Revolutionizing Malaria Diagnosis: Deep Learning-Powered Detection of Parasite-Infected Red Blood Cells

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| **Article Info** |  | **ABSTRACT** |
| ***Article history:***  Received month dd, yyyy  Revised month dd, yyyy  Accepted month dd, yyyy |  | Malaria, a disease triggered by a minuscule parasite transmitted via the bites of infected female mosquitoes, afflicts many subtropical regions lacking robust healthcare infrastructure. Traditional diagnosis relies on skilled technicians visually examining blood smears for parasite-infected red blood cells (RBCs), a method susceptible to variability in accuracy based on technician expertise. Recent automated attempts utilizing handcrafted feature extraction techniques have proven unreliable in malaria detection. However, the emergence of deep learning, particularly Convolutional Neural Networks (CNNs), offers a transformative approach. CNNs, characterized by scalability and autonomous feature extraction through hidden layers, overcome limitations associated with manual feature engineering. Our research harnesses CNNs to identify malaria-infected RBCs in segmented microscopic blood images, promising expedited diagnosis, particularly in healthcare-deprived regions. This study evaluates established deep-learning models (MobileNetV2, InceptionV3, and ResNet50) for efficient malaria detection. Furthermore, we introduce a novel CNN architecture that surpasses previously documented models, incorporating bilateral filtering and image augmentation to enhance RBC attributes and address overfitting during training. Experimental assessments conducted on the benchmark NIH Malaria Dataset substantiate the effectiveness of our proposed algorithm, showcasing notable accuracy in identifying malaria within microscopic blood smears. This research signifies a substantial stride in combating malaria by integrating the potency of deep learning with the critical requirement for precise and suitable diagnosis. |
| ***Keywords:***  Malaria detection  Red blood cells  Convolutional neural networks  Transfer learning  Bilateral filtering  Augmentation |
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1. **INTRODUCTION**

Malaria, an affliction initiated by a minuscule parasitic organism, is transmitted to humans through the piercing bites of infected female mosquitoes. Once within the human host, these parasitic invaders breach the integrity of red blood cells (RBCs), perpetuating their replication within other cellular sanctuaries [1]. The consequence of this parasitic onslaught is a debilitating illness typified by high fever, throbbing headaches, muscular agony, and profound fatigue, rendering the patient profoundly unwell [2]. Alarming statistics from the World Health Organization (WHO) underscore the global impact of malaria, with 438,000 lives succumbing to its ravages in 2015, a number that swelled to 620,000 casualties in 2017 [3]. Annually, a staggering 300-500 million individuals grapple with the affliction. In the year 2022 alone, an alarming 247 million cases of malaria were reported [4].

The primary approach in traditional diagnostic methods relies heavily on using light microscopy to confront this formidable adversary. The methodology entails a comprehensive analysis of blood films, which aids in identifying the disease and the precise classification of the parasite species [5]. Furthermore, implementing appropriate diagnostic protocols has become essential in promptly determining the existence of parasites. The tests frequently provide a recorded rate of false positives less than 10%. These tests' initial efficacy in detecting parasites' presence is commendable; however, their precision is contingent upon the test product's calibre and the targeted parasite's distinct attributes [6]. In the context of malaria evaluation, applying light microscopy entails a rigorous protocol that entails intentionally placing a small blood sample onto a meticulously prepared glass slide. The blood sample is subsequently subjected to Giemsa staining solution, enhancing the detectability of the parasites within the erythrocytes.

Moreover, the diagnostic accuracy is enhanced by employing thick and thin blood smears. The former method detects the presence of the parasite in the bloodstream, whereas the latter approach distinguishes the particular species of malaria and different phases of the parasite's life cycle [7]. The comprehensive evaluation necessitates the involvement of a skilled microscopist, who devotes a significant amount of time, 20 to 30 minutes, to analyze each blood film meticulously. Their primary objective is to meticulously examine the differences in erythrocyte morphology, chromaticity, and dimensions to quantify infectious cells [8].

Every year, countless blood smear films undergo painstaking manual examination orchestrated by seasoned pathologists. This endeavour demands an immense allocation of human resources and economic investments in the pursuit of malaria diagnosis. The crux of this arduous process hinges on the precision of parasite quantification within these blood films, a critical determinant for accurate disease classification and severity assessment [9]. A glaring consequence of imprecise diagnosis is the prescription of antibiotics when malaria is absent in the patient. Such an accidental course of action precipitates unnecessary discomfort, ranging from abdominal pain to nausea, for the afflicted individual [10].

