MicroScan: A Computer Vision Tool To Assist Malaria Microscopy Diagnosis

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The malaria parasite, Plasmodium, infects over 200 million people annually and causes over 500,000 deaths, primarily impacting developing countries. After a decline within the last decade, malaria-related cases have recently resurgence. The NIH has identified malaria diagnosis as a major challenge, stating that the current reliable technique, microscopy, is labor-intensive, time-consuming, variable in quality, and hard to implement in rural regions. The aim of this research is to solve this issue through developing a state of the art, deep learning-based algorithm that can localize and identify malaria infected cells and their stages from a thin blood smear, specifically a microscopic capture of giemsa stained patient blood. A multilayer approach was devised by implementing a faster R-CNN algorithm followed by a convolutional neural network to locate and identify each cell within a thin blood smear and identify it as a: red blood cell, white blood cell, trophozoite, schizont, ring, and gametocyte. The researcher worked with the National Institute of Malaria Research (NIMR) and publicly available data was obtained from BBBC041v1 dataset. The faster-RCNN and CNN architectures were both trained and tested on this data. The deep learning approach obtained precision, sensitivity, specificity, and recall percentages of 98.6%, 0.963%, and 0.98%, 0.844%. The solution developed in this project presents a novel method of malaria diagnosis that eliminates the issues present in the current methods. This project has the potential to be implemented in portable microscopes and can save lives and improve healthcare outcomes in developing countries.

Awards Won: