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V2SeqNet: A robust deep learning framework for malaria parasite stage classification in thin smear microscopic images

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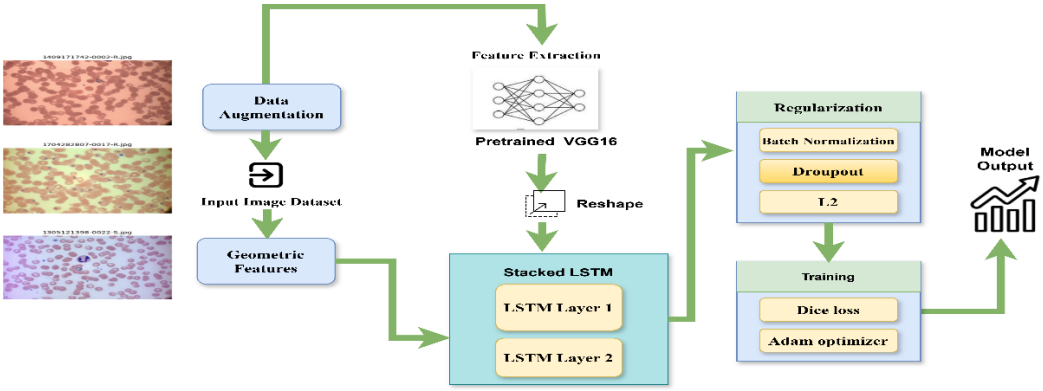
Article

ABSTRACT



Malaria is a global health problem, and it requires good diagnostic tools for early treatment. This research aims to develop an advanced deep learning-based model for the classification of malaria parasite stages using the MP-IDB dataset. Advanced preprocessing techniques such as resizing, normalization and data augmentation are used in research to enhance the quality of images and the variability of the dataset. A new architecture V2SeqNet ie VGG with 2 LSTM Layers for Sequential Classification Network combining VGG16 with LSTM layers and geometric feature extraction shows a good performance with accuracy of 99.69%, recall of 100% and precision at 98.78%. Results are compared to other state-of-the-art detection and classification models like MobileNet, EfficientNet, ResNet-50, DenseNet-121etc. Robustness, precision and scalability of the proposed model will give it an opportunity to become the best choice for automated malaria diagnosis. Future extension of the model is to identify more than one malaria species and stages, thus increasing its utility for comprehensive malaria diagnosis.

Keywords: Malaria Stage Classification, Deep Learning, Image Preprocessing, Augmentation Techniques, Automated Malaria Detection

INTRODUCTION

Malaria is a persistent threat mainly in tropical regions. This disease is produced by protozoan parasites belonging to the Plasmodium genus.[1] The primary cause is the Plasmodium parasite, which is transmitted to humans through the bite of an infected Anopheles mosquito. Five species of this parasite are existing which are P. falciparum, P. vivax, P. malariae, P. ovale, and P. knowlesi.[2] Out of these, two most prevalent species are Plasmodium falciparum and Plasmodium vivax. Even though rapid diagnostic test (RDT) has gained popularity in the last few years, examining blood smears (thin and thick) remains the most reliable method for diagnosing malaria. Earlier, laboratory technicians manually look through these smears under the microscope, locate the parasites, and count the parasitaemia. This traditional method is time-consuming since there is a need of a workforce, expertise for preparation and examination of slides to distinguish between species and development stages of parasites.

The malaria parasite undergoes several stages of development inside the mosquito as well as human host. There are four development phases that comprises of i) ring stage, ii) trophozoite stage, iii) schizont stage and iv) gametocyte stage. When infected anopheles mosquito bites human host, malaria parasites enter in its body. Initially, the parasite has a small size, single nucleus and appears as ring stage. It starts replicating in red blood cell (RBC) and as the parasites matures it enters the next stage i.e. trophozoite where they grow, and multiple nuclei are developed. It led to feeding on nutrients from the hosts' RBCs, due to which the RBCs are destroyed. After the trophozoite stage, the schizont stage comes, where parasite undergoes a technique called schizogony or asexual reproduction in which the genetic material of the parasite gets duplicated, and it divides into many daughter cells. These daughter

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cells are named merozoites which break the red blood cell of the host and migrate into the blood vessels by which they can enter some other red blood cells so that the cycle is begun again. During the schizont stage, some of the parasites moved into sexual forms called gametocytes. Even though the gametocytes are not a part of any of the asexual multiplication, they are essential for the sexual phase of the parasite's life cycle. When a mosquito feeds on the blood of an infected person, it ingests these gametocytes along with the blood.[3]

The gametocytes continue their development inside the mosquito, developing into male and female gametes. Once fertilized, it forms a zygote, which upon undergoing a series of changes eventually develop into sporozoites. It then moves to the salivary glands of the mosquito. It is through these salivary glands that the sporozoites can be transmitted from the mosquito to another human being during the next blood meal, thus starting the cycle again.[4]