In the domain of malaria diagnostics, a significant challenge emerges, demanding robustness characterized by heightened sensitivity to detect parasites across all malaria life cycle stages. This imperative seeks to minimize the risk of false negatives in diagnostic outcomes. Moreover, expedited and cost-effective diagnosis holds particular significance, especially in endemic regions where the scarcity of expert pathologists amplifies the already colossal workload associated with blood film screening. In this context, automated malaria detection methods assume paramount importance. These methods, marked by their speed, cost-efficiency, and accuracy, are a beacon of hope for many patients seeking a timely and precise diagnosis [11].

The current methods for automating the detection of malaria use complex image-processing techniques that depend on carefully designed features such as form, colour, intensity, size, and texture. Various segmentation techniques are applied to microscopic pictures to isolate red blood cells in multiple procedures [12]. Following this, a carefully chosen collection of computed characteristics is utilized to depict red blood cells accurately. Subsequently, these characteristics are used to classify segmented images into two discrete categories: infected and uninfected. Morphological-based approaches employ structural attributes to augment the distinguishing properties of erythrocytes, such as their circularity, hence enhancing the precision of classification [13]. A diversified array of methodologies, based on the historical literature encompass a wide range of methods for partitioning, identifying features, and classifying malaria diagnoses [14]. Upon completing an extensive review of conventional and contemporary methodologies employed in detecting malaria, it becomes apparent that a notable tradeoff exists between the accuracy of these approaches and the computational intricacy of the models. As the degree of precision of a model improves, there is a concomitant rise in its computational sophistication. For example, the computational efficiency of a support vector machine (SVM) is superior to that of a deep neural network. On the other hand, the latter exhibits a higher level of accuracy in comparison to SVM. The balance between accuracy and computing requirements is critical in malaria detection techniques [15].

The process of cell segmentation is a crucial and essential step in the field of automated malaria detection systems. This critical procedure creates precisely segmented discrete sections from pre-processed microscopic pictures. As mentioned earlier, the zones encompass distinct organisms, including RBCs, WBCs, malaria parasites, and various artefacts. Various image-based approaches have been used for unsupervised cell segmentation [16]. In this particular domain, there has been considerable interest and utilization of several methodologies, including hole-filling algorithms, Chan-Vese segmentation, and histogram-based approaches. When faced with situations where the contrast of a picture is significantly poor, a frequently employed technique is to extract the green channel from RGB (Red, Green, Blue) photographs to perform cell segmentation [17]. As demonstrated in previous studies [18], several alternative approaches utilize the Otsu thresholding method to segment RBCs in images that have been upgraded explicitly for this particular task. The segmentation of cells within microscopic pictures in the context of malaria detectors, as discussed in references [19,20], involves applying thresholding techniques inside the Hue-Saturation-Value (HSV) colour space. The primary emphasis of this procedure is on the saturation (S) and value (V) channels to achieve effective segmentation. The methodology employed for cell segmentation via the fuzzy convergence technique is elucidated in the scholarly publication referenced as [21].

In contrast, the implementation of a fuzzy rule-based segmentation approach for the segmentation of malaria cells across three unique colour spaces is clarified in reference [22]. Morphological-based techniques in [23] utilize grayscale granulometry to capture regional extrema, easing cell segmentation effectively. Additional innovative approaches, such as applying the Hough transform, are employed to identify RBCs by leveraging their distinctive morphologies. The study conducted by [24] proved that k-means clustering is an excellent method for segmenting cells from unlabeled data. The segmentation process becomes more intricate and challenging when cells overlap, giving rise to complex issues. The utilization of marker-controlled watershed algorithms, as elucidated in references [25,26], presents a viable approach for effectively delineating overlapping cells.

Furthermore, the authors of [27] submit a technique for cell segmentation based on graph cuts. Additional advancements in the field utilize structural, geometric, and colour data to detect white blood cells (WBCs) and gametocytes, as discussed in references [28] and [29]. Sophisticated methodologies are employed to address cell segmentation to leverage the capabilities of machine learning and neural networks, as outlined in the documentation provided in reference [30]. Identifying pertinent components from cellular images is contingent upon several pivotal factors, including erythrocytes' fundamental morphology, texture, and chromatic attributes. In the contemporary context, utilising the HSV colour space and the green channel within the RGB colour space is an advantageous technique for extracting features. This decision justifies this because stained blood images can enhance colour-related characteristics, making them more distinguishable [31]. Several techniques have been employed for feature extraction, such as local binary patterns, Haralick's texture features, Histogram of Oriented Gradients (HOG) features, and further feature-selection algorithms [32]. These methodologies are of paramount importance in collecting pertinent information from cellular images. It is worth mentioning that colour and form data are utilized to identify various parasites [33]. Morphological processes, such as thinning and grayscale granulometry, augment the feature extraction process by effectively capturing significant information derived from the intensity of picture pixels. In a particular case described in reference [34], the discriminative collection of features is utilized to classify malaria cells. This classification task is accomplished by applying robust methodologies, including SVM and Bayesian learning. These methods offer a solid basis for distinguishing between several malaria cell types.

