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Automated Malaria Detection Using Convolutional Neural Networks and Machine Learning

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ABSTRACT: Millions of people suffer from malaria, considered one of the most dangerous parasitic diseases threatening human life and cause morbidity and mortality, especially in tropical and subtropical regions. Traditional diagnostic methods such as blood smear checking, which can be achieved by using a microscope have many challenges due to the inaccuracy of manual analysis and reliance on individual skills. Therefore, utilizing machine learning or deep learning algorithms for automating malaria detection provides encouraging solutions to enhance accuracy, minimize diagnostic time, and empower scalability. This proposed research paper addresses these challenges and employs a custom Convolutional Neural Network for automating malaria detection and classification using a dataset from the National Institute of Health (NIH) that is available publicly. The proposed model achieves an accuracy of 97.5%, and excellent results are performed regarding sensitivity and specificity when compared with machine learning algorithms such as Support Vector Machine (SVM) and Decision Tree. Furthermore, the results are validated using cross-validation techniques and compared with the existing methods. The proposed CNN model can be deployed and potentially helps professionals with real-time malaria diagnosis and classification to reduce the dependency on manual analysis.

Keywords: Malaria Detection, Image Classification, Convolutional Neural Network, Machine Learning, Deep Learning.

1. INTRODUCTION

Malaria is considered one of the most common diseases that cause death, specifically in South Africa, Sub-Saharan Africa, and Southeast Asia. In 2020, the World Health Organization (WHO) reported about 241 million cases of malaria, with an estimated 672,000 deaths[1]. The disease is caused by Plasmodium parasites when transmitted through the bites of infected female Anopheles mosquitoes[2]. Although there are several species of Plasmodium, most severe cases and deaths are caused by Plasmodium falciparum[3].

Effective treatment is crucial. However, this depends on early and accurate malaria diagnoses[3]. Microscopy is often used in traditional diagnostic methods where the presence of malaria parasites in blood smears is manually examined[4]. Although it is highly sensitive, this method has disadvantages like being time-consuming, labor-intensive, and inaccurate due to human factors such as fatigue and lack of experience[5]. Rapid diagnostic tests used as alternative diagnostic methods may lack the sensitivity of microscopy, especially in cases with low parasite density, despite offering faster results[6, 7].

Malaria diagnosis has developed rapidly when machine learning and deep learning techniques offer a new frontier for accuracy and efficiency[8]. It is possible to classify malaria cells as infected and uninfected automatically by training a machine learning or deep learning model on image datasets[9]. This will help improve the accuracy and reduce the cost and effort[10]. This paper proposes a machine-learning model for malaria classification using Convolutional Neural

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Networks that process image data efficiently[11, 12]. The performance of the suggested model is compared with traditional machine learning algorithms such as Support Vector Machine (SVM) and Decision Trees applied to the NIH dataset[13].

1.2. MOTIVATION AND CONTRIBUTIONS

In this paper, we propose an approach for automatic detection and classification of malaria using Convolutional Neural Network (CNN). The main contribution for this paper is to enhance diagnostic accuracy and minimize the dependency on personal skills and ensure scalability. The key contributions of this paper include:

- Develop a model using a custom Convolutional Neural Network for malaria detection and classification depending on NIH dataset
- Enhance model generalization by employing advanced augmentation techniques.
- Compare the proposed model with traditional machine learning models such as support vector machine (SVM) and Decision tree.
- Use the cross validation to validate the model performance to ensure reliability and robustness.

2. RELATED WORK

The field of medical image classification has significantly progressed by applying machine learning techniques over the last few years[14]. The detection and classification of diseases such as malaria, cancer and tuberculosis are automated by utilizing Convolutional Neural Network (CNN) when researchers have leveraged deep learning methods [14].

2.1. MALARIA DIAGNOSIS USING MACHINE LEARNING

In (2017), a deep learning framework to detect malaria parasites in blood smear images was developed by Dong et al. This model was a multilayer Convolutional Neural Network (CNN) and achieved an accuracy of 96.5%.[15] Although their study showed important results, it focused on CNN architecture and missed out on the comparison with other machine-learning techniques. Furthermore, there are many concerns regarding model generalization due to the absence of cross-validation methods.

In (2018), Rajaraman et al. scrutinize the application of pre-trained CNN feature extraction models in malaria diagnosis. They employed CNNs trained on the ImageNet dataset and finetuned them on the NIH malaria dataset. Their model distinguished between the parasitized and uninfected cells and achieved a classification accuracy of 95%, showing the effectiveness of transfer learning in medical applications[9]. However, this model may not always generalize well to certain medical datasets because of heavy reliance on finetuning pre trained architectures. Therefore, malaria detection tasks need further optimization and customization.

Another work was implemented (2019) by Liang et al. so that various machine learning for malaria diagnosis were compared, including Convolutional Neural Network (CNN), Random Forest (RF), and Support Vector Machine (SVM). They found that Models using CNN architectures exceeded the traditional machine learning algorithms, achieving an accuracy of 93%[11]. The study emphasized the dominance of CNNs for diagnosis tasks in medical images and noted that the deeper architectures and better data augmentation techniques could enhance the performance.

2.2. USE OF CNNS IN MEDICAL IMAGE CLASSIFICATIONS

There was widely adoption of Convolutional Neural Networks CNNs in medical imaging due to their ability to extract features from images automatically[15]. Many tasks, such as lung disease detection, diabetic retinopathy, and breast cancer identification, have shown the remarkable success of CNNs. State of the art performance in these areas has been achieved using pivotal CNNs architectures such as AlexNet, VGGNet, and ResNet[16].

In (2017), Esteva et al. used a CNN to classify skin cancer, achieving performance like what human dermatologists can accomplish[17]. Their study indicated the potential of CNNs to develop image-based medical diagnosis by improving accuracy and reducing diagnosis time, particularly in areas with limited healthcare resources. Our work for malaria classification based on CNNs is built on these successes. We use custom architecture design, data augmentation, and hyperparameter tuning for optimization. Additionally, we aim to comprehensively compare the CNNs with traditional machine learning models while using cross-validation techniques to validate the model performance[18].

3. METHODOLOGY

The methodology section of this paper is used to build and design a model that utilize CNN to detect and classify malaria efficiently and accurately. It includes several stages: dataset description and preparation, data preprocessing, model architecture design, and evaluation of performance. Common challenges in medical image classification are addressed through carefully designed of each stage such as small size of dataset, class disproportion and the required model generalization. This section provides a detailed description of the processes, emphasizes the techniques utilized to improve performance and ensure that the proposed solutions are robust and reliable.

3.1. DATASET DESCRIPTION

The NIH malaria dataset is used in this study. It is one of the most extensive datasets used for malaria classification tasks that is publicly available. This dataset belongs to the National Institutes of Health and contains (27,558) cell images of thin blood smears. The images are divided into two groups: parasitized (malaria-infected) and uninfected (healthy) cells[19]. Figure (1) shows the NIH dataset sample.

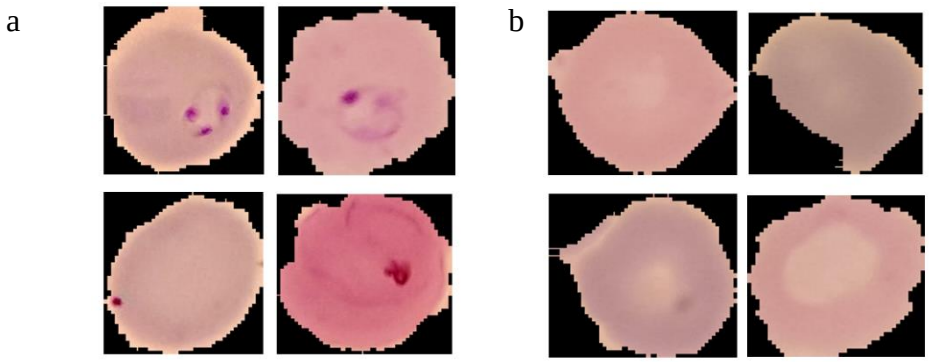

FIGURE 1. - (a) Parasitized; (b) Uninfected

The sizes of images in the dataset are slightly and they have three color channels (RGB)[20]. The two classes are evenly distributed in the dataset, with 13,780 parasitized cell images and 13,778 uninfected cell images as shown in table (1) and figure (2). The dataset was collected from various clinical settings to ensure the diversity in the representation of parasitic morphology.

