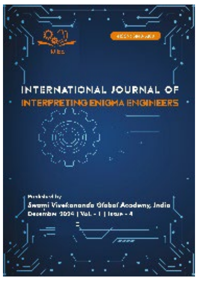
International Journal of Interpreting Enigma Engineers (IJIEE)
https://ejournal.svgacademy.org/index.php/ijiee/
OPEN ACCESS

MALARIA DIAGNOSIS BY TRANSFER LEARNING ANALYSIS OF PARASITIZED AND UNINFECTED RED BLOOD CELL IMAGES USING VGG16, DENSENET201, VGG21, AND VGG19



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Original Article

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Abstract

Malaria is still a major worldwide health concern, and effective treatment depends on early discovery. Using well-known deep learning models like VGG16, DenseNet201, VGG21, and VGG19, this study focuses on applying transfer learning techniques to diagnose malaria by examining photos of red blood cells. To identify malaria-infected cells, the dataset's red blood cell images—both parasitized and uninfected—are processed. With the intention of offering a more dependable and approachable malaria diagnostic technique, the objective is to assess the effectiveness of these predictive models in terms of accuracy, precision, and computational performance. This strategy ensures improved performance. Different methods were tried, and all classifiers' outputs were combined using an ensemble technique. The suggested technique outperformed the individual machine learning classifiers and ensemble methods employed in this study in terms of accuracy, precision, and sensitivity, with rates of 96.94%, 96.94%, and 96.94%. Furthermore, the association between the factors was investigated, showing each factor's contribution to malaria occurrence. The findings show that the suggested approach may efficiently anticipate malaria outbreaks.

Keywords: Malaria, Machine learning, Accuracy, Predictive Models, Transfer Learning

Introduction

Plasmodium parasite-caused malaria remains a public health concern, especially in tropical areas. Blood smears must be examined by skilled professionals using microscopy, the conventional way of diagnosing malaria. But this procedure takes a long time and is prone to human mistake[1][2]. Automating the diagnosis procedure has gainedpopularity as deep learning and artificial intelligence have advanced. Potential solutions include transfer learning, which reduces the requirement for large labeled datasets by adapting previously trained models for new tasks. Using well-known deep learning architectures such as VGG16, DenseNet201, VGG21, and VGG19, this study explores the use of transfer learning to automatically identify malaria from photos of red blood cells. In order to detect malaria-infected cells, the dataset is processed to contain pictures of both parasitized and uninfected red blood cells.[4] In order to develop a more dependable and approachable malaria diagnosis technique, the effectiveness of these models needs to be assessed in terms of accuracy, precision, and computational performance.

This study explores the choice and training of a variety of base models, including conventional machine learning techniques and convolutional neural networks (CNNs). The ensemble is designed to take advantage of each model's advantages, guaranteeing a thorough method of malaria identification. The goal of the research is to address the difficulties caused by the different clinical manifestations of malaria, such as variations in severity, relapse patterns, and prevalence across different geographic areas.[5]

Ensemble techniques incorporate a variety of basic models, each of which brings a distinct viewpoint to the process of making decisions as a whole [6]. Ensemble approaches aim to improve the detection system's robustness and lessen the drawbacks of individual models by aggregating the predictions of several models. The variety of base models is essential in the field of malaria detection in order to capture the subtleties that are specific to each Plasmodium species, including the intensity of symptoms, distinct presentations, and regional variances[8].

Therefore, the current issue may be effectively resolved with the help of an automatic diagnostic system. By applying picture segmentation and extraction, plasmodium in blood samples is found. Image pre-processing, image smoothing, image segmentation, and supported image acquisition are complete. To extract the characteristics of cells with malaria, a significant amount of effort has been done. An extensive discussion has been held over the extraction and optimization of malaria cell characteristics.[9] This type of virus detection may be somewhat automated, but it still takes skilled professionals to manually extract the feature vectors for the specific datasets. Nevertheless, a robust feature extraction method will improve detection accuracy.