Recently, there has been a notable increase in the application of deep learning (DL) methods for the automation of malaria diagnosis, resulting in remarkable detection rates. One distinguishing characteristic of deep learning models is their ability to eliminate the requirement for manually designed features [35]. In contrast, these models utilize their latent layers to independently extract characteristics by thoroughly examining the available data [36]. The efficacy of deep learning models hinges on the availability of substantial datasets for training neural networks, a prerequisite for enhancing model accuracy [37]. However, medical applications, such as malaria identification, frequently grapple with the inherent challenge of limited datasets. This is primarily due to the difficulties involved in gathering annotated data. Successfully executing this procedure requires the active involvement and specialized knowledge of pathologists, who may not be easily accessible [38]. To tackle the issue of limited data availability, recent progress has included image augmentation methods into deep learning models, thereby promoting enhanced generalization and alleviating the problem of over-fitting. Image augmentation is a technique employed in data preprocessing to increase the size of a dataset by generating multiple variations of the original images. This is achieved by applying diverse transformations, including but not limited to rotation, shear, and translation [39]. The process of augmenting data facilitates the achievement of enhanced accuracy in models. CNNs are extensively utilized in classification tasks owing to their computational efficiency, making them a prominent component within the array of deep learning techniques [40]. Delgado-Ortet et al. [41] utilize a deep learning CNN model to perform cell segmentation. Additionally, they employ deep belief networks to classify images as either malaria-infected or uninfected.

This study aims to evaluate the effectiveness of different well-established deep-learning models in the specific setting of malaria detection using microscopic images of blood samples. In addition, we introduce an innovative and practical deep-learning approach for distinguishing between malaria-infected cells and uninfected ones. The fundamental basis of this innovation is grounded in a tailored algorithm that utilizes a CNN. The performance of this method surpasses that of other extensively examined deep learning models. The methodology described in this study uses bilateral filtering to improve image quality.

Additionally, image augmentation techniques are incorporated to boost the generalization capabilities of the model. The architectural architecture of our model consists of a simplified CNN that includes five convolutional and pooling layers. A comprehensive assessment of this particular methodology is performed using a benchmark dataset on malaria, and the outcomes are carefully compared with those of current similar approaches. The comparative assessment demonstrates the exceptional efficacy of our proposed solution, consistently surpassing its counterparts.

The remainder of this paper unfolds as follows: Section 2 provides a comprehensive exposition of our proposed deep learning model in conjunction with an array of transfer learning models employed for comparison. This section encompasses the incorporation of the dataset, preprocessing procedures, and the intricate details of model implementation. Section 3 is dedicated to assessing our proposed model's performance alongside a comparative analysis of various deep learning models. Here, we delve into a detailed examination of the outcomes of our research, shedding light on the strengths and weaknesses of each approach. Finally, in Section 4, we conclude our investigation, summarizing our findings and their implications and articulating potential directions for future work in this domain.

1. **MATERIALS AND METHODS**

This section delves into the intricate technical facets of our research, encompassing pivotal components such as the meticulous definition of the dataset, a thorough examination of preprocessing methodologies, and a comprehensive exposition of the architecture we have devised, along with its integral components. To facilitate rigorous comparison and evaluation, a diverse set of deep learning techniques renowned for their efficacy in image processing, including MobileNetV2, InceptionV3, and ResNet50, has been thoughtfully enlisted and will be scrutinized.

**2.1. Proposed Deep Learning Model**

This part introduces a novel neural architecture explicitly created for the detection of malaria utilizing microscopic thin blood smear pictures. Three steps make up the methodology: feature extraction, classification, and data preprocessing. Figure 1 shows the suggested deep-learning model for the architectural layout for malaria detection.

