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"Identification of Plasmodium Vivax in Blood Smear Images Using CNN and SVM with Otsu Thresholding Algorithm"

[1,*] Nurul Huda, [2]Lathifatul Aulia, [3]Maulany Citra Pandini
[1]Institut Teknologi Statistika dan Bisnis Muhammadiyah, Semarang, Indonesia
[1]Universiti Muhammadiyah Malaysia, Perlis, Malaysia
[2]Institut Teknologi Statistika dan Bisnis Muhammadiyah, Semarang, Indonesia
[3]Institut Teknologi Statistika dan Bisnis Muhammadiyah, Semarang, Indonesia
[1,*] Nurul.huda@itesa.ac.id, p5240024@student.edu.umam.my [2]lathifatul.aulia@itesa.ac.id,
[3]maulanycitra26@gmail.com
[*] Correspondence email

Abstract

In this research, we explore the efficacy of Convolutional Neural Networks (CNN) and Support Vector Machines (SVM) in identifying Plasmodium vivax from blood smear images. We utilized a dataset comprising images of Plasmodium vivax and non-infected cells, applying CNN for deep feature extraction and SVM with otsu's thresholding for segmentation. The dataset was preprocessed and augmented to enhance model performance. The CNN architecture, consisting of multiple convolutional and dense layers, achieved an accuracy of 98.46% on the validation set. For comparison, features extracted using Otsu's Thresholding were fed into an SVM classifier, yielding an accuracy of 82%. Confusion matrix was generated to evaluate the classification performance of both models. The CNN model demonstrated superior accuracy and robustness in classification tasks compared to the SVM model. This study underscores the potential of deep learning frameworks in medical image analysis and highlights the importance of feature extraction and selection techniques in improving machine learning model performance.

Keywords: CNN, malaria, plasmodium vivax, SVM

INTRODUCTION

Plasmodium-parasite malaria persists as a significant global health issue, particularly in tropical and subtropical regions. Plasmodium vivax is a very prevalent species that is responsible for causing this disease. Despite improvements in Plasmodium vivax diagnosis and treatment, the precise and immediate identification of this parasite remains challenging, particularly in low-resource settings where traditional microscopic examination methods may not be practical or trustworthy [1]. The labor-intensive nature of current approaches and the requirement for qualified technicians emphasize the need for accurate and automated diagnostic tools to aid malaria detection and elimination efforts [2].

Current malaria diagnoses have identified computational effectiveness as a significant barrier. To tackle this difficulty, current research has investigated the use of deep learning methods for malaria identification. Despite the common practice of identifying Plasmodium parasites through microscopic examination of blood samples, this method is prone to errors and misdiagnoses. As a result, the advancement of computer-aided diagnostic (CAD) systems has significantly increased. Several studies have shown promising outcomes, such as Naïve Bayes classifiers achieving accuracies of 97.29% for P. vivax and 98.36% for P. falciparum. Nevertheless, conventional classifiers such as Perceptron have exhibited subpar performance, attaining a mere 81.08% accuracy [1]. This article presents a method for identifying and organizing the several developmental phases of Plasmodium vivax in digital microscopy images of thin blood.

