Malaria Disease Diagnosis using Machine Learning Techniques

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Abstract - *Malaria is a major infectious disease of humans, with roughly 200 million cases worldwide and more than 400,000 deaths per year. Malaria could be prevented, controlled, and cured more effectively if a more accurate and efficient diagnostic method was available. The standard diagnostic method for malaria is the microscopic examination of blood smears for infected erythrocytes by qualified microscopists. However, this method is inefficient and the quality of the diagnosis depends on the experience and knowledge of the microscopists. This study proposes a new and robust machine learning model based on a Convolutional neural network (CNN) to automatically classify single cells in thin blood smears on standard microscope slides as either infected or uninfected. This will help in the faster diagnosis of malaria and save valuable time for beginning the treatment.*

Key Words: (convolutional neural network, malaria, machine learning, plasmodium, Normalization)

1. INTRODUCTION

In today's world, there are several global health diseases which are serious and infectious. The disease called malaria is one of the prominent disease among them. The bite of female anopheles mosquito causes malaria. The protozoan blood parasite of the genus plasmodium makes red blood cells as host cells for its reproduction cycle. The five variety of species of genus Plasmodium are P. falciparum, P. vivax, P. ovale, P. malariae and P. knowlesi. The major species that is responsible for the malaria is plasmodium vivax. Globally, 29% of the populations is infected by malaria among all age groups and 35%among the children under the age of 5. The African region carries high share of malaria. It is the home for 90% of the malaria case and 92% of the malaria deaths. Hence, to achieve immortality, WHO recommends diagnostic procedure which is a manual microscopic diagnosis of the peripheral blood parasite. Manual diagnosis of plasmodium involves visual determination and microscopic evaluation of geimsa stained thin blood smears. The procedure involves counting of infected red blood cells against the normal red blood cells manually. However, this type of analysis involves trained and experienced person, requires man power and also time-consuming process. The accuracy of the diagnosis mainly depends on the skill and experience of the technicians. Tools and instruments required for the diagnosis may be expensive and may not be available in the poor nations. Rapid diagnostic tests (RDTs) and polymerase chain reaction tests (PCR) are some tests involved in the microscopic malaria diagnosis. Although the malaria a is both preventable and curable, the vision based manual microscopic method of evaluation of malaria may not be accurate. Manual assessment sometimes leads to errors. Even the experienced clinical experts sometimes fail to offer accurate results. To avoid these consequences and to reduce the mortality rate of the people. Consequently, technology might be used to reduce the amount of mortality and reduce the waiting time to check the specialist. This paper explored the potential of data technology within the developments of a malaria diagnostic system using algorithms that would learn from experience. This algorithm is named decision tree which is a machine learning technique utilized in the design and development of software for the diagnostic model for plasmodium. Software isn't to replace the specialists or doctors but developed to help medical practitioners in diagnosing and predicting patient condition from certain rules or experience

2. RELATED WORK

2.1. Automatic Malaria Blood Smear Classification

Machine learning has been used to detect parasitemia in images of Giemsa-stained blood smears in [7]. This early study compared the correlation between automatic and manual parasitemia detection but did not classify infected and uninfected red blood cells. In 2009, a study by Diaz et al. applied a support vector machine (SVM) to classify preprocessed blood smear images to detected infected erythrocytes. The proposed algorithm performed well, in specificity and sensitivity, on a small dataset of 450 malaria images. Unfortunately, the model performance decreases when it's applied exclusively to blood images within the infection stage [8]. In summary, the present approaches for automatic slide processing have only been evaluated on relatively small image sets. Although the reported outcomes are encouraging, all methods still need to prove their robustness and performance on a large set of images. It is fair to say that the current systems still leave much room for improvement in this regard. Therefore, we are proposing a new system based on deep learning, which exhibits robustness and good performance on a large and realistic image set.