Table 1. - Summary of Dataset

Dataset	Total images	Parasitized	Uninfected
NIH Malaria	27,558	13,780	13,778

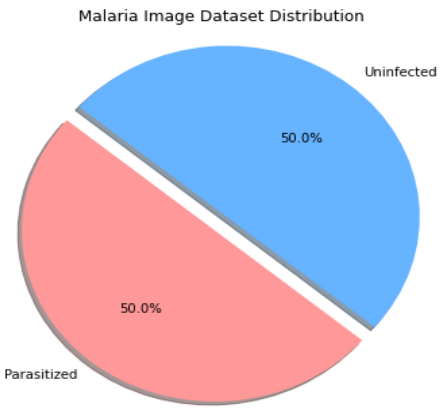

FIGURE 2. - Malaria Image Dataset Distribution

3.2. DATA AUGMENTATION

Image rotation, flipping, zooming and shifting are some data augmentation techniques employed to enhance model generalization. To reduce the risk of overfitting and increase variability, data augmentation is important when working with medical datasets, especially for deep learning models such as CNNs that need large amounts of data to generalize well[21].

3.3. PREPROCESSING

Before training the model, it is necessary to preprocess the data. First the image data is resized to 128 x 128 to ensure that all images are uniform across the dataset. Then the pixel values are converted to the range between 0 and 1. Normalization can speed up the learning process and prevent large gradients to ensure numerical stability[21].
During training, data augmentation techniques were applied to increase the size of the dataset artificially and introduce variability. Datasets are often small in medical image classifications due to the difficulty of acquiring labeled data; therefore, data augmentation is necessary.
Augmentation techniques include:

- Random zooming in and out (10%)
- Rotation by random angles (up to 40 degrees)
- Horizontal and vertical flipping
- Random brightness adjustments

3.4. MODEL ARCHITECTURE

3.4.1. CONVOLUTIONAL NEURAL NETWORK (CNN)

A custom CNN architecture has been designed to optimize the malaria classification task. The CNN architecture comprises three convolutional layers, with a max pooling layer after each to reduce the spatial dimension of the feature maps. The designed CNN includes an input layer that accepts images. The size of each image is 128x128x3. Then, it is followed by a convolutional layer, including 32 filters of size 3x3, ReLU activation, and 2x2 max pooling. The second and third convolutional layers have 64 and 128, respectively, followed by ReLU activation and 2x2 max pooling. After that, a flattening layer is coming to convert 3D feature maps into a 1D vector. Additionally, there are fully connected layers 1 and 2 containing 256 and 128 neurons, respectively, and each is followed by ReLU activation. Finally, a single neuron is used for binary classification, and a sigmoid function is employed to classify the data into parasitized or uninfected. The model was trained using Adam optimizer with a learning rate of 0. 001. Since it is suitable for binary classification. The binary cross entropy loss function was chosen, and the model was trained for 50 epochs with a batch size of 32.

Since NIH dataset consists of RGB images and each image has 3 channels, the input layer should accept three channels. The images are resized to 128x128 to ensure the uniformity in input size. This is necessary to process images in the model consistently. This size keeps the important details for a good feature extraction and balances the computational efficiency. Three convolutional layers are used to extract spatial features from image and the number of filters has been increased (32,64,128) incrementally to improve the learning ability of the model against complex patterns. The using of three Convolutional layer keeps the balance between the model complexity and the risk of having overfitting especially in this dataset. A standard 3x3 filter is used because of its efficiency in capturing features necessary to distinguish parasitized and uninfected cells such as edges, textures, and cellular structures. To provide the model with required non-linearity, the Rectified Linear Unit activation function is used to enable the model to learn complex functions between input data and output labels. ReLU also improve the training efficiency and reduce the gradients problems. The maxpooling (2x2) is used to minimize the spatial dimensions of feature maps and decrease the computational load and reduce the model complexity. The most significant features are retained by pooling operation. Translational invariance is introduced to make the model more robust to slight rotation or shift. One dimensional vector is created from multidimensional feature maps by the flattening layer. This 1D vector is required to feed data into the fully connected layer.

