

# A SLIDING WINDOW APPROACH FOR MALARIA DETECTION IN THIN BLOOD FILM IMAGES

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## Abstract

Deep Learning models have shown great success in a lot of tasks, however a reliable state-of-the-art model in biomedical imaging has not yet been achieved. In this work, we tackle the complicated task of detecting infected malaria cells in a thin blood film. One of the major drawbacks of research in biomedical imaging is the lack of standardized data. In our work, we have introduced a standardization pipeline and also defined a LeNet based sliding-window approach to identify the infected malaria cells.

## Introduction

Malaria detection is a very challenging task that conventionally involves a lot of expertise. However, due to the abundance of data available, there have been attempts to automate that process. Previous attempts to automate the process of identifying and quantifying malaria have used complex workflows for image processing and machine learning classification using features from a predetermined set of measurements (intensity, shape, and texture). However, none of these methods have gained major traction because of a lack of generalizability and difficulty of replication, comparison, and extension. Algorithms cannot be reimplemented with certainty nor extended because authors do not generally make functioning code available. Authors also rarely make their image sets available, which precludes replication of results. The lack of a standard set of images nor standard set of metrics used to report results has impeded the field.

In this work, we have presented a standardized pipeline for converting images to a standard representation using certain preprocessing techniques. We have also demonstrated the efficacy of Deep Learning models in identifying the infected malaria cells in a thin blood film image.

## Related Work

The task of segmentation is typically defined as identifying the set of voxels which make up either the contour or the interior of the object(s) of interest. Segmentation is the most common subject of papers applying deep learning to medical imaging, and as such has also seen the widest variety in methodology, including the development of unique CNN-based segmentation architectures and the wider application of RNNs.

The most well-known, in medical image analysis, of these novel CNN architectures is U-net, published by [5]. The two main architectural novelties in U- net are the combination of an equal amount of upsampling and downsampling layers. Although learned upsampling layers have been proposed before, U-net combines them with so-called skip connections between opposing convolution and deconvolution layers. This which concatenate features from the contracting and expanding paths. From a training perspective this means that entire images/scans can be processed by U-net in one forward pass, resulting in a segmentation map directly. This allows U-net to take into account the full context of the image, which can be an advantage in contrast to patch-based CNNs. Other authors have also built derivatives of the U-net architecture; [3], for example, proposed a 3D-variant of U-net architecture, called V-net, performing 3D image segmentation using 3D convolutional layers with an objective function directly based on the Dice coefficient. [1] investigated the use of short ResNet-like skip connections in addition to the long skip-connections in a regular U-net.

## Key Contributions

The objective of the project is to develop a sliding-window based Neural Network approach to performing Semantic Segmentation on Microscopy Images of Blood Samples. This study also aims at demonstrating the efficacy of the model by comparing the results with a powerful baseline. The tasks to be performed to realize the objective are as follows:

- Develop a training balanced dataset to categorise between the infected cells and non-infected regions
- Develop a sliding window approach to make the classifier work on every pixel of the entire image
- Select a simple Neural Network Image Classification Model with a simple yet powerful architecture to give accurate segmentation results

## Proposed Method

The approach basically consists of a sliding-window or a patch-based approach. The algorithm essentially consists of the following steps:

1. Apply the Stain Normalization Technique on the original input image
2. Select a patch of the image around a given pixel
3. Pass the patch through the classifier model for pixel-wise classification
4. Repeat the same process iteratively for all the pixels in the image

One may notice that depending on the size of the patch, a certain number of pixels at the border regions may be left out. This is a valid concern, but it is accounted for by the fact that in the images, none of the Objects of Interest are present at the border regions. Further, the classifications obtained at the borders can be extended to accomodate the size of the entire image.

Due to the difference in images in terms of brightness, intensity of stains, etc., we use staining techniques to ensure that all images are consistent in their appearance. We analysed the performance of our model using two staining techniques: Reinhard et al[4], Macenko et al[2] and Vahadane et al[6].

We chose LeNet as the Convolutional Neural Network architecture. LeNet is composed of 7 layers(not counting the input), all of which contain the trainable parameters (weights). The LeNet model consists of a series of Convolutional, Max-Pooling and ReLU operations, which finally gives us a 2-d Vector output.