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Employing a Naive Bayes classifier along with specific form and texture parameters achieves a classification accuracy, sensitivity, and specificity of 97.29%. Nevertheless, the utilization of microscopic image datasets requires the image preprocessing stage to be of utmost importance in enhancing accuracy performance. Image segmentation is a frequently used technique in image preprocessing. Image segmentation approaches can be categorized into three types: edge-based, region-based, and pixel-based. Thresholding is a frequently employed segmentation technique for microscopic pictures. Prior studies employed thresholding using the saturation histogram approach. The process entails examining the saturation element of a picture within the HSV (Hue, Saturation, Value) color space. The saturation component of an image shows the level of strength or purity of its colors [3]–[6]. Recent advancements in digital image processing and computer-aided diagnostics have provided a great opportunity to improve the precision and effectiveness of malaria diagnosis [7]. The Otsu thresholding segmentation approach is a useful technique for automatically identifying Plasmodium parasites in microscopic pictures of blood smears [6], [8], [9]. This technology utilizes image analysis methods to separate parasites from the surrounding blood components, making it easier to accurately identify and classify them [10]. Convolutional neural networks (CNNs) have demonstrated potential for effectively detecting malaria parasites in blood smears. However, the performance of these models might vary considerably depending on the quality and diversity of the training data. Researchers have suggested hybrid models, which integrate the advantages of various deep learning architectures, to enhance classification accuracy and resilience [11]. Recent progress in computer vision and machine learning has shown that they might be able to help with the problems that come with diagnosing malaria. For example, Convolutional Neural Networks (CNNs), a type of advanced machine learning models, have shown that they are very good at tasks like image classification and recognition. Furthermore, the field of medical diagnostics is increasingly utilizing them [4]. Nevertheless, the effectiveness of these models might differ greatly depending on the quantity and quality of the training data [12]. Proposals have recommended segmentation techniques for the pre-processing step as a means to improve the accuracy and robustness of classification by integrating the advantageous features of segmentation and deep learning algorithms. Recent advances in machine learning and computer vision have demonstrated potential for addressing malaria detection difficulties [13]. Medical diagnostics are increasingly using Convolutional Neural Networks (CNNs), a type of deep learning model, due to their remarkable precision in image recognition tasks [14]–[16]. Support vector machines (SVMs) and Otsu's threshold segmentation have demonstrated excellent synergy in many classification tasks, presenting a compelling alternative to deep learning models. These techniques employ computer algorithms to autonomously detect Plasmodium vivax in blood smear images, potentially revolutionizing the diagnostic process [17], [18]. These methods utilize computational algorithms to automatically detect Plasmodium vivax in blood smear images, potentially improving the method of diagnosis.

The study's goal is to create a complete system that compares how well CNN and SVM classifiers work when combined with Otsu's thresholding for image segmentation. This will improve both the accuracy and speed of identifying Plasmodium vivax from blood smear images. As far as we know, no one has thoroughly researched the utilization of these techniques together in the field of malaria diagnosis, setting the state of the art for this work. Prior studies have primarily focused on CNNs or SVMs separately. Nevertheless, our approach capitalizes on the advantages of both techniques to improve diagnostic accuracy. This study makes a valuable contribution by creating a hybrid model that achieves high accuracy, standard deviation, and times. As a result, this approach may be ideal for use in various healthcare contexts. We organize the manuscript as follows: The introduction offers a thorough synopsis of the study issue, proposed methods, and results. The Method section provides a comprehensive description of the dataset, preprocessing procedures, and the design of the CNN and SVM models. The Results and Discussion section provides an analysis of the data, which includes measures of accuracy, loss, and performance

comparisons. It also includes a commentary on the implications and prospective applications of the proposed system. The Conclusions section serves as a brief summary of the research contributions and provides an overview of the future directions for this work.

METHODS

Our method utilizes advanced image processing and machine learning techniques to improve the accuracy and efficiency of diagnosing *Plasmodium viva*x, a protozoan parasite that causes a large burden of malaria. The methodology utilized in this technique is derived from studies conducted on *Plasmodium falciparum*, a parasite that also causes malaria. It aims to establish a strong framework for studying *Plasmodium vivax* in microscopic blood images. This approach comprises multiple crucial phases:

Preprocessing is the first phase in the process, with the goal of enhancing the quality of the images to enable more precise analysis. This encompasses the processes of correcting lighting, enhancing contrast, and filtering noise. In addition, data augmentation techniques such as rotation, scaling, and flipping are employed to increase the size of the dataset and improve the ability of the model to generalize.

Otsu's Thresholding is utilized for segmentation due to its effectiveness in distinguishing foreground items (parasites) from the background in grayscale photos. Otsu's method is efficient as it automatically calculates the most suitable threshold by reducing the variance within each class, making it well-suited for photos with histograms that have two distinct peaks, such as those including parasite regions. The segmentation procedure generates distinct, binary masks of the regions of interest, which are essential for precise analysis and seamlessly integrate with the *Support Vector Machine (SVM)* classifier.

Convolutional Neural Networks (CNNs) and *Support Vector Machines* (SVMs) are used during the classification step. The CNN design comprises several layers, specifically three convolutional layers with 32, 64, and 128 filters, subsequent max-pooling layers, and two fully linked layers. The model employs the *Rectified Linear Unit* (ReLU) activation function, the Adam optimizer with a learning rate of 0.001, and the categorical cross-entropy loss function. This architecture is specifically developed to capture and express hierarchical features, with the goal of enhancing the accuracy of categorization. The SVM model utilizes a radial basis function (RBF) kernel, with specific parameters: a regularization parameter (C) set to 1.0 and a gamma value of 0.01. These settings are fine-tuned to achieve a balance between margin size and classification error.

Through the use of these sophisticated methods, the approach guarantees accurate recognition and categorization of *Plasmodium vivax*, thereby substantially enhancing the precision of malaria diagnosis and the formulation of treatment strategies. This holistic strategy not only improves the strength and reliability of the diagnostic process but also tackles important obstacles in malaria diagnosis using advanced algorithms and models.

Proposed Method

In this study, we present a comprehensive methodology for the identification and classification of Plasmodium vivax in microscopic blood images. Our proposed approach involves a multi-step process that begins with image preprocessing to enhance quality and facilitate accurate analysis. This is followed by the application of Otsu thresholding for effective segmentation of the parasite regions. Finally, we employ advanced machine learning techniques, specifically Convolutional Neural Networks (CNN) and Support Vector Machines (SVM), for the classification of the segmented images into various developmental stages of Plasmodium vivax. The detailed steps of our proposed methods are illustrated in figure 1.