The predictions are made by accumulate features learned by the convolutional layers through fully connected layers. Complex relationships in the high-dimensional feature space are captured by using 256 and 128 neurons that prevent the overfitting by limiting the number of parameters. The output of the model is a binary classification (parasitized or uninfected), Therefore; a single neuron with sigmoid function is ideal in this task. The output of sigmoid function is probability score that make it efficient in medical applications. The use of Adam optimizer enables the combination of adaptive learning rates and momentum resulting in faster convergence and better optimization performance. To ensure stable learning and prevent the overshooting the minimum loss, the learning rate of 0.001 is used which is widely adopted as default value. The most appropriate loss function for binary classification tasks is binary cross entropy that

measures the convergence between true labels and predicted probabilities and ensure that if the model produced incorrect classification, it will be penalized heavily. The model is trained for 50 epochs that provide enough iterations for the model to learn patterns from data and reduce the risk of overfitting by validation monitoring or early stopping. Figure (3) shows the model architecture.

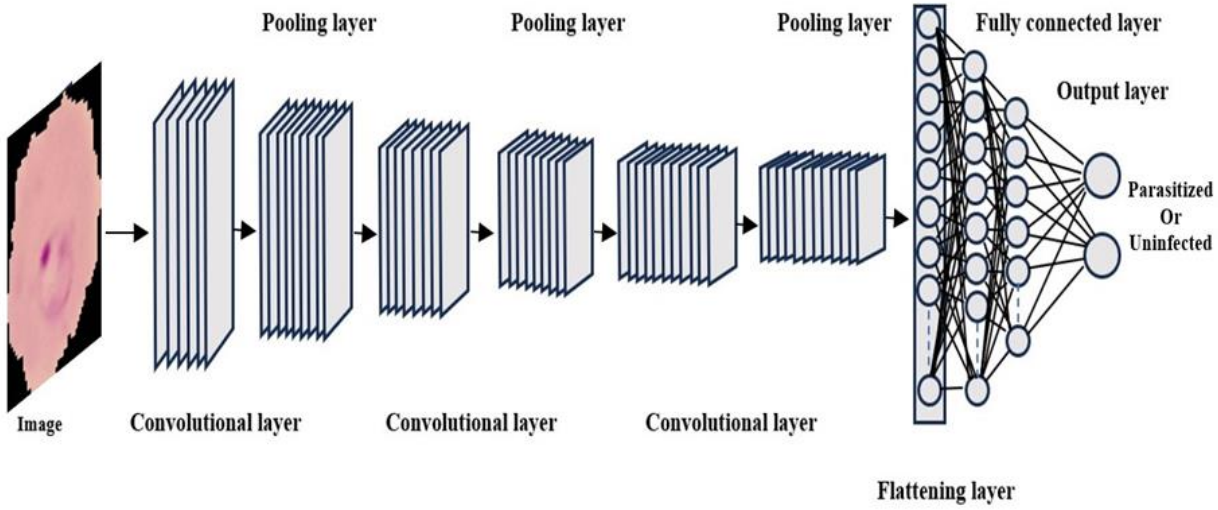

FIGURE 3. - Model Architecture

3.4.2 COMPARISON MODELS

Two traditional machine learning algorithms were implemented to compare the efficiency of convolutional neural networks.

- **Support Vector Machine (SVM):** The support vector machine was used with a radial base function (RBF) kernel effective in high dimensional spaces[22]. SVM was trained on flattened image data.
- **Decision Tree:** The Gini Impurity trains decision tree and split nodes. A decision tree can work well with a small dataset and limited features, even though it is simpler than CNNs.

3.5. TRAINING AND TESTING

The dataset was divided into two subsets, training (80%) and testing (20%), and ensured that both classes (parasitized and uninfected) were equally represented in each of the two subsets. The model was fitted using the training set, while the final evaluation was done using the test set. The Adam optimizer was used to train the model due to its ability to use adaptive learning and handle sparse gradients. Initially, the learning rate was set to 0.001, and 50 epochs with a batch size 32 were utilized to train the model. Early stopping was employed to prevent overfitting by ending the process if there is no enhancement in the model's validation loss after a certain number of epochs. The binary cross entropy was used as the loss function since the result is either parasitized or uninfected, which is useful for binary classification tasks[23]. Different metrics were used for performance evaluation, such as accuracy, sensitivity, specificity, and F1- score.