Two steps in the architectural model are used for feature extraction:
The first phase is training; the second is testing (or recognition), which aids in the identification of Plasmodium vivax. With the potential to create an automated malaria testing system, machine learning algorithms have garnered significant interest from academics lately.
To achieve 93% and 94% accuracy, respectively, SVM and Naïve Bayes classifiers were used.
In this case, however, a deep convolutional neural network (CNN) with an accuracy of over 96% was used to identify malaria in the thick blood smear sample. As opposed to those individual red blood cells clipped from complete slide pictures supported thin films, pathologists find it more challenging to distinguish between infected and non-infected samples on thick films since the difference isn't as obvious.

Background

The conventional pipeline for automated malaria diagnosis consists of four stages: pre-processing photos, cell segmentation, feature selection, and classification of infected or non-infected malaria cells.[10] For each step, several techniques are presented in the literature. Blood smear pictures are enhanced by pre-processing techniques to increase the accuracy of later processing steps such feature extraction, cell segmentation, and classification. Any kind of impurity present in the images might lead to a misclassification of malaria cells and impair the efficiency of next processing steps.[11] Using different smoothing filters, such as Gaussian, geometric mean, and median filters, is a standard way to minimize noise in microscopic images. Additionally, morphological operators have been used to remove pollutants by filling in gaps and improving cell boundaries.[12] Also used are adaptive threshold and histogram equalization to enhance the contrast and resolution of the images. The variation in cell illumination was reduced by using malaria detection methods such HSV color space and grayscale color normalization.[15] Low-pass filters have also proved beneficial in eliminating noise-related frequency components from the microscopic images. The Laplacian filter, for instance, was used in certain methods to enhance the boundaries of red blood cells (RBCs) and sharpen edges in images.[13] The Wiener filter was used to remove the blurriness in the small images generated by unfocused optics.

A number of benefits result from the paper's use of machine learning to forecast Burkina Faso malaria outbreaks. In order to enable prompt and focused intervention methods, it first offers a proactive tool for epidemic forecasting. A more effective and knowledgeable response to malaria outbreaks in the area is also fostered by the research, which advances data-driven techniques in public health.[3]

The automated identification of malaria parasites from blood smears is accomplished by the study using deep learning techniques, most likely convolutional neural networks (CNNs). This method [7] focuses on improving the efficiency and precision of parasite detection in microscopic pictures by utilizing sophisticated image analysis and classification techniques. Further expanding the practical applicability and facilitating easy-to-use malaria detection is the creation of a smartphone application.

CNNs are useful tools for categorizing image classes. Very few research have utilized deep learning to distinguish between categories with cryptic morphological variation. Deep learning algorithms called convolutional neural networks (CNNs) are adept at extracting features from a well-organized array of input, such as images. Patterns such as lines, gradients, contours, and geometries are examples of these characteristics. One advantage of neural networks, such as CNN, is its capacity to extract characteristics from unprocessed picture collections [14]. CNN extracts the required characteristics on its own, as contrast to conventional machine learning algorithms that extract specific features and send them into the training process. A portable CNN model called Mobile Net V2 was created for the implementation of mobile machine learning. The goal of the MobileNet idea is to optimize memory use and processing power.

Existing System:

In order to identify malaria parasites, a specialist looks at blood smears under a microscope using manual microscopy, which is the mainstay of traditional malaria diagnosis techniques. Although this technology is dependable, it has significant drawbacks, such as the requirement for knowledgeable specialists, the time commitment, and the possibility of subjectivity in result interpretation. Automatic systems driven by machine learning have been investigated in recent years, but these methods frequently encounter difficulties including small dataset sizes, overfitting, and high processing requirements. Advanced architectures such as VGG16, DenseNet, and VGG19 are being explored to provide more reliable and accurate systems in order to tackle these problems.

Methodology:

This technique uses deep convolutional neural networks (CNNs) in conjunction with sophisticated transfer learning techniques to identify malaria by examining pictures of both parasitized and uninfected red blood cells. By applying pre-trained models on sizable picture datasets and customizing them for malaria detection, the method investigates the use of four well-known CNN architectures: VGG16, DenseNet201, VGG21, and VGG19. A thorough explanation of the process may be found below:

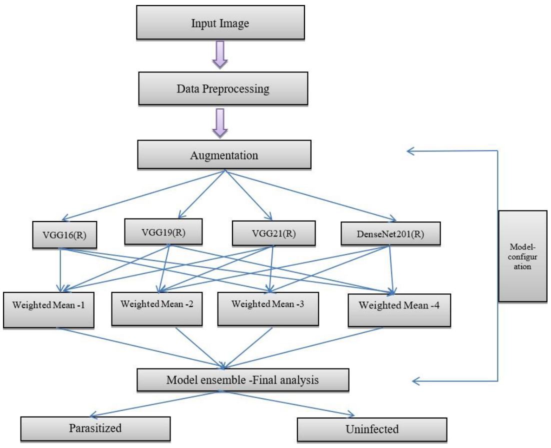

Fig 1: Proposed system architecture for malaria detection using ensemble method

Data Acquisition and Preparation:

To ensure enough variation to represent different red blood cell forms, stages of infection, and circumstances, this study employs a dataset of microscopic red blood cell images that have been classified as either parasitized (showing malaria infection) or uninfected. For this, open datasets such as the "Malaria Cell Images Dataset" are frequently used. All images are downsized to a standard resolution, usually 224x224 or 256x256 pixels, in order to standardize inputs for CNN models. This guarantees homogeneity and facilitates efficient feature extraction. To reduce biases and accelerate the model's convergence, the pixel values are normalized to a range of 0 to 1. Additionally, by producing a variety of permutations of the original dataset, data augmentation techniques like random rotations, flips, zooms, and shifts are utilized to avoid overfitting and enhance the model's capacity for generalization.

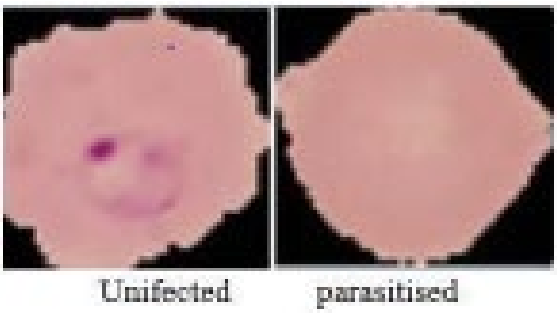

Fig 2: malaria images classified as infected and parasitised

Model Selection and Pre-training:

With the ImageNet dataset as their starting point, the research employs four convolutional neural network (CNN) architectures: VGG16, DenseNet201, VGG21, and VGG19. Red blood cell malaria detection can be accomplished using VGG16, a well-liked and uncomplicated 16-layer architecture. Its reputation for effective feature extraction—including edges, textures, and shapes—is due to its straightforward design of stacked convolutional and fully connected layers. Among its many applications in medical imaging is the elimination of parasites from red blood cells with the use of DenseNet201, a state-of-the-art model with dense connections between layers that learns more efficient and compact feature representations and thus solves problems like vanishing gradients. For the purpose of identifying minute changes in cell shape, VGG21—a 21-layer version of VGG16—is able to learn more complicated and abstract properties. Comparable to VGG16 but with 19 layers, VGG19 provides a little more depth for feature extraction and has demonstrated better performance in specific classification tasks; these qualities make it useful for assessing malaria infection in RBCs.

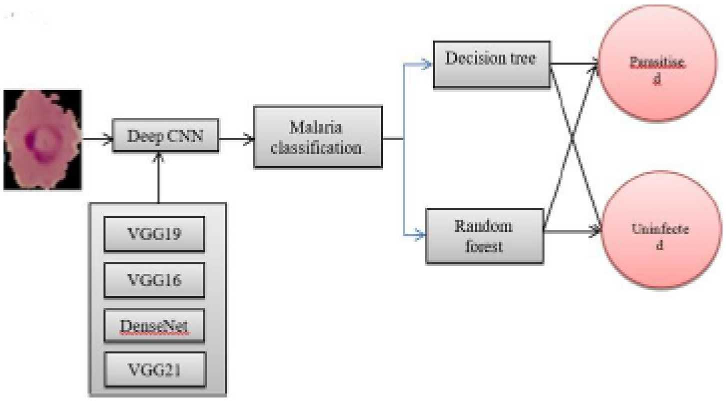

Fig 3: Convolutional Neural Network (CNN) Machine Learning Classifier model for Malaria Prediction.

Transfer Learning and Fine-tuning:

Four models—VGG16, DenseNet201, VGG21, and VGG19—that were previously trained on the ImageNet dataset are subjected to transfer learning. The procedure entails training these models to identify malaria by making use of their previously learnt features from various image datasets. In order to fine-tune the models, new layers are added to each one, initially weighted randomly, and designed for binary classification (parasitized or uninfected). The last layers are fine-tuned for the malaria detection job by training their weights with the malaria dataset; the preceding layers can be frozen to prevent this.

Model Training:

Part of training a model is splitting the dataset in two: one half goes into training the model to generalize to new data, while the other half is used for validation. Usually, 80% of the dataset is used for training, and 20% is reserved for validation. In order to ensure efficient convergence during training, the Adam optimizer is used to dynamically change the learning rate for each parameter. For this binary classification problem, categorical cross- entropy—the discrepancy between the two sets of labels—serves as the loss function. In order to train the model, it goes through a series of "epochs," or complete iterations of the dataset. Typically, a configuration with 50-100 epochs and a batch size of 32 or 64 is used, where the batch size defines the number of data processed every iteration and is determined based on available computational capabilities.

Evaluation:

Accuracy, precision, recall, sensitivity, and F1-score are some of the important performance indicators used to assess the models. Accuracy is the percentage of right predictions; precision is the percentage of parasitized cells that the model can properly identify; and recall is the percentage of parasitized instances that the model can find in the dataset. In order to provide a complete picture of the model's performance, we also use a confusion matrix to summarize the model's predictions. This matrix shows the number of correct parasitized cell identifications, the number of correct uninfected cell identifications, the number of false positives and false negatives, and the number of misclassified uninfected cells.

Model	Precision	Recall	F1 score	Accuracy
Custom CNN	0.8728	0.8721	0.8720	0.8720
VGG16 (R)	0.8456	0.8456	0.8456	0.8456
CNN-SVM	0.8214	0.8245	0.8266	0.8247
VGG19	0.9189	0.9189	0.9189	0.9189
VGG21	0.9247	0.9427	0.9427	0.9247
DenseNet201	0.9346	0.9346	0.9346	0.9346
Ensemble	**0.9694**	**0.9694**	**0.9694**	**0.9694**

Table 1: Results obtained by the proposed methodology when compared to the different models.

Ensemble Learning:

Together, the predictions from the four models (VGG16, DenseNet201, VGG21, and VGG19) are used in an ensemble technique to enhance model performance. This method aggregates the outputs of several models, reducing bias and variation and producing forecasts that are more consistent and accurate. Using a majority voting scheme, each model casts a vote on whether the image is infected or not, and the label that the majority predicts is chosen as the final classification. In general, an ensemble approach outperforms depending on any one model.

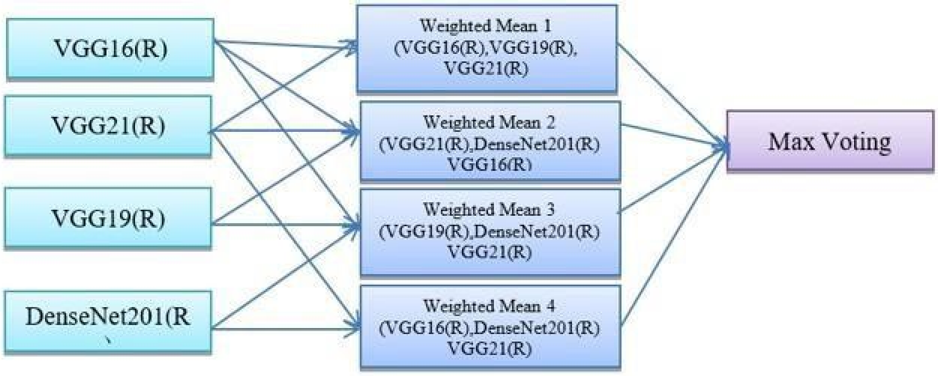

Fig 4: Ensemble method using max voting

Conclusion:

The four models used in this study-VGG16, DenseNet201, VGG21, and VGG19 are combined using an ensemble technique in order to enhance the performance of the model. More accurate and consistent forecasts are the outcome of this method's use of aggregated model outputs, which lessens bias and volatility. To get to the final classification, we employ a majority voting technique. Each model has a turn voting on whether the image is infected or not, and the result is the label that the majority predicted. In most cases, the results are better when using this ensemble method instead of depending on a single model.

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