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VL-M2C: Leveraging deep learning approach for stage detection of malaria parasites

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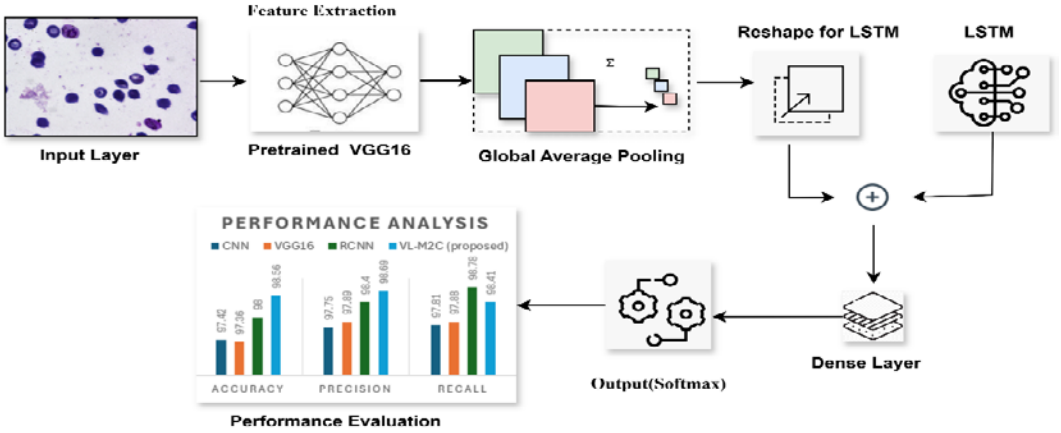
Article

ABSTRACT



Malaria is a parasitic infection that can be caused by the bite of infected anopheles' mosquitoes and can progress from mild symptoms to severe forms which make it crucial to understand its potential consequences. This study majorly focusses on multiclass classification and provides an ensemble framework for the detection of stages of malaria parasite in thin blood smears. In this study, we used publicly accessible dataset comprising 1320 images together with training and test json file. Initially pre-processing is applied to improve image quality, then key regions are extracted to retain important information during feature extraction phase. During this study, we compared different classification techniques to find the best model for multiclass classification for malaria parasite stages. Several metrics, including accuracy, recall, precision, and loss, are used to analyze the performance of the model. In this study, the ensemble method VL-M2C ie VGG LSTM Multiclass Malaria Classification has been proposed that raises the overall accuracy and robustness of the model by considering the advantages of individual classifiers. It has been compared with VGG16, CNN and RCNN. Our proposed VL-M2C has the best accuracy (98.56%) and lowest loss (0.1240), thus proves promising diagnosis system.

Keywords: Convolutional neural networks, Ensemble learning, Malaria parasite, Multiclass stage classification, Deep Learning; Diagnosis;

INTRODUCTION

Malaria is caused by the infection of plasmodium parasites on human bodies, through the infected anopheles mosquito bites which serve as their carrier host. After the plasmodium enters into the human blood system, it multiplies itself and launches assaults against red blood cells, ultimately breaking them down. The initial indicators of malaria, include chills, fever, headache and vomiting, which can be mild and may not immediately indicate the presence of the disease. However, if ignored, it can proceed significantly and have serious adverse reactions such as organ failure and even death. Therefore, it is essential to get prompt medical treatment if the disease has been detected in the human body.[1] Figure 1 depicts the five species of plasmodium that result in malaria in human beings. Plasmodium vivax and Plasmodium falciparum are the most prevalent species that causes malaria. Plasmodium falciparum is one of the most dangerous of all strain that is the primary cause of deaths related to malaria globally.[2] Under a microscope, each of the aforementioned species can be seen to have a unique appearance as they move through different stages of their growth cycle. These phases, which occur in a particular order, are the trophozoite, ring, schizont, and gametocyte stages.[3] The size, morphology, and occurrence or absence of malarial pigment determines the stage of the malaria parasite. Additionally, different species of the parasite exhibit variations in the infected cell's shape, the existence of characteristic dots and the parasite morphology at various life cycle stages. Monitoring the stages of malaria parasites helps healthcare

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workers to understand the effectiveness of their medication and identify their potential resistance.[4]

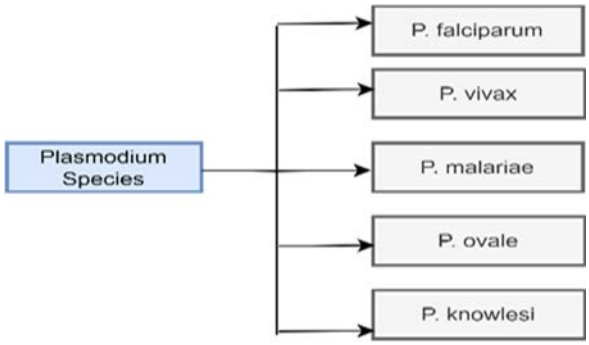

Figure 1. Types of Plasmodium Species

Diagnosing malaria accurately is very crucial for the effective treatment of disease. Various methods are available to predict malaria in human beings.[5] Some of the methods are Rapid Diagnostic Test (RDT), Light Microscopy, and molecular approaches like PCR. RDT are very quick and easy-to-use method for detecting disease and it is generally used in remote areas.[6] Molecular approaches like PCR are highly accurate but expensive as they require specialized equipment to perform testing which reduces its usage in resource-limited settings.[7] Light Microscopy is the commonly used method to detect malaria parasites in the human body [8]. In this method, a small drop of blood is carefully placed on a glass slide to form a blood smear. Then the smear is submerged in a staining solution like Giemsa stain to enhance the visibility of parasite present which can be examined under a light microscope. This technique is generally employed in identifying malaria or any other blood-borne parasites. For identifying the malaria parasites basically two types of smears are used namely, Thin and Thick smears. A drop of blood is dispersed evenly across the glass slide to create a Thin Smear. This is generally used to determine the existence of parasites, recognize the species, and also to determine stage of the development. However, in a Thick smear, a blood drop shows as a dense stain on the glass slide. This technique is used to determine whether or not human blood contains parasites.[9] It is a quicker and more precise way to determine whether a patient has malaria or not. Due to the absence of visible red blood cells in thick smears, parasites can be directly detected and counted.