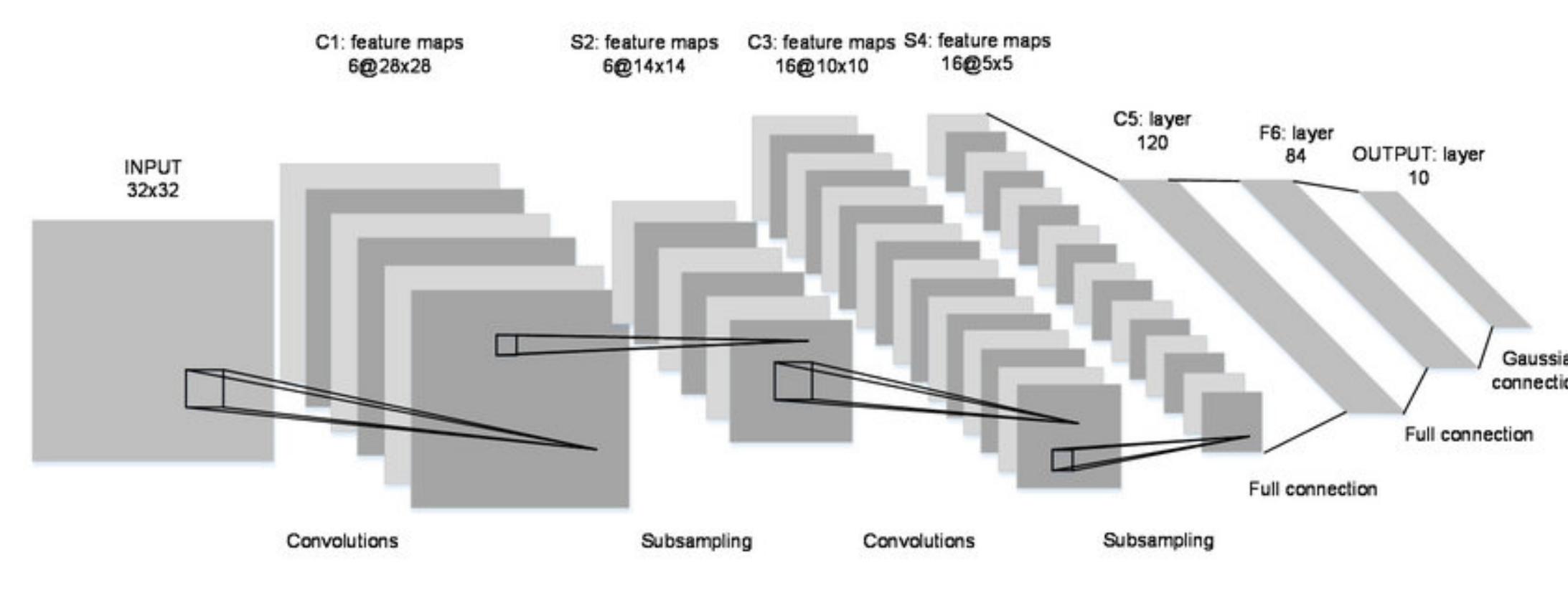


Fig. 1: LeNet Architecture

## Results and Analysis

We noticed that the dataset provided had a lot of variations in terms of the contrast of the stain color with the background, background light and stain ‘noise’. Hence, we first filter the images to select those ones which have significant contrast difference between the infected cells and normal cells which are stained. As a data preprocessing step, we applied stain normalization techniques as defined in [4], [2] and [6] separately. Then for training the model, we created patch images for each of the classes. For Malaria patches, we calculated the mid-point of the bounding boxes provided in the annotation and created a 80x80 patch around the mid-point. For the non-malaria patches, we selected pixels randomly from the non-infected regions of the image and took an 80x80 patch. This step is then repeated for all the images in the dataset. Consequently, 1502 malaria images and 1502 non-malaria images were obtained as a training set.

The LeNet model is then trained over this dataset by using Cross Entropy Loss and Stochastic Gradient Descent Optimization with default parameters for 50 epochs. For obtaining the pixel-level classification images, we iterate over all the pixels in the entire image and at each pixel, collect values of the pixels falling around the pixel in the defined patch size of 80x80. This patch is then passed through the LeNet model and the label with the maximum value is chosen as the pixel label.

