

An Evaluation of Convolutional Networks for Malaria Diagnosis Based on Empirical Data

Gouri Sankar*

Department of Vector Biology and Control, Rajendra Memorial Research Institute of Medical Sciences, Patna, Bihar, India

Editorial

Anopheles female mosquitoes carrying the parasite protozoa that cause malaria can transfer the disease to people everywhere in the world. Only the parasite Plasmodium, which is further divided into four distinct species, is responsible for its development in humans. Analyzing digital microscopic blood smears is a difficult, time-consuming and error-prone method for identifying malaria parasites. Automation of the process has therefore become more important since it facilitates the time-consuming human review and diagnostic processes. This study compares commercial designs for categorising parasite-free and parasite-affected cells, looks at the four-class classification of Plasmodium falciparum life stages and assesses the robustness of the models using cross-dataset tests on two independent datasets.

The parasite protozoa that cause malaria are conveyed to humans by female Anopheles mosquitoes that have the illness. Malaria is a disease that affects people all over the world. 2019 had an estimated 229 million cases of malaria globally, along with an expected 409,000 fatalities from the disease. Africa accounted for 94% of both malaria cases and deaths. Children under the age of five are the most susceptible group in this situation; they account for 67% of all malaria-related fatalities globally. Human malaria is brought on by parasites of the genus Plasmodium that attack red blood cells. Infected female Anopheles mosquitoes, sometimes known as "malaria vectors," bite humans to transmit the disease. Human malaria is brought on by five different parasite species: *P. falciparum*, *P. vivax*, *P. ovale*, *P. malariae* and *P. knowlesi*. The two most serious threats are *P. falciparum* and *P. vivax*.

The most accurate method for identifying leukaemia, counting blood cells and determining whether a patient has malaria is blood cell analysis on peripheral blood slides under a light microscope. Comparatively speaking, manual microscopic examination of peripheral blood smears for the diagnosis of malaria has benefits such as high sensitivity and specificity. Although a single blood sample must be examined under a microscope for roughly 15 minutes, the microscopist's experience and expertise are the only factors that affect how accurately the diagnosis is made. Without a strict framework to guarantee the accuracy of the diagnosis, the microscopist frequently works alone.

In recent years, a number of methods for the automated identification of malaria parasites have been created. They seek to lessen the drawbacks of manual analysis, which are illustrated in Section-1 and to give a more reliable and uniform interpretation of blood samples while lowering diagnostic costs, which are primarily illustrated by CAD systems. They may combine classic machine learning methods with image processing, as well as deep learning techniques, especially in light of AlexNet's convolutional neural network

*Address for Correspondence: Gouri Sankar, Department of Vector Biology and Control, Rajendra Memorial Research Institute of Medical Sciences, Patna, Bihar, India; E-mail: gourisankar86@gmail.com

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proposal (CNN). Due to the fact that malaria parasites always impact RBCs, any automatic malaria detection system must analyse the erythrocytes to determine whether or not they are infected with the parasite and, if so, to determine the parasite's kind or stage of life.

Regarding the CNN-based approaches, Rajaraman investigated the accuracy of CNN models starting from pretrained networks and proposed a novel architecture trained on a dataset made available by the National Institutes of Health, while Liang proposed a novel model for the classification of single cells as infected or uninfected (NIH). They discovered that some pre-existing networks can be more effective than networks created ad hoc by using TL. ResNet-50 in particular had the best performance. They then continued to advance using a group of CNNs. Rahman additionally tested a number of commercial CNNs in-depth to realise a binary classification by utilising TL techniques with both natural and medical pictures [1-5].

Conclusion

Training on *P. vivax* alone yielded worse outcomes than employing both kinds of parasites as source domains. Overall, the rigorous testing has shown that DenseNet-201 provides the most consistent and reliable performance, positioning itself as a key choice for more improvements and alterations.

Conflict of Interest

None.

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