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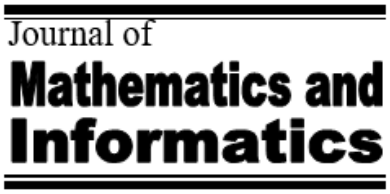


# Evaluation of the Performance of Deep Learning Classification Models in Microscopic Image Results for Malaria Disease

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***Abstract.*** Malaria is a significant public health issue, particularly in Sub-Saharan Africa, and is caused by the Plasmodium parasite, which is transmitted through mosquito bites. Traditionally, malaria diagnosis relies on the microscopic analysis of blood smears, a method that's dependable but also time-consuming and demanding in expertise. This study introduces and assesses a deep learning classification model using VGG19, aimed at automating malaria diagnosis in microscopic images. The model generated encouraging results, with a training accuracy of 97.76%, a validation accuracy of 97.00%, a processing time of 5 minutes and 20 seconds, and an F1 score of 0.4888. The study used 27,558 enhanced images, divided into training (22,046) and validation (5,512) sets to avoid overfitting and biases, adhering to an 80% training and 20% validation split. The CNN training model and VGG19 transfer learning achieved an astounding average accuracy of 97.76% for both parasitized and uninfected malaria cell images. The study emphasizes the need for collecting high-quality, abundant image data to effectively analyze contamination levels in both parasitized and uninfected individuals. It is advised that sophisticated microscopic technology be used to improve the performance, accuracy, and speed of malaria diagnosis and prediction utilizing the proposed model.

***Keywords:*** Plasmodium Parasite, Malaria detection, Microscopic Image, Deep Learning Classification, Image Pre-processing

***AMS Mathematics Subject Classification (2010):*** 62H35, 94A08

## 1. Introduction

Malaria, a potentially lethal condition that affects millions worldwide, most notably in Sub-Saharan Africa, is traditionally diagnosed through microscopic examination of blood smear samples. This procedure necessitates expertise and experience, making it time-consuming and prone to errors, particularly in areas with limited access to skilled medical experts.

Deep learning has recently shown promising results in automating the malaria diagnosing procedure. However, there remains a requirement for enhanced precision, accuracy, and quicker diagnostic speed [1,2]. This study aims to elevate the deep-learning classification of microscopic images for malaria diagnosis by implementing a set of techniques that augment classification accuracy performance and robustness [3,4]. Plasmodium is transferred to humans via infected mosquito bites [5]. Malaria remains a severe public health issue, particularly, where it contributes significantly to morbidity and mortality [6]. Data augmentation, image pre-processing, transfer learning, ensembling, and hyperparameter optimization are some of these techniques [7]. With the use of these techniques, a deep learning algorithm was created that can swiftly and accurately diagnose malaria by properly classifying malaria parasites seen in blood smears [8]. By using a series of techniques that may increase the classification's accuracy and robustness, this research intends to improve the deep learning classification in micro-scope image findings for malaria illness. The following are those techniques:

## 1.1. The following are the techniques

**1.1.1.** Preparation, refers to the set of actions and adjustments performed on raw input data before its use in a machine learning or deep learning algorithm [9].

**1.1.2.** Transfer Learning: Leveraging transfer learning can help address limitations in dataset size and diversity [10]. Pre-trained models, such as DenseNet or VGG19, can be used as a starting point and fine-tuned on malaria-specific datasets. Transfer learning enables models to benefit from previously learnt characteristics while also reducing the requirement for huge annotated datasets [11].

**1.1.3.** Ensemble Learning: Techniques like model averaging and stacking can be used to aggregate the predictions of different algorithms or models [12]. This can help mitigate individual algorithm limitations and improve overall classification performance.

**1.1.4.** Data Augmentation: By increasing the diversity and size of the training da-taset, you can improve algorithm resilience and generalization [13]. To generate more training examples, techniques such as rotation, scaling, flipping, and adding noise can be used [14]. Hyperparameters are configuration parameters predetermined before the model's training, distinct from those learned directly from the data [15].

Researchers can bridge the gaps between existing methodologies and produce more accurate, economical, and robust deep-learning models for malaria diagnosis from microscopic pictures by combining various techniques and constantly refining and optimizing the algorithms.

Deep learning classification applied to microscopic image data has the potential to automate the detection and quantification of malaria parasites in blood smears [16,17]. As a result, diagnosis accuracy and speed are improved. Deep learning algorithms have been utilized successfully in a range of medical image processing jobs because they can learn difficult patterns and characteristics from large datasets [18,19].

Researchers might also strive to close the gaps between algorithms in the context of increasing deep learning classification for malaria diagnosis using microscopic images to achieve good outcomes [20,21]. Here are a few methods that can be used. Researchers use

architecture optimization to improve performance, detection accuracy, and efficiency, experimenting with different transfer learning techniques.

However, accurate categorization of malaria parasites in blood smears remains difficult due to the parasites' varying appearances, the quality of the blood smears, and the presence of artefacts and debris (remains of something that has been destroyed). In this context, it is vital to improve the performance accuracy of malaria diagnosis by developing effective deep-learning algorithms that can reliably categorize malaria parasites.

## 2. Study background

### 2.1. Deep learning

Machine learning techniques like deep learning are being increasingly utilized for automated malaria screening, offering promising diagnostic capabilities. Originating from machine learning, deep learning draws inspiration from the information-processing methods of the human brain [22]. It represents an advanced form of multilayer neural networks capable of autonomously learning intricate data representations [23]. Often called features. This approach encourages researchers to identify distinctive features with minimal human effort and domain-specific knowledge [24].

For practical applications, the characteristics of a well-trained network are crucial. Firstly, its objectivity is paramount, highlighting the need for unbiased analysis devoid of subjective human influences. Secondly, consistency is essential, ensuring that the network consistently annotates similar features in the same manner. Lastly, the network's validity is crucial, which pertains to the precision of its outputs. In real-world scenarios, especially when training data is limited, the reliability, consistency, and accuracy of the network become pivotal. Achieving reliability and validity can be challenging in deep learning, which often requires extensive training datasets [25].

The collection of annotated training images is particularly difficult in medical contexts due to the need for expert knowledge and privacy concerns, leading to a slower adoption of deep learning in these areas [26]. However, recent advancements in this technology have significantly enhanced the efficiency and precision of large-scale computer vision tasks [27]. Consequently, the examination of microscopic images has garnered heightened attention. Specifically, Convolutional Neural Networks (CNNs), a subset of deep learning techniques, have demonstrated remarkable proficiency in various image processing tasks, including recognition, classification, and categorization [28].

### 2.2. Convolutional neural network

A Convolutional Neural Network (CNN) is a form of deep neural network that is frequently used in machine learning [29]. It is very good in processing data having a grid-like layout, such as photographs. CNNs are a cornerstone of modern computer vision technology, and they have been instrumental in many breakthroughs in image and video recognition, as well as in other areas like natural language processing. Here’s an overview of CNNs:

#### 2.2.1. Convolutional layers

The fundamental components of a CNN. Convolution operations are performed across the input data by these layers using filters or kernels. The convolution process involves sliding these filters across the input to produce feature maps, capturing spatial hierarchies and

patterns such as edges, texture or more complex shapes in images patterns such as edges, textures, or more complex shapes in images.

#### 2.2.2. Activation functions

Following convolution, an activation function, often the Rectified Linear Unit (ReLU), is added to the network to introduce non-linear features. CNNs can now handle sophisticated, non-linear data transformations.

#### 2.2.3. Pooling layers

These layers reduce the feature maps' spatial dimension, making network computing easier to operate and reducing the number of parameters. Maximum pooling and average pooling are the most popular forms.

#### 2.2.4. Fully connected layers

At the end of the network, fully connected layers integrate all the features learned by preceding layers to produce the final outcome, like class scores in tasks involving classification.

#### 2.2.5. Dropout layers

To mitigate overfitting, dropout layers may be employed, which randomly disable a portion of the neurons during the training process, encouraging the network to develop stronger, more generalizable features.

### 2.3. Related works

Several major papers and references stand out when it comes to measuring deep learning classification performance in microscopic image analysis for malaria. These publications provide insights into the efficacy, challenges, and future possibilities of employing deep learning techniques, namely convolutional neural networks (CNNs), in this specific medical discipline.

#### 2.3.1. Advancements in CNN for malaria detection

A significant study by [30], demonstrated the potential of deep CNNs in identifying malaria-infected cells from thin blood smear images. Their work highlighted not only the accuracy but also the efficiency of CNNs in medical image analysis.

#### 2.3.2. Performance metrics and validation

The work of [31], is crucial in this context. They provided a comprehensive analysis of different performance metrics such as sensitivity, deep learning models for malaria detection were evaluated for specificity and accuracy. Their findings emphasised the significance of rigorous validation approaches, such as cross-validation procedures.

#### 2.3.3. Challenges in dataset and image quality

A study by [32], addressed the challenges associated with the variability in dataset quality and image acquisition techniques. Inconsistencies in staining, picture resolution, and magnification levels, they noted, had a substantial impact on the performance of deep learning models in malaria microscopy.

#### 2.3.4. Comparison with traditional diagnostic methods

An interesting comparison was made by [33], who juxtaposed the performance of automated deep learning systems against traditional manual microscopy for malaria diagnosis. Their findings suggested that while deep learning offers promising results, it is essential to consider it as a complementary tool rather than a standalone solution.