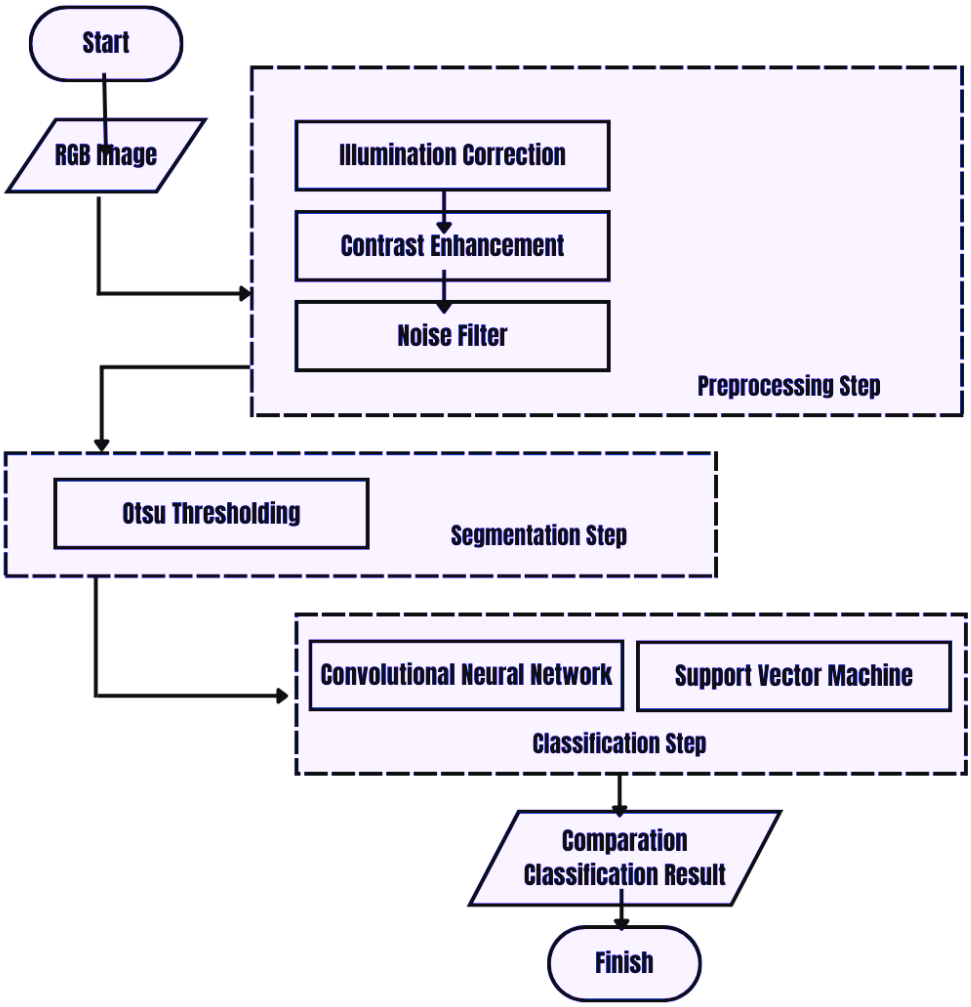

Fig. 1. The proposed method for classification plasmodium vivax

1. Preprocessing

Preprocessing is essential to enhance the quality of microscopic blood images and prepare them for further analysis.

1.1. Dataset Collection

Collect a dataset of microscopic images of thin blood smears containing Plasmodium vivax parasites. These images can be sourced from repositories Broad Bioimage Benchmark Collection, National Institutes of Health (NIH), and Kaggle [19]–[21]. The dataset includes a total of 1,404 images of Plasmodium vivax. The data consists of four classes of infected cells: gametocytes, rings, trophozoites, and schizonts. The data sample collection is shown in Figure 2. The image has a resolution of 2592×1944 pixels and a color depth of 24 bits. Figure 1.4 illustrates the cropping process from the original thin blood smear image shown in Figure 2(a) to focus on the region of interest (RoI) containing red blood cells (RBCs) infected with Plasmodium vivax. This results in an image resolution of 250×250 pixels, as seen in Figure 3(b).

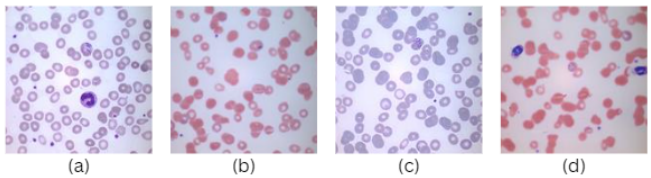

Fig. 2 Plasmodium Vivax Dataset

1.2. Image Preprocessing

The preprocessing steps undertaken to prepare the dataset for analysis are detailed below.

The initial step involves acquiring high-resolution images from the repositories. These images are then cropped to focus on the region of interest (RoI) containing red blood cells (RBCs) infected with Plasmodium vivax. The cropping process reduces the resolution to 250×250 pixels, effectively isolating the relevant sections of the blood smear images. Figure 1.4 illustrates this cropping process, transitioning from the original thin blood smear image shown in Figure 2(a) to the focused RoI.

Variations in illumination can significantly affect image analysis and classification accuracy. To standardize the lighting conditions across all images, an illumination correction step is applied [22]. This involves using techniques such as shading correction, where the image intensity is adjusted to compensate for uneven illumination. The correction ensures that the images have uniform brightness, thereby facilitating better feature extraction and classification. Following illumination correction, contrast enhancement is performed to improve the visibility of the relevant features within the images [23]. This step involves applying histogram equalization, which adjusts the contrast by redistributing the image's intensity values. By enhancing the contrast, the boundaries between different cellular components become more distinct, aiding in more accurate identification of infected cells.

The presence of noise in microscopic images can hinder accurate analysis. To mitigate this, a noise filtering step is implemented. This involves applying Gaussian blur to smooth the images and reduce high-frequency noise [24]. The Gaussian filter is particularly effective in preserving edges while eliminating random noise, resulting in clearer images that are more suitable for subsequent processing steps. To further refine the image preprocessing, Otsu thresholding is applied [6]. This technique automatically determines the optimal threshold value to separate the foreground (infected cells) from the background. By converting the grayscale images to binary images, Otsu thresholding effectively segments the images, isolating the infected regions for detailed analysis.

The preprocessing steps ensure that the dataset is standardized and optimized for feature extraction and classification tasks. The corrected, enhanced, and filtered images are then used to train and evaluate the hybrid deep learning models, contributing to the improved detection and classification of Plasmodium vivax infected cells.

