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Application of Convolutinal Neural Networks to the Classification of Malaria Infected Cells

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ABSTRACT

Malaria is a disease which, despite being present for over a century, still claims a significant number of lives every year. The advancement of artificial intelligence have opened the door to developing innovative methods in malaria treatment. Introducing machine learning approaches to this field can be beneficial in the disease prevention, detection, and therapy. In this work, convolutional neural networks for malaria detection are developed, based on the classification of thin blood smear images of the potentially infected cells. Input data was preprocessed using the image segmentation, file organization, image size standardization, color channel adjustment, and data splitting. Further, the proposed methodology included image conversion, network architecture defining, parameter tuning and network training. Various architectures of convolutional neural networks were developed and evaluated. In addition, multiple values of different network layer parameters were assessed. This study was implemented in Clojure programming language. Proposed network architecture includes two convolutional and pooling layers followed by activation functions, batch normalization and two linear layers. This convolutional neural network provided the best results and achieved an 90%% accuracy. Furthermore, this paper proposes another network model with lightweight configuration and a slight accuracy decrease.

INTRODUCTION

The first article to use Convolutional neural networks (CNN's) of deep learning for malaria diagnosis is by Liang et al., [7]. During recent years CNN based classification has shown relatively high performance for image classification. This research paper focuses on Transfer learning, a method of deep learning, for malaria cell-image classification. A performance study of Convolutional Neural Networks (CNNs) towards malaria parasite detection for thin blood smeary images is presented. A set of 94 features are computed and are later utilized to classify the images into 6 different classes using SVM and Bayesian learning. A feed-forward neural-network based classification approach is applied based on a set of features. Morphological recognition of red blood cells infected with malaria parasites is an important task in the laboratory practice. Nowadays, there is a lack of specific automated systems able to differentiate malaria with respect to other red blood cell inclusions. This study aims to develop a machine learning approach able to discriminate parasitized erythrocytes not only from normal, but also from other erythrocyte inclusions, such as Howell-Jolly and Pappenheimer bodies, basophilic stippling as well as platelets overlying red blood cells. Malaria is a life-threatening disease which is usually transmitted to people through the bite of infected female anopheles' mosquitoes. However, this article deals with the data exploration of malaria symptoms reported by 337 patients attended to at

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Federal Polytechnic Ilaro Medical center, Ogun State Nigeria. The study covers a period of four (4) weeks monitoring of patient's attendance, their consultation with physician and malaria test results as compared to their claims of malaria infection. Logistic regression was used for the basic analysis of the dataset, and it was discovered that people in the age range 38–47 years are mostly affected with malaria and that females are the most infected gender species with headache being the most significant symptom based on its Wald statistic value. This study strongly recommends the introduction of a long-lasting malaria prevention scheme that cut across all categories of ages and genders within the Nigerian community, and that self-medication should be seriously warned against as most claims of malaria were not actually found to be true upon verification.

Literature survey

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Malaria remains a major burden on global health, with roughly 200 million cases worldwide and more than 400,000 deaths per year. Besides biomedical research and political efforts, modern information technology is playing a key role in many attempts at fighting the disease. One of the barriers towards a successful mortality reduction has been inadequate malaria diagnosis in particular. To improve diagnosis, image analysis software and machine learning methods have been used to quantify parasitemia in microscopic blood slides. This paper gives an overview of these techniques and discusses the current developments in image analysis and machine learning for microscopic malaria diagnosis. We organize the different approaches published in the literature according to the techniques used for imaging, image pre-processing, parasite and cell segmentation, feature computation, and automatic cell classification. Readers will find the different techniques listed in tables with the relevant papers cited next to them, for both thin and thick blood smear images. We also discussed the latest developments in sections devoted to deep learning and smartphone technology for future malaria diagnosis.

PROPOSED ALGORITHM

Convolutional Neural Networks (CNNs) are a class of deep learning algorithms specifically designed for processing and analyzing visual data, such as images and videos. CNNs have proven to be highly effective in various computer vision tasks, including image classification, object detection, and image segmentation. Here is an overview of the key components and operations of the CNN algorithm. Convolutional layers are the heart of CNNs. They consist of a set of learnable filters (also called kernels) that slide or "convolve" across the input image. Each filter captures local patterns and features, learning to recognize specific visual patterns like edges, textures, or shapes.

During the convolution operation, each filter is applied to a small region of the input image (a receptive field), and a dot product is computed between the filter and the input pixels within that region. This process creates a feature map that highlights the presence of certain features. After the convolution operation, an activation function (typically ReLU - Rectified Linear Unit) is applied element-wise to introduce non-linearity into the model. This step helps the network learn complex and hierarchical features.

Pooling layers are used to reduce the spatial dimensions of the feature maps while retaining the most important information. Max-pooling and average-pooling are common pooling techniques that select the maximum or average value within a small region of the feature map, respectively. After several convolutional and pooling layers, one or more fully connected layers are added to the network.

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These layers perform high-level feature extraction and decision-making. They connect all the neurons from the previous layer to the current layer.

In classification tasks, a softmax layer is used as the final layer to convert the network's raw output into class probabilities. It assigns a probability score to each class, and the class with the highest probability is the predicted class. CNNs are trained using labeled data through a process called backpropagation. During training, the network's weights (parameters) are adjusted to minimize the difference between its predictions and the true labels (a loss function like cross-entropy is commonly used). Optimization algorithms like stochastic gradient descent (SGD) or its variants are employed to update the weights.

