2017 IEEE/ACM International Conference on Connected Health: Applications, Systems and Engineering Technologies (CHASE)

Malaria Parasite Detection and Species Identification on Thin Blood Smears using a Convolutional Neural Network

Kristofer E. delas Peñas[1], Pilarita T. Rivera[2] and Prospero C. Naval, Jr.[1]
[1] Department of Computer Science, College of Engineering, University of the Philippines, Diliman
[2] Department of Parasitology, College of Public Health, University of the Philippines Manila
Email: pcnaval@dcs.upd.edu.ph

***Abstract*—To aid efforts for the total elimination of malaria, effective and fast diagnosis of cases must be done. The gold standard for malaria diagnosis is microscopy. This process becomes problematic when cases are in far-flung rural areas as experts may not be present in these areas to make such diagnosis. Automation of the diagnostic process with the use of an intelligent system that would recognize malaria parasites could solve this problem. This study proposes such an intelligent system, detecting malaria parasites through images of thin blood smears. We used a Convolutional Neural Network in this research where we obtained an accuracy of 92.4% and sensitivity of 95.2% for malaria parasite detection, and an accuracy of 87.9% for identifying the two species *Plasmodium falciparum* and *Plasmodium vivax*.**

***Keywords*—Malaria, Intelligent Systems, Convolutional Neural Network**

I. Introduction

In 2012, the World Health Organization (WHO) estimated 207,000,000 cases of malaria globally, 627,000 of which resulted in deaths among African children [2]. In the Philippines, malaria is considered to be the 9th leading cause of morbidity, with 58 out of the 81 provinces being malaria-endemic [3].

Among the major obstacles for malaria eradication are the remote location of the majority of malaria cases and the lack of trained individuals that can analyze blood samples using microscopy. This is where automated systems for diagnosis come in. Instead of manually going over a blood sample and checking for the presence of malaria parasites, photographs of the sample viewed from the microscope are analyzed by an intelligent system. With such systems, the remote location of malaria cases becomes less of a problem if such systems become publicly available as trained microscopists and doctors need not be physically present to come up with a diagnosis.

This study aims to build one such system - an intelligent system can detect the presence of malaria parasites and identify the specific species in blood samples.

II. Malaria Parasites

Plasmodium vivax is the cause of most malaria cases, accounting for around 80% of the total infections in Asia and America. This species causes benign tertian malaria with frequent lapses [4].

The parasitemia of *P. vivax* is usually not heavy. In blood samples, infected erythrocytes would contain only one trophozoite, and with less than 5% of the cells being infected. In its trophozoite stage, the structure of the parasite is well-defined, having a prominent central vacuole. The cytoplasm is distinguishably blue, while the nucleus red in stained films. An infected erythrocyte would be slightly enlarged and exhibits red granulations called *Schuffner's dots* [4].

Plasmodium falciparum is most distinguishable for its sickle-shaped gametocyte. This species is the most pathogenic of all species, posing high rate of complications and fatality if left untreated [4]. The trophozoites of this species appear as tiny ring-forms usually attached near the walls of the erythrocytes. Many of the ring-forms have binucleate rings (double chromatin dots) [4].

The diagnosis of malaria is done through demonstration of malaria parasites in the blood by preparing blood smears. A thin smear is used in determining the infecting species. This type of smear is prepared from capillary blood drawn from a fingertip, applied to a slide, and stained by one of the Romanowsky stains such as *Giemsa* to highlight the parasite [4].

Figure 1 shows an example of a thin smear.

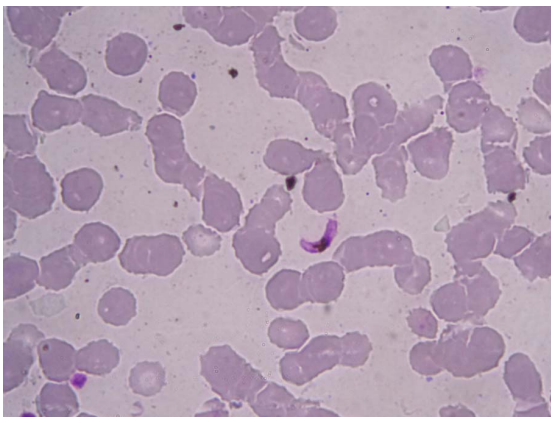

Fig. 1. A thin smear

Treating malaria requires administration of anti-malarial drugs. The infecting species of malaria parasite plays a significant role in the course of treatment. The two species *P. falciparum* and *P. vivax* are treated differently, hence the need for species identification.

