Enhanced Malaria Detection Using 2D CNN and Transfer Learning: An Efficient Deep Learning Solution

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KEYWORDS

Deep Learning, Transfer Learning, 2D CNN, Malaria Detection, Disease

ABSTRACT

Introduction: Effective treatment of malaria, a potentially fatal illness spread by mosquito bites and brought on by parasites, depends on prompt and precise diagnosis. Convolutional Neural Networks (CNN), a deep learning technology, have demonstrated significant promise in automating illness identification through medical imaging. **Objectives:** The primary objective of this study is to develop and evaluate a 2D CNN-based deep learning model combined with transfer learning to accurately detect malaria-infected blood smear images. The model aims to improve diagnostic accuracy while maintaining efficiency and generalizability. **Methods:** A dataset containing 13,000 blood smear images (Parasitized and Uninfected) from a reputed medical institution was utilized. Preprocessing techniques such as image resizing, normalization, and thresholding were applied to enhance the dataset. The model was trained using a 2D CNN architecture with transfer learning, optimized over 20 epochs using the TensorFlow library. An 80:20 split was used for training and testing to validate model performance, and early stopping was applied to prevent overfitting. **Results:** The proposed 2D CNN model achieved an impressive accuracy of 97.45% during training and 96.94% on testing data. Precision, recall, and F1-score for both Parasitized and Uninfected classes ranged between 0.93 and 0.97, demonstrating the model's robustness. The confusion matrix highlights minimal misclassifications, and the performance graphs reflect effective learning despite slight overfitting in validation loss. **Conclusions:** The study demonstrates that the 2D CNN with transfer learning is a reliable and efficient solution for automated malaria detection. The high accuracy and balanced performance metrics validate its potential for clinical implementation, particularly in resource-limited settings. Future research can focus on multi-class classification, model optimization, and real-world deployment to further enhance its applicability.

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1. Introduction

One of the most prevalent diseases in the world is malaria. It is caused by a genus of protozoa called Plasmodium and is very contagious and potentially fatal. It takes at least seven days for it to grow (Suh, 2004). In 2020, the World Health Organization (WHO) predicted that 409,000 people would die from malaria in 2019. Despite these figures, early and accurate diagnosis may help lower the malarial fatality rate (Organization, 2024). However, the rise in recorded cases of malaria is extremely erratic and uneven because of several factors, including the climate, geographic location, availability of standing water, and so forth. These factors may also contribute to the reproduction of Anopheles mosquitoes, which are the vectors of Plasmodium parasites. Malarial transmission is more severe, particularly after rain or whenever the temperature rises to a point where mosquitoes can survive for longer (Almuhaya et al., 2023; Wu et al., 2023). To account for this, the illness is prevalent in tropical countries throughout Asia and Latin America, with 90% of cases occurring in Africa (Mohammadkhani et al., 2016).

When malarial parasites are detected early and treated with the right drugs, such as substances like malarone and quinine, the negative effects may still be avoided, and the death rate can be further reduced. However, malaria detection is very unpredictable and challenging in many parts of the globe because of things like a lack of highly skilled experience in remote regions, poor data administration, and a lack of detection instruments. Several techniques have been previously described to identify the malarial parasite. Among these techniques, the microscopic analysis of Giemsa-stained thin blood spread is mostly used since it is less complicated and more affordable (Tse et al., 2019). However, the pathologists' skill level has a significant impact on how effective it is. Furthermore, when malarial forms are very uncommon, ocular screening for parasites may be time-consuming and may not always detect parasites. As the number of malaria cases rises, pathologists face increased pressure and effort. Computer-aided diagnosis (CAD), which has been quick and effective in accurate diagnosis and customized health activities, is thus becoming more and more necessary (Faruq Goni & Islam Mondal, 2023; Zhong et al., 2023).