#### 2.3.5. Data augmentation and transfer learning

The work of [34], explored how data augmentation and transfer learning could mitigate the challenges posed by limited datasets in malaria image analysis. They demonstrated that these techniques could significantly enhance model performance, especially in scenarios with scarce training data.

Each of these papers adds a piece to the jigsaw of how deep learning can be used effectively for malaria detection in microscopic images, showing the progress made, the challenges to overcome, and the possibility for future breakthroughs in this crucial field of medical study.

## 3. Materials and methods

### 3.1. Materials

To discover relevant publications published between 2020 and 2023, a thorough search was undertaken across electronic databases such as PubMed, Scopus, and IEEE Xplore. Keywords such as 'malaria,' 'deep learning,' 'classification,' and 'microscopic images,' along with their variations, were employed in various combinations to locate pertinent articles. The search was restricted to human subject's research published in English. This section discusses the application of CNN with techniques such as Vgg19, Vgg16, InceptionV3, and ResNet152 in the categorization of malaria cell images for accuracy and performance evaluation.

### 3.2. Methods

The literature search process is a critical step in conducting a comprehensive review of the existing literature on a specific topic. It involves systematically searching for relevant studies in online databases such as Kaggle and Scopus, as well as articles and other sources of information, to gather the necessary literature for the review.

The source of the accrued information involves a vast array of relevant techniques for evaluating the performance of deep learning classification in microscopic image analysis for malaria detection. The exploration was confined to works published in the timeframe of 2020 to 2023 and was carried out exclusively in English. The following keywords were used in the search: 'malaria detection,' 'performance of microscopic images

### 3.3. Dataset

**3.3.1.** In the initial phase, we present elucidations concerning several studies incorporated from widely-used databases, sourced from the National Institutes of Health (NIH). The dataset consists of 27,558 samples, comprising 13,779 parasitized and an equal number of 13,779 uninfected samples [35]. The source of this dataset is accessible through the following URL: https://ceb.nlm.nih.gov/repositories/malaria-datasets/. For a visual representation, refer to Figure 1 in the 'repositories/malaria' section.

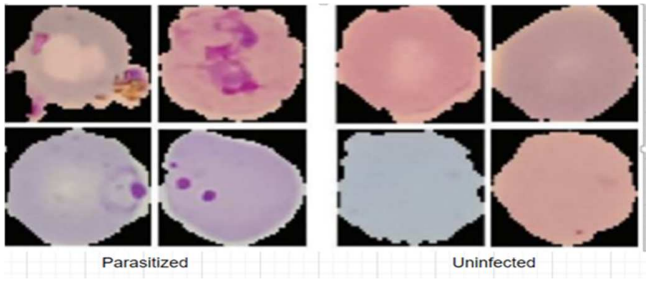


**Figure 1:** Sample of collected datasets

The term 'uninfected class' refers to image data that does not exhibit malaria infection, while the 'parasitized class' represents image data depicting parasitized blood cells.

**3.3.2.** The dataset was allocated with 80% dedicated to training and 20% to validation purposes. We utilized Vgg19 and integrated Transfer Learning with CNN-based deep learning models as feature extractors. This approach aids in distinguishing between healthy and parasitized blood cells, thus facilitating the diagnosis of diseases. The proposed model has three fully connected layers, three convolutional layers that each use three 2, 2 filters with two-pixel steps, 64 filters for the first, 32 filters for the second, and 16 filters for the third. The model input is made up of segmented cells with resolutions of 80, 80, and 3. They assessed how well pre-trained CNNs, in particular Vgg19, Vgg16, InceptionV3, and ResNet152, extracted traits from parasitized and uninfected cells. The Random Grid Search technique was used to optimize these models for hyperparameters.

## 4. Model development process

**4.1.** The technique illustrated in Figure 2 was utilized for model creation; it describes all the steps starting from tool design.

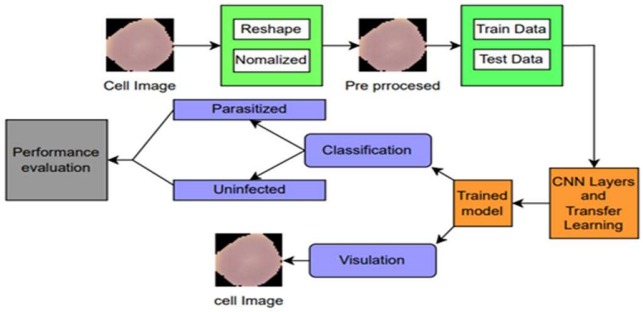


**Figure 2:** Block diagram of the model procedure for the literature review process

**4.2.** In the context of research evaluating the performance of deep learning classification in microscopic image analysis for malaria disease, the validation process is crucial in assessing the performance, accuracy, and reliability of the developed models. It involves evaluating the trained models using independent datasets and established evaluation metrics. Below is an overview of the validation process:

**4.2.1.** Splitting the dataset: The initial dataset was segmented into subsets for training, validation, and testing. The training subset facilitated the training of deep learning models,

while the validation subset aided in refining the models and optimizing hyperparameters. Finally, the testing subset was employed to assess the performance of the models.