978-1-5090-4722-2/17 $31.00 © 2017 IEEE
DOI 10.1109/CHASE.2017.51

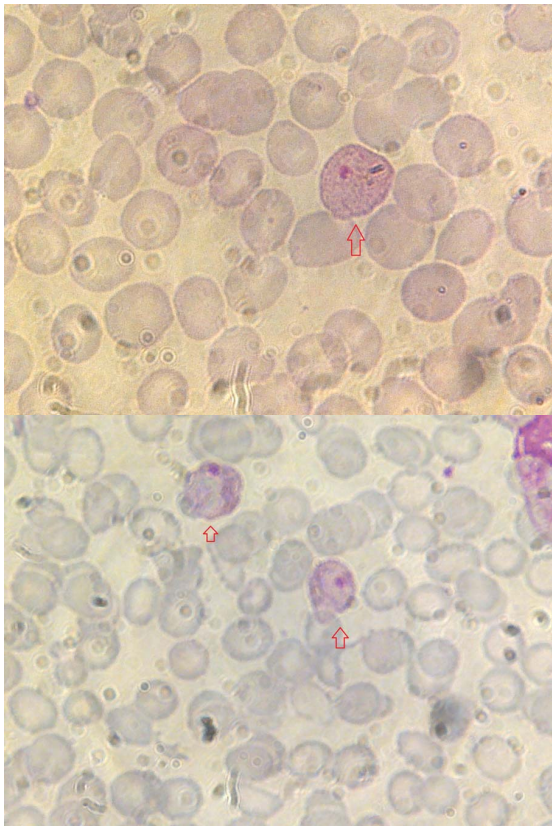

Fig. 2. Difference in background color of two images of blood smears

III. State of the Art Intelligent Systems for Malaria

Several intelligent systems for malaria have been developed that aims to automate the diagnosis and classification of blood slides, to countercheck human diagnosis, and even eliminate human errors. To do this, images of the slides viewed from a microscope need to be taken and used as input for these systems.

Various techniques in digital image processing are employed for malaria detection and classification. The initial step in detecting the presence of malaria parasites in an image of a blood sample is to segment possible regions of interest (foreground) from the background. The background for the malaria images is a large region of stained blood sample, and depending on the quality of staining performed and the image captured, the color of the background varies from a bright pink to a dull gray tone. Figure 2 shows very different background colors between two image samples. One research focused on segmentation is done by Makkapati and Rao [5]. The research addressed the problems due to variability and presence of artifacts in microscope images of blood samples. The authors used a segmentation scheme based on the HSV color space to separate the red blood cells (RBC) and parasites. This scheme focuses on detecting the parasites' chromatin within the RBCs once the segmentation was done. The HSV color space was used since the RGB color space is not intuitive for processing, unlike HSV which offers a representation that could be used to easily identify among color families even with varying image qualities. Given 55 test images, the specificity and sensitivity of this approach are 83% and 98% respectively.

A similar research was done by Anggraini, et. al [6]. The proposed algorithm does not consider for segmentation the hue of the individual pixels of the image. Instead, a global threshold was obtained by varying the contrast among pixels, and was used to classify each pixel as belonging to either foreground or background. To do this, pre-processing of the images to obtain "uniform" images was done by converting all input images to grayscale. The images were then filtered to normalize the pixel intensities around a median value before obtaining the histogram of the individual images and expanding each until the two intensity classes, foregound and background, become distinct given a threshold intensity.

Some researches employ more morphological techniques than the two previous ones. The work done by Das, et. al [7] uses thresholding, marker-controlled watershed algorithm, and Haralick textural feature extraction. Another work, by Kareem, et. al [8] also uses morphological image transformations to infer malaria parasites from Giemsa-stained blood films. First, a grayscale image is dilated and eroded to highlight the parasites and platelets (foreground). The cells and parasites are then identified based on a combination of annular ring ratio method, size, and intensity variation.

In conjunction with the techniques explored in the previously mentioned researches, machine learning techniques serve as the core for decision systems for malaria. Some, like Das et. al [7], employ generative methods such as multivariate regression models. Anggraini, et. al [6], used Bayes decision theory to classify images after segmentation.

Other researchers use discriminative models to classify malaria images. One such research was done by Barros, et. al [9]. This particular research used artificial neural networks, aside from Bayesian networks, to construct a model that can diagnose asymptomatic malaria.