4. RESULTS AND DISCUSSION

4.1. PERFORMANCE METRICS

The following metrics were used to evaluate the models:

- Accuracy: It denotes the ratio of corrected predictions (parasitized and uninfected) to the total predictions

- Sensitivity (Recall): It represents the ratio of parasitized cells identified correctly to the total number of parasitized cells. In medical diagnostics, this metric is necessary to reduce false negatives.
- Specificity: It illustrates the ratio of uninfected cells identified correctly to actual uninfected cells. These metrics confirm that no healthy cells will be classified as infected.
- F1 score: This metric describes the harmonic mean of precision and recall and gives a stable measure of model performance, particularly if the datasets are not balanced. Table (2) and figure (4) show the model performance metrics

Table 2. - Model Performance Metrics

Model	Accuracy	Sensitivity	Specificity	F1 Score
CNN	97.5%	97.2%	97.8%	97.5
SVM	91.4%	89.3%	92.7%	91.0
Decision Tree	87.2%	85.9%	88.1%	86.5

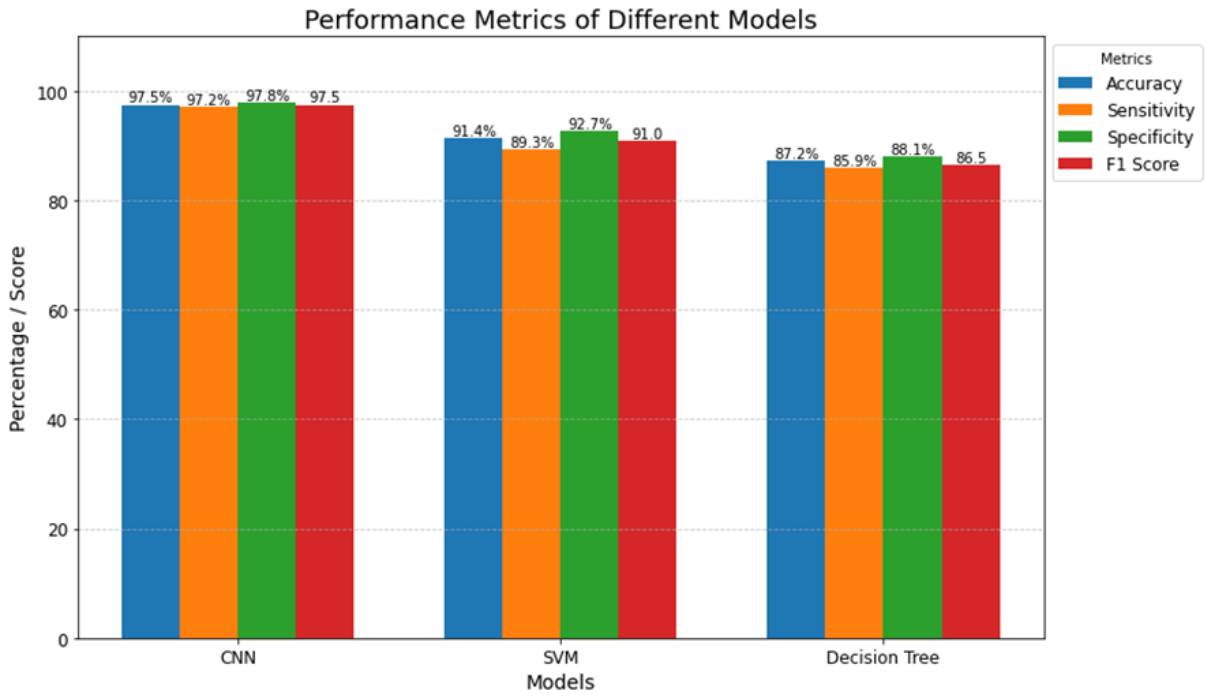

FIGURE 4. - Model Performance Metrics

When comparing performance metrics, the CNN model achieved better results than SVM and Decision Tree. Its sensitivity (97.2%) demonstrates how accurate the model is when identifying parasitized cells, which is very important in malaria diagnosis to avoid missing any infected cell. The specificity (97.8) illustrates how the model is robust and can identify the uninfected cells, reducing the probability of overdiagnosis. (91.4%) was a respectable accuracy achieved by using a Support Vector Machine (SVM); however, its sensitivity (89.3%) was less than that of CNN. This indicates that the SVM model could misclassify parasitized cells and cause a serious (false negative) issue in medical diagnosis. These results prove the dominance of deep learning when used in image classification tasks. The decision tree performance was the worst, with (87.2%) accuracy, and the sensitivity and specificity were lower than that of CNN and SVM.

