1-1-2019

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Barath Narayanan Narayanan, Redha Ali, Russell C. Hardie, "Performance analysis of machine learning and deep learning architectures for malaria detection on cell images," Proc. SPIE 11139, Applications of Machine Learning, 111390W (6 September 2019); https://doi.org/10.1117/12.2524681

Performance Analysis of Machine Learning and Deep Learning Architectures for Malaria Detection on Cell Images

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ABSTRACT

Plasmodium malaria is a parasitic protozoan that causes malaria in humans. Computer aided detection of Plasmodium is a research area attracting great interest. In this paper, we study the performance of various machine learning and deep learning approaches for the detection of Plasmodium on cell images from digital microscopy. We make use of a publicly available dataset composed of 27,558 cell images with equal instances of parasitized (contains Plasmodium) and uninfected (no Plasmodium) cells. We randomly split the dataset into groups of 80% and 20% for training and testing purposes, respectively. We apply color constancy and spatially resample all images to a particular size depending on the classification architecture implemented. We propose a fast Convolutional Neural Network (CNN) architecture for the classification of cell images. We also study and compare the performance of transfer learning algorithms developed based on well-established network architectures such as AlexNet, ResNet, VGG-16 and DenseNet. In addition, we study the performance of the bag-of-features model with Support Vector Machine for classification. The overall probability of a cell image comprising Plasmodium is determined based on the average of probabilities provided by all the CNN architectures implemented in this paper. Our proposed algorithm provided an overall accuracy of 96.7% on the testing dataset and area under the Receiver Operating Characteristic (ROC) curve value of 0.994 for 2756 parasitized cell images. This type of automated classification of cell images would enhance the workflow of microscopists and provide a valuable second opinion.

Keywords: Malaria Detection, Computer Aided Detection, Convolutional Neural Networks, Support Vector Machine

1. INTRODUCTION

Computer Aided Detection (CAD) and diagnosis in medical imaging has been a research area attracting great interest in the past decade. Detection and diagnosis tools offer a valuable second opinion to the doctors and assist them in the screening process[1]. In this paper, we propose and study the performance of various machine learning and deep learning algorithms for the detection of malaria on thin blood smeary images. Plasmodium malaria is a parasitic protozoan that causes malaria in humans and CAD of Plasmodium on thin blood smeary images would assist the microscopists and enhance their workflow.

Several machine learning and deep learning methods have been proposed in the literature for CAD in the field of medical imaging. Some of the feature-based approaches for CAD in medical imaging are presented[2-6]. A CAD system for detection of lung nodules in Computed Tomography (CT) scans is presented[2]. A set of 503 handcrafted features are computed and are later classified using a Fisher Linear Discriminant (FLD) classifier. An optimized feature selection-based clustering approach is presented for CAD of lung nodules in CT scans and chest radiographs[3]. A Fuzzy clustering-based diagnosis rules are presented for CAD of lung nodules[4]. A performance comparison of various classifiers such as the Support Vector Machine (SVM), K-nearest neighbor, quadratic and linear classifier are presented for CAD in medical imaging[5, 7]. Feature-based studies indicate that intensity, shape, and texture-based features are highly effective for classification. Research work[8-11] proposes certain deep learning approaches that have been effectively applied for CAD.

Automated approaches for the detection of malaria are presented[1, 12-14]. Various established segmentation, feature extraction techniques, and machine learning based approaches are utilized for classification of images[1]. A performance study of Convolutional Neural Networks (CNNs) towards malaria parasite detection for thin blood smeary images is presented[12]. A set of 94 features are computed and are later utilized to classify the images into 6 different classes using

Applications of Machine Learning, edited by Michael E. Zelinski, Tarek M. Taha, Jonathan Howe, Abdul A. S. Awwal, Khan M. Iftekharuddin, Proc. of SPIE Vol. 11139, 111390W
 · doi: 10.1117/12.2524681

SVM and Bayesian learning[13]. A feed-forward neural-network based classification approach is applied based on a set of features[14].

