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Automated Life Stage Classification of Malaria Using Deep Learning

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Abstract

INTRODUCTION: Malaria, an infectious illness spread by mosquitoes, is a serious hazard to humans and animals, with an increasing number of cases recorded yearly. Prompt and precise diagnosis, as well as preventative actions, are critical for effectively combating this condition. Malaria is now diagnosed using standard techniques. Microscopy of blood smears, which consists of small pictures, is used by trained specialists to identify diseased cells and define their life phases. The World Health Organisation (WHO) has approved this microscopy-based malaria diagnostic method. Drawing a blood sample from the finger, pricking it, spreading it onto a clean glass slide, and allowing it to dry naturally are all steps in the method. Thin blood smears were previously used to identify parasites under the microscope, but thick blood smears are utilized when parasite levels are low.
OBJECTIVES: Due to its reliance on medical knowledge, high prices, time-consuming nature, and unsatisfactory outcomes, this technique has significant disadvantages. However, as deep learning algorithms progress, these activities may be completed more effectively and with fewer human resources.
METHODS: This study demonstrates the usefulness of transfer learning, a type of deep learning, in categorizing microscopic pictures of parasitized versus uninfected malaria cells. Six models were evaluated using the publicly accessible NIH dataset, proving the usefulness of the suggested technique.
RESULTS: VGG19 model fared better than its competitors, obtaining 95.05% accuracy, 92.83% precision, 96.88% sensitivity, 93.46% specificity, and 94.81% F1-score.
CONCLUSION: This categorization of malaria cell photos will benefit microscopists in particular, as it will improve their workflow and provide a viable alternative for detecting malaria using microscopic cell images.

Keywords: Deep Learning, Malaria microscopic cell images, life stage classification, Blood smear

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1. Introduction

Malaria is a major public health hazard caused by parasites spread by mosquito bites, mainly female Anopheles mosquitoes. According to the World Health Organisation's (WHO) World Malaria Report 2020, there were 229 million recorded cases of malaria in 2020, with 409,000 deaths [1]. The parasites establish themselves and multiply within human liver cells before infecting red blood cells. Understanding the parasites' present life cycle within patients is critical for developing successful treatment techniques. To detect the presence or absence of infection in humans, accurate evaluation of infected and uninfected human cells and meticulous analysis of thick and thin blood smears are required. Examining erythrocytes with a peripheral blood smear and microscope can help determine the existence of the illness [2]. A peripheral blood smear or blood film, also known as a little amount of blood, applied or spread on a microscope slide, is then stained to enable microscopic inspection of the different blood cells [3]. However, this

procedure is time-consuming, labor-intensive, and repetitive, necessitating a high degree of skill from those engaged. Deep learning-based algorithms, which display accuracy, fault tolerance, and non-exhaustive capabilities, provide a viable answer to these difficulties. Our study focuses on the critical need to address the issue of malaria cell imaging, especially considering the severity of the disease in impoverished nations.

The sickness takes the lives of children, particularly those under the age of five, as well as pregnant mothers. According to statistics, children are more sensitive to malaria, resulting in one kid's death every minute. As shown in Table 1, global statistics from 2000 to 2019 showed a total of 409,000 malaria-related fatalities. Malaria symptoms include fever, headache, nausea, vomiting, joint pain, and muscular stiffness [4], with more severe instances including seizures and comas, which can be fatal [5]. The typical time frame for the onset of malaria symptoms is 7 to 30 days following a mosquito bite. The disease can be efficiently treated with the deployment of suitable safeguards and strategic measures, largely centered on early parasite diagnosis [6].

Malaria treatment options include a variety of drugs. Despite this, the lack of contemporary equipment and dependence on manual blood cell counts have resulted in an alarming increase in death rates. Traditional malaria diagnosis and prediction approaches, which require skilled radiologists, time-consuming and expensive diagnostic instruments, and limited effectiveness, are regarded as insufficient. Deep learning (DL) provides a solution by entrusting pathologists' jobs to computers [7]. DL is mostly concerned with creating instruments and algorithms for precise illness diagnosis in medicine [8].