Pinkaew et. al explored the use of Support Vector Machines in malaria classification [10]. Their work used statistical measurements such as mean intensity, standard deviation, kurtosis, skewness and entropy to characterize regions of interest. Training on 40 *P. falciparum* and 25 *P. vivax* images, the study's SVM model with radial basis kernel gained an accuracy of 85.71% in identifying *P. falciparum* and 78.72% in identifying *P. vivax*.

IV. Convolutional Neural Network

Convolutional Neural Networks or CNNs (shown in Figure 3) are very similar to ordinary artificial neural networks having trainable weights on sets of neurons given some inputs and expected outputs. One key difference is that in CNNs, layers of convolution and pooling are employed. These layers create feature maps that are sensitive to certain patterns that characterize the input images.

Different architectures over the few years of active research on CNNs were proposed. These architectures mainly differ on the number of layers for each type used [11]. GoogLeNet employs the Inception architecture that aims to lessen the computation complexities of its precursor architectures. For

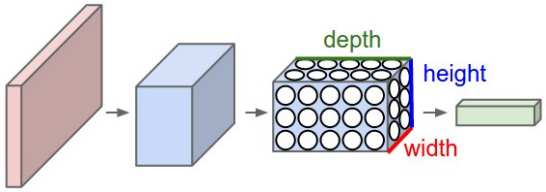

Fig. 3. Convolutional Neural Network
Source: CS231n Convolutional Neural Networks for Visual Recognition.
URL: *http://cs231n.github.io/convolutional-networks/*

Number of Images in Dataset	363
Image Resolution	2592 x 1944 pixels
P. *falciparum* : P. *vivax* ratio	221:142

TABLE I. THE DATASET USED IN THE STUDY

example, AlexNet uses 60 million parameters while VGGNet requires 3x more. This large set of parameters directly translates to large computational cost, slower training and classification [12, 13].

Inception tries to minimize the set of parameters by factorizing convolutions with large filter size into a set of multiple convolutions with small filter sizes. For example, a convolution of 5x5 convolution is replaced by two 3x3 convolutions in Inception. The developers of Inception have shown that this replacement is indeed less computationally complex than the original convolution. With only around 13 million parameters, Inception (version 3) outperformed VGGNet, with only 3.58% top-5 error and 17.2% top-1 error. [13]

V. Methodology and Results

A. Dataset

The dataset used is composed of 363 images. The smears used for the images were obtained during a field study done in Palawan, Philippines conducted by some researchers of the College of Public Health, University of the Philippines. Images were taken using a digital single-lens reflex camera attached to a microscope with a resolution of 2592 x 1944 pixels at 100X magnification using an oil immersion objective lens.

To fully capture the entire erythrocytic schizogony of malaria parasites, key lifecycle stages (trophozoite and gametocyte) were represented in the dataset.

Images of *P. vivax* (142 images) were included in the dataset to effectively discriminate between *P. falciparum* (221 images) from this species.

Table I summarizes the information on the dataset used in this study.

B. Data Preprocessing

Makkapati and Rao [5] have shown that the HSV color space is than the RGB color space for the segmentation task. In this study, the saturation channel was used since it gives the best contrast between parasite and non-parasite regions in the images.

A series of morphological transforms were done for data preprocessing to enhance the digital images before segmentation.

Each image underwent image opening and closing using a circular structuring element. This step ensures that salt-and-grain noise that would otherwise register as candidate regions were removed.Figure 4 shows one image before and after image opening and closing.