4.2. VALIDATION AND CROSS-VALIDATION

To avoid overly dependency on a specific train-test split, 5-fold cross-validation was performed. The dataset was partitioned into five subsets to train and evaluate the model five times. Each time, the distinct subset was used for

validation, and the remaining subsets were used for training. 97.1% accuracy is achieved through the 5 folds on average, indicating the generalization of the CNN model, and there is no over-sensitivity to a specific training set. Figure (5) shows the cross-validation results (accuracy per fold)

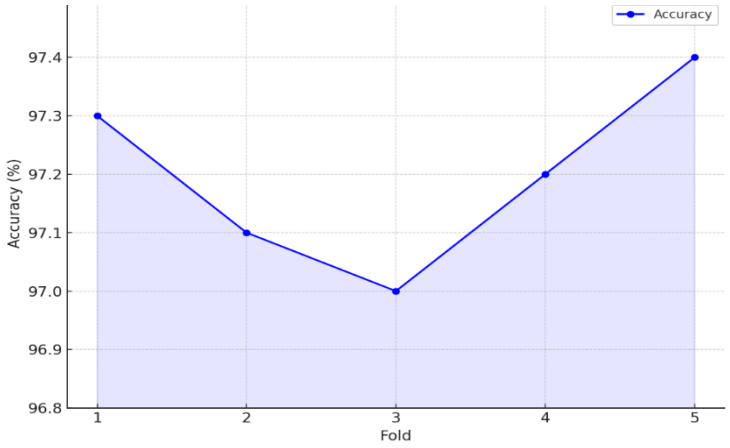

FIGURE 5. - Cross-Validation Results (Accuracy per Fold)

4.3. COMPARISON WITH EXISTING METHODS

The proposed CNN model accomplished a higher accuracy of 97.5% when compared with the Rajaraman et al. (2018) model, which achieved 95%, and Liang et al. (2019) reported (93%) accuracy when using a hybrid approach. This enhancement demonstrates the optimized architecture and the importance of the data augmentation techniques that improve the model generalization. Rajaraman's model had a sensitivity of 94%, while our CNN achieved 97.2%. Therefore, the proposed model achieved better sensitivity and specificity than models in previous studies, and the probability of having a false negative in malaria diagnosis would be lower. Table (3) and figure (6) show the comparison with previous works.

Table 3. - Comparison with Previous Works

Study	Model	Accuracy	Sensitivity	Specificity
Rajaraman et al. (2018)	CNN (Transfer Learning)	95%	94%	95%
Liang et al. (2019)	CNN + RF + SVM	93%	91%	93%
This Study	CNN	97.6%	97.2%	97.8%