2. Segmentation

Following the image preprocessing steps, which include illumination correction, contrast enhancement, and noise filtering, the Otsu thresholding technique is utilized for effective image segmentation. Otsu's method is an adaptive thresholding technique designed to automatically determine the optimal threshold value for converting a grayscale image into a binary image [25]. This technique is particularly advantageous for images exhibiting a

bimodal histogram, where pixel intensities are distributed across two distinct peaks representing the foreground and background.

The Otsu thresholding process encompasses several key steps:

a. Grayscale Conversion: The preprocessed color images are first converted to grayscale, simplifying the computational complexity by focusing solely on intensity values, which are crucial for thresholding [22]. In grayscale images, each pixel value represents light intensity, with values ranging from 0 (black) to 255 (white).
b. Gaussian Blurring: To mitigate noise and minor intensity variations, a Gaussian blur is applied to the grayscale image [26]. This smoothing operation helps in reducing high-frequency noise while preserving significant edges. The blur is achieved by convolving the image with a Gaussian function.
c. Histogram Calculation: The histogram of the blurred grayscale image is computed, reflecting the distribution of pixel intensities [26].
d. Within-Class Variance Calculation: Otsu's method aims to determine the threshold value that minimizes the within-class variance, which is the weighted sum of the variances of the two classes—foreground and background [8], [22], [25]. For each potential threshold value *t*, the image is divided into two classes: C_1 (pixels with intensity values less than or equal to ttt) and C_2 (pixels with intensity values greater than *t*). The within-class variance $\sigma\frac{w}{2}(t)$ is calculated as:

$$\sigma w2(t) = w1(t)\sigma 12(t) + w2(t)\sigma 22(t) \quad (1)$$

where:

• w1(t)w_1(t)w1(t) and w2(t)w_2(t)w2(t) are the probabilities (weights) of the two classes, calculated as:

$$w1(t) = i = 0\sum tP(i) \quad (2)$$

$$\text{w2(t)=i=t+1}\sum \text{L}-1\text{P(i)} \quad (3)$$

Here, P(i)P(i)P(i) is the probability of intensity level iii, and LLL is the number of intensity levels (256 for an 8-bit image).
σ12(t) and σ22(t)\sigma_2^2(t)σ22(t) are the variances of the two classes, calculated as:

$$\sigma 12(t)=w1(t)\sum i=0t(i-\mu 1(t))2\cdot P(i) \quad (3)$$

$$\sigma 22(t)=w2(t)\sum i=t+1L-1(i-\mu 2(t))2\cdot P(i) \quad (4)$$

where μ1(t)\mu_1(t)μ1(t) and μ2(t)\mu_2(t)μ2(t) are the means of the two classes, calculated as:

$$\mu 1(t)=w1(t)\sum i=0ti\cdot P(i) \quad (3)$$

$$\mu 2(t)=w2(t)\sum i=t+1L-1i\cdot P(i) \quad (4)$$

Optimal Threshold Selection:
The optimal threshold t^* is the value that minimizes the within-class variance σw2(t)\sigma_w^2(t)σw2(t):

$$t*= argtmin\sigma w2(t) \quad (5)$$

Fig. 3 shows segmented infected region.