In traditional methods, an extensive workforce and skilled macroscopic observers were required to analyze malaria slides and identify malaria parasites. Presently, however, automated technologies are being created to reduce human labour and increase the precision of the outcomes. Malaria diagnosis plays a very essential role in the treatment of malaria infection. Early diagnosis of the disease empowers one to fight the disease effectively. It is required to plan proper treatment and ensure the well-being of a patient. Thus, Artificial Intelligence in disease diagnosis plays a vital role in achieving safe and effective patient care. This paper presents a deep Learning technique to diagnose and detect the stage of malaria in the blood.

The Research contribution of this paper is:

- Most of the papers are based on the binary classification which tells the absence and presence of Malaria parasite but this paper introduces an innovative automated system to perform multistage classification of malaria disease that leverages the computer vision as well as Deep learning approaches. The suggested system has the potential to substantially improve the efficiency as well as accuracy of diagnosis.
- The study presents an ensemble-based approach by integrating classifiers VGG16, and LSTM and demonstrating how combining different model's strengths can enhance overall accuracy and reliability of the system.
- By addressing gaps in current methodologies, this study will provide the foundation for future research along with the advancements in the field, aiming to enhance patient care and improve health outcomes in malaria-affected regions.

This paper is organized into several key sections, each contributing to a proposed ensemble technique comprehensive exploration for malaria parasite detection. Section 1 Introduction, sets the stage by highlighting the significance of accurate parasite stage detection in the context of malaria diagnosis, emphasizing the need for an improved and automated ML approach. Examining previous research, the literature review establishes a basis for comprehending current approaches and points out gaps that our investigation seeks to fill. The Methodology section details the dataset, pre-processing steps, and the ensemble technique, elucidating the experimental setup for a transparent and reproducible study. In the Experimental Setup and Results sections, we present the specifics of our approach and provide a thorough comparison of classifiers, showcasing performance metrics. It also analyses the obtained results, drawing connections between our findings and the research objectives. The conclusion encapsulates key insights and implications of our research and also throw light on future directions.

Related Work

Automatic detection of malaria parasite has been extensively studied.[10–14] However most of these studies focus on binary classification i.e. presence of malaria parasite. In exploring the landscape of related work, it is essential to comprehend the current methodologies employed for malaria parasite detection and stages of malaria parasite that will lay the foundation for our novel ensemble-based approach. This section provides recent advancements in malaria stage detection with performance analysis of various techniques used for the multi class classification i.e. stages of malaria parasite of different species has been detected.

To address the subjective nature of visual parasitemia quantification, G. Díaz et al.[15] proposed a novel method for the classification of erythrocytes infected with Plasmodium falciparum. The approach involves pre-processing for luminance correction, segmentation utilizing normalized RGB color space, and an inclusion-tree representation to identify erythrocytes. A two-step classification process, aided by user intervention when needed, achieves specificity of 99.7% and 94% sensitivity for infected erythrocytes. The classification of infection stage shows an average sensitivity of 78.8%.

A comprehensive approach for the identification and categorization of malaria-infected stages utilizing microscopic pictures of thin blood smears is presented by D. K. Das et al.[16] Leishman-stained blood slide imaging, reduction of noise, lighting, erythrocyte segmentation, correction, and feature selection for classification of the machine are all included in the methodology. The marker-controlled watershed technique outperforms the other segmentation algorithms in boundary detection, especially in overlapping configurations. To distinguish between infected and non-infected erythrocytes, microscopic features at the texture, intensity and levels of morphology were obtained. To find possible features, feature selection methods such as information gain criterion and the F-statistic were used. For every feature subset, 888 erythrocytes were employed to train and evaluate five classifiers: multilayer perceptron neural network, Naive Bayes, logistic regression, classification and regression tree (CART), and RBF neural network. The performance evaluation demonstrates the multilayer perceptron network's effectiveness in the recognition and classification of malaria-infected erythrocytes along with the infected stages. The findings show that for the purpose of classifying malaria-infected stages, the top 60 features ordered by gain of information and the top 90 features ranked by F-statistic produce the best overall specificity, accuracy, sensitivity, and positive predictive values.

A. Nanoti et.al.[17] present an automated method for detecting and classifying malaria parasites and their life cycle stages in thin blood smear microscopic images. The proposed method involves acquiring images at 100x magnification, pre-processing, separating infected cells using k-means clustering in the Lab color space, and extracting shape and textural features for classification. The algorithm focuses only on infected cells, enhancing speed and efficiency. The K-nearest neighbor (KNN) classifier was trained with 300 images, achieving 90.17% accuracy and 90.23% sensitivity for detecting three life cycle stages across four malaria species. Features were ranked using one-way ANOVA, and KNN outperforms SVM in classification.

N. Abbas et al.[18] focused on improving the detection along with classification of malaria parasites in thin blood smear images using digital image processing. They have discussed two approaches: the first one uses k-NN, Naïve Bayes and Multi-Class SVM classifiers based on HOG and LBP features to classify the life cycle stages of malaria parasites. The second approach employs k-NN, SVM and Naïve Bayes classifiers to grade parasites based on their life phases and uses HOG and LBP features for accurate classification. The proposed methods show high sensitivity (96.75%) and specificity (94.59%) when tested on a benchmark dataset. The study emphasized an economical solution for malaria parasite grading in extensive testing.

Authors R.R Manku et al.[19] introduced a two-layer framework for malaria diagnosis, utilizing a Faster-RCNN for infected cell detection in the first layer and a separate neural network for classification in the second layer. The dataset, BBBC041v1 from the Broad Bioimage Benchmark Collection, contain 1364 images of blood smears with different cell classes. Layer 1 used Faster RCNN for infected cell detection, while Layer 2 employed a pretrained ResNet-50 for classification based on the detected cells' features. The two-layer approach overcomes issues with feature loss and achieved better accuracy.

S.S. Abbas et al.[20] proposed a computer-based framework using segmentation of images along with life stage classification with a RF classifier. The approach is evaluated on a dataset of Giemsa-stained images from 16 patients infected by the Plasmodium falciparum. The two-step process involved pixel classification for segmentation and subsequent classification of parasite life stages. The segmentation method outperformed the Otsu method, achieving a Dice coefficient of 0.82. Overall life stage classification accuracy is reported at 58.8%, improving to 82.7% when focusing on three main stages (ring, trophozoite, schizont).

Kittichai et al.[5] address the economic threat posed by avian malaria (Plasmodium gallinaceum) to the poultry industry. It introduced computer-aided diagnosis using deep CNNs (Darknet, Darknet19, Darknet19-448, Densenet201) to classify blood stages of the parasite. The models exhibit high accuracy, with Darknet outperforming others. The methodology employed a two-stage model involving YOLOv3 for object detection and subsequent classification using selected neural networks. Vijayalakshmi A et al.[2] introduced a novel approach for identifying infected falciparum malaria parasites using a VGG-SVM model, combining VGG networks and SVM through transfer learning. The proposed model achieves a high classification accuracy of 93.13% in identifying infected falciparum malaria, outperforming existing CNN models. The transfer learning strategy involved using pre-trained VGG layers as expert learning along with SVM as domain-specific learning, overcome class distribution mismatches. The method utilized digital microscopic images of stained blood smears for malaria diagnosis, showcasing the potential of transfer learning in medical image analysis.

The study by M.S. Davidson et.al.[21] introduced an automated image analysis approach to enhance the accuracy as well as standardization of malaria diagnosis through microscopic blood smear examination. A machine learning (ML) approach, incorporated Faster R-CNN for RBC detection and a residual neural network-50 model for infected cell classification. The model achieved high accuracy in cell segmentation and parasite detection, offering a practical route to automated malaria diagnosis. The user-friendly web tool, PlasmoCount, facilitated result review and quality assurance.

A. Molina et al.[22] emphasised on optimal deep learning model architecture selection for malaria-infected red blood cells (RBCs) classification from normal and other inclusion types. Based on extensive evaluation criteria such as sensitivity, positive predictive value, and overall accuracy, VGG-16 was the preferred model. Sequential CNN called VGG-16 has an easy structure that demonstrated the best results in those factors and was chosen the classification model for further testing purposes. The proposed deep learning system aimed at enabling efficient identification of malaria-infected RBCs that embodied excellent outcomes in single-cell recognition and feasibility of automatic identification. This approach separated malaria parasites and other RBC inclusions thereby providing rapid and objective morphological analysis. S. Li et al.[23] gave an approach to recognition of multi-stage malaria parasite using unsupervised learning and transfer learning from

source images with discriminative morphology through DTGCN. It proved to be a promising solution for automated low-cost diagnosis of malaria by showing its effectiveness across different stages.

The research by P. Krishnadas et.al.[24] focuses on automating malaria diagnosis by utilizing object detection models, YOLOv5, and scaled YOLOv4, to classify the type and stage of malaria parasites in Giemsa-stained blood smears. Two datasets were employed one for parasite classification with 172 images, including Vivax, Falciparum, Ovale, and Malariae classes, and another for stage classification with 1330 images indicating ring, trophozoite, RBC, gametocyte, schizont, leukocyte and difficult stages. While both models proved effective, scaled YOLOv4 outperformed YOLOv5 in accuracy.

To address inconsistencies in the manual inspection as well as staging, a framework integrating image processing as well as ML have been reported by T. Aris et.al.[25] Using thresholding and clustering, a standardized segmentation framework was developed to accurately identify the stages of P. falciparum & P. vivax parasites. Experimental Outcomes revealed the efficacy of thick smear image segmentation, achieving 99.86% accuracy with Phansalkar thresholding. Enhanced k-means (EKM) clustering, utilizing variance and a new transferring process, achieved a remarkable 99.20% accuracy and 0.9033 F1-score for segmenting all malaria stages Moreover, 86.89%, 98.82%, and 90.78% accuracy rates for parasite detection, species recognition, and staging are attained by an RF. This proposed framework lays the foundation for future improvements across a range of malaria species and enables flexible malaria parasite detection as well as staging. It also yields an interactive outcome.

Various deep-learning models were applied to classifying 4 classes of malaria parasite datasets by B. Kakkar et.al.[26] NASNetLarge and the Hybridized model of DenseNet201 and ResNet152V2 attained the greatest accuracy during the training phase, both reaching 99.9%. Conversely, DenseNet121 exhibited the best loss value of 0.001, showcasing superior performance. During validation, MobileNetV2 achieved the greatest accuracy, while ResNet152V2 obtained the best loss value of 0.005. However, DenseNet121, found a decrease in accuracy on the validation dataset suggesting overfitting during training.

The methods discussed in the state-of-art achieved high sensitivity, accuracy and specificity, demonstrating the potential of digital image processing and machine learning in this domain. However, many studies faced limitations such as high computational cost, dependency on extensive labeled datasets, overfitting and challenges in handling overlapping erythrocytes and classifying multiple parasite stages accurately. Our approach, utilizing a combination of VGG16 and LSTM, addresses these limitations by leveraging the powerful feature extraction capabilities of VGG16 and the sequence learning strength of LSTM. VGG16, pre-trained on ImageNet, effectively captures spatial features from blood smear images, while LSTM model's temporal dependencies, improving the accuracy of stage-wise parasite classification.

PROPOSED FRAMEWORK ENSEMBLE DEEP LEARNING

3.1 Dataset Description

The dataset P. vivax (malaria) is publicly available at https://bbbc.broadinstitute.org/BBBC041/ and consists of 1364 images i.e. collected from 3 different sources and labeled by malaria expert. A sample image of this dataset shown in Figure 2. There are total of six classes, consisting of 2 classes of uninfected cells comprising RBC as well as leukocytes and 4 phases of infected cells that include gametocyte, ring, trophozoites and schizonts stages. Figure 2 displays segmented images of infected cell. Two JSON files testing.json and training.json are also provided that serves as a structured way to link images with their corresponding class labels. A class label and set of bounding box coordinates were given for each cell.

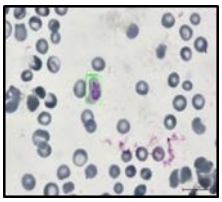

Figure 2(a) Sample dataset

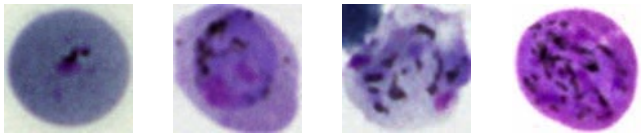

Figure 2. (a) Sample of dataset, (b-e) After Segmentation (b) Ring (c)Gametocyte(d)Schizont(e)Trophozoite

To enhance the quality of the image and to address the artifacts that can affect the further analysis, the pre-processing of the dataset is employed. This includes resizing of images, normalization and noise reduction to ensure a consistent dataset. Different feature extraction techniques can be used to extract the relevant features that can be used for the accurate identification of different stages of malaria parasite.

Design and implementation of the ensemble technique, integrating individual classifiers to leverage their strengths and enhance overall accuracy. This involves combining the outputs of multiple classifiers to make a consensual decision on the malaria parasite stage. Implementation and training of various classification techniques, including VGG16, CNN, and LSTM to establish baseline performance metrics. Each classifier is individually evaluated on the dataset.

3.2 Ensemble Model Design

Convolutional Neural Network (CNN) for Feature Extraction

The basic CNN model for image classification applied using Tensor Flow is shown in Figure 3. The model starts with an input dataset with images and a JSON file containing the image path and category label associated with each image. One hot encoding has been applied to convert the categorical labels into numerical

vectors. Each image is pre-processed, resized to fixed size pixels of 128x128 to maintain consistency and then normalized to bring it in the range of 0-1. The data is split into training as well as validation set to ensure the evaluation of the model on the unseen data. The model in which the layers are stacked one after another are referred as sequential model. Three convolution layers are used to extract the features from the data. These layers use filters of different sizes {3x3} to detect patterns at various scales within the images.

Each convolutional layer is followed by a ReLU activation function that introduces non-linearity and helps the model learn complex features. ReLU is Rectified linear unit [27] which is an activation function applied element by element to the convolution operation's output. Mathematically, ReLU is defined in equation (1) which means if input is greater than 0 then output is considered as x but if input is less than or equal to 0 output is considered as 0.

$$ReLU(x) = Max(0, x) \quad (1)$$

Max pooling layers [28] are also inserted after each convolutional layer which is use to downsample the feature maps by taking the maximum value within a specific window size (2x2). In Equation (2) M represent the output of max pooling operation, F represent feature map and W is window size say 2x2, then max pooling operation at a specific position (x, y) in the output can be expressed as:

$$M[x, y] = \max(F[i, j]) \text{for i in range}(x, x+), j \text{ in range}(y, y + W) \quad (2)$$

The max pooling layer preserves key features while assisting in lowering the spatial dimensionality of the data. The data is flattened into a 1D vector that can be fed into fully connected layers after the final convolutional and pooling layers. Two fully-connected layers are also used for further feature learning and classification. Initially, the dense layer has 128 neurons with ReLU activation for additional feature extraction. In the output layer, the final dense layer is used that has a number of neurons equal to the numbers of category labels present in the dataset.

It utilizes SoftMax activation to generate probabilities for each category, essentially predicting the class an image belongs to Adam optimizer is used in the compilation of the model with a categorical loss function suitable for multiclass classification. During training, the model iterates through the training data, updates its internal weights and biases to minimize the loss function to accurately classify images. After training, the model is evaluated on validation set.

VGG16 with Transfer Learning for Feature Extraction

A pre-trained VGG 16 model with transfer learning[29] is applied for feature extraction as shown in Figure 4. The model is pre-trained on ImageNet dataset which means it has been trained on massive dataset of millions of images and has learnt powerful feature representation for the visual recognition task. In this architecture, base layer of the model excluding the classification are frozen so that it is not retrained during training process as it has already learnt a powerful feature for the classification.

A custom classification head is added on top of the pre-trained VGG16 model which includes Global Average pooling layer which reduces the feature maps' spatial dimensions from the pre-trained model.It also includes the Dense layer with ReLU Activation which adds a hidden layer with 128 neuron and ReLU activation for further feature extraction. The model is fine-tuned by updating only weights in custom head classification layer so that model can adapt our specific classification problem. In this model, we have split the dataset into training as well as validation set which is further converted into TensorFlow dataset. The pre-processing function is applied on each image of the dataset which will read the image file, decode the image and resize the image to a fixed size of (224x224) pixels to match the input size of pretrained VGG16 model. Normalization of pixel values is also done by dividing it with 255 i.e converting it into a range from 0.0 to 1.0. A batch function has been utilized to group the data into batches for efficient training .In this model, prefetch function is also used to prefetch the data asynchronously which will in turn increases the speed of the training.

Label encoding is done to convert the category labels into numerical values for the model. In the output layer, it has the same number of units as the number of categories i.e. number of malaria stages available in dataset.

It uses SoftMax activation to predict the probability of each category of an image. This model is appropriate for multi-class classification problems because it has been compiled by utilizing the Adam optimizer and a sparse categorical cross-entropy loss function. The model is evaluated by utilizing primary metrics on the validation data after a predetermined number of iterations on the training set.

R-CNN for Malaria Parasite Detection

R-CNN is a region with convolution neural network which is a two-stage object detection model. In the first stage it proposes candidate regions that may contain objects in an image. In the second stage, the model classifies each proposal and refines its bounding box for accuracy. R-CNN utilizes pre-trained CNN for feature extraction, making it powerful for object detection tasks. In this research, we have utilized a pre-trained ResNet50 model[30] as the base model for feature extraction. This will exclude the top classification layer of ResNet50. Again, the base model is set non-trainable i.e. the weights are freezed to focus on learning in the following layers. In our model, we utilize a simplified RCNN that uses a pretrained model for feature extraction and focuses on classification based on pre-generated

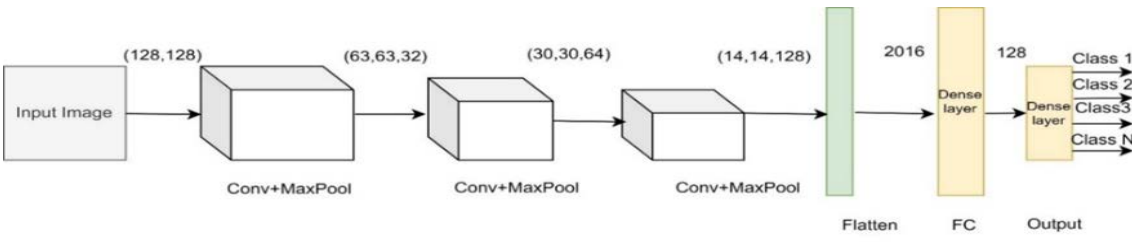

Figure 3. Convolution Neural Network

region proposals that would be distinct step in a full R-CNN implementation.

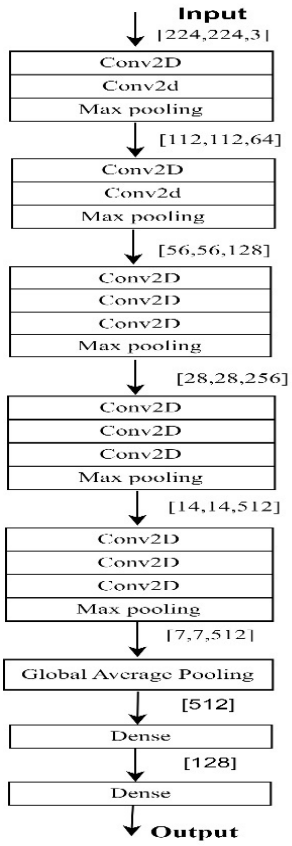

Figure 4. VGG16 with Transfer Learning

Proposed VL-M2C Model

In the proposed model VL-M2C, malaria stage classification is done using combination of VGG16 and LSTM as shown in Figure 5. JSON file is used to check the image path and category labels showing the stage of malaria parasite in the image. Images are pre-processed by decoding the jpeg image with 3 channels (RGB). It also incorporates data augmentation techniques that include flips (left-right, up-down), contrast adjustment, brightness adjustment, saturation adjustment and hue adjustment. These transformations are generally applied to increase data artificially and to improve the model robustness on the variation of real-world images. Images are also resized to 224x224 pixels to match VGG16 input size and normalize pixel values to the range [0,1] by dividing it with 255.The dataset has been then split into training and validation set utilizing train_test_split method of scikit-learn library. Label encoder is used to convert string category labels into numerical values.

A VGG16 model is pretrained on ImageNet dataset. Weights of the VGG16 layers are frozen to prevent them from being updated at the time of training and which leverages the learned features for image recognition . The VGG16 base model's last few layers are fine-tuned during training. This allows the model to adapt the pre-trained features specifically for the malaria classification task, all layers except the last 4 are frozen. Convolution layer is applied to an input image data to extract features. Mathematically, it can be represented with below equation (3) where i, j, k are the output feature map dimensions and m, n, l are the dimensions of the filter being applied.

$$Output[i,j,k] = \sum(Input[m,n,l] * Filter[i-m, j-n, l, k]) + Bias[k] \quad (3)$$

Global Average Pooling is applied to the output of the VGG16 to reduces the spatial dimensions i.e. height and width, while maintaining the channel dimension. This will recapitulate the features extracted by VGG16 into fixe-sized vector. Output received from global average pooling layer is reshaped to prepare it for the LSTM layer.

LSTM layer [31] will process the features extracted by VGG16 in a sequential manner. This is useful for capturing temporal dependencies that is useful in detecting stages of malaria parasite. To add non-linearity and decrease the dimensionality of the aggregated features, a fully connected layer with 128 neurons as well as ReLU activation is applied.