In our study, we did a comparative examination of eight distinct transfer learning mechanisms [9]. This article describes a quick and accurate approach to diagnosing malaria. The Adam optimization technique is used to optimize the parameters of the proposed strategy, which employs a transfer learning model. Our work made the following notable contributions:

- The results are assessed using several statistical methods, and the proposed algorithm is compared to the competing state-of-the-art.
- Our goal is to develop an AI-based automated system that is extremely accurate and trained to identify malaria in stained blood cell pictures in a short period.

Section 2 of this report contains a collection of relevant research publications. Section 3 expands on the approach utilized, providing information regarding the dataset and the experimental setting. Section 4 delves into the results and analysis in the Results and Discussion section. Finally, Section 5 summarises the important results of this study.

Table 1. Recorded Cases and Deaths

Year	Recorded Cases	Recorded Deaths
2000	238000	736000
2001	244000	739000
2002	239000	736000
2003	244000	723000
2004	248000	759000
2005	247000	708000
2006	242000	716000
2007	241000	685000
2008	24000	638000
2009	246000	620000
2010	247000	594000
2011	239000	545000
2012	234000	517000
2013	225000	487000
2014	217000	471000
2015	218000	453000
2016	226000	423000
2017	231000	422000
2018	228000	411000
2019	229000	409000

2. Related Research Work

In this part, we will look at some current research on the issue. [10] presented a transfer learning approach for malaria cell image identification in one such work. The authors used a pre-trained ResNet50 model that included a fully linked layer as well as a pre-trained ResNet50 layer. The model was trained for ten epochs and scored 95.40 percent on testing. Another study [11] proposed a novel CNN model that was specially built to distinguish between native and parasitized cells. Three convolutional layers, max pooling, and two fully linked layers were used in this model. The writers received 95% on the test photographs.

[12] did an experimental study in which their 16-layered CNN model outperformed transfer learning approaches, attaining a model accuracy of 97.37% in recognizing cell pictures. Throughout the investigation, the suggested model's performance was compared to that of a pre-trained CNN. The CNN model also surpassed transfer learning, which obtained 91.99% accuracy on the same picture dataset, according to the researchers, across all performance parameters, including specificity, recall, F1 Score, precision, and Matthews correlation coefficient.

A unique and strong machine learning (ML) model related to CNN was suggested in a relevant article [13] to categorize parasite or uninfected individual microscopic cell pictures through thin blood smears. In their research examination, the contributors reported a model accuracy of 97%. Furthermore, [14] investigated the performance of different transfer learning models, including AlexNet, VGG-16, ResNet50, Xception, and DenseNet-121, as well as a custom-built model, to discover the ideal layer for feature extraction from underlying malaria parasite data.

[17] examined several deep-learning techniques for the automated recognition of cells harboring malarial infections. Three CNN-based models, LeNet, AlexNet, and GoogLeNet, were specifically examined. According to the data, LeNet had

an accuracy rate of 96.18%, AlexNet had an accuracy rate of 95.79%, and GoogLeNet had an accuracy rating of 98.13%. These findings show that these models outperform the SVM model, which had an accuracy rate of just 91.66%.

For malaria detection, it is proposed in [18] to use a Deep Learning model, namely ResNet based on CNN. ResNet, which has 152 layers, is a dense network. The model was constructed by the study team to be computationally efficient, resulting in a training time of less than 5 hours and an accuracy rate of 98%. The model not only produced very accurate results, but it also required less training time and used fewer hardware and memory resources.

[19] proposes a method that combines an SVM classifier and Inception v3, a Transfer Learning model. Inception v3 is used in this system to extract classification-related features, which are subsequently input into the SVM classifier for prediction. The third version of Google's Deep Learning Architecture includes the Deep Convolutional Network Inception. When the model reached the bottleneck layer, which comes before the completely linked layer, it stayed frozen. The model has a 93% accuracy during training and a 94.8% accuracy during testing.

[20] outlines a study that uses Transfer Learning algorithms to classify images from thin blood smears. The ResNet50 model is used for classification in the recommended approach. As layers in the proposed model, a fully linked dense layer with a sigmoid activation function and a pre-trained ResNet layer is proposed. The input data is sent to the ResNet50 layer, which employs back-propagation to capture important properties using pre-trained weights. The model has a training accuracy of 95.91%.

The fundamental aim of this research is to identify and evaluate a deep-learning model for identifying malaria parasites in thin blood smear pictures. The goal is to identify whether or not parasites are present in the blood samples. To do this, a carefully considered dataset is chosen, and a publicly available malaria dataset was used. The study seeks to determine the best model architecture and design for reliable malaria detection, to enhance the model's overall performance.