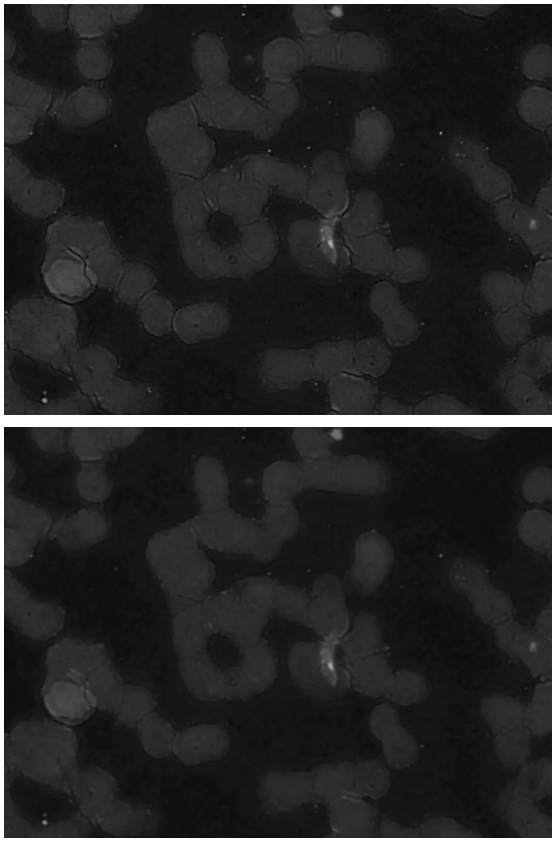

Fig. 4. Image before and after image opening and closing

The mean and standard deviation of each image is then computed and subtracted from the image. Figure 5 shows one image before and after subtraction of mean and standard deviation.

Finally, binary thresholding was done. Figure 6 shows one image before and after thresholding.

Figure 7 shows an image before and after all preprocessing steps.

C. Image Segmentation

After the preprocessing step, segmentation was done through Connected Components Analysis. For each region with area greater than 500 pixels, a square bounding box was used for segmentation. Figure 8 shows some segmented regions. These regions vary in size and required rescaling to a standard size of 299x299 pixels for the succeeding steps.

D. Data Augmentation

As is to be expected, segmentation would yield far numerous non-malaria regions than malaria regions. This poses a

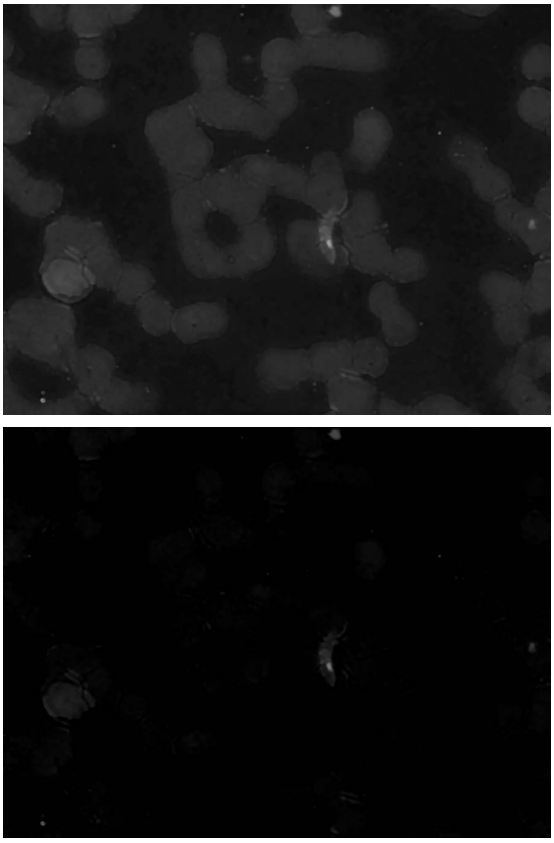

Fig. 5. Image before and after subtraction of mean and standard deviation

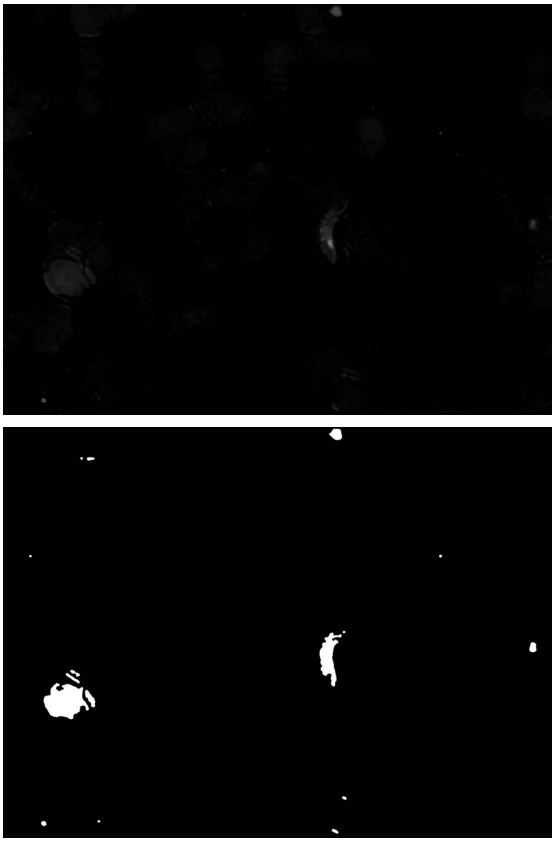

Fig. 6. Image before and after binary thresholding

problem especially for classifiers relying on minimization of some loss function. This imbalance could result in converging to a local minimum. However, data augmentation helps prevent this by artificially creating additional instances through transformations such as rotation, translation, and scaling. To augment the dataset, rotation by 15 degree increments were done on all malaria regions. Figure 9 shows a malaria region rotated 23 times to produce additional malaria instances.