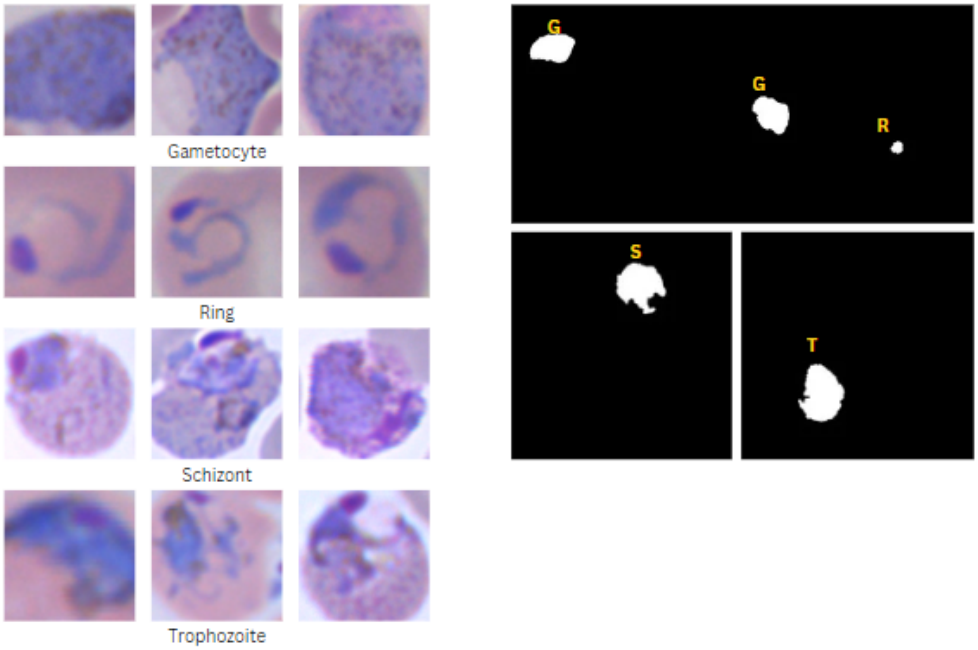

Fig. 3. Segmented Infected Region by Plasmodium Vivax

3. Classification

The final stage of this research is to classify images using the Convolutional Neural Network (CNN) and Support Vector Machine (SVM) methods. CNN is one of the deep learning classification methods that has the potential for high-accuracy results [12], [27]–[29]. CNN consists of three main layers: "convolution", "pooling", and "fully connected". Figure 3 illustrates the CNN algorithm.

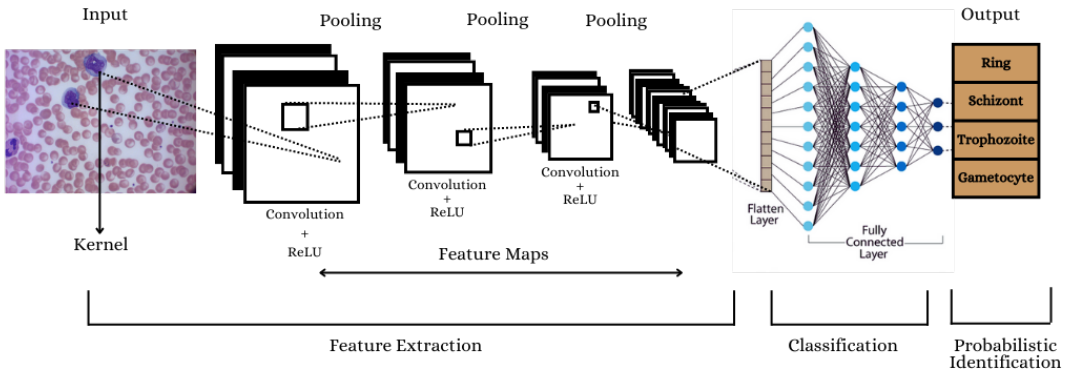

Fig. 3. Convolutional Neural Network Architecture

SVM classifiers (linear and RBF) are currently applied within the detection framework due to their exceptional generalization capabilities and reputation for achieving high accuracy in training datasets. This method is based on statistical learning theory and the principle of structural risk minimization [26]. The classification strategy aims to find the optimal separating hyperplane with the maximum margin between classes, focusing on the training samples located at the edges of the class distribution. The system's performance will be evaluated using a Confusion Matrix to obtain accuracy. Below is the equation for measuring the effectiveness of the system [2], [30]–[32].

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN} \tag{6}$$

RESULT AND DISCUSSIONS

When comparing some classification methods for achieving high accuracy, we conducted experiments on convolutional neural networks (CNN) and support vector machines (SVM). The Convolutional Neural Network (CNN) demonstrated superior performance compared to the Support Vector Machine (SVM), with an accuracy of 98.46% as opposed to the SVM's 82%. CNN's deep architecture, adept at acquiring and generalizing intricate data patterns by capturing hierarchical feature representations, accounts for its exceptional performance. CNNs are highly suitable for tasks that require complex data structures, where precise feature extraction and pattern identification are crucial.