CNNs are effective for classification of malaria parasite detection[12] and have provided good performance for various imaging applications which includes text, handwriting, and natural images. CNNs provide state-of-the-art performances for various visualization tasks[15-19]. We adopt the same in this paper. We present a fast CNN architecture that would classify thin blood smeary images as either parasitized or uninfected. In addition, we study the performance of transfer learning approaches[15] using AlexNet[16], ResNet[17], VGG-16[18] and DenseNet[19]. We also study the performance of bag-of-features model coupled with SVM[20]. Overall probability of a cell image being parasitized is determined based on the average of probabilities provided by all the classification architectures implemented in this paper. Our proposed algorithm provides an overall accuracy of 96.7% on a publicly available testing dataset comprising 5512 cell images (2756 parasitized and 2756 uninfected) and area under the Receiver Operating Characteristic (ROC) curve value of 0.994 for the detection of parasitized samples.

The remainder of the paper is organized as follows. Section 2 describes the database utilized for this research. Section 3 presents the proposed fast CNN architecture. Section 4 presents the transfer learning approaches. Experimental results obtained using the proposed approaches are presented in Section 5. Finally, conclusions are offered in Section 6.

2. MATERIALS

In this research, we make use of a publicly available dataset provided by the National Institutes of Health (NIH) [21,12]. A level-set based algorithm to detect and segment the red blood cells is presented as well[12]. All these images were manually annotated by an expert slide reader at the Mahidol-Oxford Tropical Medicine Research Unit. The dataset contains a total of 27,558 cell images with equal instances of parasitized and uninfected cells[13]. Figures 1 and 2 represent certain sample images of parasitized and uninfected cells. We randomly split the dataset into 80% for training and 20% for testing samples belonging to each class. We further divide the (randomly chosen) training dataset into groups of 90% and 10% for training and validation purposes respectively. Table 1 presents the distribution of the images belonging to each class for training, validation and testing.

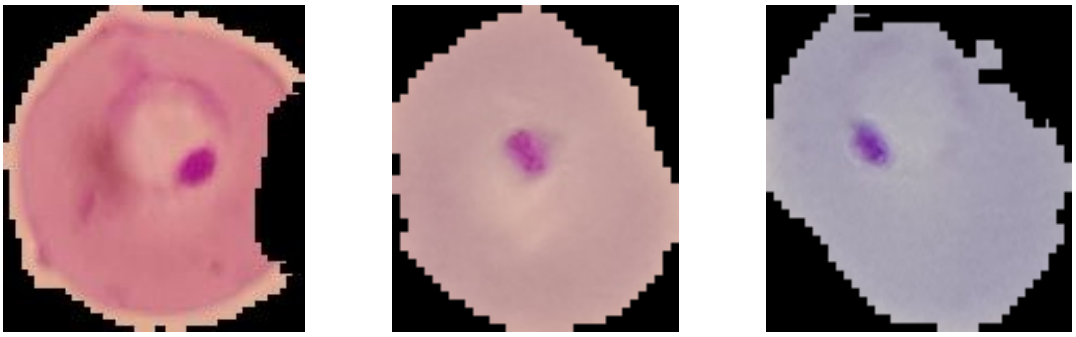

Figure 1. Sample images annotated as ‘Parasitized’ by Expert Slide Readers.

