

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

Introduction:

Point of care diagnostics using microscopy and computer vision methods have been applied to a number of practical problems, and are particularly relevant to low-income, high disease burden areas. In general, deep learning has recently revolutionised the field of computer vision, in some cases surpassing human performance for other object recognition tasks. 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.

Objective:

The objective is to evaluate the performance of deep convolutional neural networks on three different microscopy tasks: diagnosis of malaria in thick blood smears, 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. Finally the intestinal parasites images were captured from slides of a wet preparation, i.e. a portion of stool sample mixed in a drop of normal saline and examined under x400 magnification. The laboratory experts identified bounding boxes around each object of interest in every image. 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 Hymenolepis nana were annotated (162 objects in 1217 images).

CNN Architecture:

For this classification they have designed a CNN architecture with convolution (2 layers), maxpooling and fully connected layers. The input layer is followed by a convolution layer whose size of filters will be 3x3 which consists of 7 filters. The output from convolution will be given to the maxpooling of order 2x2. The following layer will be a convolution

layer whose order is 2×2 with 12 filters in that. After this this is connected to the fully connected layer which consists of 500 neurons. This can be represented as:

1. Convolution layer-I : 7 filters of size 3×3 .
2. Pooling layer: max: pooling, factor 2.
3. Convolution layer-II : 12 filters of size 2×2 .
4. Fully connected layer - 500 neurons.