3. Methodology

The technique used to detect malaria parasites is described in this section. Deep Learning approaches rely on a systematic set of activities that must be carried out in a certain order to produce a strong and trustworthy model [19]. The majority of these approaches begin with data collection. Predictions are produced using photos of stained blood smears in the current Deep Learning approach. For professionals in computer vision and human analysis, the staining process is critical. The first step in implementing automated diagnosis using digital image processing is to gather pictures or datasets of blood smears.

3.1. Dataset Description

We used a dataset from the National Library of Medicine's website [20], which is freely available, for this component of the study investigation. There are a total of 27,558 cell pictures in the collection. Among them, 13,779 photos show malaria parasite-free cells, whereas the remainder shows parasite-infected cells. As a result, this research may be considered a binary classification problem. In our tests, we labeled the parasitized/infected class as 1 and the uninfected class as 0. We split the data using the scikit-learn into training (80% dataset), testing (10% dataset), and validation (10% dataset) sets to ensure proper training and assessment.

3.2. Pre-Processing

The initial stage of image processing is pre-processing. Data preparation is the process of converting raw data into useful data for a classification model. Real-world data is typically noisy, has missing values, or is in a format that prevents direct use in deep learning (DL) models. As a result, it cannot be utilized in DL models directly. Data pre-processing is crucial for increasing the overall efficacy of deep learning models. Furthermore, we employ a variety of pre-processing techniques to improve image quality and obtain a reasonable degree of accuracy.

This section focuses on increasing the image's size and quality. Furthermore, it emphasizes the low quality of the original image, explicitly highlighting difficulties such as the brightness and darkness of objects seen during transmission. The initial processing steps try to improve the image's quality so that it may be used in a variety of additional applications. It is vital to highlight that diverse image processing issues necessitate distinct techniques, and no single solution can cover all obstacles.

The images were resized and normalized in our pre-processing module. Resizing was done to maintain data uniformity, and all photos were resized to a similar size. The input layer chose this size since many pre-trained models use 224x224-pixel pictures. As a result, the pictures were reduced to 224 x 224 pixels. Normalization was also performed by dividing the pixel values of the photos by 255. The goal of this normalization technique was to reduce the difference between an image's top and lowest pixel values while maintaining all of the critical information.

3.3. Pre-trained DL models

Following the completion of the pre-processing stage, the next step is to train a model capable of associating the retrieved characteristics with the pictures. The pre-processed normalized picture is then supplied to the classification algorithm for parasite life stage prediction. Given that cell pictures frequently lack distinguishing characteristics that may considerably improve classification accuracy, we included a variety of transfer-learning strategies in our classification model.

Pretrained networks have shown tremendous success, notably in image processing. As a result, they are extensively employed in models and applications of transfer learning. Transfer learning is the application of a previously trained machine learning model to a different but related issue. This method makes use of prior knowledge to boost generalization in a new activity. The notion of transfer learning is used in this study since it is successful in recognizing malaria parasites in microscopic cell pictures derived from blood smears.

Various deep learning approaches trained on the massive ImageNet dataset have made considerable improvements in image classification and object recognition jobs. The use of pre-trained models in transfer learning, in particular, has become a frequent strategy, particularly in areas with minimal labeled data, such as biological picture recognition. Transfer learning allows deep learning models trained on large-scale datasets to be applied to smaller, domain-specific datasets, improving performance in instances with restricted data availability. Transfer learning models VGG (16, 19), ResNet (50, 101), and DenseNet (121, 169) were used for malaria diagnosis in this suggested study with 20 epochs, 32 batch sizes, Adam optimizer, and Categorical cross-entropy loss function.

VGG. K. Simonyan and A. Zisserman created the VGG16 model, which won the 2014 ImageNet competition. It has 16 layers in total, including five maximum pooling levels, three deep layers, and thirteen convolution layers. The term "VGG16" refers to the fact that it contains 16 layers. VGG19 is an enhanced version of the VGG16 model, with 16 convolutions, 5 max-pooling layers, and 3 dense layers. The primary distinction between VGG16 and VGG19 is the number of layers used in the deep neural network: VGG16 has 16 layers, whereas VGG19 has 19. The VGG19 model is being used to successfully execute the model for this project and image training.