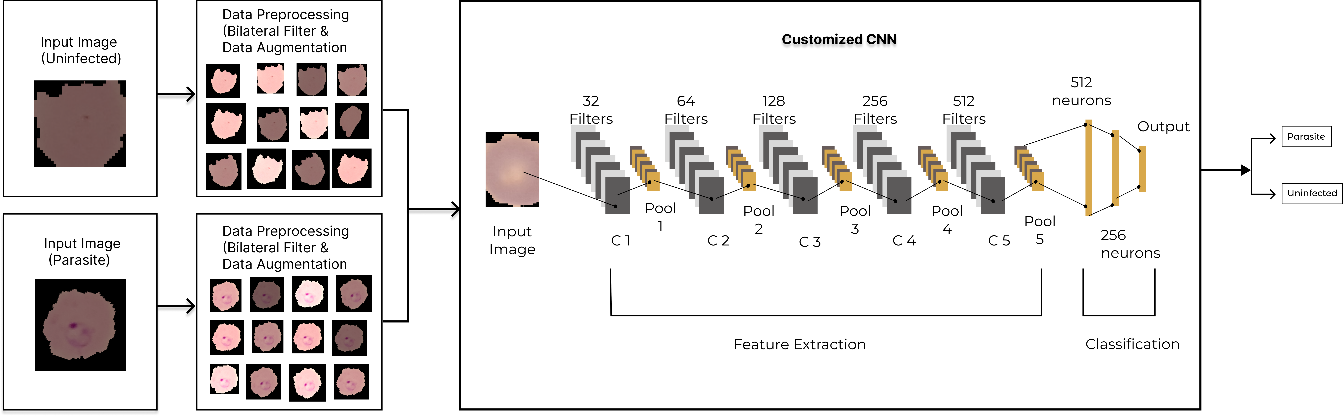


Figure 1. Block diagram illustrating the model suggested for the detection of malaria.

Before delving into the intricacies of our proposed DL model, we embark on a two-fold journey: acquiring and exploring the dataset. Subsequently, we initiate a data preprocessing step, a pivotal endeavour to enhance the images' overall quality. This preparatory phase serves as the bedrock for our subsequent analysis.

**2.1.1. Description of the Dataset**

To evaluate the efficacy of the models being compared, we employed the publicly available NIH Malaria dataset, which can be accessed on the official website of the National Institute of Health (NIH). The dataset utilized in this research comprises a complete assemblage of 27,558 cellular photographs. The collection has been carefully and systematically balanced, containing 13,779 photos representing parasitized cells and an equivalent number of images showcasing uninfected cells. It is essential to recognize that the cellular pictures exhibit variances in colour distribution, which can be related to inherent differences in bloodstains encountered during the data collection procedure.

The images in Figure 2 depict segmented images of red blood cells acquired from the NIH Malaria dataset, illustrating examples of both parasitized and uninfected cells. This visual representation serves to provide a clear depiction of the dataset. The equipped models offer a limited perspective on the range of ideas that comprise the dataset and provide the foundation of our evaluation.

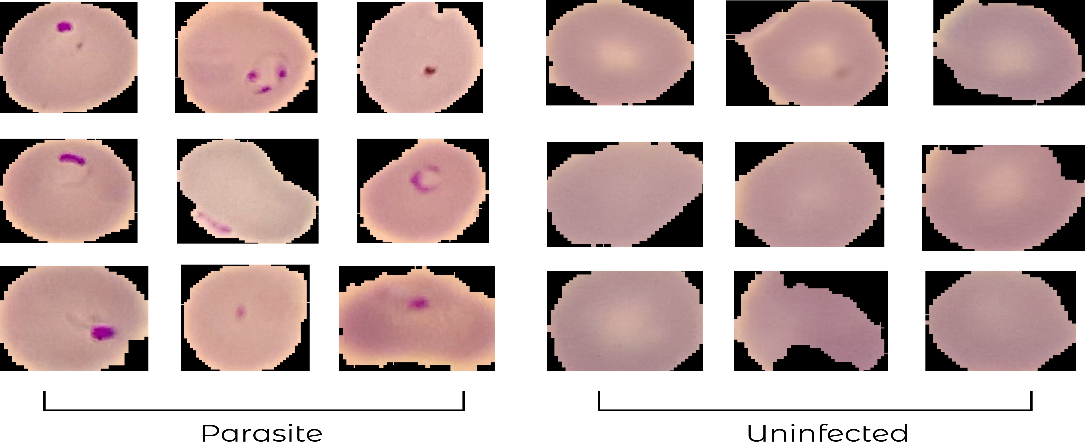


Figure 2. Images of uninfected and parasitized RBCs

**2.1.2. Data Preprocessing**

During data acquisition, images are susceptible to contamination from various sources of noise, which may manifest as distortions arising from factors such as camera angles and microscope positions [42]. The scientific community has proposed diverse noise removal techniques to restore image integrity in response to these challenges. The range of techniques encompasses fundamental blurring operators, such as the averaging filter, and more sophisticated non-linear filters, such as the median filter.

Within the particular framework of our scenario, the scans of red blood cells (RBCs) exhibit a diminished level of detail and inherently include significant data about the manifestation of parasites. Applying conventional blurring methods runs the risk of degrading or obliterating this vital structural information embedded within the images. Therefore, the imperative arises for an image-denoising technique that can effectively eradicate noise while preserving the structural intricacies of the picture.