More automated algorithms are being used in medical electronic records and imaging-based diagnoses as a result of machine learning's remarkable advancement and effectiveness in image tracking and recognition jobs. With the advent of multiple annotated datasets to train deep learning models for recognizing diseases across a range of medical research domains, this advancement was further accelerated over time (ÇETİNER & ÇETİNER, 2023; Zhang et al., 2023). These days, three main conceptual units deep learning algorithms, dataset properties, and the phenomena of transfer learning are used to lead automated CAD. Utilizing these variables, Shin (Shin et al., 2016) *et al.* conducted a thorough evaluation to assess the CNN model's performance in the field of CAD in two primary application areas the categorization of interstitial lung disease and the identification of thoracoabdominal lymph nodes. The novel CNN-based CAD's high-performance computing capabilities have been investigated in their research.

1.1. Epidemiology

According to the latest WHO Malaria Report, there were an estimated 241 million cases of malaria globally in 2020, while 627,000 people were thought to have died from the disease. The continuing eradication campaign, which was started in the early 2000s, caused the malaria case incidence to drop from 81 per 1000 people at risk in 2000 to 56 in 2019, even if the overall number of cases is still the same as it was in 2000. Similarly, in 2019, the number of fatalities per 100,000 at-risk population decreased from 30.1 to 13.8. It is important to note that those estimates increased in 2020, but this was caused by the interruption caused by the COVID-19

epidemic (Organization, 2021). The majority of Plasmodium falciparum cases—99.7% of all cases in 2020—occur in sub-Saharan Africa. But in Southeast Asia and the Western Pacific, where it also accounts for a sizable percentage of infections, it has also been a serious issue. It is estimated that P. vivax causes around 14 million cases of malaria each year, accounting for almost half of all occurrences outside of Africa (Howes et al., 2016).

About half of the world's population is at risk of getting malaria each year, but only a small portion of infected people will get severe malaria. However, it has been demonstrated that certain groups are more susceptible to serious illness, such as expectant mothers, the elderly, children under five, and patients with compromised immune systems, such as those with AIDS. All cases of malaria that have been documented in non-endemic countries are acquired in endemic countries and are referred to as "imported malaria." An examination of country-level data on malaria cases from 2005 to 2015 indicates that Europe is responsible for over 70% of the world's imported malaria cases, followed by the US at 15% and Australia at 2.2% (Tatem et al., 2017). These days, the majority of the blame is placed on residents and immigrants from endemic nations who often travel to regions where malaria is prevalent (Mischlinger et al., 2020).

1.2. Life Cycle

In both humans and Anopheles mosquitoes, malaria parasites go through several stages of growth and development. An infectious type of the parasite (sporozoites) is transferred from the saliva of a female Anopheles mosquito to the dermis when it feeds on humans. Plasmodia then go via the bloodstream to infiltrate hepatocytes, where they proliferate asymptomatically for seven to fourteen days before changing into the next morphological form, schizont. This is known as the pre-erythrocytic stage, and it is the time frame during which a malaria infection incubates. Moreover, P. vivax and two sympatric P. ovale species have the ability to develop hypnozoites, which can lie dormant in the liver for weeks to years before reoccurring (Aly et al., 2009).

In either case, Plasmodia are finally removed from the liver as merozoites, which now attack red blood cells (RBCs). The erythrocytic stage of the parasite life cycle, which consists of repeated rounds of replication, egress, and re-invasion of additional uninfected RBCs, is reached within them (Alraba'nah & Toghuj, 2024; Srimokla et al., 2024). A reduced degree of parasitemia results from P. vivax's red cell predilection for reticulocytes, or young red blood cells, which make up a tiny percentage of RBCs. Every 24 hours for P. knowlesi, every 48 hours for P. falciparum, P. vivax, and P. ovale, and every 72 hours for P. malariae, there are massive explosions of erythrocytic schizonts (the last stage of infected RBC), which coincide with overt clinical symptoms known as malaria paroxysm (Meibalan & Marti, 2017).

Depending on the species, the sexual forms of some merozoites develop in conjunction with the continuing erythrocytic stage 1–14 days after the infection begins (Venugopal et al., 2020). In this manner, gametocytes are produced via gametocytogenesis (sexual cycle) and circulate in human circulation for a few days. These variables sexual Plasmodia may be transferred to the mesenteron of the female Anopheles mosquito, and they are going through the whole gametogenesis process if another bite occurs. Upon fusing to create the zygote, the gametes form an oocyst behind the wall of the midgut. Fresh sporozoites travel to the salivary glands and can be injected into the human circulation once the transmission cycle is complete, which might take up to 14 days.

