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

[Re-Written Paper]

INTRODUCTION -

Microscopy method of medical diagnostics is used for various disease diagnostics purpose with various medical condition of patients. There are numerous many methods of detections of diseases which can be considered quite costly when compare to microscopy method of detections of diseases. But this method of detection requires more skilled persons for correct accurate medical diagnostics of samples which is being tested at lab of various patients.

In this “Deep Convolutional Neural Networks for Microscopy-Based Point of Care Diagnostics” paper they are trying to automate the process of microscopic detection & diagnostics with deep-learning technique. This approach of paper with visual recognition & detection which is non-existing one.

OBJECTIVE -

Implementation of Microscopy-Based Point of Care Diagnostics using DCNN for diagnosis of malaria in thick blood smears, tuberculosis in sputum samples, and intestinal parasite eggs in stool samples.

METHODOLOGY -

Using DCNN deep convolutional neural networks to learn to distinguish the characteristics of pathogens in different types of sample images of malaria in thick blood smears, tuberculosis in sputum samples, and intestinal parasite eggs in stool samples.

HARDWARE DESIGN -

3D structure of mobile holding stand which would be fitted over Microscope focusing mobile camera on lens of microscope. As shown in below figure -

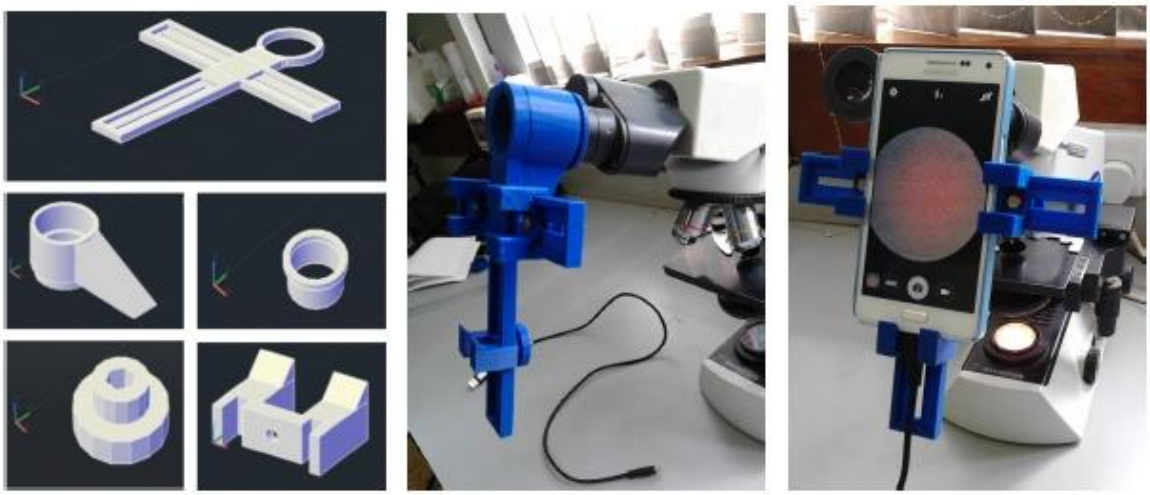

Figure 1: Microscope smartphone adapter: design of components (left), 3D-printed adapter mounted on microscope (center), smartphone inserted into adapter (right).

COMPUTER RECONITION & DETECTION -

Sample images annotated by the skilled lab technicians are used as the training and testing samples. Image recognition accuracy is compared with the testing samples once training is done with the training samples.

CNN model is used on every image related problem. It is also successfully applied to recommender systems, natural language processing and more. The main advantage of CNN compared to its predecessors is that it automatically detects the important features without any human supervision.

CNN is also computationally efficient. It uses special convolution and pooling operations and performs parameter sharing. This enables CNN models to run on any device, making them universally attractive.

All in all this sounds like pure magic. We are dealing with a very powerful and efficient model which performs automatic feature extraction to achieve superhuman accuracy (yes CNN models now do image classification better than humans). Hopefully this article will help us uncover the secrets of this remarkable technique.

A CNN model can be thought as a combination of two components: feature extraction part and the classification part. The convolution + pooling layers perform feature extraction.

Convolution: this method creates a convolutional layer. The first parameter is the filter count, and the second one is the filter size. We use *relu* non-linearity as activation. We also enable padding.

MaxPooling: creates a maxpooling layer, the only argument is the window size. We use a window as it's the most common. By default stride length is equal to the window size, so we don't change that.

Flatten: After the convolution + pooling layers we flatten their output to feed into the fully connected layers .

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.

Architecture -

DCNN Model 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.

Implementation over GPU for Lasagne Python -

Training/Testing split - 50/50

Training epochs - 500 (each dataset).

Tuberculosis Model -

Neural Network with 27448 learnable parameters

Layer information

#	name	size
0	input	3x20x20
1	conv1	7x18x18
2	pool1	7x9x9
3	lstm	7x50

4 output 2

Intestinal Parasite Model -

Neural Network with 356234 learnable parameters

Layer information

name size

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0 input 3x60x60

1 conv1 7x56x56

2 pool1 7x28x28

3 lstm 7x100

4 output 2

Plasmodium Model -

Neural Network with 386046 learnable parameters

Layer information

name size

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0 input 3x20x20

1 conv1 7x18x18

2 pool1 7x9x9

3 conv2 12x8x8

4 hidden3 500

5 output 2

Generation of training/testing set data -

Each image collected was downsampled and then split up into overlapping patches, with the

downsampling factor and patch size determined by the type of pathogen to be recognised

in each case.