Malaria poses a significant threat to public health, especially in tropical and subtropical areas. For its effective treatment, and accurate diagnosis is essential.[5] The development of automated systems for malaria diagnosis, using image classification methods, has gained significant attention.[6] Two different blood smears are examined for the identification of malaria parasite- a) thick smear, primarily used to detect the presence of malaria parasite and b) Thin smears help not only to confirm the presence of malaria parasites but also to identify their species and stages.[7]

The manual classification of malaria parasite stages requires skilled workforce and can be error prone. An automated system can help us to overcome these problems. Current Deep learning approaches face significant challenges related to image quality, lighting variability and noise in microscopic images. Poor-quality images, often affected by artifacts or low contrast, can lead to incorrect classifications, potentially hindering proper treatment and patient care. Pre-processing techniques applied to input images significantly impact the performance of classification algorithms. Recent studies have introduced several transfer learning techniques in diagnosis malaria through microscopic images. By using Deep learning techniques, extraction and evaluation of relevant information from raw data without human intervention becomes easier and convenient. Unlike ML techniques, which requires features to be extracted manually, the deep learning techniques extract the features automatically from the raw data. It then processes the data and classify them efficiently and more accurately.[8]

This research introduces a novel approach to malaria parasite stage classification by integrating advanced deep learning architectures with geometric feature extraction techniques. The main contributions of this work are as follows:

- The study incorporates sophisticated preprocessing methods such as resizing, normalization and synthetic mask generation, coupled with extensive data augmentation (rotation, scaling, brightness adjustments) to improve image quality and enhance model generalization.
- A novel architecture V2SeqNet (VGG with 2 LSTM Layers for Sequential Classification Network) is proposed by combining VGG16, LSTM layers and geometric features (area and perimeter), achieving state-of-the-art performance metrics, including 99.69% accuracy, 98.78% precision and 100% recall, significantly surpassing other models.
- The research provides an in-depth comparison of the proposed model with widely used architectures, including MobileNet, EfficientNet, ResNet-50, and DenseNet-121, validating the superior performance of the V2SeqNet model on the MP-IDB dataset.

LITERATURE *SURVEY*

Over the years, several research studies have considered innovative methods for classifying malaria parasite stages using various advanced computational techniques. In the following review, various research papers have been considered, focusing on methodologies, preprocessing techniques and classification models to improve accuracy and reliability in malaria diagnosis. Preprocessing plays a critical role in disease detection through microscopic images, notably in malaria diagnosis. Besides this, this enhances the model's performance and helps the health workers distinguish between the parasite's stages correctly at an initial stage.

Author I.M.L Chaharou et al. [9] applied processing technique of image cropping to enhance the effectiveness of different deep learning model like DenseNet, LeNet-5, CNN. This method can maximize the region of interest by emphasizing the image's key features. Using the proposed pre-processing technique, DenseNet achieved an accuracy of 97.50%, significantly higher than the 81.26% accuracy obtained using the Canny filter for contour detection.

Mosabbir Bhuiyan et al.[10] introduced an ensemble learning approach, combining ResNet50, Inception, and DenseNet201, to improve malaria detection accuracy from RBC images. Using diverse Deep learning methods and data augmentation techniques, the proposed model achieves 96.87% precision, outperforming individual models and effectively addressing overfitting challenges. Several models are tested, including a custom-built CNN, Transfer Learning, and a hybrid CNN-Machine Learning classifier. Additionally, classification is performed using algorithms like Random Forest, Support Vector Machine (SVM), K-Nearest Neighbour (KNN) and Decision Tree.

Antora Dev et al.[11] introduced hybrid deep learning models designed for malaria detection, emphasizing the use of cascading RNN classifiers. The CNN-LSTM-BiLSTM model achieved 96.20% accuracy, while CNN-BiLSTM-GRU minimized type-II errors. It clearly ensures deep learning model hods enormous potential in advancement of diagnosis of malaria.

Ozbilge E. et al. [12] investigated the use of deep learning-based object detection models for identifying malaria parasites in blood smear images. Their study utilized 1,081 thin blood smear samples from patients in Cyprus and compared advanced models like YOLOv8, achieving a mean Average Precision (mAP@0.5) of 0.9031. Ensemble strategies improve accuracy even further, up to 0.9324 using the non-maximum weighted method. This is novel contribution through model combination, optimization of detection strategy, and pioneering work on YOLOv8 in malaria detection.

In the study author Thaqifah Ahmad Aris et al. [13] offered a machine learning framework in the detection of malaria parasites, Plasmodium species, and staging in P. falciparum and P. vivax from both thick and thin blood smears. The study utilized sophisticated

techniques such as Phansalkar thresholding and EKM clustering and the results are promising. The Random Forest classifier obtained an accuracy of 98.82% species recognition accuracy and 90.78% staging accuracy. It has much potential in its future applications to perform an automated malaria diagnostic.