A fully connected layer employed in the output layer has as many neurons as there are categories in the dataset. In addition, the probabilities for every category are generated using SoftMax activation. The model has been compiled using the Adam optimizer and sparse categorical cross-entropy loss function for multiclass classification with integer labels. It is evaluated on the validation set and trained on the training dataset to test its performance based on several key criteria. In order to prevent overfitting, an early stopping callback is also implemented to monitor the validation loss. If the validation loss remains unchanged for a predetermined period of epochs, the training is halted.

EXPERIMENTS AND RESULTS

The suggested VL-M2C model effectiveness for identifying malaria parasite stages in thin blood smear data is examined in this section. In order to determine the efficiency of the model, it is analyzed using a range of performance metrics, such as accuracy, loss, precision, recall, and F1-score. The suggested VL-M2C model

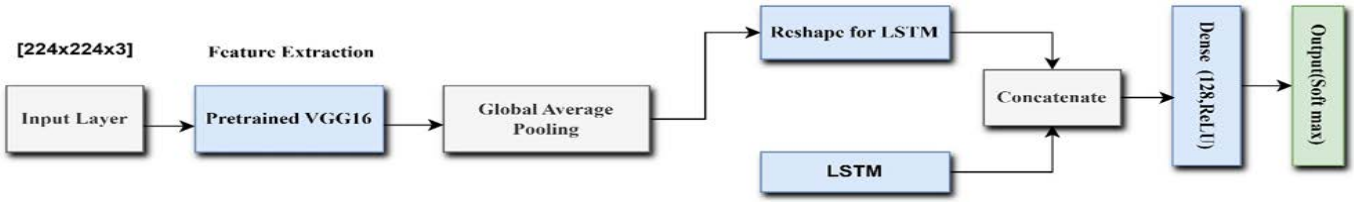

Figure 5. Proposed VL-M2C Model

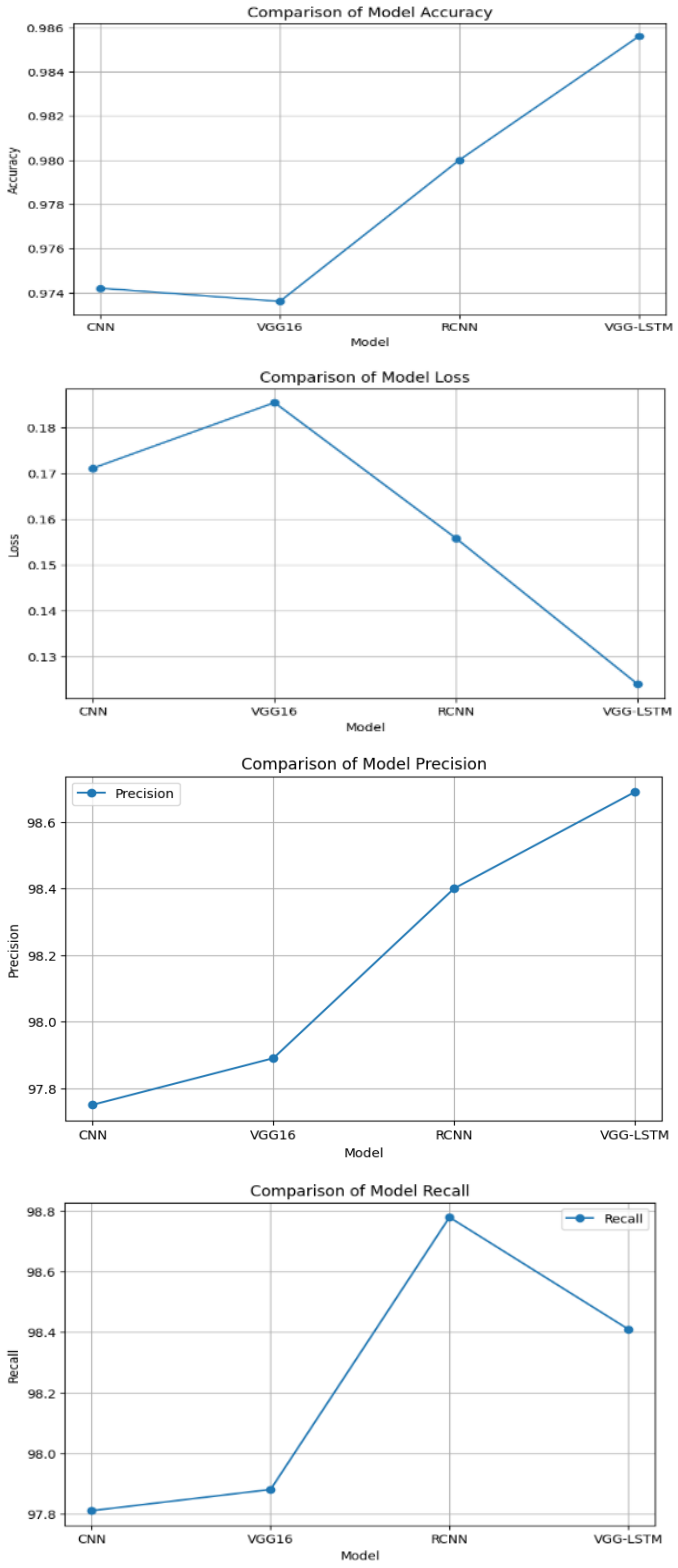

Figure 6. Graphical analysis of different models

in medical image processing achieves remarkable accuracy and efficiency by merging the advantages of LSTM and CNNs. Assessing the outcomes in Table 1, we could see that VL-M2C attained the highest accuracy of 98.56 among the evaluated models CNN, VGG16 and RCNN which obtained the accuracy of 97.42, 97.36 and 98 respectively.