**4.2.2.** Training of Models: The training dataset was used to educate deep learning models through the application of pertinent algorithms, including Convolutional Neural Networks (CNN). This process involved utilizing architectures like VGGNET, INCEPTIONV3, and RESNET, along with optimization methods such as Stochastic Gradient Descent (SGD), Data Augmentation, and Transfer Learning. In order to attain accurate performance and classifications, these models adapt their internal parameters based on the data they process.

**4.2.3.** Hyperparameter Optimization: In the stage of validating the models, there is a precise adjustment of the hyperparameters to enhance overall performance. This step includes the organized modification of settings like learning rate, batch size, regularization techniques, and the structure of the network to ascertain the best possible configuration.

**4.2.4.** Assessment of the Validation Set: The validation set, separate from the training data, was used to evaluate the trained models. This step is crucial for assessing how well the models generalize to new data and for detecting problems such as overfitting or under fitting. Metrics used for this evaluation include accuracy, precision, recall, F1-score, and the area under the receiver operating characteristic curve (AUC-ROC).

**4.2.5.** Evaluating Model Performance: The performance of the models is gauged using the previously mentioned metrics. Successful completion of the final testing phase by the models indicates they have achieved the set performance criteria. Should the performance be subpar, modifications in the architecture, hyperparameter settings, or data augmentation methods might be necessary.

**4.2.6.** Testing Set Evaluation: The final evaluation of the models' performance is conducted using an independent testing set, which was not used during training or validation. This ensures an unbiased assessment. The models' predictions for the testing set are evaluated, and metrics are calculated to measure performance on unseen data.

**4.2.7.** Cross-Validation (Optional): In some cases, a cross-validation approach may be employed to further validate the models.

**4.2.8.** The validation process ensures that the developed deep learning models are reliable, accurate, and capable of effectively classifying microscopic image results for malaria disease. It provides an objective assessment of the models' performance on both seen and unseen data, contributing to the overall validity and trustworthiness of the research findings.

