



## APPLICATION OF DEEP LEARNING TO SMARTPHONE BLOOD SMEARS FOR IDENTIFICATION OF MALARIA PARASITES

Mrs. S. Mounasri<sup>1</sup>, Dr. V. Anantha Krishna<sup>2</sup>, Devarshetty Bhavani<sup>3</sup>, Chatrathi Mahalakshmi<sup>4</sup>, Begari Bhargavi<sup>5</sup>

**Article History:** Received: 14.02.2023

Revised: 31.03.2023

Accepted: 15.05.2023

### Abstract

In this study, we use smartphones to examine the prospect of automating the identification of malaria parasites amid heavy stains of blood. We developed the deep learning method which is first technique (superset of machine learning) capable of recognizing malarial parasite in thick blood stain images on mobile devices. Below is how our two-stage processing works. To begin, we use a Recursive Global Minimum Screen (IGMS) technique that rapidly screens a thick smear picture for parasite candidates based on intensity. Finally, each potential candidate is assigned to the parasite or background category employing an established Deep Neural Network (CNN). With this publication, the academic community now has access to 1819 images of thick smears or stains taken from 150 patients. In this research, we demonstrate how we fed this data set into our deep learning framework for training and testing purposes.

Results: In a cross- evaluation which is five-folded at the patient level, the tailored CNN model performed exceptionally well in terms of accuracy (93.46percent ) of the respondents 0.32%), region under the curve (98.39percent ) of the respondents 0.18%), sensitivity (92.59percent ) of the respondents 1.27%), specificity (94.33percent ) of the respondents 1.25%), precision (94.25percent ) of the respondents 1.13%), and a negative predictive value (92.74percent ) of the respondents 1.09%). At both the image and patient levels, the automatic parasite identification and ground truth exhibited high correlation coefficients (>0.98), demonstrating the system's effectiveness.

<sup>1</sup>Assistant Professor, Computer Science and Engineering, Sridevi Women's Engineering College, Hyderabad, India

<sup>2</sup>Professor, Computer Science and Engineering, Sridevi Women's Engineering College, Hyderabad, India

<sup>3</sup>Computer Science and Engineering, Sridevi Women's Engineering College, B.Tech IV Year, Hyderabad, India

<sup>4</sup>Computer Science and Engineering, Sridevi Women's Engineering College, B.Tech IV Year, Hyderabad, India

<sup>5</sup>Computer Science and Engineering, Sridevi Women's Engineering College, B.Tech IV Year, Hyderabad, India

Email: <sup>1</sup>swecmouna@gmail.com, <sup>2</sup>krishnaananthav@gmail.com, <sup>3</sup>bhavanidevarshetty516@gmail.com,

<sup>4</sup>mahalakshmi.chatrathi35@gmail.com, <sup>5</sup>begaribhargavi@gmail.com

**DOI: 10.31838/ecb/2023.12.s3.330**

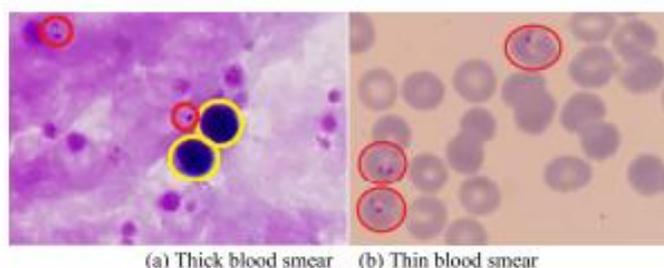
## 1. Introduction

The potential for automating the detection of plasmodium falciparum in thicker blood smears is investigated in this project. We developed the first deep learning method that works on mobile devices and can recognize plasmodium in images of thick plasma smears. Below are the details of our two-stage processing system.

