Diagnosis of Malaria with a Lightweight Deep Convolutional Neural Network on a Raspberry Pi

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Malaria is a parasitic infection spread via mosquito bites. It is a major health threat. According to the World Health Organization's 2019 World Malaria Report, there were 228 million cases of malaria in 2018 which caused an estimated 405,000 deaths in total. However, most cases of malaria happen in Sub-Saharan Africa and Southeast Asia, places which do not have adequate medical care and experienced personnel. The traditional method of diagnosis is by visually reviewing blood cell image under a microscope. However, the current diagnosis method is inefficient, and the accuracy and consistency of the diagnosis depends on the experience of the individual microscopist. Therefore, a high-accuracy, low-cost, and high-efficiency malaria diagnosis system was created using a Convolutional Neural Network implementing MixNet-S, an architecture which uses a mix of different kernel sizes with a depthwise separable convolution to minimize the parameters and computations while achieving high accuracy. The model was trained on data from the National Institute of Health's Malaria Screener Research Activity. After designing an architecture implementing MixNet, fully-connected layers and Gaussian dropout, the model was trained using grid search hyper-parameter optimization. In the end, the diagnosis accuracy per blood cell is 97.02%, an astounding result given the size of the model. The technology was integrated onto the Raspberry Pi to further reduce cost and ease implementation of the model. The system took 0.5 seconds to diagnose each image, and costed around 91 dollars. The exceptional performance of the model given its small size shows that it can be deployed to rural malaria-endemic areas to ease diagnosis of malaria from blood slides.

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