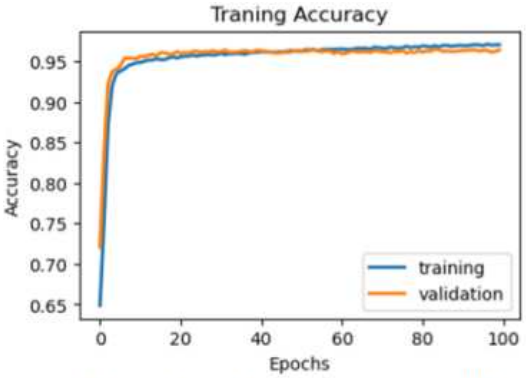


Figure 3: The training accuracy of the CNN and VGG19 transfer learning model

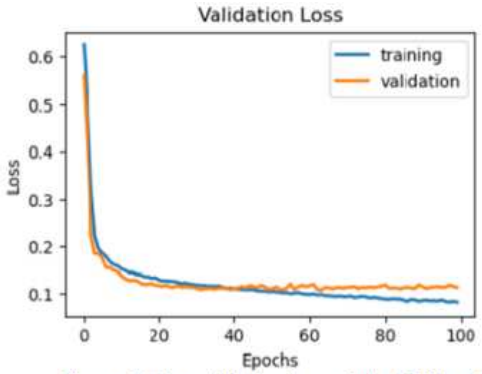


Figure 4: The validation loss of the CNN and VGG19 transfer learning model

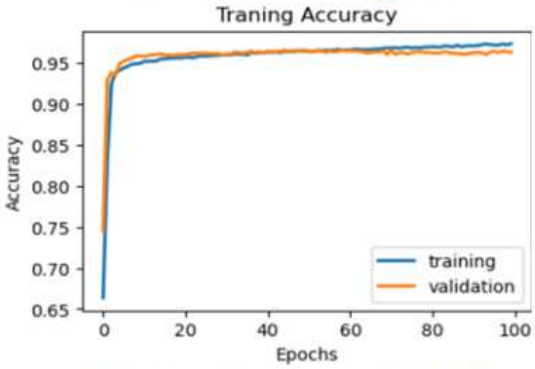


Figure 5: The training accuracy of the CNN and VGG16 transfer learning model

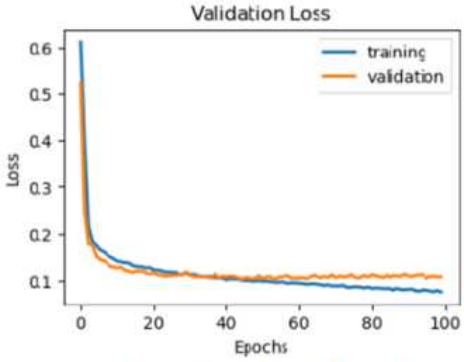


Figure 6: The validation loss of the CNN and VGG16 transfer learning model

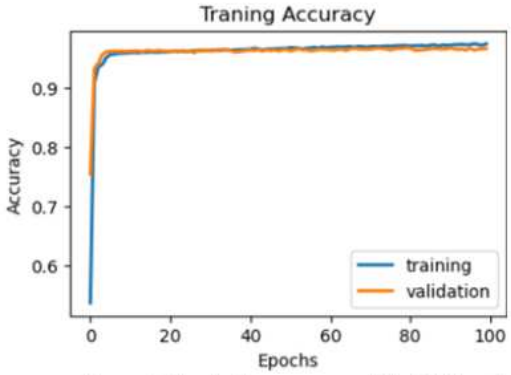


Figure 7: The training accuracy of the CNN and InceptionV3 transfer learning model

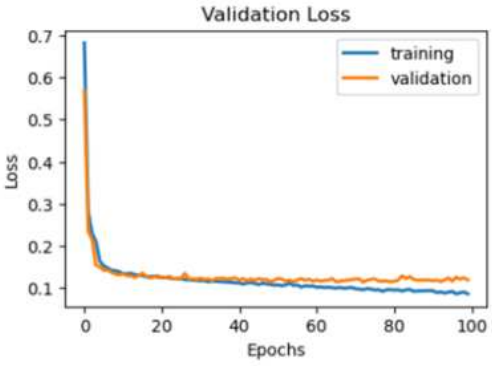


Figure 8: The validation loss of the CNN and InceptionV3 transfer learning model

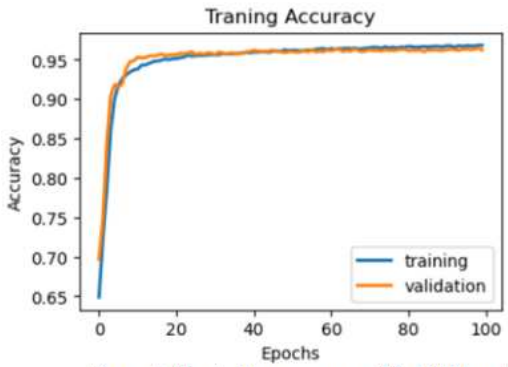


Figure 9: The training accuracy of the CNN and ResNet152 transfer learning model

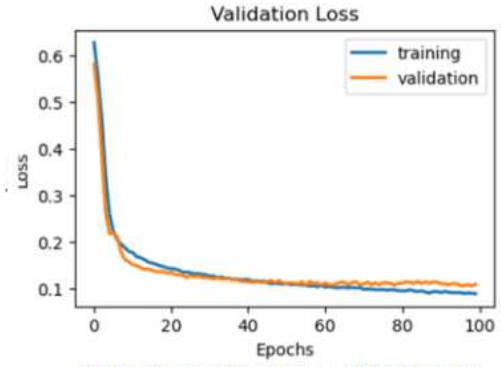


Figure 10: The validation loss of the CNN and ResNet152 transfer learning model

## 5. Results and discussion

### 5.1. Results

The initial search revealed 27,558 cell pictures, with 13,779 parasitized cells and 13,779 uninfected ones. Several tactics were used in the preliminary operations. To improve the dataset's quality, numerous pre-processing procedures were performed on the photos before they were fed into our deep learning model.

**5.1.1.** Image Rescaling: All images were resized to a uniform size of 80x80 pixels. This resizing ensured that the model could process images of a consistent size efficiently.

**5.1.2.** Data Augmentation: To mitigate potential overfitting and enhance the model's robustness, we implemented data augmentation techniques. These included random rotations (up to 20 degrees), horizontal flips, and brightness adjustments.

**5.1.3.** Normalization Process: Each image's pixel values were scaled down to a [0, 1] range by dividing them by 255. This normalization was crucial for enhancing the training efficiency and convergence of the model.

**5.1.4.** Dataset Division: The dataset was split into two segments - 80% of the images were allocated for training, and the remaining 20% formed the test set. This separation allowed for the evaluation of the model's effectiveness on new, unexposed data.Ensuring Dataset Quality: By executing these pre-processing steps, we ensured that our deep learning model had access to a standardized and diverse dataset. These measures helped mitigate common issues associated with image-based data, such as variations in image sizes and lighting conditions.

