CLASSIFICATION AND DETECTION OF *Plasmodium Vivax* INFECTED CELLS IN BLOOD SMEARS IMAGES

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Paper under double-blind review

ABSTRACT

In Guatemala, the current techniques used for the diagnosis of *P. Vivax* malaria parasite are not very efficient causing a delay in the diagnosis, these techniques are the microscopic examination of the protozoan through two types of blood films: thick blood smear and peripheral smear. The research carried out consisted of creating an automatic detection system in images containing four of the *P. Vivax* parasite, using two different CNN architectures (YOLO and U-Net). The results were satisfactory and the convolutional architecture YOLO managed to classify the trophozoite, schizont and gamete phases of the *P. Vivax* parasite present in blood smear images. Code is available: `https://github.com/ErickDiaz/bioinformatic_thesis_project/tree/dev`

1 INTRODUCTION

According to the World Health Organization (WHO) report, malaria caused 435,000 deaths worldwide in 2017 (WHO, 2018). Currently, the standard method for detecting and diagnosing malaria is through using a microscopic under observation through an extended and smear of Blood colocated on a slide (WHO, 2015). In Guatemala, this type of diagnosis (*P Vivax malaria*) has several disadvantages, trained and experienced microscopist personnel are needed to identify and quantify the parasite in the thick drop (gold standard) and blood smears. There is also a high workload for the staff on the area in which the disease is concentrated; high estimated time in observation of blood films, on average a trained person observes a thick blood film for 10 to 20 minutes, in endemic areas a health center can receive between 200 and 300 weekly blood films, producing ocular fatigue, which is usually is the most influential factor in an incorrect diagnosis. Automation test through CNN networks it could accelerate diagnoses, increase the efficiency and performance of specialists.

2 DATASET

We used image set *P. Vivax* (malaria) infected human blood smears, accession number BBBC041 version 1, available from the Broad Bioimage Benchmark Collection (Ljosa et al., 2012). The images in the dataset contains 1,364 images, with a total of 80,113 labeled cells, different researches contributed labeling each cell in the dataset. These images were contributed by Jane Hung of MIT and the Broad Institute in Cambridge, MA. Each cell in the biological images has a class label an the bounding box coordinates, for the infected cell he have four classes gametocytes, rings, trophozoites and schizonts.

3 METHODOLOGY

We are running multiple experiments using two different CNN architectures and different sets of configurations for each model. For image segmentation, we are using U-Net (Ronneberger et al., 2015) and for object detection and classification, we decided to experiment with YOLO(Redmon et al., 2015). For U-Net we developed the architecture using TensorFlow, for the loss function of the model we used Bray–Curtis dissimilarity and IoU for the cost function. For the training of YOLO model, we used the original repository, after the model was trained with the original dataset we use transfer learning to continue the training with the augmented datasets.

3.1 DATA AUGMENTATION

To increase the training data and remove the imbalance of the dataset for one of the classes and improve the generalization ability of the models, we fist cropped all parasites form images using the bounding box location and augmented these images with rotations, then we generated a method that randomly adds parasites into the training images that had less than four parasites, the method always add the parasite class that has fewer occurrences this runs until the different classes are close to be balanced.

4 RESULTS

In table 1 there is a quantitative comparison of the model results on the test dataset.

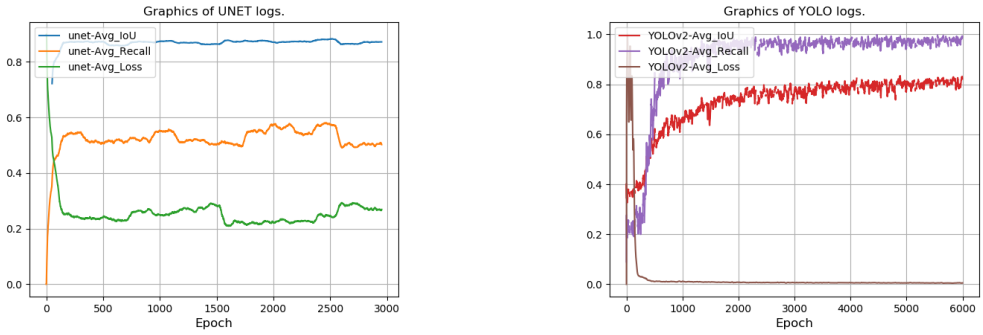

Figure 1: Training models metrics.

Table 1: Quantitative comparison of the architectures.

Model	IoU	Precision	Recall	F1 Score
U-Net	71.1%	27.81%	44.29%	34.16%
YOLO	77.17%	45.41%	3.77%	6.96%
YOLO 1st augmented dataset	77.19%	41.56%	4.08%	7.44%
YOLO 2nd augmented dataset	84.85%	57.26%	5.13%	9.42%
YOLO 3rd augmented dataset	83.66%	46.71%	7.16%	12.42%

5 CONCLUTIONS

We were able to detect malaria parasites in the images, training the models with augmented datasets helped to improve the performance. In the future, we plan to extend this work, gathering our dataset, will be an important step, also creating an ensemble prediction using both models; we will also experiment with different novel models. Once we reach better performance measures we plan to automate the whole process using a robotic arm for manipulating the blood samples, the goal is to automate the complete process.

ACKNOWLEDGMENTS

We thank Jane Hung of MIT and the Broad Institute in Cambridge, for publishing and making available this dataset, and all the researchers that prepared the images.
We thank to BIOCANET ISCB (USA).

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