Author G. Díaz et al[14] introduced a paradigm that differentiate the three life phases of Plasmodium falciparum, namely Ring, Trophozoite or Schizont stage. A model suggested integrates pre-processing for removal of variations in brightness using local adaptive low-pass filter. Then comes three-phase recognition. The color-based approach is segmentation or color-based clustering, where pixels are classified by a specific color space. Each pixel would then be tagged foreground or background. To suppress background pixels and for erythrocytes detection, background pixels are gathered in one streamlined inclusion tree. For complete quantification, foreground objects need separation when their largest area is greater than or equal to a threshold because they are assumed clumped erythrocytes. In the overall sense, the purpose of parasitic quantification is to separate healthy from infected erythrocytes. Here, the classification of the parasites is divided into two stages: first, the classification was used to determine the infection status of an erythrocyte, and then the type was identified using a set of classifiers.

Author N. Abbas et al. [15] presents a significant contribution to automated malaria parasite detection and classification. Employing k-nearest neighbor, Naïve Bayes, and multi-class SVM classifiers based on HOG and LBP features, the approach achieves commendable sensitivity (96.75%) and specificity (94.59%). The segmentation method improves quantification of RBC by better handling clumps through concavity region analysis. With the independent focus on factors such as RBC morphology, the study is able to expand in scope, offering an economical and accurate solution to grade malaria parasites in large-scale testing.

Authors Manku et al [16] designed a two-layer framework for malaria diagnosis, The first layer used a Faster-RCNN for infected cell detection and a second layer used a separate neural network for classification. 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 feature loss issues are overcome using the two-layer approach and this model achieves better accuracy.

Davidson et al. [17] introduced an approach of automated image analysis that improved the accuracy along with the standardization of diagnosis of malaria through microscopic blood smear examination. A machine learning (ML) approach incorporated Faster R-CNN for the detection of RBC and a residual neural network-50 model for infected cell classification. The model provided high accuracy in cell segmentation and parasite detection.

The literature highlights the significant advancements that have been achieved in malaria parasite detection and classification through the innovative preprocessing techniques and sophisticated deep learning models. Major methodological areas focus on data augmentation, the concept of hybrid deep learning architectures and the inclusion of ensemble strategies for improved model performance.

Our research focus on the spatial-temporal dependencies and take advantage of local and global features to achieve the highest accuracy and reliability in diagnosing malaria. This makes our work a substantial contribution to the automated detection and classification of malaria, overcoming difficulties in imbalanced datasets, overfitting and stage differentiation.

RESEARCH METHODOLOGY

The research methodology is based upon the development of a robust framework for malaria parasite stage classification. It begins with Dataset Description that involves the origin, composition and relevance of the dataset. It also accommodate preprocessing techniques such as ROI Extraction that obtains the important region for improve classification and Contour Extraction that extracts the geometric features. Data Augmentation introduces transformations that enhance the model's robustness against variations. The methodology incorporates the VL-M2C Model [18] that unites visual learning and geometric features, so comprehensive analysis is provided and lastly, Enhanced Architecture is designed that optimizes the pipeline for high-accuracy and computation. This systematic approach ensures precise and reliable malaria parasite detection.

Dataset Description

In this study, thin blood smear images are collected from open-source MP-IDB datasets, ensuring a variety of samples with different quality levels. All images in MP-IDB are saved in a JPG format, of 2592 x 1944 pixels resolution and a 24 bits color depth, with about 717 MB of total file size.

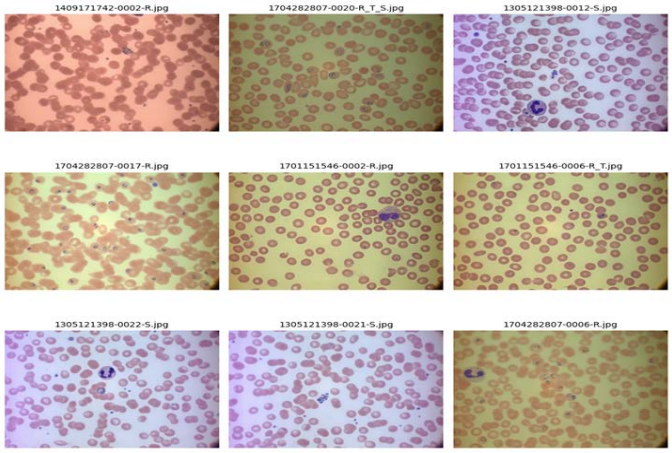

Figure 1. Sample thin blood smear images from the MP-IDB dataset

The data was solely collected from thin blood smears stained with Giemsa, as explained in [19]. Figure 1 shows the sample thin blood smear images from the MP-IDB dataset for further processing to detect the different stages of the malaria parasite.