In contrast, the Support Vector Machine (SVM), although resilient and effective in dealing with both linear and non-linear decision boundaries, exhibited lower levels of accuracy. The limitations of the SVM in capturing intricate correlations within the dataset likely hindered its performance, compared to the sophisticated capabilities of CNN. This disparity highlights CNN's superiority in situations that require the use of deep learning methods to attain greater accuracy in classification. An in-depth examination of the confusion matrix reveals that the CNN not only obtained greater overall accuracy but also displayed superior standard deviation and times across a number of classes, showing its ability to identify between diverse types of data.

The SVM may have limitations due to its sensitivity to kernel parameter selection and its challenges in effectively handling extremely intricate data without significant adjustment. Investigating different kernel functions, performing more rigorous hyperparameter optimization, and integrating feature scaling approaches can enhance the performance of SVM.

Overall, these results highlight CNN's dominance in this application, showcasing its ability to attain greater classification accuracy in comparison to conventional machine learning methods such as SVM. Figures 4, 5, and 6 depict the graphical outcomes, while Table 1 provides a comparative table of findings with prior investigations.

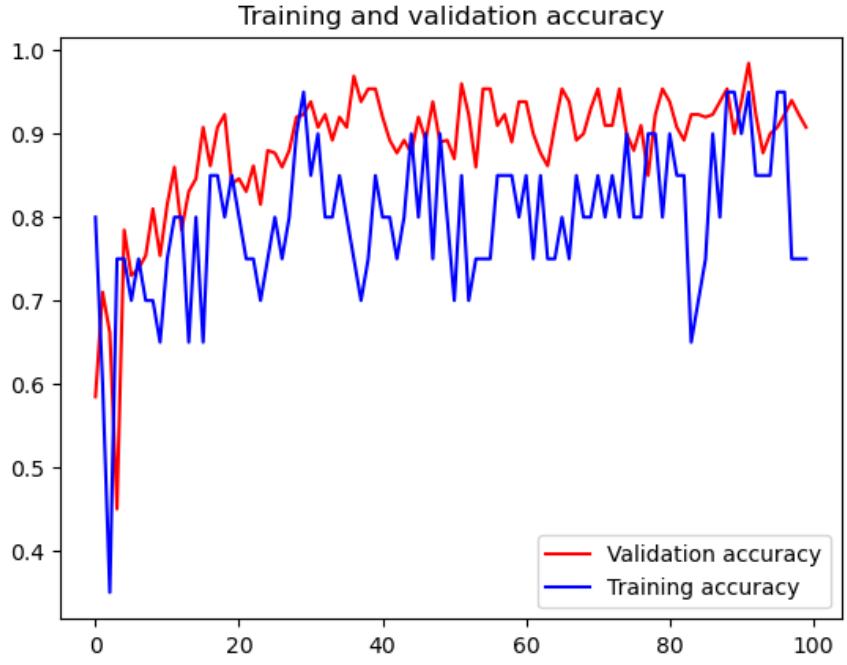

Fig. 4. Accuracy of CNN Algorithm

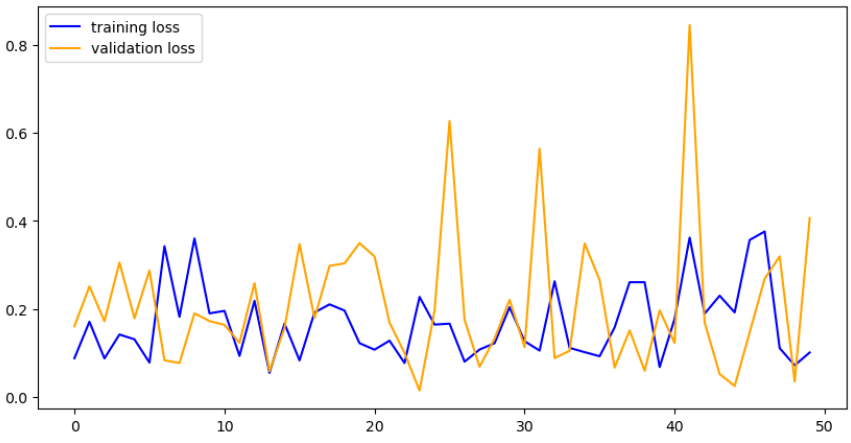

Fig. 5. Accuracy for SVM Algorithm

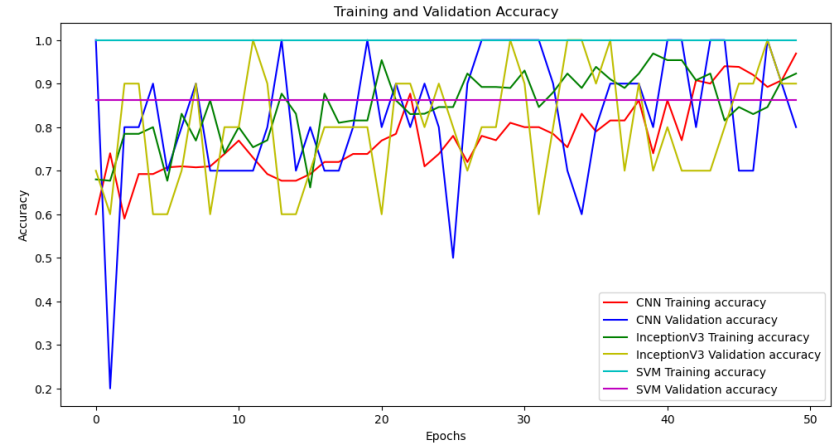

Fig 6. Comparison of Algorithms

Table 1. The Comparison Result of Classification Methods for Plasmodium Vivax

Author	Results			
	Methods	***Accuracy***	***SD***	***Time***
Maysanjaya et al	Naïve Bayes	97.29%	-	-
	Percepton	81.08%	-	-
Nugroho et al	GLCM Feature Extraction + Naïve Bayes	97.29%	-	-
Proposed Method	Otsu Thresholding + CNN	98.46%	±1.2%	5s
	Otsu Thresholding + SVM	82%	±1.5%	14s

CONCLUSIONS