We first use an approach called Iterators Global Minimum Screen (IGMS), which quickly eliminates low-intensity parasite candidates from a thick smear image. At last, a Convolutional Neural Network that has been trained divides potential voters into parasite and host categories (CNN). This publication makes accessible to the scholarly community 1819 images of thick smears collected from 150 patients. In this study, we show how we

fed this data into our deep learning training and evaluation process.

Results: Excellent metrics of the customized CNN model's capacity to differentiate among favourable (parasitic) as well as negative image patches in a five-fold cross-evaluation at the patient level include accuracy (93.46percent ) of the respondents 0.32%), the curve's area under the curve (98.39percent ) of the respondents 0.18%), sensitivity (92.59percent ) of the respondents 1.27%), specificity (94.33percent ) of the respondents 1.25%), precision (94.25percent ) of the respondents 1.13%), as well as negative predictive value (92.74percent ) of the respondents 1.09%). Our system's effectiveness was shown by the Automatic parasite detection yielded very strong correlation coefficients ( $>0.98$ ), both in terms of picture quality and patient health.



Examples of thick and thin blood smears. Red circles are parasites and yellow circles are white blood cells.

life cycles of parasite species. Both thick and thin blood smears need different processing processes when looking for parasites. Evidence of the both lymphocytes i.e., white blood cells (WBCs) either Erythrocytes i.e., red blood cells (RBCs). An early stage in automated parasite detection in thin stains is RBC segmentation, followed by RBC classification as untreated [5-7]. Blood stains that are thicker yet only show off the nuclei of the red and white cells. This necessitates a method for directly detecting parasites, with a typical approach being to preselect candidates before labelling these as parasitic infections or noise. It's not easy to identify parasites since the nucleus of white blood cells as well as other non-parasitic elements may absorb stain.

## 2. RELATED WORK

### "Using repeated blood film testing to confirm a malaria diagnosis,"

If a blood film test comes out negative, current recommendations for diagnosing and ruling out malaria state that further blood film preparation should be done. To determine those who were tested with malaria, we went back 14 years to a state-wide collection of blood results. The majority of patients

or sufferers (93%) were given a diagnosis after the first blood test. Almost seven percent of sufferers had a negative blood film test but later got a positive result. Plasmodium falciparum was found in 66% of sufferers with ms on the first blood film, whereas P. vivax was found in 78% of individuals with an immediate negative blood film result. The majority of the 7 percent group were Australian military personnel who would have been given malaria chemoprophylaxis. Most cases of malaria may be diagnosed with only one positive blood film. Yet, a single blood film examination would miss a substantial number of malaria cases. There is not enough clinical and epidemiological data available at this time to determine who should have one or three blood film exams. Those who have symptoms consistent with malaria should have three blood films taken.

### "Malaria detection using image processing and machine learning,"

More than 400,000 people lose their lives every year, and malaria continues to be a severe threat to public health on a global scale. Contemporary computer technology is playing an important part in many initiatives to combat the illness, alongside biological research and political activities.

Inadequate diagnosis of malaria has been one of the main obstacles to significant mortality reduction. Parasite numbers on microscopic blood slides have been quantified using analysis of image tools and machine learning techniques in an effort to enhance diagnosis. This piece gives a summary of these methods and talks about recent advances in the use of image analysis as well as machine learning to diagnose malaria in microscopic samples. We classify the various methods used in the literature by their respective imaging, image processing, pathogen identification and cell segment, feature calculation, and automated cell categorization methods. Both the thick and thin blood smear imaging methods are described, with references provided for further reading in the accompanying tables. The newest innovations in machine learning and smartphone advanced features for malaria detection in future were also presented.