In this pursuit, our investigation led us to the bilateral filter, which has proven particularly productive in the given scenario, as demonstrated in previous work [43]. This filter shows a notable capacity to remove noise from the images while safeguarding the essential structural information for our analysis.

In conventional methods of image blurring, the determination of a pixel's value is affected by its proximity to the central point of the filter. Nevertheless, the bilateral filter deviates from this pattern by integrating two independent components into its filter weights. One of the primary components of this phenomenon relates to the spatial proximity of the pixel in question to the filter. This aspect assumes a crucial part in the introduction of a specific degree of blurriness to the image. The second feature that sets the bilateral filter apart is its consideration of variations in pixel colour or intensity ranges. This particular component plays a crucial role in achieving the primary goal of the filter, which is to retain the fundamental structural details of the image effectively, ensuring their preservation while reducing noise [44,45].

Let represent an input picture with dimensions P×Q that undergoes bilateral filtering with a filter size of (2d + 1) × (2d + 1). The computation of the value of pixel (i, j) is expressed in equation (1).

(1)

In the given expression, we have the term which represents the intensity value at the pixel location (i+x, j+y) in the image. where represents the filtered image, *N* denotes the normalization factor, and represents the range kernel. The range kernel, as computed in equation (1), is given by the following expression in (2)

(2)

The variable represents the Euclidean distance between the pixel coordinates (x, y) and the center pixel coordinates (i, j). The equation (3) for is derived by evaluating the exponential function of the negative of the sum of the squares of l and m, divided by twice the square of the standard deviation .

(3)

The variance parameters are denoted as and . Equation (1) is applied to filter all photos, followed by resizing them to uniform dimensions (125×125). This standardization of input shape is necessary for the deep learning models to process all images in the dataset consistently.

The dataset on malaria, made available by the National Institutes of Health (NIH), has a balanced composition, with an equal representation of 13,779 photographs depicting parasitized cells and an equivalent number of images portraying uninfected cells. To comprehensively evaluate our deep learning models, we employ a meticulous approach of partitioning the dataset into distinct subsets that are purposefully designated for training, testing, and validation purposes. The process of partitioning is conducted before the implementation of data augmentation techniques. To achieve this goal, a proportion of 70% of the available data is allocated to the training phase. In contrast, a subset comprising 10% of the dataset is earmarked explicitly for validation. A portion of 20% of the dataset is designated for evaluating the performance and generalization abilities of the trained model. This segment is deliberately reserved and excluded from the training procedure.

Table 1 provides a comprehensive and precise overview of the unique partitioning details of the dataset, serving as a valuable resource for clarity and reference.

Table 1: Partitioning dataset into training, testing and validation datasets

|  |  |  |
| --- | --- | --- |
| **Partition** | **Parasitized** | **Uninfected** |
| Training | 9647 | 9647 |
| Testing | 2754 | 2754 |
| Validation | 1378 | 1378 |

Data augmentation approaches are widely recognized as a practical approach for improving the precision of deep learning models in the academic field. The primary purpose of their role is to introduce diversity and variety into the dataset, hence enhancing the performance of the model. Extensive datasets are widely recognized as beneficial for neural networks, as they improve their generalization ability and reduce the likelihood of overfitting [46]. The ImageDataGenerator module from the Keras package (https://keras.io/, retrieved on June 27, 2023) was utilized after resizing the photos in our dataset. The utilization of this module facilitated the enhancement of the training data for malaria cell images through the implementation of image modification operations. The actions above consisted of a zoom value of 0.1, a rotation of 25 degrees, a shear range 0.05, and a horizontal flip. In addition, a translation of (0.1, 0.1) was implemented to modify the width and height dimensions.

It is important to emphasize that the selective exclusion of image augmentation from the testing and validation datasets was motivated by our primary goal of assessing the model's performance within these subsets. The data augmentation method led to a substantial increase in the size of our training dataset, resulting in a final count of 173,700 training photos.

**2.1.3. Architecture of the proposed CNN model**

In our pursuit to augment the effectiveness of malaria detection by classifying images depicting infected and uninfected RBCs, we introduce an innovative CNN model. The present model has been created to handle input photos with dimensions of 125×125×3.

The architectural design of our proposed noble Convolutional Neural Network (CNN) model is illustrated in Figure 3. The architecture is distinguished by a network configuration that includes five convolutional layers, five max-pooling layers, and two fully-connected layers. The arrangement of these layers has been carefully designed to address the intricacies associated with malaria detection effectively. The model integrates a kernel size 3×3 and employs the Rectified Linear Unit (ReLU) activation function in all convolutional layers. The number of filters applied to these layers progressively increases, with the sequence being 32, 64, 128, 256, and culminating at 300 filters for the five layers. This strategic choice in layer architecture and filter configuration is central to the overall effectiveness of our proposed model in the context of efficient and accurate detection of deadly malaria.