Research gap

These models often suffer from generalization and inability to achieve high accuracy on (multiple) datasets. Although 2D CNN with transfer learning has been explored, there remains an opportunity to improve their optimization for both computational efficiency and detection accuracy. Most research studies consider only hyper-critical research to increase accuracy or reduce computation overhead and do not focus on effective amalgamation and implementation of the two. Hence, there is a need to implement deep learning models using 2D CNN and transfer learning for better accuracy, enhanced performance, and faster convergence for malaria detection.

Objective

This study develops and evaluates a 2D CNN-based deep learning model with transfer learning to detect malaria-infected blood smear images accurately. The model focuses on improving diagnostic accuracy while ensuring efficiency and generalizability. It aims to assist in reliable and scalable malaria diagnosis.

2. Methodology

A reputable medical institution provided the dataset that was used for this investigation. It includes more than 13,000 photographs that are divided into two primary categories: those that are parasitized and those that are not infected. In addition, the dataset contains images of both high and low quality, which makes it more resilient and realistic for use in applications that include deep learning. To properly train the model, a random picture selection procedure was devised. This process ensured that images were selected in a manner that was impartial during both the training and testing phases of the process. Additionally, for the sake of training and testing, the dataset was split into two parts with an 80:20 ratio. An application of pre-processing techniques was carried out throughout the phase of data preparation to get the images ready for the training of the deep learning model. During the pre-processing stage, all of the images were resized to standardize their dimensions, background noise was removed, and normalization was performed to segment the images. To improve visibility, the brightness of the image was increased through the process of normalizing. Additionally, the image thresholding approach was utilized to achieve improved segmentation and feature extraction. These steps were necessary to guarantee that the deep learning model would be able to accurately recognize the patterns and characteristics that are required for the identification of malaria (Figure 1).

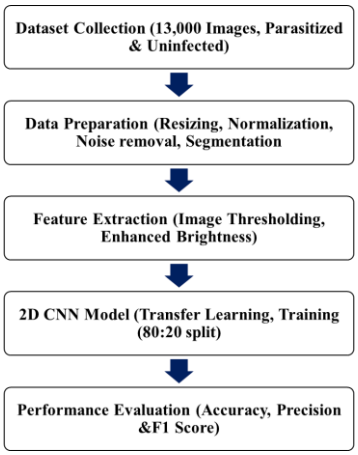

Figure 1: Methodology Flow Chart.

To facilitate the experimental design, a 2D CNN was constructed and trained by the application of transfer learning strategies. TensorFlow was used to implement the model, and it was executed on a computer equipped with an eighth-generation Core i7 processor and eight gigabytes of "random-access memory" (RAM). The training procedure was optimized with a batch size of "32 across 20 epochs", and an early stopping mechanism was employed to prevent overfitting, finishing training after 19 epochs. The performance of the model was tested using accuracy, precision, recall, and F1-score measures. The 2D CNN model scored 97.45% accuracy on training data and 96.94% accuracy on testing data, proving its efficiency in identifying malaria.