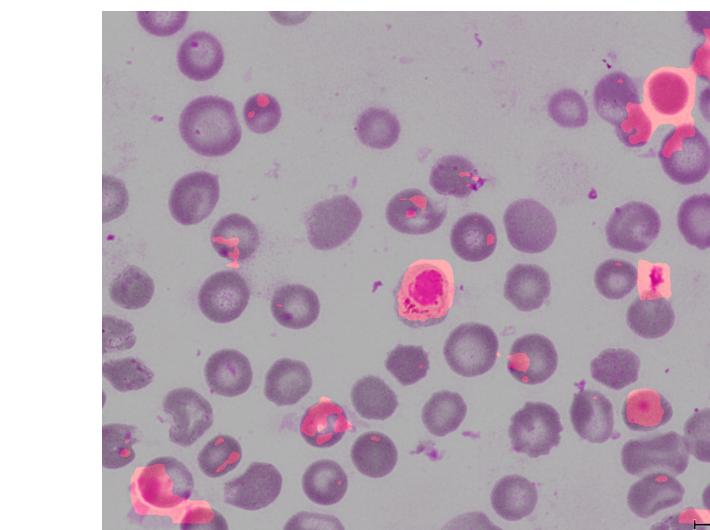


Fig. 2: Macenko

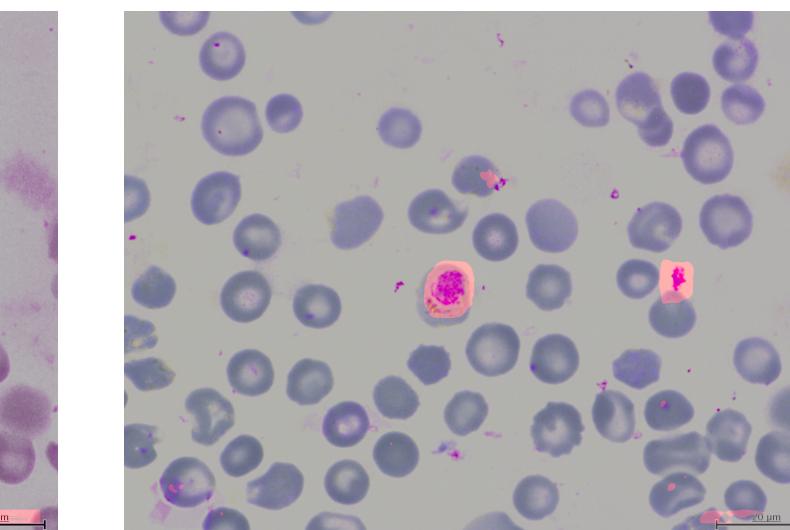


Fig. 3: Reinhard

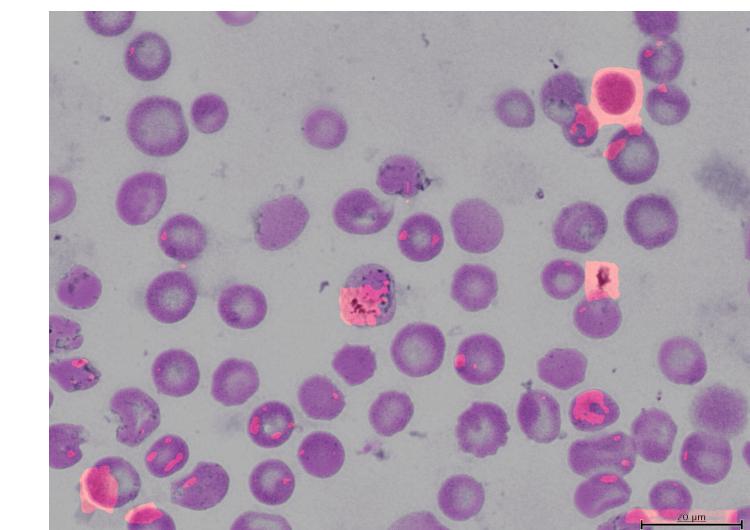


Fig. 4: Vahadane

## Conclusion and Future Works

In this report, the results of the patch-based LeNet architecture for the task of semantic segmentation of Malaria Cells in Thin Blood Films is presented. The results under different stain normalization techniques were compared and the one under Vahadane et al.[6] were found to be the best. In the future, we plan to extend this work by developing image-based approaches rather than patch-based approaches, which will give results near instantaneously.

## References

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