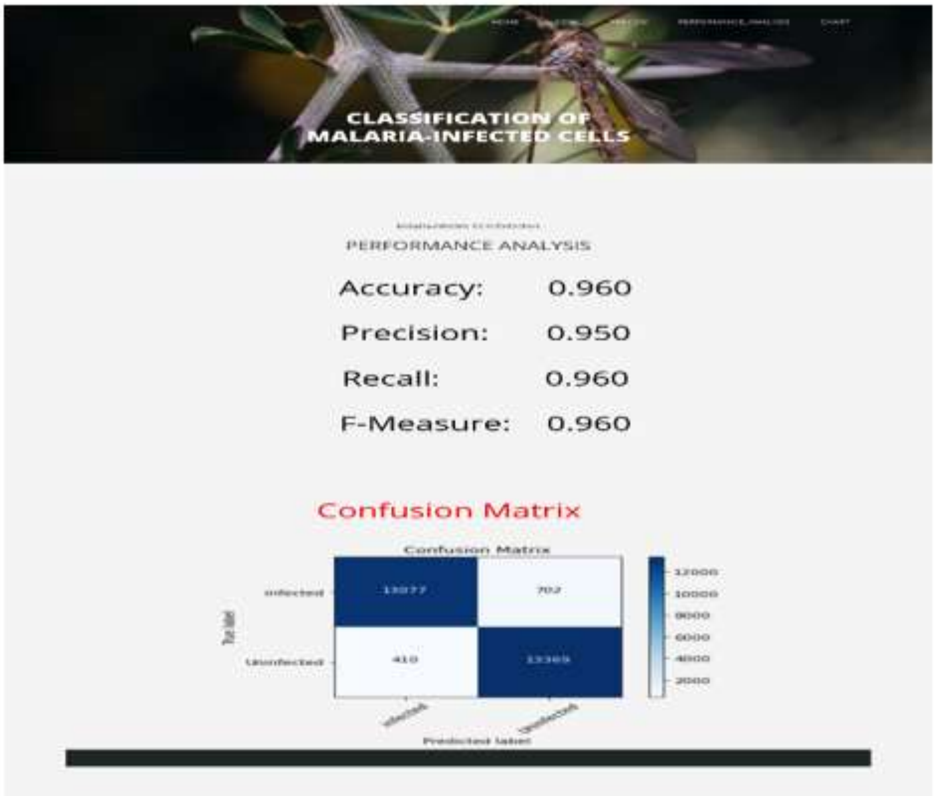
CNNs are particularly effective for tasks where the spatial arrangement of features in the input data is important (e.g., image recognition) due to their ability to capture hierarchical patterns. CNNs automatically learn and extract meaningful features from data, reducing the need for manual feature engineering. CNNs learn features at different levels of abstraction, from simple edges to complex objects, making them powerful for complex tasks. CNNs have achieved state-of-the-art performance in various computer vision tasks, including image classification and object detection. Convolutional Neural Networks have revolutionized the field of computer vision and have had a significant impact on various other domains by enabling the development of highly accurate and efficient models for visual data analysis.

PROPOSED SYSTEM CONFIGURATION

The application of Convolutional Neural Networks (CNNs) to the classification of malaria-infected cells has shown tremendous promise in the field of medical image analysis and disease diagnosis. Malaria is a life-threatening disease caused by the Plasmodium parasite and is transmitted through infected mosquito bites. Early and accurate diagnosis is crucial for timely treatment and prevention of complications. Here's how CNNs are employed in this context: Researchers collect a dataset of microscopic images of blood smears or thin blood films containing red blood cells (RBCs) infected with malaria parasites (Plasmodium falciparum or Plasmodium vivax) and uninfected RBCs. To improve model generalization, data augmentation techniques like rotation, flipping, scaling, and brightness adjustments are often applied to increase the diversity of the training dataset. Images are preprocessed to enhance features and reduce noise. Common preprocessing steps include resizing, normalization, and contrast adjustment.

CNNs are chosen due to their ability to automatically learn hierarchical features from images. Common architectures such as VGG, ResNet, or custom CNN architectures are used. The CNN model is trained on the labeled dataset. During training, the model learns to distinguish between infected and uninfected cells by adjusting its internal parameters. The model is evaluated on a separate test dataset to assess its accuracy, sensitivity, specificity, and other relevant metrics. Interpretability techniques like gradient-based class activation maps (CAM) or attention mechanisms can help identify the regions of the image that contributed to the classification decision. This can aid in understanding the model's reasoning. Once the CNN model demonstrates high accuracy in classifying infected and uninfected cells, it can be deployed in clinical settings. It can assist healthcare professionals in diagnosing malaria quickly and accurately.

CNNs have proven to be highly accurate in detecting malaria-infected cells, often outperforming traditional image analysis methods. CNNs can provide fast results, which is crucial in a clinical context where timely diagnosis is essential. Once trained, CNN models can be automated, reducing the burden on healthcare workers and improving consistency. CNN models can be scaled to handle large datasets, making them suitable for population-scale screening programs. the application of CNNs to the classification of malaria-infected cells demonstrates the potential for AI-driven solutions to improve the accuracy and efficiency of malaria diagnosis, ultimately contributing to better patient outcomes and the global fight against this infectious disease.



CONCLUSION

Malaria is a disease that has been present for a long time, but even though various traditional methods for prevention, identification, and treatment have been developed, the mortality rate from this disease is still high. The development of artificial intelligence enabled modern practices and applications for the suppression of this disease. In this research, several CNNs were developed in order to obtain a network that will classify the cell image into healthy or malaria-infected with high accuracy. The final results showed that the CNN with two convolutional and two pooling layers followed by ReLU activation functions achieved the highest accuracy. This paper offers a straightforward and rapid solution for malaria-infected cell classification. The proposed networks demand low memory and time requirements and achieve satisfactory results.

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