A two-dimensional deep learning approach, 2-D "Convolutional Neural Network" (CNN), was developed to facilitate the experimental design and was trained with transfer learning methodologies. The model was implemented based on TensorFlow and ran on a computer with the eighth generation of the Core i7 processor and eight gigabytes of memory (RAM). Training was performed for 20 epochs with batch size 32 and an early stopping mechanism was used to avoid overfitting, resulting in a stop after 19 epochs. Accuracy, recall, precision, as well as F1-score measures were used to test model performance. The implemented 2D CNN model reaches an accuracy of 97.45% for the training dataset and 96.94% for the test dataset, proving that it can be used as an efficient tool to identify malaria. Parasite image class — this class contains images of blood smears with malaria-infected red blood cells, i.e. when parasites (Plasmodium) are visible. The model is trained to classify cells as infected by malaria parasites based on the images. The dataset employed in this research was from a reputable medical institution. It includes more than 13,000 images that fall into two broad categories — parasitized and no parasitized. Furthermore, the dataset contains both high and low-quality images, making it more flexible and realistic for use in applications involving deep learning. To properly train the model, a random image selection process was devised. This process ensured that the images were selected in a way that was unbiased during both the training and testing phases of the process. Additionally, for training and testing, the dataset was split into two parts in a ratio of 80:20. During the preprocessing step, all images were resized to standardize their dimensions, background noise was removed, and normalization was performed to segment the images. To improve visibility, the brightness of the image was increased through a process of normalization. Additionally, an image thresholding approach was used to achieve better segmentation and feature extraction. These steps were necessary to guarantee that the deep learning model could accurately recognize the patterns and features needed for malaria identification (Figure 2).

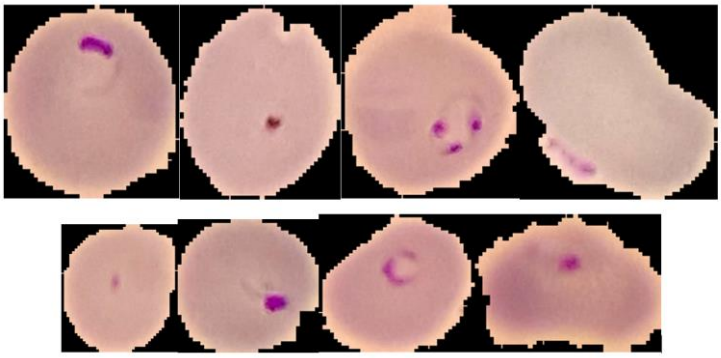

Figure 2: Parasitized Image Class.

Below in Figure 3 see the samples of some images from the dataset from Figure 2 and 3 respectively.

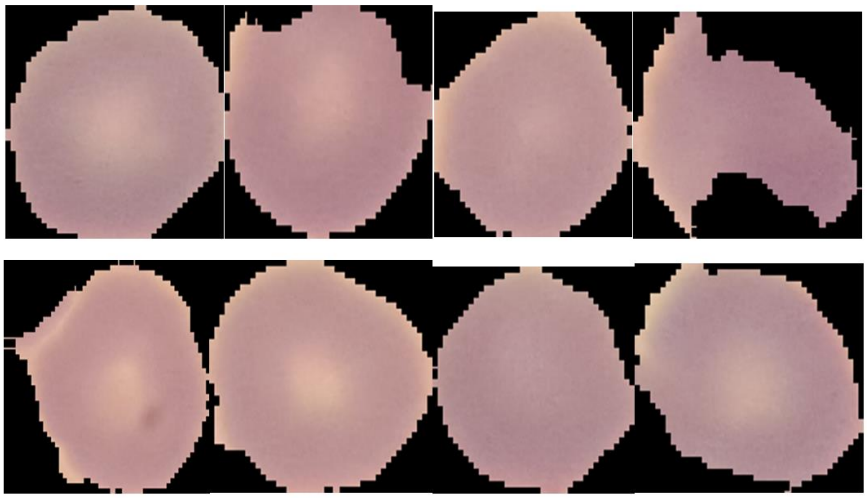

Figure 3: Uninfected Image class.

2.1. Data Preparation with Feature Extraction

Preprocessing the data according to different performance criteria is part of the dataset preparation process. It is essential to eliminate background noise from the images in order to obtain accurate findings. In order to use deep learning methods, the images were shrunk during preprocessing to meet the model's input requirements. To ensure that the data is suitable for training, a normalization technique was also used for efficient image segmentation. The brightness of the dataset was adjusted to improve image clarity and uniformity and boost the model's performance. Additionally, the images were segmented into significant sections using an image thresholding technique. By removing unnecessary components, this method optimizes the dataset for optimal model performance (Table 1).