Table 1. Performance analysis of different models

Model	Accuracy	Loss	Precision	Recall
CNN	97.42	0.1711	97.75	97.81
VGG16	97.36	0.1854	97.89	97.88
RCNN	98	0.1558	98.40	98.78
VL-M2C (proposed)	98.56	0.1240	98.69	98.41

It's noteworthy that CNN, a simpler model frequently used as a baseline, achieved a competitive accuracy of 97.42. This suggests that CNN captured significant discriminative features within the images. However, VL-M2C's edge over CNN highlights the potential benefits of incorporating an LSTM layer. LSTMs are adapting at learning temporal dependencies, which could be particularly useful if the image data exhibits sequential information or relationships between image elements. The impressive performance of the VL-M2C model, with a precision of 98.69 and a recall of 98.41 is demonstrated in Table 1 By expressing the percentage of accurately detected parasite stages among all projected positives, precision quantifies the accuracy of the model's positive predictions. The recall of the model quantifies its capacity to recognize actual positive cases. The high precision and recall scores of VL-M2C indicate its effectiveness in accurately detecting parasite stages and minimizing false positives, making it a reliable tool for malaria diagnosis. RCNN, on the other hand, demonstrates a good balance between accuracy of 98.00 and loss of 0.1558.

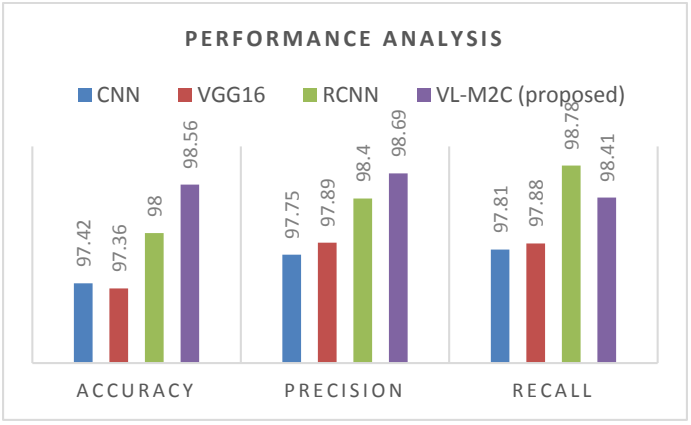

Figure 7. Analysis of model performance metrics

It is possible that RCNN effectively localized relevant image regions using its region-based approach, leading to a good overall performance. VGG16, while having a slightly lower accuracy of 97.36 compared to CNN, might have encountered challenges in capturing specific features crucial for optimal classification in this dataset. Figure 6 depicts the graphical analysis of the models discuss in this study.

Delving deeper into the results, we can observe that VL-M2C also achieved the lowest loss of 0.1240 when analyzed alongside

with the other models CNN, VGG16, RCNN. The discrepancy between the actual labels along with the model's predictions is represented as loss. The model's predictions and the actual data are more closely aligned when the loss value is smaller. This indicates that VL-M2C efficiently learned the patterns within the training data, minimizing errors during the classification process. Figure 7 indicates VL-M2C's superior ability to correctly classify image data compared to the other individual classifiers.

CONCLUSION AND FUTURE SCOPE

A detailed analysis of existing literature divulges strengths and limitations in current approaches, setting the stage for our proposed ensemble-based technique. The research focuses on a publicly available P. vivax (malaria) dataset of 1320 images, employing pre-processing and feature extraction to optimize image quality. The findings indicate the effectiveness of our proposed model VL-M2C in image classification. VL-M2C outperformed other models in terms of accuracy and losses, suggesting that it can learn distinct features and make accurate predictions. A solid experimental design ensured a reliable assessment, which has been supported by statistical analysis to show significant differences. The integration of individual classifiers is part of an ensemble technique whose goal is to completely revolutionize multi-stage malaria parasite detection. In order to improve its performance, it would be interesting for future work to investigate how hyperparameter tuning affects VL-M2C and probably explore different LSTM architectures. Additionally, applying VL-M2C to various image classification tasks would provide further insights into its generalizability and effectiveness across different datasets. This research moves towards closing some gaps in the field, thus providing useful information for future advances in multi class classification malaria diagnosis

CONFLICT OF INTEREST STATEMENT

Authors do not have any conflict of interest related to this work.