Preprocessing Techniques

In this study, a variety of pre-processing techniques have been applied to raw microscopic images of malaria-infected blood smears before feeding them into classification model. Preprocessing is critical for enhancing the quality of the images and ensuring that features extracted from them are robust and informative.

Region of Interest (ROI) Extraction for Enhanced Malaria Parasite Classification

Extraction is done to concentrate on the region of interest (ROI)[20]. This ensures that only the regions of interest are processed. The method is very useful in isolating the area where malaria parasites exist, thus reducing irrelevant regions that may introduce noise or irrelevant data during classification. Focusing on the key sections of the image can enhance the performance of feature extraction and classification models by downsizing irrelevant details and extraneous parts.

For cropping, pixel coordinates are used to slice the image. In eq(1), $I(x, y)$ is the image matrix where x and y represent pixel coordinates.

$$I_{cropped} = I(x_1 : x_2, y_1 : y_2) \quad (1)$$

Where (x_1, y_1) and (x_2, y_2) are the top left & bottom right coordinates of the region to be cropped.

Figure 2 showcases the sample of cropped images from each malaria parasite stage. The images have been cropped to focus on the ROI, allowing better visualization of parasite morphology at each stage. Here, R, S, T, and G represent Ring, Schizont, Trophozoite, and Gametocyte, respectively [21].Table 1 will show the number of images per stage extracted from given dataset after image cropping.

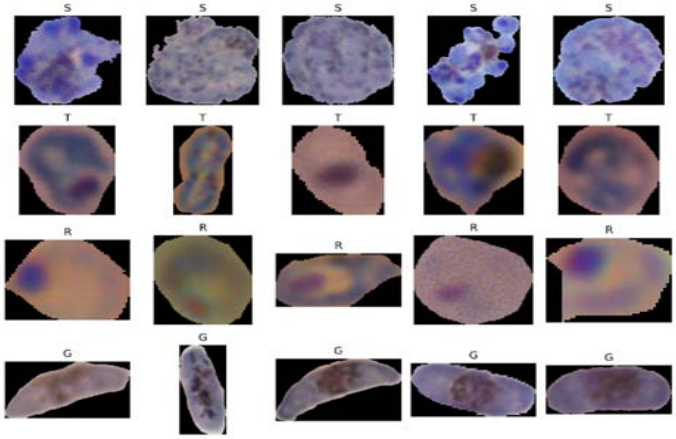

Figure 2. Extracted sample images focusing on the region of interest (ROI) for each malaria parasite stage

Once the images are pre-processed, the necessary features are extracted for classification process[22]. This process requires segmentation or detection techniques to identify regions of interest (ROIs) in the image, which are then used for further analysis and classification[23]. In this work, after preprocessing, we extract geometric features based on the contour of the detected objects in the image.

Contour Extraction

Image contours are boundaries or outlines in an image formed by a boundary of an object. This could be said as the curve connected to all the continuous points along the boundaries of an object, thus serving to differentiate this object from another object. Contour extraction usually proceeds from binary images, in which objects are separately taken out against the background. Contours are extracted from the image [24] using OpenCV's findContours function, which captures the boundary of objects in a binary image. Contours are significantly used to play a major role in feature extraction and object recognition tasks. Contours have been used to analyze the shape and pattern of malaria parasites in the images that have undergone pre-processing. The contours are features that can calculate geometric features like area and perimeter which may make classification and analysis easier. Given a contour C, the area A and perimeter P of the contour can be calculated by using the following:

$$A(C) = \sum_{(x,y)\in C} Area\ of\ enclosed\ pixels \quad (2)$$

$$P(C) = \sum_{(x_i,y_i)(x_{i+1},y_{i+1})\in C} \sqrt{(x_{i+1} - x_i)^2 + (y_{i+1} - y_i)^2} \quad (3)$$

Weighted area and perimeter add more feature values for a complete representation of the detected objects and hence improve the performance of the classification model. Weighted Area highlights the larger components, and Weighted Perimeter is the area-weighted average of the perimeters of all components C_i, calculated by dividing the sum of the product of each component's area and perimeter by the total area. Weighted area and Perimeter can be defined with below mathematical equations.

$$Weighted\ Area = \frac{\sum_{i=1}^{n} A(C_i)^2}{\sum_{i=1}^{n} A(C_i)} \quad (4)$$

$$Weighted\ Perimeter = \frac{\sum_{i=1}^{n} P(C_i).A(C_i)}{\sum_{i=1}^{n} A(C_i)} \quad (5)$$

.

Where $A(C_i)$ and $P(C_i)$ represent the area and perimeter of the i^{th} contour respectively, and n is the total number of contours detected.

This part focused on extraction of geometric features of malaria parasite images by preprocessing it for contour-based analysis. Boundary detection for calculating the area and perimeter helped in attaining some major key features which are descriptive in explaining the shapes and structures of parasites. A further refinement of these features is made by the weighted combination of area and perimeter for the objects to achieve a more precise representation. The extracted features play a significant role in the next classification step since they improve the distinguishing capability of the machine learning model between the different stages of malaria parasites.

Data Augmentation for Robustness

The key role that data augmentation [25] plays in enhancing the performance and robustness of deep learning models, especially in imbalanced datasets. In this study, the augmentation techniques were used to balance the malaria parasite life stages' distribution of the MP-IDB (P. falciparum) dataset [19] for enhancing the generalization ability of the model. Augmentation methods included random rotations up to ±10°, horizontal and vertical flipping, and random zooming with the retention of 80% of the image area. These transformations significantly enhanced the diversity of the training data without losing the biological relevance of the images. The data set was made balanced by adding more

underrepresented classes, equalizing the number of samples at every stage, which includes Ring, Trophozoite, Schizont, and Gametocyte. This reduced overfitting and increased the accuracy of classification. This also gives a robust and reliable model for automated detection of malaria parasite stages. Table1 presents a summary of the augmentation process by showing the initial number of images, the number of augmented images generated, and the total images after augmentation at each stage. Augmentation processing time was variable because it was contingent on the number of images that needed to be added to attain the target number, and more augmentation was needed for Gametocyte (G) and Schizont (S) since the initial sample size was small for both stages. This augmented the dataset with a balance to increase the model's generalization capacity across all stages.

Table1: Augmentation Statistics for Balancing Malaria Parasite Life Stage Dataset

Stage	Images Before augmentation	Augmented Images	Total Images After Augmentation	Processing Time
G	7	14,993	15,000	3 minutes 57 seconds
R	1,230	13,770	15,000	2 minutes 50 seconds
S	18	14,982	15,000	3 minutes 57 seconds
T	42	14,958	15,000	3 minutes 13 seconds

Designed Model

The proposed V2SeqNet model, namely, VGG with 2 LSTM Layers for the Sequential Classification Network, as seen in Figure 3, has a better capacity for segmentation and precise classification of the malaria parasites stages. The architecture applies regularized convolutional layers using batch normalization that helps to stabilize the activation in training stability while promoting convergence. The model involves the VL-M2C Model by uniting visual learning along with geometric features to ensure extensive analysis while bringing optimized architecture into the design of high accuracy coupled with low computation. This systematic approach ensures precise and reliable malaria parasite detection. The VL-M2C model is designed for multiclass malaria classification, enhanced with spatial and temporal features to boost accuracy and robustness. By combining VGG16's feature extraction capabilities with LSTM's sequential modeling, superior performance is observed compared to traditional methods.

The process begins with data preparation, where the malaria parasite image dataset is loaded, and synthetic ground truth masks [26] are generated if unavailable. These masks simulate segmentation labels, marking regions with malaria parasites. Images are preprocessed by resizing to a fixed input size (e.g., 256x256 pixels) and normalizing pixel values to [0, 1]. Synthetic masks with variations simulate malaria parasite presence, and data augmentation techniques such as rotation, scaling, shifting, flipping, and color adjustments are applied to increase dataset variability and reduce overfitting.

Feature extraction is performed using a pre-trained VGG16 model [27], fine-tuned to extract spatial features from images. The top classification layers of VGG16 are removed, retaining only convolutional layers to extract deep hierarchical features. These features are flattened and reshaped for input into an LSTM network.

For sequential modeling, flattened features are passed through LSTM layers [28] to capture long-range spatial dependencies across images. These layers enable the model to recognize sequential relationships within images. A dense layer with sigmoid activation predicts an output mask, improving the localization process. The output is reshaped to match the input image dimensions, resulting in the final segmentation mask. The Dice Loss function 29, measuring overlap between predicted and ground truth masks, is used to handle imbalanced datasets effectively. The model is compiled with the Adam optimizer and a learning rate of 0.0001. The configurations used in the V2SeqNet model are detailed in Table 2. During training, data augmentation is dynamically applied using ImageDataGenerator, and the model's performance is monitored on the validation set after each epoch.

Table2: Configurations used in the **V2SeqNet** Model

Parameter	Value/Description
Input Shape	(256, 256, 3)
Conv2D Filters	[64, 128, 256]
Kernel Size	(3, 3)
Activation Function	ReLU
Kernel Regularizer	L2 (1e-4)
MaxPooling Size	(2, 2)
Dropout Rates	[0.2, 0.3, 0.4]
LSTM Units	[128, 64]
LSTM Dropout Rate	0.3
Dense Layer Activation	Sigmoid
Optimizer	Adam
Learning Rate	0.0001
Loss Function	Dice Loss
Batch Size	16

For prediction, the trained model generates segmentation masks for unseen images. Thresholding probabilities converts them into binary masks depicting segmented regions. These predictions and corresponding segmentation masks are saved for further analysis. The test set is used to evaluate the classification model and a confusion matrix examine its performance in classifying parasite stages.