ResNet. Deep neural networks, such as VGG16 and VGG-19, have excelled in large-scale picture classification challenges. However, because of the issue of vanishing gradients, training deep neural networks may be extremely difficult. To overcome this issue, researchers created the notion of skip connections, which allow specific layers of the network to be ignored. This method attempted to solve the vanishing gradient problem. ResNet-50, and ResNet-101 models with skip links were used in the proposed study to increase training efficiency and performance.

DenseNet. We used two DenseNet models in our study: DenseNet121, and DenseNet169. DenseNet models are a sort of convolutional neural network that was created to solve the problem of disappearing gradients in deep networks. All layers in DenseNet models are directly connected through skip connections, allowing for enhanced information flow and gradient propagation during the backpropagation process.

DenseNet121 is made up of 121 layers, and DenseNet169 is made up of 169 layers. The models get more complicated and comprise a larger number of layers as the number of layers increases. Transfer learning is advantageous since all DenseNet models were already trained on the ImageNet dataset for malaria diagnosis, providing a strong starting point.

4. Results and Discussion

Following extensive descriptions of the suggested strategy, this portion of the paper concentrates on presenting the experimental results and analyzing the quantitative data gathered in this study. This section discusses several categorization methods and the statistical studies that go with them. To begin, we evaluate and compare the performance of several models using the malaria NIH dataset. Second, we compare the proposed models to previous studies.

Our proposed model looked at five key performance metrics: accuracy, recall, specificity, precision, and F1 score. Several measures were created using the obtained confusion matrices to assess the model's performance. The confusion matrix presented in Table 2 displays the count of:

True positives. True positives are tiny malarial cell pictures that were successfully detected as infected even though they were not anticipated to be**.**

True negatives. True negatives are uninfected malarial cell pictures that were appropriately recognized as such.

False positives. False positives happen when a tiny cell picture is wrongly labeled as infectious, notwithstanding the initial prognosis.

True positives. False negatives are malarial cell pictures that were incorrectly identified as uninfected, even though the original forecast indicated that they were infected.

Table 2. Confusion Metrics Design

	Estimated	**Real**
Parasitized/ Infected	True Positive (TP)	False Positive (FP)
Unparasited/Uninfected	False Negative (FN)	True Negative (TN)

The categorization outcomes of the used model are shown in the confusion matrix (see Fig. 1). We calculate several assessment metrics, such as specificity, sensitivity, precision, accuracy, and F1 Score, to evaluate the performance of the suggested model [21]. Table 3 displays these assessment indicators. The assessment measures utilized were generated from the confusion matrix. Table 4 displays the results.

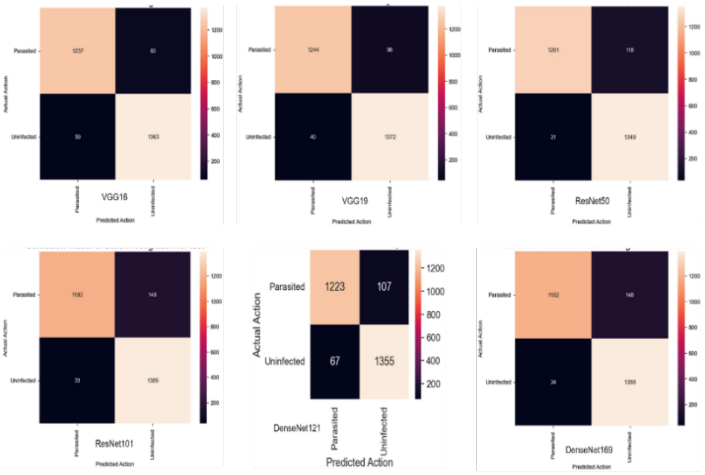

Figure 1. Confusion Matrix of Action Recognition for Test

Table 3. Metrics Measures

Metrics	Measures
Accuracy	$\frac{TP + TN}{TP + FP + FN + TN}$
Precision	$\frac{TP}{\mathrm{TP} + \mathrm{FP}}$
Sensitivity or Recall	$\frac{TP}{TP + FN}$
Specificity	$\frac{TN}{\mathrm{TN} + \mathrm{FP}}$
F1 Score	$\frac{2 * TP}{2\mathrm{TP} + \mathrm{FP} + \mathrm{FN}}$