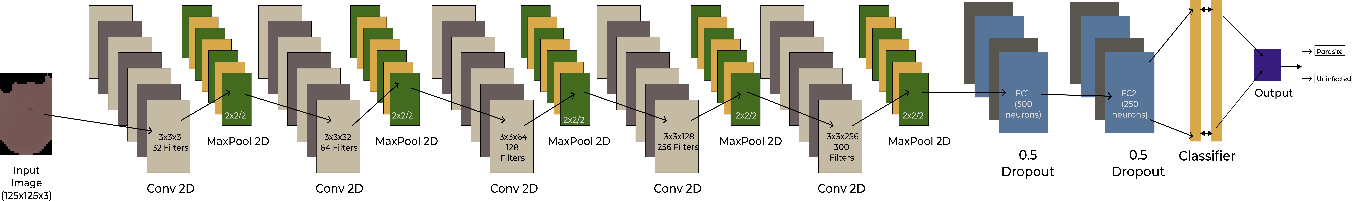


Figure 3. The architecture of the proposed CNN mode.

This research paper introduces a novel approach to the detection of malaria, as illustrated in Figure 3. The proposed model employs a consistent methodology in all max-pooling layers following convolutional layers. The coatings under analysis have a pooling size of 2x2 and a stride of 2 pixels. The primary rationale for implementing this strategy methodology is to enhance the accuracy and comprehensibility of the feature maps generated by the preceding convolutional layers. The input to the subsequent fully connected (FC) layers is derived from the output of the fifth pooling layer. A dropout mechanism is implemented next to each FC layer, wherein a dropout rate of 0.5 is employed to mitigate overfitting. The output of the fully connected layer is subsequently passed onto the sigmoid classifier, which plays a crucial part in the classification process. In the training phase, a specific set of hyperparameters, which encompasses a batch size of 64, is utilized. The training procedure is conducted throughout 50 epochs. The ADAM optimizer is frequently employed in conjunction with bidirectional cross-entropy loss, while a dropout ratio of 0.5 is utilized to regularise. The selection of this specific dropout ratio is consistent with recognized recommendations derived from previous research endeavors. Including dropout layers are of utmost importance in addressing the issue of overfitting, hence enhancing the model's ability to generalize its outcomes properly.

**2.1.4. Details Implementation**

The experimental procedures were performed using Google Colaboratory, which utilized a GPU runtime infrastructure with 28 GB of RAM and a 512 GB SSD capacity. Machine learning models were employed using Python 3.6, employing the DL package Keras in conjunction with TensorFlow. The architectural designs of the CNN-based transfer learning models were obtained from publicly accessible online resources. Subsequently, these models were fine-tuned with a specified set of hyperparameters. These hyperparameters encompassed configurations such as batch sizes ranging from 32 to 64, learning rates spanning the range of 1×10-4 to 1×10-5, training throughout 50 epochs, and using ADAM optimizers.

Additionally, the models were trained with binary cross-entropy loss, and a dropout ratio varying between 0.3 and 0.5 was incorporated to facilitate regularization. In terms of their initialization, the models commenced training with random weights. This training process was executed leveraging the TensorFlow library, a key component in the deep learning framework.

The application of cross-validation methodology is systematically employed to assess the effectiveness of machine learning models on data that has yet to be encountered. This approach involves partitioning the original dataset into k unique subsets, with each subset being utilized for training and validation cyclically. To assess the predicted accuracy of our models, we performed a five-fold cross-validation procedure, which entailed using five separate test sets.

Within each dataset partition, 2,756 samples were allocated for testing purposes, whereas the training set consisted of 24,802 samples. The training dataset was partitioned into five subsets of equal size using a random process. One of these subsets was allocated for validation testing, while the remaining four subsets were used for training the model. The cross-validation procedure was repeated five times for our proposed model, guaranteeing that each of the five subsets was used as the validation data once. The outcomes of these validations are later aggregated using an average methodology, yielding a singular score that represents the model's performance throughout all five validation iterations. This comprehensive technique guarantees a thorough and complete evaluation of the model's predictive capacities.

**2.2. Transfer Learning Models for Comparison**

The outstanding ability of CNNs in image categorization has been widely recognized due to its numerous hidden layers and vast parameter base. These networks have a high level of proficiency in detecting spatial patterns in images while also showing the ability to remain invariant to translation and effectively identify complex visual characteristics [47]. Prominent CNN-based transfer learning designs such as ResNet, MobileNet, and Inception have gained significant recognition for their exceptional performance in the ImageNet Large Scale Visual Recognition Challenge (ILSVRC). Nevertheless, it is crucial to recognize that developing a network architecture is time-consuming and precise, requiring significant dedication and exertion. A wide range of architectural blueprints have been carefully designed to address the complexities of specific challenges.