### **“The Use of Convolutional Neural Networks in Malaria Diagnosis,”**

Worldwide, malaria poses a significant threat to public health. The gold for diagnosing malaria is looking for plasmodium red blood cells in blood smears under a microscope. This method is inefficient, and it relies on the examiner's ability and knowledge to provide an accurate diagnosis. In the past, machine learning-based automated image recognition systems were employed to diagnose malaria from blood stains. The performance in real-world applications has been subpar, unfortunately. In order to automatically distinguish between infections and uninfected single cells in microscopic blood stains on standard microscope slides, this study presents a unique and strong deep learning technique based on the utilisation of convolutional neural networks (CNN). Using 27,578 single-cell images and 10 rounds of cross-validation, our innovative 16-layer CNN model achieved an accuracy of 97.37%. When applied to the same images, a transfers training model achieves just 91.99% accuracy. The CNN model is worthier than the transfer learning model in several respects, including sensitivity (96.99percent ) of the respondents vs. 89.00%), specificity (97.75percent ) of the respondents vs. 94.98%), precision (97.73percent ) of the respondents vs. 95.12%), F1 score (97.36percent ) of the respondents vs. 90.24%), and Matthews correlation coefficient (94.75% vs. 85.25%).

### **3. METHODOLOGY**

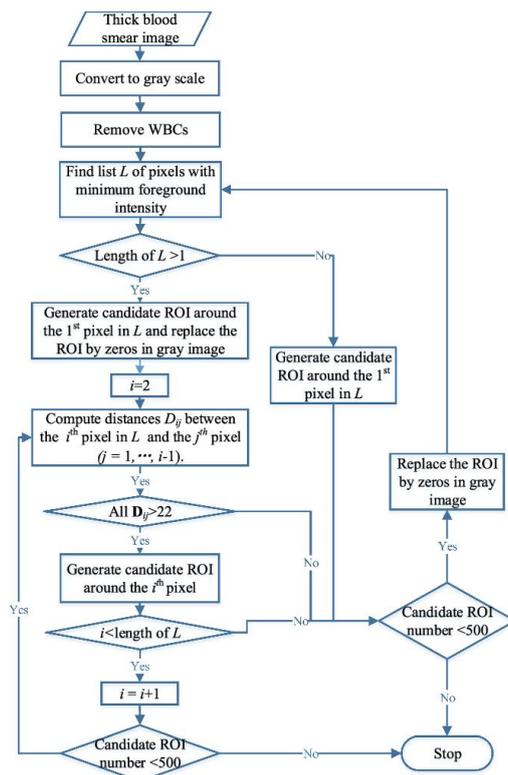
Since we only need to make predictions on a limited subset of pixel patches, we can handle the issue more quickly by decomposing it into a screen and classification phase. sum total processing price. we show how our process flows.

#### **The Parasite Application Process, Part A**

The screening phase narrows the search field and eliminates less probable possibilities before moving on to the next phase. Using a histogram analysis, the parasite candidates with the darkest nuclei are chosen (Fig. 3(a)), while usage of the fact that parasite and WBC nuclei are darker in intensity than the background. We remove WBCs using a filter before we screen for parasite candidates to make sure they don't interfere.

Thus, we generate parasite candidates and use a WBC detection technique to test for them using an intensity-based screening approach. First, the picture of white blood cells (WBCs) is filtered. The parasite option generator then generates regions of interest by isolating minute differences in a very diffuse blood smear.

1) White Blood Cell Detection Figure 3 displays a typical smear picture (a). To begin, we do a color-to-grayscale conversion on the picture. We next use Otsu's approach [29] to the grayscale picture to transform it into a binary mask M1. A broad region of interest (ROI) matching to a field of view appears white (foreground) and white blood cells (WBCs) appear black (background) in this multimodal mask M1 (b). The field of vision mask M2 in Fig. 3 is obtained by plugging the holes in the big ROI region (c). To isolate WBCs, we remove the ROI masks M2 from the ternary mask M1. By filtering out localized noise, we may get clean WBCs. The outcome of this process is seen in Fig. 3(e). To continue with the process of detecting parasites, the values of the WBCs' pixels are cleared to zero. Parasite selection before treatment with Iterative Global Minimum Screening (IGMS): In order to find potential RGB parasites, IGMS first finds the grayscale image's lowest intensity values and works backwards. If just a single pixel can be pinpointed, a 22-pixel-radius circular area is taken from the initial RGB picture and considered for selection as the parasite. A new infection possibility is introduced when all the ranges between the *i*th picture and the previously picked pixels are greater than 22. After a parasite has been suspected, the brightness values inside that area of the grayscale picture will be set to zero in order to ensure that the IGMS procedure converges. After a certain threshold is reached, the screening process is complete.