Geometric features like area and perimeter capture contextual information, while the LSTM layer captures temporal or sequential dependencies. This would make LSTM learn how the parasite stages change with time, enhancing its classification performance. For instance, as the parasites grow, their perimeter and area do change, and LSTM learns the temporal relations of these quantities for better stage progression understanding.

The combination of geometric features with those of VGG16-based features improves the discriminative power of the model. Both fine image details and global information about shape and size allow this model to distinguish between stages with higher accuracy. Geometric features like area and perimeter differentiate morphologically distinct stages, while VGG16 captures deeper hierarchical features such as textures and shapes. Passing area and perimeter values provide additional structural context, which makes the model more sensitive to variations in morphology of parasite.

The enhanced architecture uses regularized convolutional layers with batch normalization to stabilize activations, improve the stability of training, and enhance convergence. Dropout regularization rates are set between 0.2 and 0.4, and L2 regularization is applied to prevent overfitting.

Spatial-temporal analysis is carried out where the convolutional feature maps are reshaped in a sequence format used for the LSTM layers. Stacked LSTM layers capture spatial relationships and reduce dimensionality further for efficient local spatial pattern and sequential dependency analysis. Dice loss ensures precise segmentation of small regions in imbalanced datasets.

Variations in masks over synthetic ground truth allow the model to test predictive capabilities. Several data augmentation techniques, including geometric transformations, color adjustments, and large-scale improvements in the robustness of unseen data, are used. The process of artificially repeating synthetic images with masks reduces the likelihood of overfitting by enhancing generalization. A learning rate of 0.0001 enables gradual convergence in the training process with an Adam optimizer for fine-tuning [30]. Its performance is measured in terms of precision, recall, and accuracy.

RESULT

The MP-IDB dataset is a collection of annotated images of malaria-infected red blood cells used in the evaluation of several deep learning models for the classification of the malaria parasite stage. In this section, the proposed V2SeqNet model is compared against state-of-the-art architectures on key metrics, including accuracy, precision and recall. These are very important in estimating the reliability and effectiveness of the models to distinguish malaria parasite stages.

The V2SeqNet model proposed in this work was better than the rest of the architectures, with an accuracy of 99.69%, precision of 98.78%, and recall of 100%. Table 3 gives a detailed comparison of the performance metrics. The comparative analysis shows that V2SeqNet can be a reliable and precise tool for the computer-aided diagnosis of malaria due to its ability to produce superior classification results.

Table 3. Performance comparison of various deep learning models for malaria parasite stage classification on the MP-IDB dataset

Model	Accuracy	Precision	Recall
MobileNet [31]	95.67	88.51	98.72
EfficientNet [31]	90.71	84.07	98.08
ResNet-50 [31,32]	94.4	88	99.36
Vgg16 [31,32]	92.49	80.31	99.36
DenseNet-121[31,33]	95.55	92.68	97.44
AlexNet [31]	94.91	84.7	99.36
Proposed Model	**99.69**	**98.78**	**100**

Although MobileNet and DenseNet-121 had similar accuracy levels at 95.67% and 95.55, respectively, DenseNet-121 had higher precision at 92.68%, which would mean that DenseNet-121 is more suitable for applications requiring high precision in classification.

