Deep Convolutional Neural Networks for Microscopy-Based Point of Care Diagnostics

INTRODUCTION

Point of care diagnostics can be applied to different practical problems.The problems may addresses to low income,high disease burden areas all such problems can be solved using the microscopy based point of care diagnostics. Here we evaluate the performance of deep convolutional neural networks on three diﬀerent microscopy tasks: diagnosis of malaria in thick blood smears, tuberculosis in sputum samples, and intestinal parasite eggs in stool samples. Microscopy is particularly well adapted to low-resource, high disease burden areas, being both simple and versatile; even for diagnostic tasks for which newer technologies are available, e.g. based on ﬂow cytometry or molecular biology, the cost of specialised equipment may render it impractical in such places. In this work, we focus on the development of point-of-care (POC) diagnostics which utilise two relatively common resources: microscopes and smartphones. Smartphones are widely owned across the developing world, and have the capacity to capture, process and transmit images. In principle, any microscopical assessment can be automated with computer vision methods, within the limits of camera optics and the accuracy of image analysis methods. The ﬁeld of computer vision has been signiﬁcantly advanced recently by the emergence of deep learning methods, to the extent that some object recognition tasks can now be automated with accuracy surpassing human capability (He et al., 2015). Rather than relying on the extraction of image features hand-engineered for a particular task, a standard approach in medical imaging, such methods learn eﬀective representations of input images automatically, with successive layers in the model representing increasingly complex patterns. This paper demonstrates the application of deep learning to microscopy-based POC diagnostics, with particular focus on the end-to-end application of these methods in a resource-constrained environment, using images captured by a low cost smartphone microscope adapter developed for this study. We provide experimental results for three diagnostic tests: malaria (in blood smear samples), tuberculosis (in sputum samples) and intestinal parasites (in stool samples). In order to deploy computer vision methods for decision support and automated diagnostics, a suitable deployment platform is needed. While there are a range of digital microscopes and imaging solutions, they tend to be costly, or limited to particular models of microscope, and therefore not well suited to this task.

OBJECTIVE

The objective is to evaluate the performance of deep convolutional neural networks on three diﬀerent microscopy tasks: diagnosis of malaria in thick suited to this task. : diagnosis of malaria in thick blood smears, tuberculosis in sputum samples, and intestinal parasite eggs in stool samples.

DATASET DESCRIPTION

Malaria images were taken from thick blood smears and stained using Field stain at x1000 magniﬁcation. The TB images were made from fresh sputum and stained using ZN (Ziehl Neelsen) stain. These were examined under x1000 magniﬁcation. In thick blood smear images, plasmodium were annotated (7245 objects in 1182 images); in sputum samples, tuberculosis bacilli were annotated (3734 objects in 928 images), and in stool samples, the eggs of hookworm, Taenia and Hymenolepsis nana were annotated (162 objects in 1217 images).

ARCHITECTURE

Convolutional neural networks (CNNs) are a form of neural network particularly well adapted to the processing of images. Rather than densely connected layers in traditional networks such as the classic multi-layer perceptron structure, the sharing of weights between many locally receptive ﬁelds means that the number of parameters is relatively low. These locally receptive ﬁelds are convolutions over a small region of the input. Diﬀerent convolution ﬁlters respond to the presence of diﬀerent types of patterns in the input; in the initial layers, these responses may be to edges, blobs or colors, whereas in higher levels, the responses can be to higher-level, more complex patterns. CNNs generally include some combination of the following types of layers.

• Convolution layers are computed by taking a sliding window (the receptive ﬁeld) across the input, calculating the response function at each location for each ﬁlter. Multiple ﬁlters capture diﬀerent types of patterns

• Pooling layers reduce the size of the input, merging neighbouring elements e.g by taking the maximum. This reduces the number of parameters, and hence the amount of computation, as each pooling is done.

• Fully connected layers have connections from all activations in the previous layer to all outputs. This is equivalent to a convolutional layer with one ﬁlter, the same size as the input. A fully connected layer is typically used as the last layer in a CNN, with the output having one element per class label.

In this work, we used networks with four hidden layers: 1. Convolution layer: 7 ﬁlters of size 3×3. 2. Pooling layer: max-pooling, factor 2. 3. Convolution layer: 12 ﬁlters of size 2×2. 4. Fully connected layer, with 500 hidden units.

A particular conﬁguration of layers deﬁnes a loss function for the CNN. This loss function can be computed for a training data set, and minised using optimisation methods. We used the Lasagne1 Python CNN implementation to accomplish this, running on a GPU server. A 50/50 training/testing split was used, and training run for 500 epochs on each dataset.