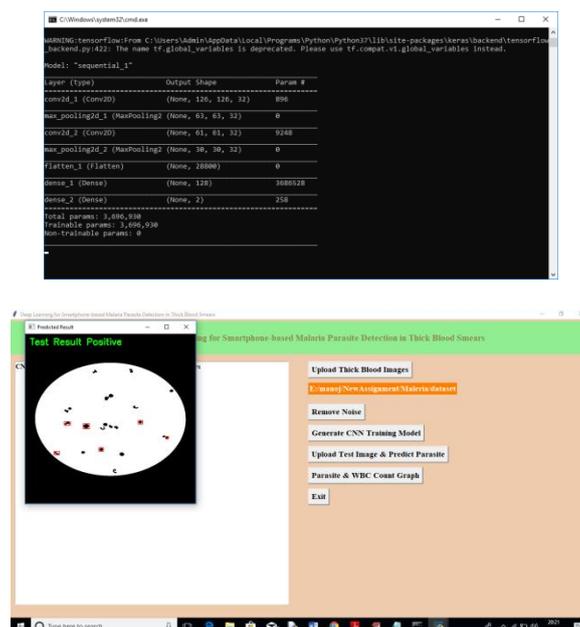


#### 4. RESULT AND DISCUSSION

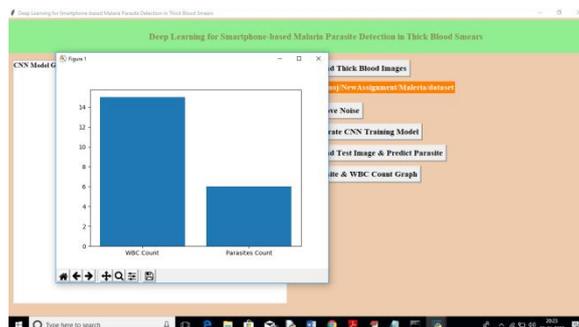
This research describes an idea for employing a Convolution Neural Network (commonly known as "deep learning") to recognize illustrations of parasites of malaria on thick blood stains which runs on mobile phones, but we're creating this solution in Python for the PC platform since we

will not have access to every APIs or mobile sensing equipment.

The accompanying screenshot shows the whole progression of the 7-layer CNN model creation process. To create the first layer, a picture with dimensions of 126 pixels on each side and a color depth of 32 should be used. To submit a test picture and make a disease prediction after developing a model, choose the option to do so.



The uploaded test picture is positive; the red spots indicate parasites and the other colors are white blood cells. We shall treat as parasitic any points whose pixels are too thick. Now choose the "WBC & Parasite Count Graph"



Here, the x-axis illustrates the significant cell types while the y-axis illustrates the total cell count.

## 5. CONCLUSION

In this project, we use deep learning to create an app for smartphones that can detect malarial parasite in thick stain images. Our method for the automated identification of parasites consists of a screening step and a classification step. A quick screening of the whole thick stain image is the first stage in producing parasite candidates utilizing vividness Iterative Globally Minimal Screening (IGMS). Following that, a CNN model created specifically for the task determines whether or not a certain person is a parasite. This method for automated process of malarial parasites identification is validated by experimental data. This is just the second work to build a smartphone for thick blood stain images screening [18], but to the extent possible, it is the first to apply deep learning algorithms for parasite identification in thick stain using smartphone, including assessment at the patient level. In an attempt to remedy the scarcity of training examples for automated malaria analysis in thin blood stain images, we make available our dataset comprising of 1819 photos from 150 patients as a government assistance to the science organization. The next phase of our research will include applying network ensemble techniques to our existing automated parasite identification system for mobile devices.