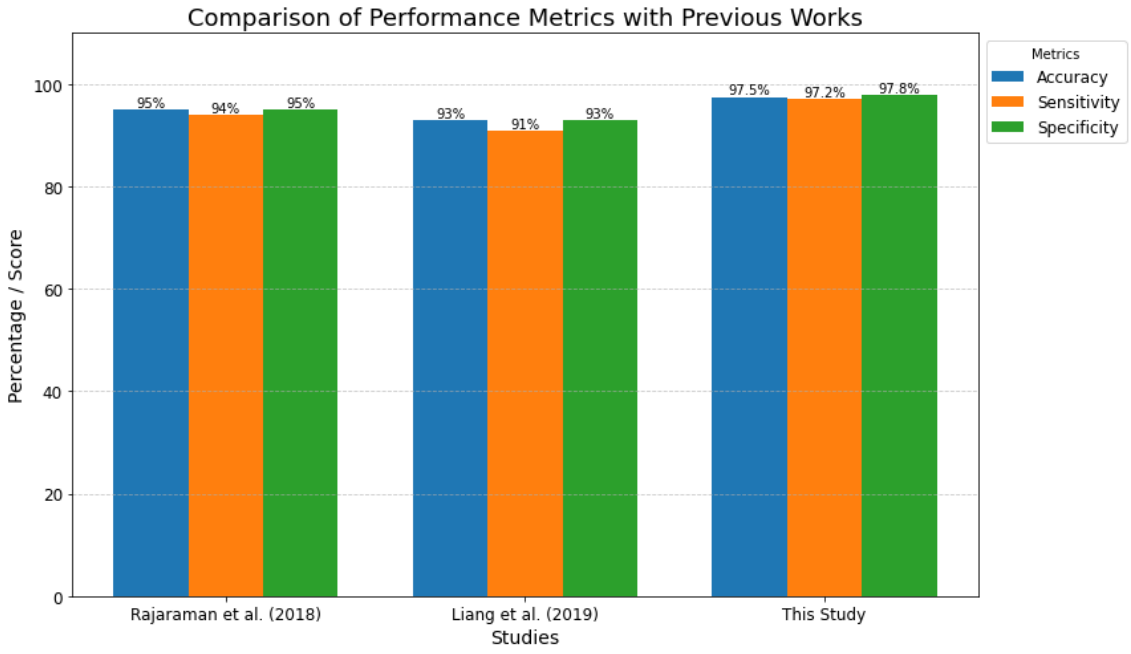

FIGURE 6. - Comparison with Previous Works

The optimization of the model's hyperparameters, such as learning rate and batch size, in addition to the early stopping that was used to prevent overfitting, led to improvements in performance. Furthermore, the simple architecture of the model, compared to other transfer learning methods like VGG or ResNet, which are considered as pre-trained models, makes it very efficient in terms of computation and suitable for real-time diagnostic applications.

4.4. LIMITATIONS

Although the proposed model achieved high accuracy, some limitations can be noticed in the study. First, the real-world clinical data is vast, while the dataset used was relatively small. Data Augmentation approaches were employed to reduce this drawback. However, the setting in real clinical data can differ. Second, the dataset has only two classes (parasitized and uninfected), while the stages of malaria infection may be multiple or mixed. In such ways, the classification process may be more difficult.

5. CONCLUSION

This research paper presents an automated system to diagnose malaria using a convolutional neural network to provide an efficient approach to classify parasitized and uninfected blood smear cells using the deep learning-based model. Across all validation folds, the proposed model achieved high accuracy, showing the reliability and effectiveness of malaria detection and classification. The model successfully reduces the challenges that result from imbalanced and limited medical data by integrating data augmentation with a convolutional neural network that offers generalization for new samples.

This approach provides many advantages compared to traditional microscopy methods, reducing human error and processing time and ensuring scalability for deployment in resource-limited environments. The performance metrics, which include accuracy, precision, recall, and F1-score, demonstrate that the model has promising achievements when used in automated diagnosis systems and real-world applications. These results may overcome other similar outcomes from previous models and prove the effectiveness of CNN when used in medical image classification tasks.

Further improvements could be explored in the future, such as using a more diverse and larger dataset, tuning the hyperparameter, and integrating attention mechanisms. Additionally, the system can be interpreted by medical professionals if methods of demonstrating ability are incorporated. Overall, this research contributes to supporting and improving the use of machine learning in healthcare, especially the detection of malaria through scalable and efficient diagnostic tools.

In the future, we can utilize additional blood smear images to expand the dataset depending on other sources and use more complex pre-trained models to explore transfer learning approaches such as ResNet or DenseNe so that more improvements in accuracy may be achieved. Furthermore, different stages of Plasmodium infection or co-infections with other pathogens can be identified by developing a multiclass classification model. Finally, the model deployment could happen when there is an integration in real-time diagnostic tools, such as mobile applications, to be used in resource-limited settings.

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