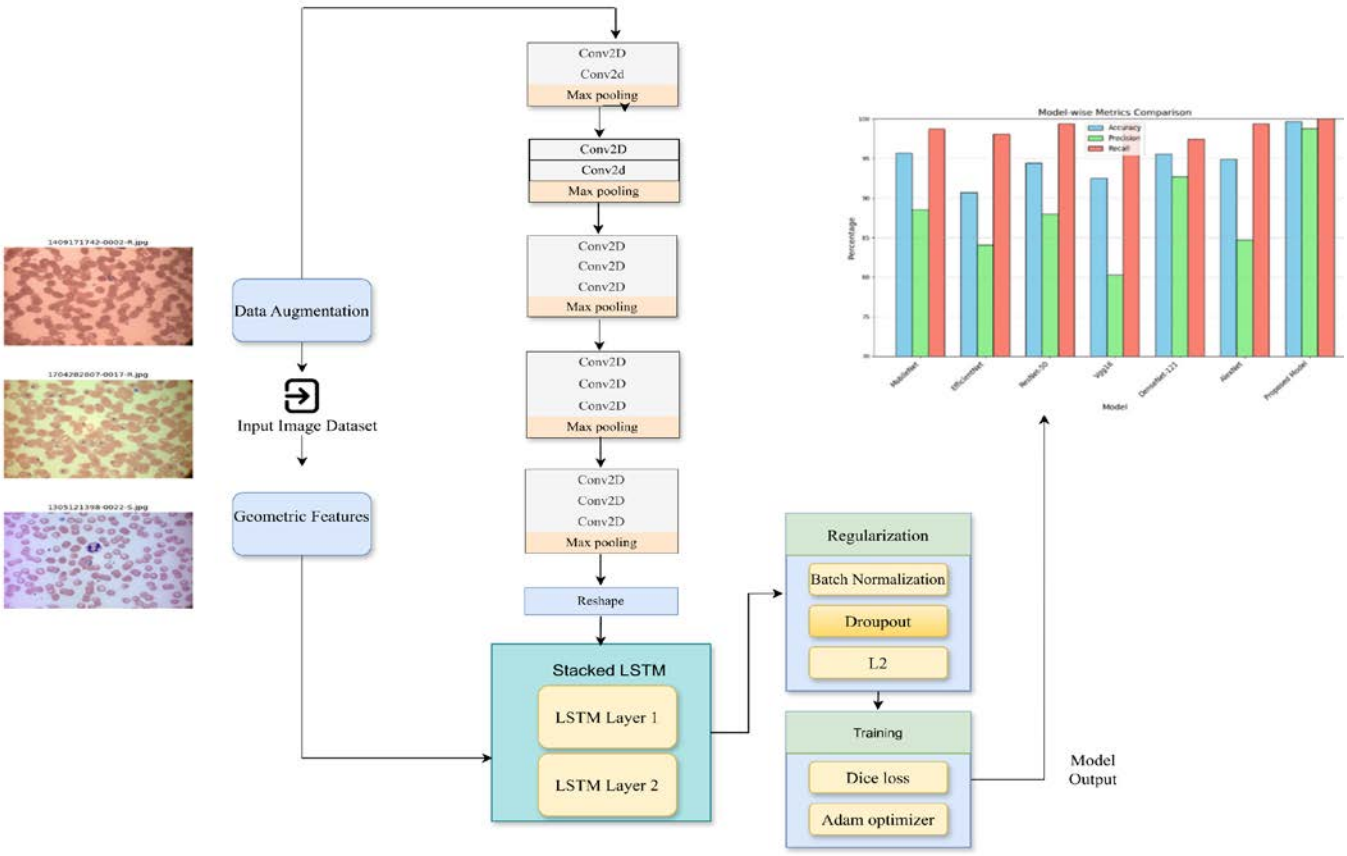

Figure 3. V2SeqNet - VGG with 2 LSTM Layers for Sequential Classification Network

MobileNet, though less precise, had a very good recall at 98.72%, indicating that it could effectively detect malaria parasites.

ResNet-50 and AlexNet have high recall values of 99.36%. This is a good indication that the models can detect malaria parasite effectively.However, their lower precision values of 88.00% and 84.70%, respectively indicate the inability of the models to distinguish between the different stages of the parasite. The EfficientNet and VGG16 models recorded the lowest accuracy and precision, with EfficientNet achieving 90.71% accuracy and 84.07% precision. These results indicate that these models are less effective for the classification of malaria parasite stages, likely due to limitations in capturing intricate spatial and temporal dependencies.

Figure 4 demonstrates the outstanding performance of the V2SeqNet model which exploits a newly designed architecture tailored for malaria stage classification. It is constructed with an entirely new architecture that employs geometric features, better regularization techniques, and optimized learning parameters. This kind of architecture allows the model to realize the critical spatial and temporal dependencies so that it gives accurate and reliable stage classification. The achieved results establish that the proposed V2SeqNet model is an extremely effective tool for automated malaria parasite stage classification and diagnosis.

The proposed V2SeqNet model further improves the ability to capture long-range dependencies through the integration of sequential learning via LSTM layers, which is a critical aspect for accurate malaria stage classification. These layers enable V2SeqNet to efficiently consider long-range dependencies in the image data, a necessity for good classification of malaria stages. In this regard, these advanced techniques ensure that the model not only surpasses other state-of-the-art models but also answers the primary concerns of malaria parasite stage classification, which are variability in image quality, uneven illumination, and overlapping features.

The importance of the V2SeqNet model goes beyond its numerical metrics. Its design shows a deep understanding of the problem domain, with both spatial and sequential learning improving its classification capabilities. Geometric features add additional contextual information, regularization techniques and optimized parameters ensure that the model is robust against overfitting. All these features enable the model to generalize well across different datasets and conditions.

The results presented in this study show tremendous potential for V2SeqNet as a revolutionary tool for the diagnosis of malaria. High accuracy, precision and recall values that the model exhibits ensure reliability for real-world application settings wherein accurate and timely diagnosis is crucial. Its capacity to consistently do better than any other architectures signifies robustness and adaptability, making it a good addition to the field of automated malaria diagnosis.