## 6. REFERENCES

- "World malaria report," WHO, Geneva, Switzerland, 2018.
- WHO, Guidelines for the Treatment of Malaria, 3rd ed. Geneva, Switzerland: World Health Organization, 2015.
- K. S. Makhija, S. Maloney, and R. Norton, "The utility of serial blood film testing for the diagnosis of malaria," *Pathology*, vol. 47, no. 1, pp. 68–70, 2015.
- WHO, Malaria Microscopy Quality Assurance Manual. Geneva, Switzerland: World Health Organization, 2016.
- M. Poostchi, K. Silamut, R. J. Maude, S. Jaeger, and G. Thoma, "Image analysis and machine learning for detecting malaria," *Transl. Res.*, vol. 194, pp. 36–55, Apr. 2018.
- Z. Liang et al., "CNN-based image analysis for malaria diagnosis," in *Proc. IEEE Int. Conf. Bioinf. Biomed.*, Shenzhen, China, 2017, pp. 493–496.
- S. Rajaraman et al., "Understanding the learned behavior of customized convolutional neural networks toward malaria parasite detection in thin blood smear images," *J. Med. Imag.*, vol. 5, no. 3, Jul. 2018, Art. no. 034501.
- L. Rosado, J. M. Correia da Costa, D. Elias, and J. S. Cardoso, "A review of automatic malaria parasites detection and segmentation in microscopic images," *Anti-Infective Agents*, vol. 14, no. 1, pp. 11–22, Mar. 2016.
- P. A. Pattanaik and T. Swarnkar, "Comparative analysis of morphological techniques for malaria detection," *Int. J. Healthcare Inf. Syst. Inform.*, vol. 13, no. 4, pp. 49–65, Oct. 2018.
- S. Kaewkamnerd, A. Intarapanich, M. Pannarat, S. Chaotheing, C. Uthaiyibull, and S. Tongsima, "Detection and classification device for malaria parasites in thick-blood films," in *Proc. IEEE Int. Conf. Intell. Data Acquisition Adv. Comput. Syst.*, Prague, Czech Republic, 2011, pp. 435–438.
- N. S. M. M. Hanif, M. Y. Mashor, and Z. Mohamed, "Image enhancement and segmentation using dark stretching technique for Plasmodium Falciparum for thick blood smear," in *Proc. Int. Colloq. Signal Process Its Appl.*, Penang, Malaysia, 2011, pp. 257–260.
- K. Chakrabortya, "A combined algorithm for malaria detection from thick smear blood slides," *J. Health Med. Inform.*, vol. 6, no. 1, pp. 179–186, Jan. 2015.

