeling using convolutional neural network," in *2023 International Conference on Network, Multimedia and Information Technology, NMITCON 2023*, IEEE, Sep. 2023, pp. 1–5. doi: 10.1109/NMITCON58196.2023.10275862.

[21] D. R. Loh, W. X. Yong, J. Yapeter, K. Subburaj, and R. Chandramohanadas, "A deep learning approach to the screening of malaria infection: automated and rapid cell counting, object detection and instance segmentation using Mask R-CNN," *Computerized Medical Imaging and Graphics*, vol. 88, p. 101845, Mar. 2021, doi: 10.1016/j.compmedimag.2020.101845.

[22] S. Y. Chaganti, I. Nanda, K. R. Pandi, T. G. Prudhvith, and N. Kumar, "Image classification using SVM and CNN," in *2020 International Conference on Computer Science, Engineering and Applications, ICCSEA 2020*, IEEE, Mar. 2020, pp. 1–5. doi: 10.1109/ICCSEA49143.2020.9132851.

[23] M. Masud *et al.*, "Leveraging deep learning techniques for malaria parasite detection using mobile application," *Wireless Communications and Mobile Computing*, vol. 2020, pp. 1–15, Jul. 2020, doi: 10.1155/2020/8895429.

[24] S. Rajaraman, S. Jaeger, and S. K. Antani, "Performance evaluation of deep neural ensembles toward malaria parasite detection in thin-blood smear images," *PeerJ*, vol. 7, p. e6977, May 2019, doi: 10.7717/PEERJ.6977.

[25] S. Kumar, S. Priya, and A. Kumar, "Malaria detection using deep convolution neural network," *ArXiv Preprint*, 2023, [Online]. Available: http://arxiv.org/abs/2303.03397

[26] F. A. Shewajo and K. A. Fante, "Tile-based microscopic image processing for malaria screening using a deep learning approach," *BMC Medical Imaging*, vol. 23, no. 1, p. 39, Mar. 2023, doi: 10.1186/s12880-023-00993-9.

[27] J. G. Kotwal, R. Kashyap, and P. M. Shafi, "Artificial driving based efficientnet for automatic plant leaf disease classification," *Multimedia Tools and Applications*, Oct. 2023, doi: 10.1007/s11042-023-16882-w.

[28] V. D. P. Jasti *et al.*, "Computational technique based on machine learning and image processing for medical image analysis of breast cancer diagnosis," *Security and Communication Networks*, vol. 2022, pp. 1–7, Mar. 2022, doi: 10.1155/2022/1918379.
[29] M. H. D. Alnussairi and A. A. İbrahim, "Malaria parasite detection using deep learning algorithms based on (CNNs) technique," *Computers and Electrical Engineering*, vol. 103, p. 108316, Oct. 2022, doi: 10.1016/j.compeleceng.2022.108316.
[30] H. Yu *et al.*, "Patient-level performance evaluation of a smartphone-based malaria diagnostic application," *Malaria Journal*, vol. 22, no. 1, 2023, doi: 10.1186/s12936-023-04446-0.
[31] "NIH malaria dataset," National Library of Medicine, National Institutes of Health. [Online]. Available: https://lhncbc.nlm.nih.gov/LHC-downloads/downloads.html#malaria-datasets. (accessed: Nov. 08, 2023).

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