E. Classification

A Convolutional Neural Network was used for malaria species classification. Utilizing transfer learning on Inception v3 convolutional neural network, a model was built to classify the Plasmodium species. After creating bottleneck values from the convolutional layers of the network, the fully-connected layers was retrained to classify the species.

Train accuracy	94%
Cross entropy	0.22
Validation accuracy	87.6%

TABLE II. TRAINING AND VALIDATION RESULTS OF THE MODEL TRAINED TO DETECT PLASMODIUM PARASITES

Figure 10 shows the training accuracy per epoch of the CNN trained to classify species. Table II shows the training results of the model. Positive detection was simplified to classification to any from one of the three classes: vivax, falciparum gametocyte and falciparum ring-form. The model obtained a training accuracy of 94% in detecting parasites on images and with a 87.6% validation accuracy.

Running on the test set, the model obtained an accuracy of 92.4% for parasite detection (with 95.2% sensitivity and 84.7% specificity) and 87.9% in species identification. Table III shows the confusion matrix of the CNN trained to identify species on the test set.

	VIVAX	FALCIPARUM GAMETO-CYTE	FALCIPARUM RING-FORM	NEGATIVE
VIVAX	1654	46	92	80
FALCIPARUM GAMETO-CYTE	33	1214	1	24
FALCIPARUM RING-FORM	111	11	1460	129
NEGATIVE	88	26	161	1526

TABLE III. CONFUSION MATRIX FOR CNN TRAINED TO IDENTIFY PLASMODIUM SPECIES

VI. CONCLUSION AND RECOMMENDATION

This study has shown that malaria parasites can be effectively recognized on thin blood smears using a Convolutional Neural Network. The features generated from the convolutional neural network are discriminant attributes for the detection of malaria parasites on images of thin blood smears, obtaining an accuracy of 92.4%. Moreover, the study has also built a

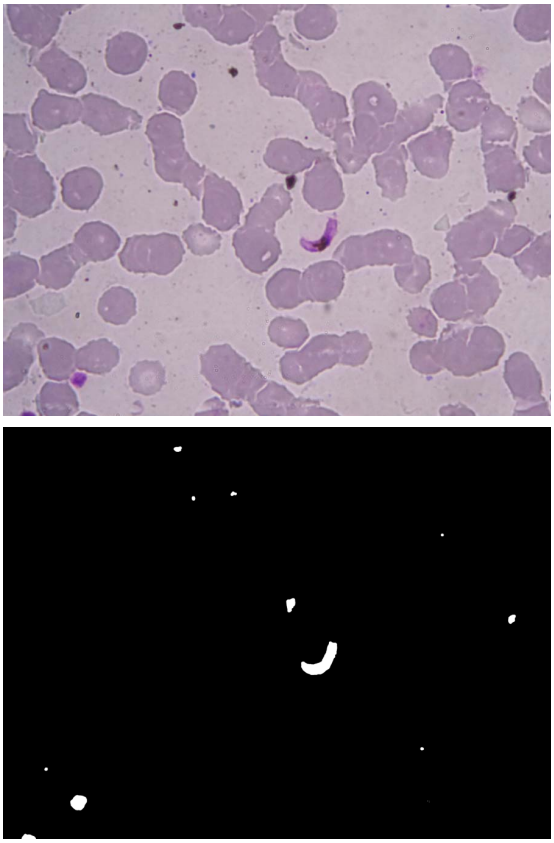

Fig. 7. An image before and after preprocessing

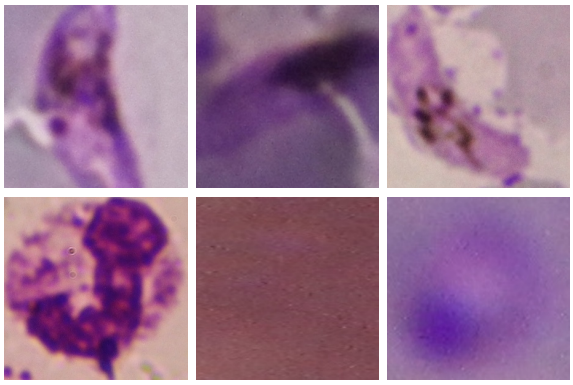

Fig. 8. Some segmented regions

model using Inception v3 Convolutional Neural Network that goes beyond parasite detection to identify the species in the blood smear as either *Plasmodium falciparum* or *Plasmodium vivax* with an accuracy of 87.9%.