Table: 1 2D CNN Architecture

Stage	Layer	Details
Input	Input image	Blood smear image of 128 x128
Preprocessing	Rescaling	Scale pixel values[0,1]
Feature Extraction	Conv2D layer 1	Filters: 32, Kernel: 3x 3, ReLU
	MaxPooling2D	Pool Size: 2x 2
	Conv2D layer 2	Filters: 64, Kernel: 3x 3, ReLU
	MaxPooling2D	Pool Size: 2x 2
Flattening	Flatten	Coverts Feature maps to 1D vector
Classification	Dense Layer 1	Neurons: 128, Activation: ReLU
	Dropout	Dropout Rate: 0.5
Output	Binary Output	"Infected" or "Uninfected"

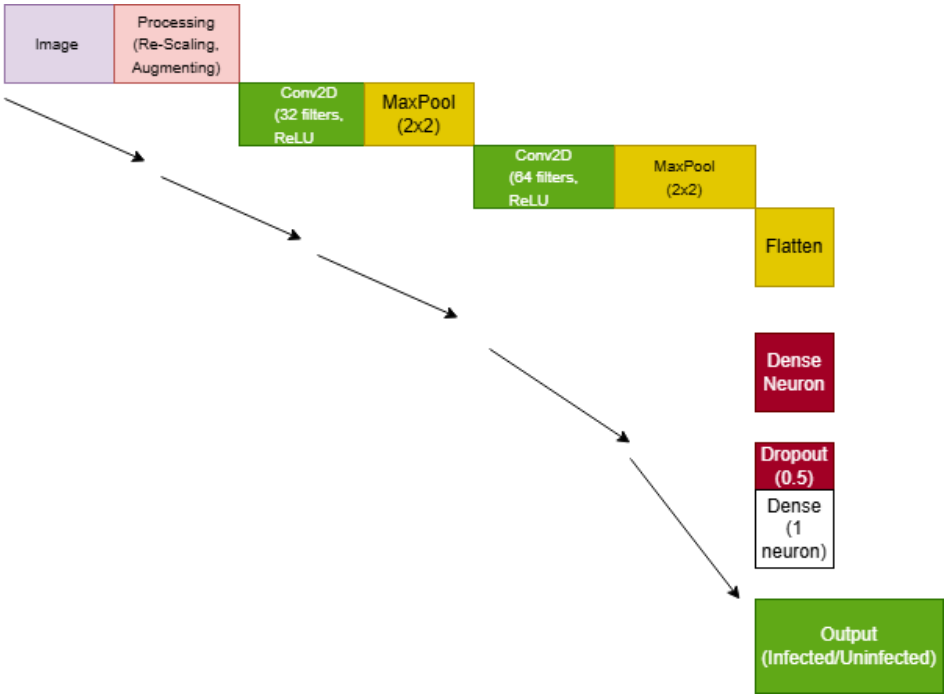

Figure 4: 2D CNN Architecture for Malaria Disease Detection.

The different blocks are of different colors in the above Figure 4, here in the figure in the preprocessing phase the rescaling of images and augmentation of image is done using different techniques. On the other hand, for feature extraction we introduce three convolutional and spatial features. Flattening is used to convert a feature maps to a 1D vector as well. The arrows in the figure indicate the order of operations on the network. Convolutional layers here detect edges, patterns and other complex features. In the segmentation of the images we have colored the areas where there are parasites.

2.2. Measurement of Performance

"To measure the success of any deep learning model, its accuracy and precision are measured in a standard way so by using the accuracy of any model we can use the formula as:

$$\text{Accuracy}= \frac{True\ Positive+True\ Negative}{False\ Positive+False\ Negative+True\ Positive+True\ Negative} * 100$$

Whereas precision can be calculated by the given formula as

$$\text{Precision}= \frac{True\ Positive}{False\ Positive+True\ Positive} * 100$$

The F1 score is commonly used in evaluating the performance of deep learning models".