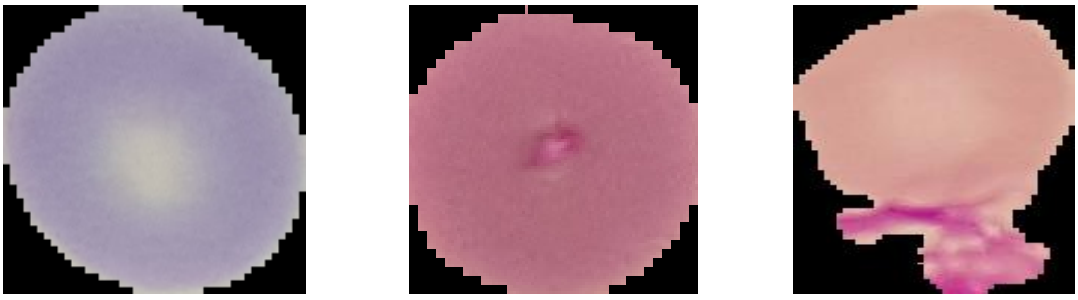

Figure 2. Sample images annotated as ‘Uninfected’ by Expert Slide Readers.

Table 1. Dataset Distribution.

Type of Dataset	Number of Parasitized Samples	Number of Uninfected Samples
Training	9921	9921
Validation	1102	1102
Testing	2756	2756

3. FAST CONVOLUTIONAL NEURAL NETWORK ARCHITECTURE

In this section, we present the fast CNN architecture proposed for the classification of cell images as parasitized and uninfected. At first, we spatially re-sample all the images to 50 × 50. Later, we preprocess them using color constancy technique to ensure the perceived color of the image remains the same under different illumination conditions[22]. Figure 3 presents the results obtained using the color constancy technique for cell images. The top row in Figure 3 presents the sample images in the dataset and bottom row presents the results obtained using the color constancy technique.

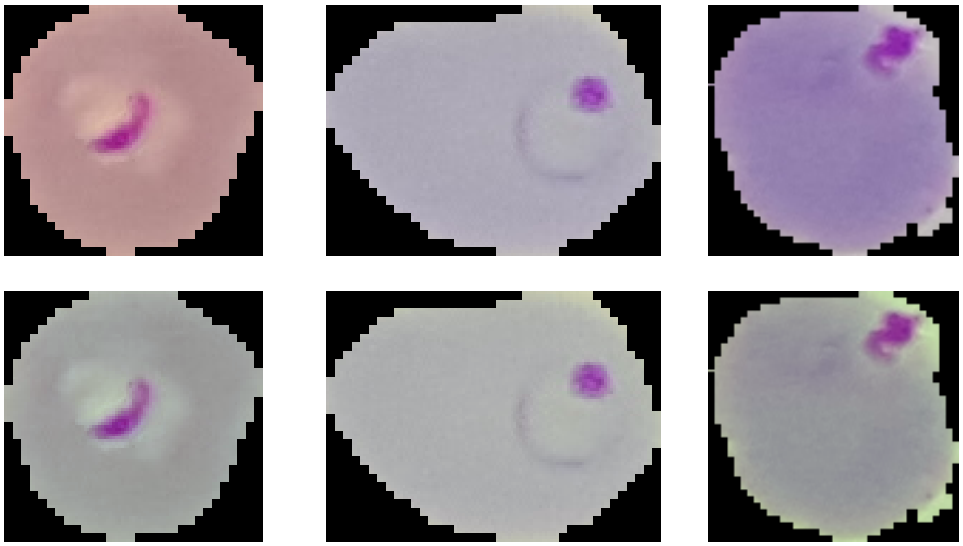

Figure 3. Results obtained using Color Constancy.

Figure 4 presents the fast CNN architecture presented for the classification of cell images. Each convolutional layer present in the architecture is comprised of 3 × 3 convolution operation, batch normalization, Rectified Linear Unit (ReLU) and maximum pooling layer of window size 2 × 2 with a stride of 2 as shown in Figure 5. Number of convolution filters present in each convolutional layer is presented in Table 2. Hyperparameters for the proposed fast CNN architecture are determined solely based on the training dataset. We choose 'gradient descent with momentum' optimization technique with a mini batch size of 64 and an initial learning rate of 0.0001.