REFERENCES

1. H. Caraballo, K. King. Emergency department management of mosquito-borne illness: malaria, dengue, and West Nile virus. *Emerg. Med. Pract.* **2014**, 16 (5), 1–23; quiz 23–24.
2. Vijayalakshmi A, Rajesh Kanna B. Deep learning approach to detect malaria from microscopic images. *Multimed. Tools Appl.* **2020**, 79 (21–22), 15297–15317.
3. World Health Organization. Compendium of WHO malaria guidance: prevention, diagnosis, treatment, surveillance and elimination; World Health Organization, Geneva, **2019**.
4. S. Shambhu, D. Koundal, P. Das, et al. Computational Methods for Automated Analysis of Malaria Parasite Using Blood Smear Images: Recent Advances. *Comput. Intell. Neurosci.* **2022**, 2022, 1–18.
5. V. Kittichai, M. Kaewthamasorn, S. Thanee, et al. Classification for avian malaria parasite Plasmodium gallinaceum blood stages by using deep convolutional neural networks. *Sci. Rep.* **2021**, 11 (1), 16919.
6. A. Moody. Rapid Diagnostic Tests for Malaria Parasites. *Clin. Microbiol. Rev.* **2002**, 15 (1), 66–78.
7. K.A. Mangold, R.U. Manson, E.S.C. Koay, et al. Real-Time PCR for Detection and Identification of *Plasmodium* spp. *J. Clin. Microbiol.* **2005**, 43 (5), 2435–2440.
8. P. Dahal, B. Khanal, K. Rai, et al. Challenges in Laboratory Diagnosis of Malaria in a Low-Resource Country at Tertiary Care in Eastern Nepal: A Comparative Study of Conventional vs. Molecular Methodologies. *J. Trop. Med.* **2021**, 2021, 1–9.
9. Stefan R. Jaeger, PhD Sameer Antani, PhD Mahdieh Poostchi, PhD Sivaramakrishnan Rajaraman, PhD Feng Yang, PhD Hang Yu. Malaria Screening: Research into Image Analysis and Deep Learning. In *A Report to the Board of Scientific Counselors*; **2018**.
10. G. Marques, A. Ferreras, I. de la Torre-Diez. An ensemble-based approach for automated medical diagnosis of malaria using EfficientNet. *Multimed. Tools Appl.* **2022**, 81 (19), 28061–28078.
11. T. Jameela, K. Athotha, N. Singh, V.K. Gunjan, S. Kahali. Deep Learning and Transfer Learning for Malaria Detection. *Comput. Intell. Neurosci.* **2022**, 2022, 1–14.
12. T. Banerjee, A. Jain, S.C. Sethuraman, et al. Deep Convolutional Neural Network (Falcon) and transfer learning-based approach to detect malarial parasite. *Multimed. Tools Appl.* **2022**, 81 (10), 13237–13251.
13. B. Qin, Y. Wu, Z. Wang, H. Zheng. Malaria Cell Detection Using Evolutionary Convolutional Deep Networks. In *2019 Computing, Communications and IoT Applications (ComComAp)*; IEEE, Shenzhen, China, **2019**; pp 333–336.
14. Z. Liang, A. Powell, I. Ersoy, et al. CNN-based image analysis for malaria diagnosis. In *2016 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*; IEEE, Shenzhen, China, **2016**; pp 493–496.
15. G. Díaz, F.A. González, E. Romero. A semi-automatic method for quantification and classification of erythrocytes infected with malaria parasites in microscopic images. *J. Biomed. Inform.* **2009**, 42 (2), 296–307.
16. D.K. Das, A.K. Maiti, C. Chakraborty. Automated system for characterization and classification of malaria-infected stages using light microscopic images of thin blood smears. *J. Microsc.* **2015**, 257 (3), 238–252.
17. A. Nanoti, S. Jain, C. Gupta, G. Vyas. Detection of malaria parasite species and life cycle stages using microscopic images of thin blood smear. In *2016 International Conference on Inventive Computation Technologies (ICICT)*; IEEE, Coimbatore, India, **2016**; pp 1–6.
18. N. Abbas, T. Saba, A. Rehman, et al. Plasmodium life cycle stage classification based quantification of malaria parasitaemia in thin blood smears. *Microsc. Res. Tech.* **2019**, 82 (3), 283–295.
19. R.R. Manku, A. Sharma, A. Panchbhai. Malaria Detection and Classificaiton. arXiv November 29, 2020.
20. S.S. Abbas, T.M.H. Dijkstra. Detection and stage classification of Plasmodium falciparum from images of Giemsa stained thin blood films using random forest classifiers. *Diagn. Pathol.* **2020**, 15 (1), 130.
21. M.S. Davidson, C. Andradi-Brown, S. Yahiya, et al. Automated detection and staging of malaria parasites from cytological smears using convolutional neural networks. *Biol. Imaging* **2021**, 1, e2.
22. A. Molina, J. Rodellar, L. Boldú, et al. Automatic identification of malaria and other red blood cell inclusions using convolutional neural networks. *Comput. Biol. Med.* **2021**, 136, 104680.
23. S. Li, Z. Du, X. Meng, Y. Zhang. Multi-stage malaria parasite recognition by deep learning. *GigaScience* **2021**, 10 (6), giab040.
24. P. Krishnadas, K. Chadaga, N. Sampathila, et al. Classification of Malaria Using Object Detection Models. *Informatics* **2022**, 9 (4), 76.
25. T. Aris, A. Nasir, W. Mustafa, et al. Robust Image Processing Framework for Intelligent Multi-Stage Malaria Parasite Recognition of Thick and Thin Smear Images. *Diagnostics* **2023**, 13 (3), 511.
26. B. Kakkar, M. Goyal, P. Johri, Y. Kumar. Artificial Intelligence-Based Approaches for Detection and Classification of Different Classes of Malaria Parasites Using Microscopic Images: A Systematic Review. *Arch. Comput. Methods Eng.* **2023**, 30 (8), 4781–4800.
27. V. Nair, G. Hinton. Rectified linear units improve restricted boltzmann machines. In *In Proceedings of the 27th international conference on machine learning (ICML-10)*; pp 807–814.
28. J. Nagi, F. Ducatelle, G.A. Di Caro, et al. Max-pooling convolutional neural networks for vision-based hand gesture recognition. In *2011 IEEE International Conference on Signal and Image Processing Applications (ICSIPA)*; IEEE, Kuala Lumpur, Malaysia, **2011**; pp 342–347.
29. S. Sharma, K. Guleria, S. Tiwari, S. Kumar. A deep learning based convolutional neural network model with VGG16 feature extractor for the detection of Alzheimer Disease using MRI scans. *Meas. Sens.* **2022**, 24, 100506.
30. H. Kaiming, Z. Xiangyu, S. Ren, S. Jian. Deep Residual Learning for Image Recognition; Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR), **2016**; pp 770–778.
31. F. Gers. Long short-term memory in recurrent neural networks. Doctoral dissertation, Verlag nicht ermittelbar. **2005**.