2.2 Convolutional Neural Network

A convolutional neural network (CNN) is a specific deep learning architecture suitable for image recognition. A CNN model processes input data by its multiple layers and is characterized by four key features: local connections,

shared weights, pooling, and the use of many layers. The early applications of CNN can be traced back to the 1990s for speech recognition and text recognition. Its use is then extended to handwriting recognition and later to natural image recognition. The performance of CNN models for natural image classification received another boost by the introduction of ImageNet by Alex Krizhevsky, thus also known as AlexNet, in 2012. AlexNet is considered a breakthrough application of CNNs to multi-categorical classification. In the ILSVRC-2012 competition, ImageNet composed of seven convolutional layers successfully classified the ILSVRC-2012 sets with 10,184 categories and 8.9 million images with a top-5 error of 15.3%. Following this initial success, the top-5 error has been reduced to 14.8% by ZFNet in 2013, then to 6.7% by GoogLeNet in 2014, and to 3.6% by ResNet in 2015.

2.3. Challenges for CNN Applications

The idea of CNNs is to apply smaller convolutional kernels (or filters) in combination with a deep network architecture to capture the discernable image features as much as possible. However, a more complex CNN architecture will inevitably increase the demand for more powerful computing resources. New technologies such as GPU and cluster computing can effectively improve the training efficiency but they are unable to ensure the performance of classification. Other factors such as data preprocessing and size of the training dataset strongly affect the classification accuracy, however. Since the CNN classification accuracy depends on the amount of training data, small data sets such as those used in earlier approaches are not large enough for training a deep model with its many parameters. As a compromise, the method of transfer learning has been introduced where a pre-trained network model is used to extract features that a conventional classifier, such as a SVM, can use for a fine-tuned classification [18]. Transfer learning can be used as a shortcut to deep learning where time for training is saved at the cost of performance, which may be lower but still acceptable. It can be used as a temporary replacement when large training data is not immediately accessible. In this study, we will implement deep learning by both training a newly configured CNN model and applying transfer learning in order to evaluate its use for malaria blood smear classification.

3. CONFIGURATION OF A CONVOLUTIONAL NEURAL NETWORK

The architecture of a CNN will largely determine the final net performance after training. The basic mechanism of deep learning is to apply a multi-layer network to map the input space by transforming it at the hidden nodes. Using a series of transformations, the network tries to learn the optimal mapping of the input data through a process called back-propagation. In this process, the partial derivative or gradient of the input parameters is computed from the partial derivative of the output, given an objective function, by applying the chain rule. Thus the changes of one layer can be computed recursively by measuring the changes of the following layer connected to it. Learning of a CNN model consists of two inverse computations: the feed-forward and the said back-propagation. The feedforward propagation computes the output of all units in each layer, where for each unit a non-linear activation function f is applied to the weighted sum of all inputs from the preceding layer. The activation function can be a rectified linear unit (ReLU), hyperbolic tangent (tanh), logistic function etc. Backpropagation is applied to train or fine-tune the deep network by optimizing the parameters/weights of each layer. By applying the above propagation mechanisms, a CNN can create a model of the input data when sufficient training data enters and propagates through the whole network.

3.1. CNN Architecture for Malaria Image Classification

Based on the above discussion, we apply a 17-layer CNN model for the malaria blood smear classification task. Note that the network is organized by blocks of similar layers where the width and height of the feature maps are 1x1 and the depth of the feature representations is 256 at the last fully connected layer. The sandwich design with one convolutional layer plus one ReLU layer allows enhanced learning.

4. MODEL EVALUATION

4.1. Data Source

We used archived blood smear images acquired from Chittagong Medical College Hospital, Bangladesh, and segmented the visual region of the erythrocytes from the first images. Our data set contains 27,578 erythrocyte images where the ratio of infected cells to uninfected cells is 1:1. All images are normalized to the median width and height for the training and classification experiments, at 44*44 pixels, with three color channels.

4.2 Data Preprocessing

Data Pre-processing refers to some artificial transformations to the raw dataset (including training, validation and testing datasets) in order to make the dataset more clean, more featureful, more learnable and in a uniform format. The data pre-processing is done before feeding the data to the data to the CNN model. In a

convolutional neural, network it is a fact that the performance of CNN is directly proportional to the amount of data used to train it, i.e. good pre-processing, always increases accuracy of the model. But on the other side, a bad pre-processing can also reduce the performance of the model.