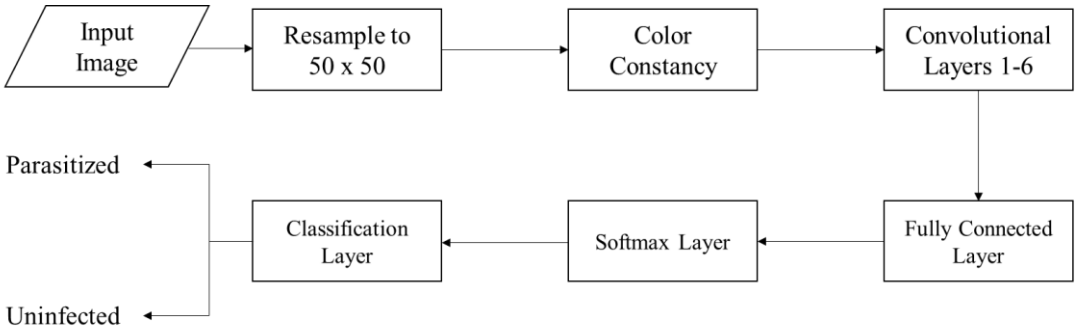

Figure 4. Fast CNN architecture.

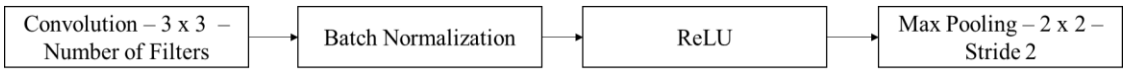

Figure 5. Convolutional Layer Structure.

Table 2. Number of convolution filters present in each convolutional layer.

Convolutional Layer #	Number of Filters
Layer #1	8
Layer #2	16
Layer #3	32
Layer #4	64
Layer #5	128
Layer #6	256

4. TRANSFER LEARNING METHODS

In this section, we present transfer learning approaches applied in this research for classification of cell images. As implemented in Section 3, we spatially re-sample all images to a particular size depending on the classification architecture implemented and later apply color constancy preprocessing technique. Aforementioned, we study the performance of AlexNet, ResNet, VGG-16 and DenseNet transfer learning approaches. Figure 6 presents the top-level block diagram of the transfer learning approach implemented in this study. These approaches have proven to be highly effective especially for image-based classification problems[16-19]. Moreover, study of such transfer learning approaches could provide us with insights about the cell images and would help us understand the effectiveness of such approaches for medical imaging-based classification problems.

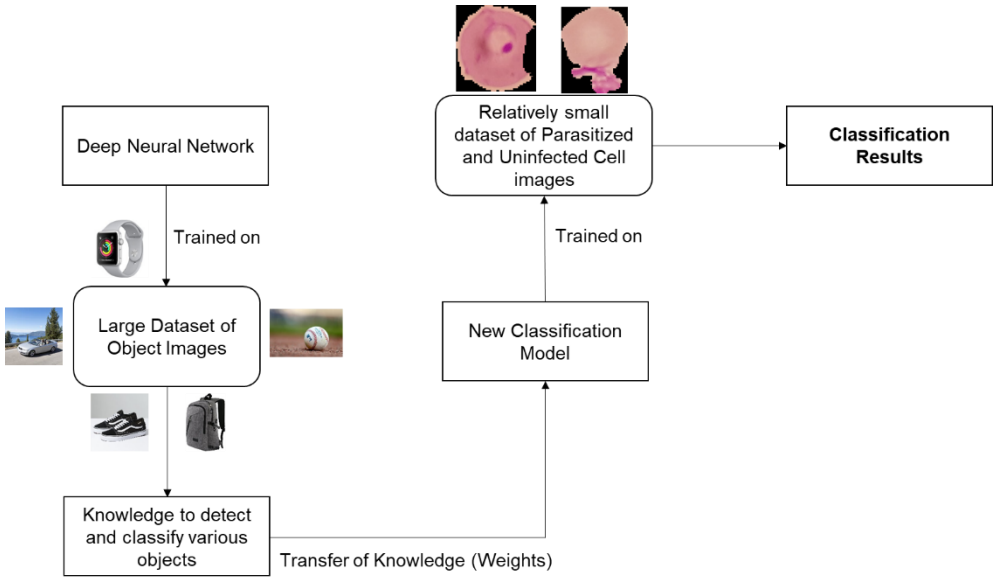

Figure 6. Top Level Block Diagram of Transfer Learning Approach.