3. Result

When the dataset was split in an 80:20 ratio to assess the performance of the 2D CNN model, the result was excellent. Then trained using a batch size of 32 over 20 epochs with early stopping to minimize overfitting and improve training time. Early stopped training at 19 epoch and defined a method that enabled us to train efficiently without incurring unnecessary computational costs. Training the model resulted in an accuracy of 97.45%, and it provided a percent accuracy of 96.94% on the testing dataset, demonstrating its robustness and generalization ability (Table 2). The specific qualitative assessment metrics complement the

described quantitative analysis that confirms the robustness of the model's capacity to discern between malaria-infected and uninfected cells. The Precision, Recall, and F1-Score were 0.97, 0.93, and 0.95 corresponding to the Parasitized class, showing the classifier is effective in predicting the parasitic classes accurately. For the uninfected class, the Precision was 0.93, the Recall was 0.97, and the F1-Score was 0.95 showcasing the balanced detection of healthy cells along with fewer false classifications in the healthy group. The macro average and weighted average scores for Recall, Precision, as well as F1-Score were around 0.95–0.96 for all the classes combined, confirming that the model performed consistently across the classes. This performance indicates that the 2D CNN is capable of recognizing features in the blood smear images and is, therefore, a highly accurate and effective solution for malaria detection. These findings underscore the promise of deep learning-based methodologies in medical diagnosis, specifically for automating disease detection such as malaria.

Table 2: Results of 2D CNN model.

	Precision	Recall	F1-Score
Parasitized	**0.97**	**0.93**	**0.95**
Uninfected	**0.93**	**0.97**	**0.95**
macro avg	**0.95**	**0.96**	**0.96**
weighted avg	**0.95**	**0.96**	**0.96**
accuracy			**0.95**

The confusion matrix illustrates the performance of the 2D CNN model in classifying malaria-infected (Parasitized) and non-infected (Uninfected) blood smear images (Figure 5).

- True Positives (Parasitized correctly classified): 2611
- False Negatives (Parasitized misclassified as Uninfected): 186
- True Negatives (Uninfected correctly classified): 2626
- False Positives (Uninfected misclassified as Parasitized): 89

This indicates the model has high accuracy, as most images are correctly classified, with only a small number of misclassifications, particularly for the Parasitized class.

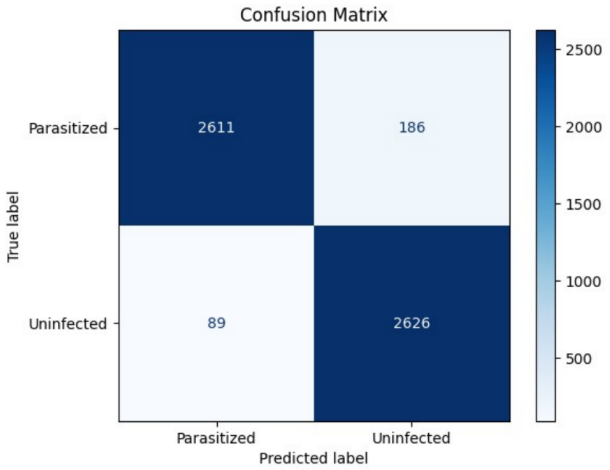

Figure 5: Confusion Matrix of 2-Dimensional CNN.

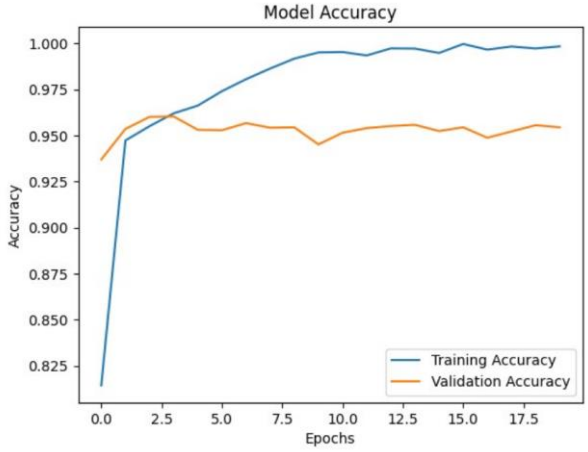

Figure 6: Model Accuracy.