In the context of our research focused on detecting malaria-infected cells, we undertake a comprehensive examination of the performance of various CNN architectures, specifically ResNet, MobileNet, and Inception. These architectures are briefly introduced in the subsequent sections to provide a foundational understanding of their structural and functional attributes.

**2.2.1. ResNet**

The Residual Neural Network (ResNet) is highly regarded in convolutional neural networks because of its exceptional ability to train numerous layers, effectively leading to outstanding performance outcomes. The described strategy is a novel methodology for tackling the pervasive problem of the vanishing gradient phenomenon, a frequently encountered obstacle in deep neural networks. The primary approach for training neural networks is the iterative back-propagation method, which employs gradient descent to minimize the loss function and optimize the model's weights. However, as the depth of the neural network increases, a significant issue occurs - the gradients begin to diminish and may vanish due to recurrent multiplicative interactions. The empirical evidence indicates that adding each layer results in a decline in performance [48].

ResNet effectively addresses the challenge with the incorporation of identity skip links. These connections facilitate bypassing one or more layers, allowing the utilization of feature maps obtained from earlier layers within the network. The strategic application of "skipping" effectively reduces the network's size, expediting the learning process. Throughout the training procedure, the layers within the network demonstrate a dynamic expansion, which facilitates the active extraction of more subtle properties from the source image by the residual components of the network. The ResNet architecture manifests in various iterations, encompassing ResNet-152, ResNet-101, and ResNet-50. ResNet-V1 distinguishes itself from ResNet-V2 by including batch normalization preceding every weight layer. The adaptation process plays a crucial role in enhancing the performance and convergence of the network [49].

**2.2.2. Inception**

The Inception deep neural network, which Google built, has notably influenced the progress of convolutional network classifiers. The Inception framework employs a comprehensive strategy that amalgamates various innovative methodologies to improve the model's performance, encompassing accuracy and processing speed. The core of the Inception architecture lies in the incorporation of inception modules, specifically built to perform convolutional operations on the input data. These operations involve using varying-size filters, such as 1×1, 3×3, 5×5 kernels, and max-pooling. The network consists of four separate layers, which include three convolutional layers and one pooling layer. The outputs from these layers are concatenated and then given to the subsequent inception module. One notable approach employed by Inception to address the computational burden of the network involves the incorporation of 1×1 convolutions before utilizing the more computationally demanding 3×3 and 5×5 convolutions. The deliberate incorporation of 1×1 convolutions in this strategy serves the dual objective of enhancing computing efficiency and mitigating the proliferation of input channels [50].

The Inception family encompasses several variations, each denoted by a version label, such as Inception-v1, Inception-v2, and Inception-v3. The continual evolution of the Inception model is rooted in advanced factorization methods designed to diminish the computational cost of convolution operations. Furthermore, these techniques mitigate the risk of representational bottlenecks, a scenario where information loss occurs due to the compression of input data dimensions. In the case of Inception-v3, the model features 11 inception modules, reflecting the ongoing refinement and expansion of the architecture [51].

**2.2.3. MobileNet**

MobileNet, a lean and efficient deep neural network, distinguishes itself by its streamlined architecture featuring a reduced parameter count. Yet, it excels in classification performance compared to its deep neural network counterparts. To bolster its classification capabilities, MobileNet incorporates the concept of dense blocks, a strategy conceived and envisioned in Dense Nets. The fundamental objective of integrating thick blocks into MobileNet is to simultaneously decrease the overall number of network variables and improve classification accuracy. When embedded within the MobileNet framework, these dense blocks are characterized by convolution layers possessing dimensions equivalent to those of the input feature maps. This architectural decision further alleviates computational constraints and reduces overheads, all while maintaining high-performance standards. MobileNet networks are further optimized by adopting a modest growth rate [52].

Within the realm of Dense-MobileNet models, two notable configurations emerge: Dense1-MobileNet and Dense2-MobileNet. Through extensive experimentation, it has become evident that Dense2-MobileNet, despite employing fewer parameters and computational resources, surpasses the recognition accuracy achieved by MobileNet. This is a testament to the effectiveness of MobileNet's efficient design and strategic integration with dense blocks [53].