5. EXPERIMENTAL RESULTS

In this section, we present the results obtained for approaches presented in Sections 3 and 4. In addition, we also study the performance of the bag-of-features model using SVM with linear kernel for classification. Performance is measured in terms of overall accuracy and ROC curve. We believe, overall accuracy is a good indicator as the testing dataset utilized in this study is distributed uniformly (in terms of images belonging to each category). ROC would assist the microscopists in choosing his/her operating point in terms of false positive and detection rate. We utilize the composition presented in Table 1 for training, validation and testing purposes respectively. Figure 7 presents the ROC curves obtained for the detection of Plasmodium (parasitized category). Later, we combine all the CNN architectures presented in this paper by averaging the probabilities of an image belonging to parasitized category estimated by each approach. We term this method as 'Average of All'. Table 3 presents the performance measure in terms of accuracy and area under the ROC curve (AUC). Figure 9 presents the training time consumption for each CNN method along with its overall accuracy.

Table 3. Performance Measure of Classification Algorithms for CAD of Plasmodium.

Classification Approach	Overall Accuracy	AUC
Bag of Features and SVM	85.6%	0.932
Proposed Fast CNN	96.0%	0.991
AlexNet	96.4%	0.992
ResNet	96.0%	0.992
VGG-16	96.5%	0.993
DenseNet	96.6%	0.991
Average of All	**96.7%**	**0.994**

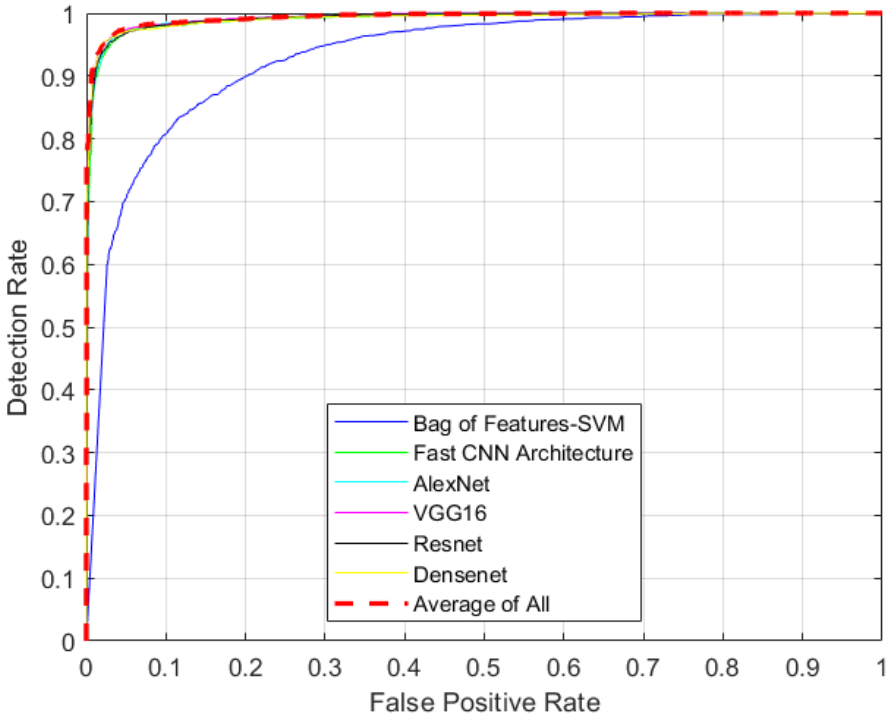

Figure 7. ROC curve obtained for various classification algorithms for CAD of Plasmodium.