The comparison of convolutional neural networks (CNN) and support vector machines (SVM) revealed that CNN outperformed SVM with a significantly higher accuracy rate of 98.46% compared to SVM's accuracy rate of 82%. This discrepancy highlights CNN's sophisticated ability to handle intricate data patterns and extract intricate features. In order to expand upon these discoveries, further investigations should concentrate on enhancing CNN structures, possibly by employing methods like transfer learning and implementing CNNs on a wider array of datasets. Furthermore, incorporating sophisticated kernel techniques or creating hybrid models could enhance the performance of SVM approaches. Assessing these methods in practical scenarios can offer a more profound understanding and help improve the precision of classification.

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AUTHORS BIBLIOGRAPHY

NURUL HUDA was born in Pekalongan, Central Java, Indonesia, in 1985. She received her M.S. degree in Information Technology from Dian Nuswantoro University, Semarang, Central Java, Indonesia, and is currently a Ph.D. candidate in Information Technology at Universiti Muhammadiyah Malaysia.
She began her career as a lecturer and researcher at Stikubank University, Semarang, Indonesia, from 2007 to 2010. Subsequently, she joined a Korean company as a staff member in 2010 and served as a General Manager from 2014 until 2021. In 2021, she returned to academia as a lecturer and researcher. Since 2022, she has authored several articles, with six of them indexed by SINTA and Scopus. Her research focus is on image processing, particularly in medical imaging.

LATHIFATUL AULIA The author was born in Demak on February 1, 1995. The author is a permanent lecturer at the Actuarial Science Study Program, Faculty of Science and Technology, Institut Teknologi Statistika dan Bisnis Muhammadiyah Semarang. She completed his undergraduate education at the Department of Mathematics, Universitas Diponegoro and continued his Masters at the Department of Mathematics, Universitas Diponegoro. Now, I often teach in Linear Algebra, Calculus, Discrete Mathematics, and Mathematical Statistics courses. The author pursues analysis and applied mathematics.

MAULANY C. PANDINI was born in Semarang, Central Java, Indonesia, in 2000. She is currently pursuing a bachelor's degree in Software Engineering at Institut Teknologi Statistika dan Bisnis Muhammadiyah Semarang. During her studies, she participated in a student exchange program at University of Mataram for one semester in her third semester.
She is actively involved in various on-campus and off-campus activities. In 2023, she authored a module book on basic Python programming, which is registered with HaKI.