**5.2.** In the trials, deep learning models such as Convolutional Neural Networks (CNNs) were used. Transfer learning approaches involving Vgg19, Vgg16, InceptionV3, and ResNet 152 were used for malaria categorization utilising microscopic pictures.

| Model | Train Accuracy | Test Accuracy | Epochs | Time | Loss |
|---|---|---|---|---|---|
| VGG19 | 97.76% | 97.00% | 97 | 5m 20s | 0.065 |
| VGG16 | 97.37% | 96.34% | 100 | 4m 12s | 0.0764 |
| INCEPTIONV3 | 97.36% | 96.28% | 97 | 3m 22s | 0.0861 |
| **RESNET152** | 96.86% | 96.50% | 99 | 3m 77s | 0.0906 |

### 5.2.1. Training accuracy

The accuracy of the model on the training dataset is shown in Table 1. The fraction of correctly categorised samples in the training set is measured by this metric. A high training accuracy suggests that the model matches the training data effectively.

### 5.2.2. Test accuracy

As indicated in Table 1, this refers to the model's accuracy on a separate dataset that it has not encountered during training, often referred to as the test or validation set. This metric is crucial as it indicates how well the model generalizes to new, unseen data.

**Table 2:** Comparison of model performance using transfer learning models

| Model | F1-Score | Sensitivity(Recall) |
|---|---|---|
| VGG19 | 0.4888 | 0.9776 |
| VGG16 | 0.4869 | 0.9737 |
| INCEPTIONV3 | 0.4868 | 0.9736 |
| RESNET152 | 0.4843 | 0.9686 |

**5.2.3.** Table 2 features the F1-Score, also referred to as the F1 Measure, which serves as a statistical tool for gauging the efficacy of the classification model. This metric, representing the harmonic mean between precision and recall, offers a balanced evaluation of both these aspects. The calculation of the F1-Score is done using the following formula:

$$F1 - score = 2 \times \frac{precision \times recall}{precision + recall}$$

**Where;**

Precision is calculated as the proportion of correct positive predictions (true positives) to the overall number of positive predictions made (which encompasses both true positives and false positives). The formula for calculating precision is as follows:

$$Precision = \frac{True\ positive}{True\ positives + False\ positive}$$

**and;**

Recall, also known as Sensitivity, is the measure of true positives relative to the total of true positives and false negatives. It evaluates the model's capacity to correctly identify all positive cases.

$$Recall = \frac{True\ positive}{True\ positives + False\ negatives}$$

The F1-Score is especially beneficial in circumstances with unequal class distribution, when it is critical to strike a compromise between precision and recall. It has a value between 0 and 1, with a greater value indicating a better balance of precision and recall.

### 5.3. Discussion

The comparison of model performance revealed that CNN-based architectures were widely used and consistently demonstrated superior performance in malaria classification tasks. Models such as VGGNet, InceptionNet, and ResNet were extensively used among these architectures, displaying good accuracy, sensitivity, and specificity in differentiating between malaria-infected and uninfected cells.

Image pre-processing techniques were discovered to be significant in boosting the accuracy of deep learning models for malaria classification in a review of the literature. Image enhancement, noise reduction, contrast correction, and image normalisation are all common pre-processing techniques. These strategies aid in the improvement of the quality and visibility of malaria-infected cells, allowing for more accurate feature extraction and categorization.

Convolutional Neural Networks (CNNs) emerged as the most extensively utilised deep learning architecture for malaria categorization. CNNs outperformed humans when it came to automatically learning and extracting relevant characteristics from tiny images. Various CNN architectures were used, including VGGNet, ResNet, and InceptionNet, with modifications tailored to the unique needs of malaria classification.

Feature extraction methods, such as transfer learning, which involves leveraging pretrained models, showed promise in improving classification performance by utilizing knowledge learned from large-scale datasets. Additionally, ensemble learning techniques, such as bagging and boosting, were explored to further enhance the accuracy and robustness of deep learning models.

## 6. Conclusion and recommendation

### 6.1. Conclusion

According to the research data, CNN-based transfer learning outperforms other deep learning architectures in terms of performance accuracy in classifying malaria-infected cells in microscopic pictures, especially when combined with the VGG19 design.

However, the choice of model and its performance can be influenced by various factors, including dataset characteristics, hyperparameter optimization, and pre-processing techniques. Further research is needed to investigate the generalization of models across different datasets, their robustness against variations in image quality, and the integration of these models into clinical practice

### 6.2. Recommendations

Based on the findings and outcomes of our research evaluating the performance of deep learning classification in microscopic image results for malaria disease, we propose the following recommendations for future studies and practical applications:

Further Research on Diverse Data Sets: Conduct additional research using diverse and comprehensive data sets to enhance the robustness and generalizability of deep learning models for malaria classification. This includes incorporating data from different geographical regions, various levels of disease severity, and diverse populations.