4.2.1Normalization

In Normalization, the data sample's (Belonging from both train, validation and test dataset) dimension by dividing each dimension by its standard deviations.

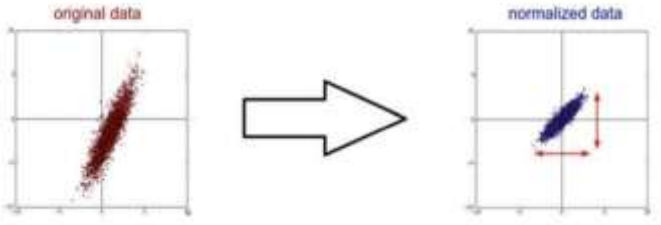

Fig-1 Normalization of data

4.3CNN Model Training

In order to train and evaluate our CNN model, we implement a ten-fold cross-validation on the whole data set, where 90% of the images are used for training, and 10% are used for testing. In model training, 90% of the images are separated from the training set for the actual training and the remaining 10% are used for back-propagation validation. The performance evaluation criteria are the average accuracy, sensitivity, specificity, precision, F1 score, and Matthews correlation coefficient over the ten-fold crossvalidation. A pre-trained AlexNet based on the CIFAR-100 data set is applied as the feature extractor for transfer learning. It is linked to a conventional SVM classifier to implement transfer learning as a comparison to our CNN model.

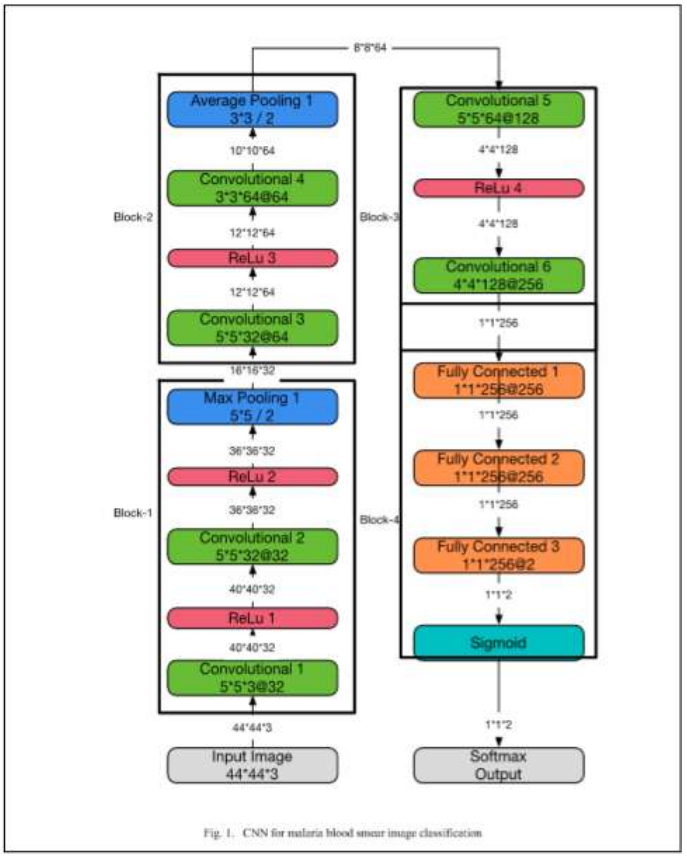

Fig-2 CNN for malaria blood smear image classification

5. CONCLUSIONS AND DISCUSSIONS

Based on the above experiment, we conclude that our newly designed convolutional neural network model is a suitable solution for blood smear classification. Compared to transfer learning and other similar studies, the CNN model shows much better classification performance after training with more than 27,000 images. Its performance is affected by both the architecture and the volume of training data. We expect that deep learning will significantly improve the working efficiency and accuracy of malaria diagnosis and other health-related applications, following our previous studies on deep learning for genomics.

6. REFERENCES

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