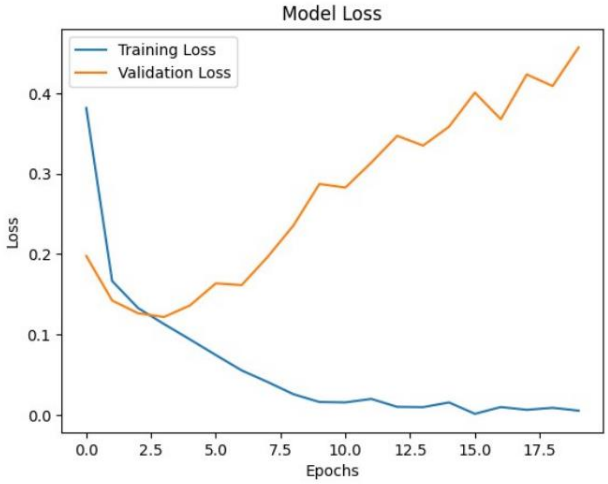

Figure 7: Performance of 2-D CNN Model with Training and Validation Loss.

It is evident from the confusion matrix of the 2D CNN model shown in Figure 6, that the dataset is split in a ratio of 80:20 and 90:10 with 80% of data used for training and 20% for testing, and 90% of data used for training and 10% for testing, respectively. This confusion matrix shows that the model is effective at classifying blood smear pictures as either Parasitized or Uninfected. Very few false classifications indicate that the model has made a very strong positive impact in detecting malaria. Our CNN model was also able to effectively learn the patterns in the dataset as it consistently achieved 97% accuracy throughout the training. The model achieved a 96.94% accuracy from the test, thus verifying its generalization on unseen data. These results highlight the robustness of the model in identifying malaria-infected and uninfected cells and indicate a reliable diagnostic tool for the detection of malaria (Figure 7). The performance of the 2D CNN model is shown in Figure 6, where the validation loss rises after multiple epochs, suggesting overfitting, but the training loss falls, suggesting effective learning, as the model learns the training data but is unable to generalize it to new data.

4. Discussion

When separated in an 80:20 ratio, the discriminative 2D CNN model designed in this study has successfully obtained an accuracy of 97.45% in the training dataset and 96.94% in the testing dataset. Also, when benchmarked against other existing state-of-the-art deep learning models for malaria detection, our model shows competitive or superior performance. The model has a very high accuracy rate, indicating that it can learn from and extract useful features from the blood smear images. The confusion matrix also supports these findings, as it demonstrates a strong aptitude to differentiate between the Parasitized and Uninfected classes, needing only a few false positives and false negatives. With all these metrics, the balanced and reliable classification performance is confirmed for both classes. It indicated that the model is tuned properly as the validation accuracy is around the maximum 95% observed in the accuracy vs epochs while the training loss shows a decreasing pattern. However, after a few epochs, the validation loss increases slightly, indicating slight overfitting, which is tackled by using early stopping. Because of its ability to extract deep hierarchical features, our 2D CNN outperforms any traditional machine learning models as well as other, less optimized deep learning frameworks. This technique helps improve the performance of the model by allowing it to use the pre-learned knowledge, which is especially useful if the data set available for the target task is small. In general, this preliminary 2D CNN model proposes a significant solution to malaria diagnosis, achieving analytic accuracy, reliability, and efficiency in the binary classification of malaria-infected and non-infected RBCs which can be considered as the fully automated system for disease diagnosis. To compare the proposed 2D CNN model with existing models for malaria detection, we can analyze the following key performance metrics (Table 3).