Investigating Transfer Learning with Pre-Trained Models: Examine the utility of transfer learning and pre-trained models in the classification of malaria. Using knowledge from previously trained models on large-scale picture datasets can help to accelerate the creation of accurate and efficient deep learning models for malaria classification.

Addressing Class Imbalance: When training deep learning models, the imbalance in the distribution of malaria-positive and malaria-negative samples can provide difficulties. To address class imbalance and increase model performance, consider strategies such as oversampling, under sampling, or employing class weights.

Collaboration and Data Sharing: Encourage collaboration and data sharing among academics and institutions working on deep learning malaria categorization. Collaborative efforts can result in larger and more diversified datasets, algorithm benchmarking, and enhanced model performance.

Ethical Considerations: Continuously address and navigate the ethical considerations associated with deep learning classification in malaria disease. Ensure the privacy and confidentiality of patient data, address biases and fairness in algorithmic decisions, and obtain informed consent from participants.

Validation and External Evaluation: Assess the generalizability and robustness of deep learning models by validating and evaluating their performance on external datasets and in different healthcare settings. External validation helps to prove the models' dependability and correctness across a wide range of populations and contexts.

Continuous Monitoring and Improvement: Monitor and improve deep learning models for malaria classification continuously as new advancements and techniques emerge. Stay up-to-date with the latest developments in deep learning and regularly reassess and refine models to enhance their performance.

By implementing these recommendations, researchers can advance the field of deep learning classification in microscopic image analysis for malaria disease, ultimately leading to improved diagnostic accuracy, efficient screening processes, and better management of malaria worldwide.

The analysis of the literature illustrates the increased interest and progress in improving deep learning classification for malaria detection using microscopic pictures.. The application of deep learning techniques, combined with appropriate preprocessing, feature extraction, and classification algorithms, holds significant potential for accurate and automated malaria diagnosis. However, further research is needed to address challenges such as limited dataset availability, generalization across different malaria strains, and integration into clinical practice. Continued efforts in this area can contribute to improved malaria diagnosis, ultimately aiding in better disease management and control.

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**Conflicts of Interest.** The authors state that there are no conflicts of interest in relation to this study.

**Authors' contributions.** All authors contributed equally to this work.

## REFERENCES

1. A.Negi, K.Kumar and P.Chauhan, Deep learning-based image classifier for malaria cell detection, *Mach Learn Health Appl*, (2021) 187–197. https://doi.org/10.1002/9781119792611.ch12
2. L.E.Fitri, T.Widaningrum, A.T.Endharti, et al, Malaria diagnostic update: From conventional to advanced method, *J Clin Lab Anal*, 36 (2022) 1–14. https://doi.org/10.1002/jcla.24314
3. N.Singla and V.Srivastava, Deep learning enabled multi-wavelength spatial coherence microscope for the classification of malaria-infected stages with limited labelled data size, *Opt Laser Technol*, *130* (2020). https://doi.org/10.1016/j.optlastec.2020.106335
4. KKK, et al., An efficient image classification of malaria parasite using convolutional neural network and ADAM optimizer, *Turkish J Comput Math Educ.* 12 (2021) 3376–3384. https://doi.org/10.17762/turcomat.v12i2.2398
5. G.Arora, Y.M.Chuang, P.Sinnis, et al., Malaria: influence of Anopheles mosquito saliva on Plasmodium infection, *Trends Immunol*, 44 (2023) 256–265. https://doi.org/10.1016/j.it.2023.02.005
6. E.O.Kolawole, E.T.Ayeni, S.A.Abolade, et al., Malaria endemicity in sub-Saharan Africa: Past and present issues in public health, *Microbes Infect Dis*. 4 (2023) 242–251. https://doi.org/10.21608/MID.2022.150194.1346
7. A.Rahman, H.Zunair, M.S.Rahman and J.Q.Yuki, Improving malaria parasite detection from red blood cell using deep convolutional, *Neural Networks*, 1–33.
8. F.J.P.Montalbo and A.S.Alon, Empirical analysis of a fine-tuned deep convolutional model in classifying and detecting malaria parasites from blood smears, 15 (2021) 147–165.
9. M.Schuld and F.Petruccione, *Supervised Learning with Quantum Computers* (2019).
10. K.T.Chui, B.B.Gupta, M.Zhao, et al., Enhancing electrocardiogram classification with multiple datasets and distant transfer learning, *Bioengineering* 9 (2022) 1–21. https://doi.org/10.3390/bioengineering9110683
11. C.Tan, F.Sun, T.Kong, et al., A survey on deep transfer learning. Lect Notes Comput Sci (including Subser Lect Notes Artif Intell Lect Notes Bioinformatics) (2018) 11141 LNCS:270–279. https://doi.org/10.1007/978-3-030-01424-7_27