Table 4. Evaluation Measures

	Accuracy	Precision	Sensitivity	Specificity	F1 Score
VGG16	94.47%	93.00%	95.44%	93.61%	94.21%
VGG19	95.05%	92.83%	96.88%	93.46%	94.81%
ResNet50	94.59%	91.44%	97.60%	91.95%	94.42%
ResNet101	93.42%	88.87%	97.28%	90.37%	92.88%
DenseNet121	93.67%	91.95%	94.80%	92.68%	93.35%
DenseNet169	93.38%	88.87%	97.20%	90.36%	92.85%

From Table 4, The percentage of parasitized malarial cells accurately recognized is indicated by sensitivity. The results demonstrate that ResNet50 properly recognized 97.60% of the parasitized cells, compared to 95.44%, 96.88%, 97.28%, 94.80%, and 97.20% sensitivity for VGG16, VGG19, ResNet101, DenseNet121, and DenseNet169. As a result, ResNet50 is somewhat better at accurately identifying positives, which in this case are parasitized malarial cell pictures.

Specificity tells us how many unparasitized malarial cell pictures were successfully recognized. The results demonstrate that VGG16 accurately recognized 93.61% of the unparasitized cells, compared to 93.46%, 91.95%, 90.37%, 92.68%, and 90.36% specificity for VGG19, Resnet50, ResNet101, DenseNet121, and DenseNet169. As a result, VGG16 is marginally better at detecting unparasitized malarial cell pictures.

Precision is the proportion of positively identified parasite malarial cell pictures. The results demonstrate that VGG16 successfully detected 93.00% of parasite cells, compared to 92.83%, 91.44%, 88.87%, 91.95%, and 88.87% for VGG19, Resnet50, ResNet101, DenseNet121, and DenseNet169. As a result, VGG16 is marginally better at detecting parasite malarial cell pictures.

On a dataset, the F1 Score evaluates model accuracy. With a percentage of 94.81%, our proposed model, VGG19, performed better on the dataset than VGG16, Resnet50, ResNet101, Dense-Net121, and DenseNet169, which scored 94.21%, 94.42%, 92.88%, 93.35%, and 92.85%. The outcomes show that VGG19 outperforms other models and is a suitable alternative for malaria detection.

Accuracy assesses the model's overall performance. The suggested model VGG19 achieved a better classification accuracy of 95.05% when compared to VGG16, Resnet50, ResNet101, DenseNet121, and DenseNet169, which achieved 94.47%, 94.59%, 93.42%, 93.67%, and 93.38% accuracy, respectively. This demonstrates that our model VGG19 outperforms all other models.

The results demonstrated that our suggested strategy achieved successful results in performance matrices. The suggested model, as shown in Table 5, outperforms several state-of-the-art models, according to statistical data.

Table 5. Comparative Analysis

Reference	Model	Accuracy
[11]	Custom CNN	95%
[17]	Inception + SVM	94.8%
[22]	VGG19	85.18%
[23]	Custom model with ResNet50 and ResNet101 base.	94%
[24]	Bayesian Network	81%
[25]	CNN	95%
[26]	Deep Belief Network (DBN)	89.9%
Proposed	**VGG19 Accuracy** **F1 Score**	**95.05%** **94.81%**

5. Conclusion

The detection of malaria parasites from cell pictures is critical because it can save lives. Deep neural network models provide intriguing answers to this problem. In light of this, six classification models for detecting malaria parasites have been created. This study presents a malaria illness detection method based on pre-trained models. The outcomes of six pre-trained models were compared using a dataset of blood smear pictures.

Among all models, the VGG19 model had the greatest accuracy and F1 score. The ResNet50 model has the second-highest accuracy and F1 score but ranks first in sensitivity, whereas the VGG16 model ranks third in accuracy and F1 score but first in precision and specificity. In conclusion, the healthcare business has a lot of promise for using Deep Learning and Computer Vision models. There is a potential to lessen the stress on medical professionals and the reliance on expensive and sophisticated medical equipment by automating the diagnosis procedure. Furthermore, because these programs are user-friendly, people with minimal technological and medical competence may give greater support to their superiors. As a result, more research in this sector is critical and extremely important.

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