Because most of each image does not contain pathogen objects, the potential number of negative patches is usually disproportionately large compared to the number of positive examples.

Two measures were taken to make the training and testing sets more balanced.

First, negative patches were randomly discarded so that there was at most 100 times the number of positive patches.

Second, new positive patches were created by applying all combinations of rotating and flipping, giving 7 extra positive examples for each original.

Detection of pathogen objects in test images -

Many overlapping patches for each actual object in the test image, with a small stride is used while creating the patches, with high degree of overlap. For this reason, non-maximum suppression is used with the aim of having one activation per object within the test image. This works by first finding overlaps amongst the selected patches in the test image, then for those which overlap beyond a certain extent, choosing the one with the highest probability and suppressing the others.

DATASET DESCRIPTION -

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),

In stool samples, the eggs of hookworm, Taenia and Hymenolepsis nana were annotated (162 objects in 1217 images).

Annotation objects in .xml file for .jpg file correspondingly.

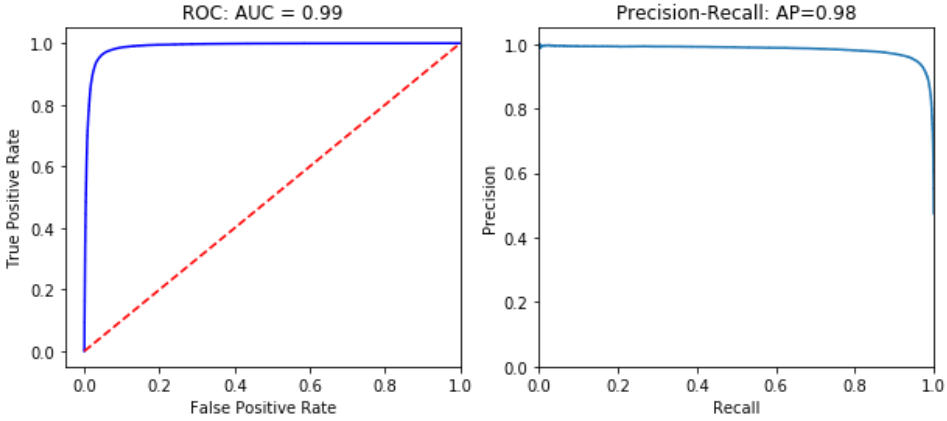
RESULTS -

The trained networks is used in test sets data.

Receiver Operating Characteristics and Precision-Recall curves are shown for each case is given below -

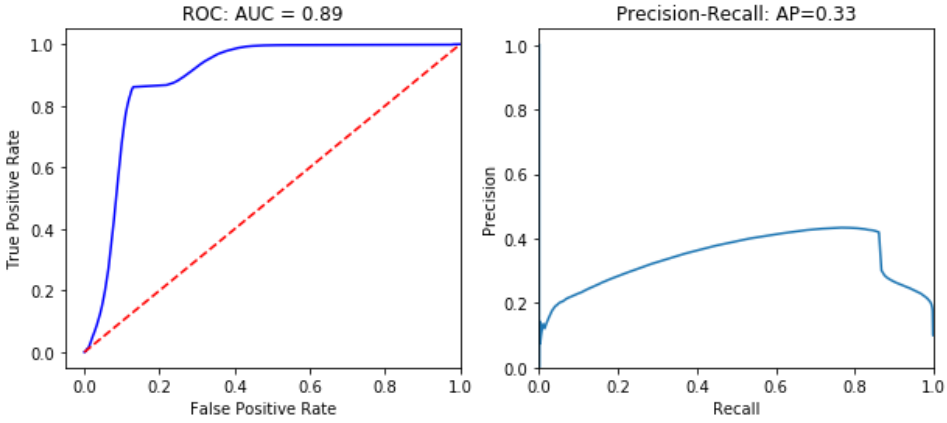
Tuberculosis Model -

Tuberculosis -> 315,142 test patches (9.0% positive)



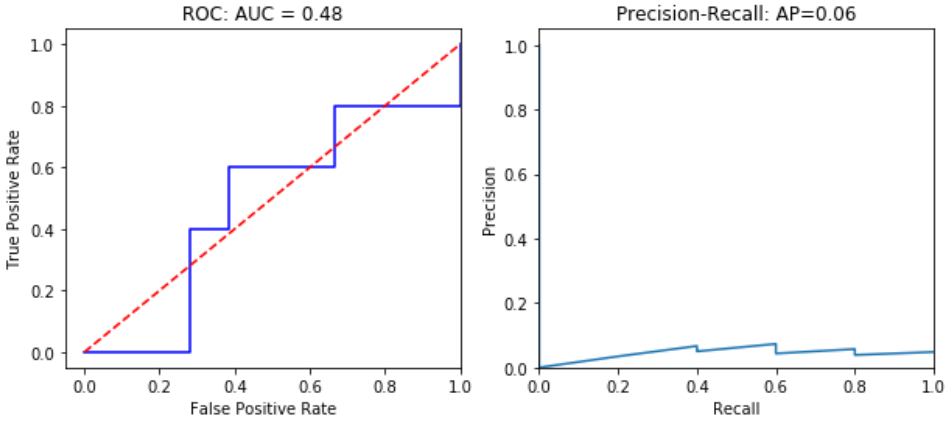
Plasmodium Model -

Plasmodium detection -> 261,345 test patches (11.3% positive)



Intestinal Parasite Model -

Hookworm -> 253,503 patches (0.4% positive).



REFERENCE -

[1.]

Title -

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

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,William, Lubega ,Alfred Andama

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