12. S.Rajaraman, S.Jaeger and S.K.Antani, Performance evaluation of deep neural ensembles toward malaria parasite detection in thin-blood smear images, *PeerJ* 7 (2019) https://doi.org/10.7717/PEERJ.6977
13. P.T.Jackson, A.Atapour-Abarghouei, S.Bonner, et al., Style Augmentation: Data Augmentation via Style Randomization (2018).
14. R.Blaser and P.Fryzlewicz, Random rotation ensembles, *J Mach Learn Res*. 17 (2016) 1–26.
15. F.Hutter, *Parameter Optimization* (2017).
16. K.M.F.Fuhad, J.F.Tuba, M.R.A.Sarker, et al., Deep learning based automatic malaria parasite detection from blood smear and its smartphone-based application, *Diagnostics*, 10 (2020). https://doi.org/10.3390/diagnostics10050329
17. A.Maqsood, M.S.Farid and M.H.Khan, *Applied Sciences Deep Malaria Parasite Detection in Thin Blood Smear Microscopic Images* (2021).
18. M.Imaging, Survey of deep learning applications to medical image analysis, *Med Imaging Technol* 35 (2017) 212–226.
19. J.Ker, L.Wang, J.Rao and T.Lim, Deep learning applications in medical image analysis, *IEEE Access*, 6 (2017) 9375–9379. https://doi.org/10.1109/ACCESS.2017.2788044
20. K.Hemachandran, A.Alasiry, M.Marzougui, et al., Performance analysis of deep learning algorithms in diagnosis of malaria disease, *Diagnostics*, 13 (2023). https://doi.org/10.3390/diagnostics13030534
21. L.Rosado, J.M.Correia Da Costa, D.Elias, J.S.Cardoso, A review of automatic malaria parasites detection and segmentation in microscopic images, (2016) 1–12
22. H.Wang and B.Raj, *On the Origin of Deep Learning*, (2017) 1–72
23. K.Kumar, G.S.M.Thakur, Advanced applications of neural networks and artificial intelligence: a review, *Int J Inf Technol Comput Sci*., 4 (2012) 57–68. https://doi.org/10.5815/ijitcs.2012.06.08
24. M.MacLeod, What makes interdisciplinarity difficult? Some consequences of domain specificity in interdisciplinary practice, *Synthese*, 195 (2018) 697–720. https://doi.org/10.1007/s11229-016-1236-4
25. B.Adlam, M.D.Hoffman, N.Houlsby, et al., Underspecification Presents Challenges for Credibility in. (2020) 23:1–61
26. S.Lebovitz, N.Levina, H.Lifshitz-Assaf, Is AI ground truth really true? The dangers of training and evaluating AI tools based on experts' know-what, *MIS Q Manag Inf Syst.*, 45 (2021) 1501–1525. https://doi.org/10.25300/MISQ/2021/16564
27. N.O.Mahony, S.Campbell, A.Carvalho, et al., *Advances in Computer Vision*, (2014) https://doi.org/10.4324/9781315802145
28. A.Krizhevsky, I.Sutskever, G.E.Hinton, ImageNet classification with deep convolutional neural networks, *Commun ACM*, 60 (2017) 84–90. https://doi.org/10.1145/3065386

29. B.Madhu, M.Z.Islam, L.A.Ershad, Depth motion maps and log-gabor features based human action recognition using support vector machine, *J Math Informatics*, 17 (2019) 73–89. https://doi.org/10.22457/jmi.149av17a7
30. R.Nakasi, E.Mwebaze, A.Zawedde, et al., A new approach for microscopic diagnosis of malaria parasites in thick blood smears using pre-trained deep learning models, *SN Appl Sci*, 2 (2020) 1–7. https://doi.org/10.1007/s42452-020-3000-0
31. K.Sharif, P.David, M.Omar, et al., *Deep Learning in Coeliac Disease : A Systematic Review on Novel Diagnostic Approaches to Disease Diagnosis*, (2023) 1–13.
32. Inferring characteris cs of malaria infec on of two plasmodium strains, (2019).
33. C.Ikerionwu, C.Ugwuishiwu, I.Okpala, et al., Application of machine and deep learning algorithms in optical microscopic detection of Plasmodium: A malaria diagnostic tool for the future, *Photodiagnosis Photodyn Ther*, 40 (2022) 103198. https://doi.org/10.1016/j.pdpdt.2022.103198
34. D.O.Oyewola, E.G.Dada, S.Misra, R.Damaševičius, A novel data augmentation convolutional neural network for detecting malaria parasite in blood smear images, *Appl Artif Intell*, 36 (2022). https://doi.org/10.1080/08839514.2022.2033473
35. B.N.Narayanan, R.A.Ali and R.C.Hardie, Performance analysis of machine learning and deep learning architectures for malaria detection on cell images, 29 (2019). https://doi.org/10.1117/12.2524681