The proposed V2SeqNet model is a significant improvement in malaria parasite stage classification. It overcomes the limitations of the existing models and introduces innovative design elements, which sets a new benchmark for performance in this domain. The results validate the effectiveness of V2SeqNet as a precise, reliable, and efficient tool for automated malaria diagnosis, paving the way for its integration into clinical workflows and further research.

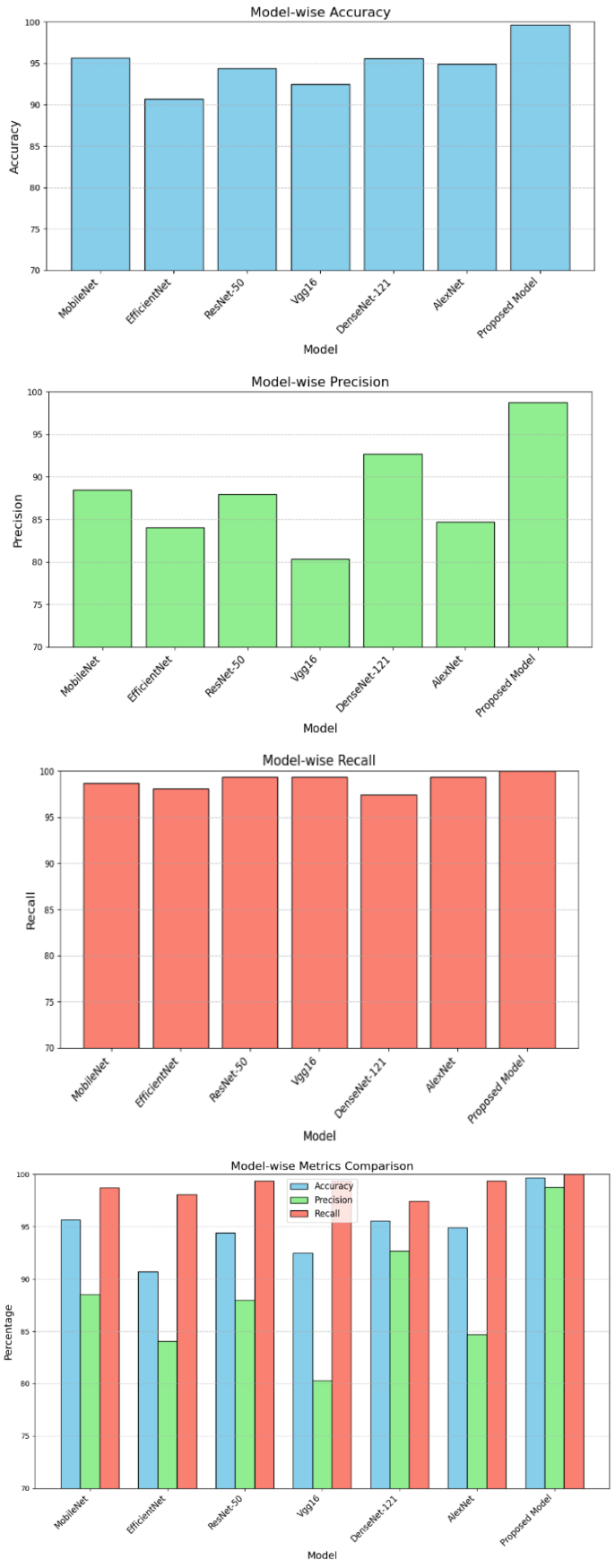

Figure 4 Comparison of accuracy, precision, and recall (%) across multiple models for malaria parasite stage classification.

CONCLUSION

This research could prove the efficiency of advanced deep learning models and pre-processing techniques for classifying malaria parasite stages with the MP-IDB dataset. A proposed model called V2SeqNet proven to be a better alternative model compared to those in existence, achieved 99.69% accuracy, 98.78% precision, and 100% recall. The results display the robust and reliable nature of the model in terms of dealing with complex variations in malaria parasite morphology. Incorporation of geometric features, extraction through deep learning, and using sequential models as applied in this study provides an integrated approach toward classification of stages of malaria parasites. This spatial-temporal geometry architecture allows integration of spatial and temporal features at higher accuracy medical image analysis. The proposed model has great promise for real-world applications.

Its integration with mobile applications or web-based platforms in real-time diagnostic tools can significantly aid healthcare workers in resource-poor settings, ensuring timely and accurate malaria diagnosis. Further, the model shows excellent generalization and robustness across populations and imaging conditions. Future extensions would include multi-class classification to diagnose multiple malaria species and their stages to make the model more useful in comprehensive malaria diagnosis. This upgrade would make it a valuable model for global health initiatives.

CONFLICT OF INTEREST STATEMENT

Authors do not have any known conflict of interest for this work.

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