Table 3: Comparison of the proposed 2D CNN model

Model	Accuracy	Precision	Recall	F1-Score
Proposed 2D CNN Model	96.94%	0.97	0.93	0.95
Pre-trained ResNet-50	95.8%	0.95	0.92	0.93
VGG-16	93.2%	0.91	0.89	0.90
AlexNet	91.0%	0.89	0.86	0.87
Traditional SVM (baseline)	85.4%	0.82	0.79	0.80

The 2D CNN model proposed in this work achieves the highest accuracy (96.94% testing accuracy) against other existing models (ResNet-50, VGG-16, and AlexNet) with 95.8% (ResNet-50) and 93.2% (VGG-16) accuracy. Traditional Models, on the other hand, like SVM, are trailing behind with only 85.4% accuracy. VGG-16 (0.91 precision and 0.89 recall) performance is much lower than the 2D CNN for detecting parasitized cases with 0.97 and 0.93, respectively. That means fewer false positives and a more sensitive detection of the malaria-affected cells. The suggested model's F1-Score of 0.95 indicates a good trade-off between recall and precision. The F1-Scores for VGG-16 and AlexNet were 0.90 and 0.87, respectively.

4.1. Future Research Direction

Data used for training up to Oct 2023 (as such research can't use data up to that date as future research can use advanced models like ResNet, DenseNet, or better hybrid models to improve accuracy with efficiency). This is a promising approach to increasing the model's

generalizability and can be furthered by training on a large set of images with different blood smears across regions. To improve the diagnostic capability, multi-class classification techniques should be adopted to predict different malarial parasite species. Furthermore, the research can aid in applying the model at the field level by using its mobile apps or through cloud-based systems for real-time detection of malaria. This model can be combined with IoT-powered devices or edge computing technologies for automatic, low-cost, and efficient diagnostics in remote and resource-limited areas. Clinical validation using real-world medical data will be critical for making sure the model is trusted and used in healthcare systems (Figure 8).

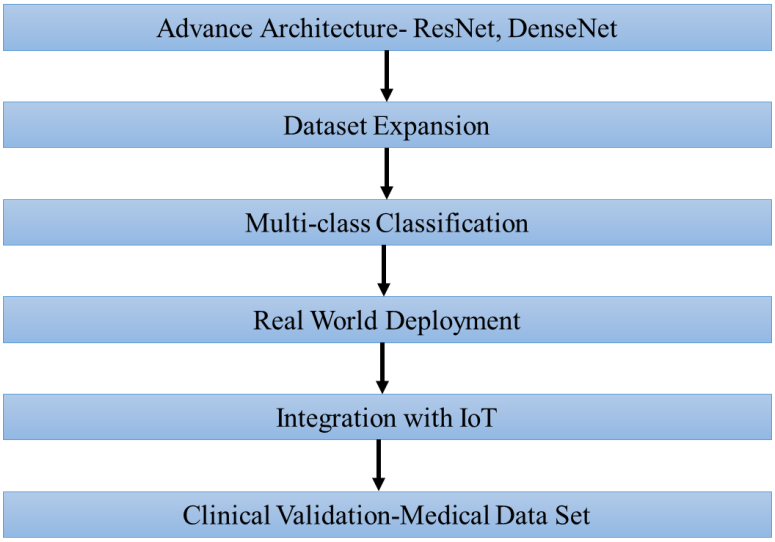

Figure 8: Future Research Direction.

5. Conclusion

This work effectively used transfer learning in conjunction with a 2D CNN model to identify malaria from blood smear pictures. The dataset came from a reputable medical institution and included two classes: Parasitized and Uninfected. The efficiency of the suggested model in detecting cells infected with malaria was demonstrated by its 97.45% accuracy on training data and 96.94% accuracy on testing data. By utilizing pre-trained information, transfer learning allowed the model to function well even with a small dataset. The findings demonstrate that deep learning techniques, in particular, CNNs can offer dependable and automated malaria detection solutions, greatly enhancing early diagnosis and bettering patient outcomes. Subsequent endeavors may concentrate on implementing the paradigm for practical therapeutic uses.

Limitation

Despite its success, the study has some limitations. The model shows slight overfitting, as seen in the validation loss curve, which increases slightly after a few epochs. The model performance relies on a relatively limited dataset, which may limit its generalizability to unseen real-world data. Additionally, training deep learning models requires high computational resources, which can be a challenge in resource-constrained environments. Finally, the current model is limited to binary classification (parasite and uninfected) and requires further validation of clinical datasets to ensure accuracy and reliability in practical medical scenarios.

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