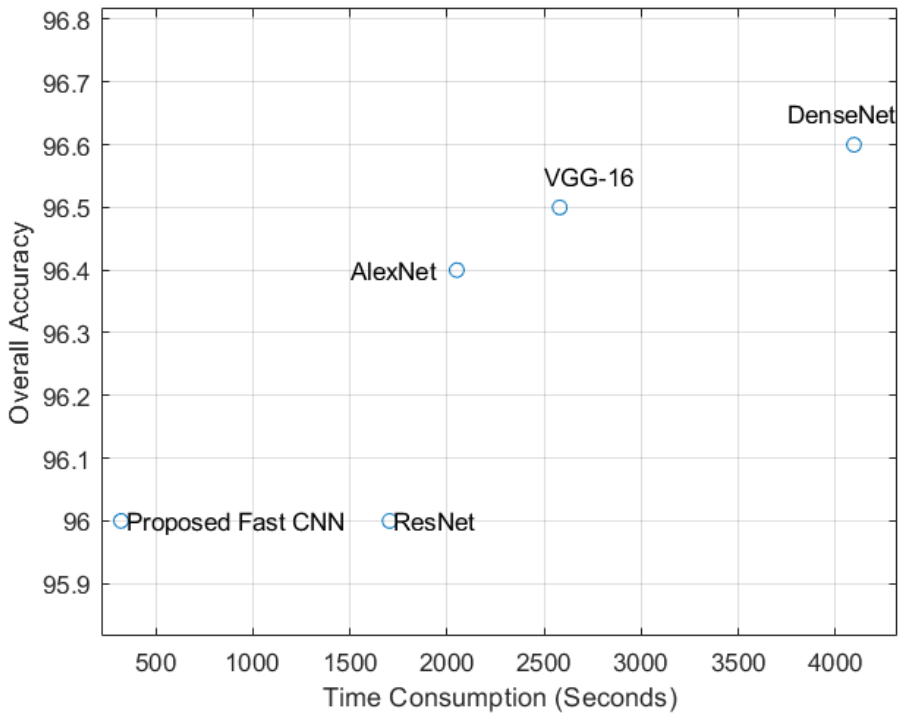

Figure 8. Performance comparison in terms of training time consumption and overall accuracy.

6. CONCLUSIONS

In this research, we have presented several deep learning-based classification approaches for CAD of Plasmodium. All the classification algorithms presented in this paper performed relatively well with minimum performance being 86% and 0.932 in terms of overall accuracy and AUC respectively. All the deep learning and transfer learning-based approaches performed better than bag-of-features and SVM based classification model. Implementation of CNN based architectures for categorizing the cell images as parasitized and uninfected is proven to be effective. Transfer learning-based algorithms provided similar performance with VGG-16 performing the best in terms of AUC (0.993) and DenseNet being the best in terms of overall accuracy (96.6%). Performance of transfer learning approaches clearly reiterates the fact that CNN based classification models are good in extracting features. Figure 9 illustrates that proposed fast CNN architecture provided comparable performance and it is the least in terms of time consumption among the deep learning architectures presented in this paper. Note that, this level of accuracy is achieved for the fast CNN with images of size 50 × 50 which helps in reducing memory consumption as well. With reduced training time, algorithm can be easily re-trained with new sets of labeled images to enhance the performance further. Combining the results of all these architectures provided a boost in performance both in terms of AUC and overall accuracy. A comprehensive study of these algorithms both in terms of computation (memory and time) and performance provides the subject matter experts to choose algorithms based on their choice. CAD of Plasmodium would be of great help for the microscopists for malaria screening and would help in providing a valuable second opinion.

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