- I. R. Dave and K. P. Upla, "Computer aided diagnosis of malaria disease for thin and thick blood smear microscopic images," in Proc. Int. Conf. Signal Process. Integr. Netw., Noida, India, 2017, pp. 4–8.
- M. Elter, E. Hasslmeyer, and T. Zerfass, "Detection of malaria parasites in thick blood films," in Proc. IEEE Eng. Med. Biol. Soc., Boston, MA, USA, 2011, pp. 5140–5144.
- I. K. E. Purnama, F. Z. Rahmanti, and M. H. Purnomo, "Malaria parasite identification on thick blood film using genetic programming," in Proc. Int. Conf. Instrum., Commun., Inf. Technol., Biomed. Eng., Bandung, Indonesia, 2013, pp. 194–198.
- L. Yunda, "Automated image analysis method for p-vivax malaria parasite detection in thick film blood images," Rev. S&T, vol. 10, no. 20, pp. 9–25, Mar. 2011.
- J. A. Quinn, A. Andama, I. Munabi, and F. N. Kiwanuka, "Automated blood smear analysis for mobile malaria diagnosis," in Mobile Point-of-Care Monitors and Diagnostic Device Design, W. Karlen and K. Iniewski, Eds., Boca Raton, FL, USA: CRC Press, 2014, pp. 1–20.
- L. Rosado, J. M. C. Da Costa, D. Elias, and J. S. Cardoso, "Automated detection of malaria parasites on thick blood smears via mobile devices," Procedia Comput. Sci., vol. 90, pp. 138–144, Dec. 2016.
- A. Krizhevsky, I. Sutskever, and G. E. Hinton, "ImageNet classification with deep convolutional neural networks," in Proc. Advances Neural Inf. Process. Syst., Dec. 2012, pp. 1–9.
- Y. Sun, X. Wang, and X. Tang, "Deep learning face representation from predicting 10,000 classes," in Proc. IEEE Conf. Comput. Vision Pattern Recognit., Columbus, OH, USA, 2014, pp. 1891–1898.
- S. Ren et al., "Rich feature hierarchies for accurate object detection and semantic segmentation," in Proc. IEEE Conf. Comput. Vision Pattern Recognit., Boston, MA, USA, 2015, vol. 794, pp. 1–15.
- C. B. Delahunt et al., "Automated microscopy and machine learning for expert-level malaria field diagnosis," in Proc. IEEE Global Humanitarian Technol. Conf., Seattle, WA, USA, 2015, pp. 393–399.
- J. A. Quinn, R. Nakasi, P. K. B. Mugagga, P. Byanyima, W. Lubega, and A. Andama, "Deep convolutional neural networks for microscopy-based point of care diagnostics," in Proc. Mach. Learn. Healthcare Conf., Los Angeles, CA, USA, 2016, pp. 271–281.
- C. Mehanian, M. Jaiswal, C. Delahunt, and C. Thompson, "Computerautomated malaria diagnosis and quantitation using convolutional neural networks," in Proc. IEEE Int. Conf. Comput. Vision Workshops, Venice, Italy, 2017, pp. 116–125.
- K. Torres et al., "Automated microscopy for routine malaria diagnosis: A field comparison on Giemsa-stained blood films in Peru," Malaria J., vol. 17, no. 1, pp. 339–350, Sep. 2018.
- K. He, X. Zhang, S. Ren, and J. Sun, "Deep residual learning for image recognition," in Proc. IEEE Conf. Comput. Vision Pattern Recognit., Las Vegas, NA, USA, 2016, pp. 770–778.
- K. Simonyan and A. Zisserman, "Very deep convolutional networks for large-scale image recognition," presented at the 3rd Int. Conf. Learn. Representations, San Diego, May 7–9, 2015, arXiv1409.1556.
- C. Szegedy et al., "Going deeper with convolutions," in Proc. IEEE Conf. Comput. Vision Pattern Recognit., Boston, MA, USA, 2015, pp. 1–9.
- S. Ioffe and C. Szegedy, "Batch normalization: Accelerating deep network training by reducing internal covariate shift," in Proc. Int. Conf. Mach. Learn., Lille, France, 2015, pp. 81–87.
- N. Srivastava, G. Hinton, A. Krizhevsky, I. Sutskever, and R. Salakhutdinov, "Dropout: A simple way to prevent neural networks from overfitting," J. Mach. Learn. Res., vol. 15, pp. 1929–1958, Jun. 2014.
- S. Ren, K. He, R. Girshick, and J. Sun, "Faster R-CNN: Towards real-time object detection with region proposal networks," IEEE Trans. Pattern Anal. Mach. Intell., vol. 39, no. 6, pp. 1137–1149, Jun. 2017.
- J. Redmon, S. Divvala, R. Girshick, and A. Farhadi, "You only look once: Unified, real-time object detection," in Proc. IEEE Conf. Comput. Vision Pattern Recognit., Las Vegas, NV, USA, 2016, pp. 779–788.
- N. Otsu, "A threshold selection method from gray-level histograms," IEEE Trans. Syst., Man., Cybern., vol. SMC-9, no. 1, pp. 62–66, Jan. 1979.