As the dataset used is limited to only the trophozoite and gametocyte stages of the malaria parasites, future research may include images of the full schizogony of the parasites to build a more representative and discriminative model for species identification.

Fig. 9. Dataset augmentation by rotation of segmented image by 15 degree increments

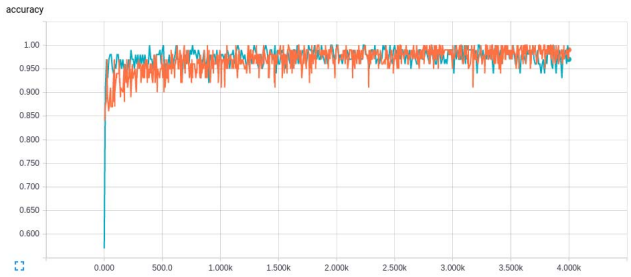

Fig. 10. Training accuracy per epoch of the CNN trained to classify trophozoite species

REFERENCES

[1] .

[2] World Health Organization. *Malaria Factsheet*. 2014. URL: http://www.who.int/mediacentre/factsheets/fs094/en/ (visited on 10/01/2014).

[3] Philippines Department of Health. *Malaria Control Program*. 2014. URL: http://www.doh.gov.ph/node/1072.html (visited on 10/01/2014).

[4] CK Jayaram Paniker. *Paniker's Textbook of Medical Parasitology*. Ed. by S. Ghosh. Seventh. New Delhi, India: Jaypee Brothers Medical Publishers (P) Ltd, 2013. Chap. 6, pp. 63–83.

[5] V. Makkapati and R. Rao. "Segmentation of Malaria Parasites in Peripheral Blood Smear Images". In: 2009, pp. 1361–1364.

[6] D. Anggraini, A. S. Nugroho, C. Pratama, I. E. Rozi, V. Pragesjvara, and M. Gunawan. "Automated status identification of microscopic images obtained from malaria thin blood smears using bayes decision: A study case in plasmodium falciparum". In: *2011 International Conference on Advanced Computer Science and Information Systems*. 2011, pp. 347–352.

[7] D. Das, M. Ghosh, C. Chakraborty, A. K. Maiti, and M. Pal. "Probabilistic prediction of malaria using morphological and textural information". In: *2011 International Conference on Image Information Processing*. 2011, pp. 1–6. DOI: 10.1109/ICIIP.2011.6108879.

[8] S. Kareem, I. Kale, and R. C. S. Morling. “Automated malaria parasite detection in thin blood films:-A hybrid illumination and color constancy insensitive, morphological approach”. In: *2012 IEEE Asia Pacific Conference on Circuits and Systems*. 2012, pp. 240–243. DOI: 10.1109/APCCAS.2012.6419016.

[9] A. M. Barros, A. A. Duarte, M. B. Netto, and B. B. Andrade. “Artificial Neural Networks and Bayesian Networks as supportting tools for diagnosis of asymptomatic malaria”. In: *The 12th IEEE International Conference on e-Health Networking, Applications and Services*. 2010, pp. 106–111. DOI: 10.1109/HEALTH.2010.5556584.

[10] A. Pinkaew, T. Limpiti, and A. Trirat. “Automated classification of malaria parasite species on thick blood film using support vector machine”. In: *2015 8th Biomedical Engineering International Conference (BMEiCON)*. 2015, pp. 1–5. DOI: 10.1109/BMEiCON.2015.7399524.

[11] Andrej Karpathy. *CS231n: Convolutional Neural Networks for Visual Recognition*. Stanford University. 2016. URL: http://cs231n.github.io/convolutional-networks/.

[12] Christian Szegedy, Vincent Vanhoucke, Sergey Ioffe, Jonathon Shlens, and Zbigniew Wojna. *Rethinking the Inception Architecture for Computer Vision*. 2015. URL: http://arxiv.org/abs/1512.00567.

[13] C. Szegedy et al. “Going deeper with convolutions”. In: *2015 IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*. 2015, pp. 1–9. DOI: 10.1109/CVPR.2015.7298594.