1. **EXEPRIMENTAL RESULTS AND EVALUATIONS**

This section focuses on thoroughly assessing several deep learning architectures, specifically in the domain of malaria detection, utilizing the reliable NIH Malaria dataset. Furthermore, we do a comprehensive comparative analysis, evaluating the effectiveness of our suggested methodology compared to established malaria identification algorithms. This comparative evaluation explores a range of statistical metrics, offering a detailed comprehension of the strengths and weaknesses inherent in each methodology.

3.1. Performance Evaluation and Comparison

The evaluation process in binary deep learning models hinges on using a confusion matrix, a comprehensive tool for encapsulating prediction outcomes when tested against labelled data. This evaluation gives rise to four distinct and consequential effects:

True-Positives (TP): These instances denote the accurate identification of infected cells as infected, reflecting the successful diagnosis of positive cases.

False-Positives (FP): In contrast, this category encompasses uninfected cells that are inaccurately classified as infected, representing cases where the model erroneously predicts a positive outcome.

True-Negatives (TN): This category signifies the correct identification of uninfected cells as uninfected, capturing the accurate diagnosis of negative cases.

False-Negatives (FN): Finally, this group encompasses infected cells erroneously classified as uninfected, highlighting cases where the model fails to identify a positive instance, resulting in a pessimistic prediction.

These four distinct outcomes serve as the cornerstone of assessing the model's performance and ability to classify instances into binary categories accurately. The models under consideration underwent extensive training and testing, adjusting various parameters, including the number of epochs and batch size. Notably, the number of ages represents a critical hyperparameter, signifying the count of complete passes or iterations through the training phase encompassing the entire training dataset.

The outcome of this rigorous evaluation process is vividly presented as confusion matrices for each model, namely MobileNetV2, InceptionV3, ResNet50, and the proposed CNN, as visually depicted in Figures 4 through 7. A close examination of these confusion matrices reveals a compelling performance by the proposed CNN, which emerges as the frontrunner, boasting the highest accuracy rate and an impressive 100%. This underscores the effectiveness and superiority of the proposed CNN model in achieving outstanding results in the context of malaria detection.

|  |  |
| --- | --- |
| Figure 4. Confusion matrix of MobileNetV2 | Figure 5. Confusion matrix of InceptionV3 |
| Figure 6. Confusion matrix of ResNet50 | Figure 7. Confusion matrix of the proposed CNN |

Various parametric and nonparametric statistical metrics evaluate performance, encompassing Specificity, Sensitivity, Precision, Accuracy, and F1 score.

Specificity, also called the "true negative rate," gauges the percentage of correctly predicted true negatives among an algorithm's overall count of actual negative observations. This metric is calculated using the mathematical expression outlined in Equation 4.

(4)

Sensitivity, often termed the "true positive rate" or "Recall," is a metric to assess an algorithm's ability to accurately detect actual positive instances from the entire pool of positive observations. Its mathematical representation is provided by equation 5.

(5)

Precision is a measure that quantifies the level of accuracy exhibited by an algorithm in terms of producing good outcomes. The calculation involves determining the proportion of actual positive instances about the overall count of positive observations shown in equation 6.

(6)

The accuracy metric evaluates the algorithm's capacity to accurately differentiate between those who are healthy and those who are diseased. In the specific domain of a malaria diagnosis model, optimal performance is attained when the classification accurately identifies infected cell images as infected and uninfected cell images as clean. The accuracy can be determined by employing the following equation: 7.

(7)

The F1 score is a mathematical metric that combines precision and recall metrics in a weighted harmonic mean. The evaluation comprehensively analyses the model's efficacy, considering both favourable and unfavourable predictions. The statistic is frequently regarded as more dependable than accurate and precise. A high F1 score signifies a well-balanced classification model that exhibits robust precision and recall in extremely unbalanced data situations. The F1 score may be computed using the following equation 8.

(8)

The performance indicators provided enable a comprehensive evaluation of the model's capacity to distinguish between positive and negative cases, a crucial component of malaria detection. The metrics for each deep learning architecture are computed individually, and the summarized findings are displayed in Table 2. The results demonstrate the superiority of the malaria detection method utilizing the suggested convolutional neural network (CNN) framework, outperforming other deep learning models in the comparative evaluation. The approach provided in this study demonstrates a noteworthy level of accuracy and an F1 score of 1, highlighting its excellent efficacy.

Table 2: Performance comparsion between the proposed model and other DL models

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **Precision** | **Accuracy** | **Specificity** | **Sensitivity** | **F1 Score** |
| InceptionV3 | 0.82 | 0.80 | 0.88 | 0.80 | 0.80 |
| MobileNet | 0.94 | 0.94 | 0.96 | 0.94 | 0.94 |
| ResNet | 0.98 | 0.97 | 0.99 | 0.97 | 0.97 |
| **Proposed** | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |

The improved performance of the proposed Convolutional Neural Network (CNN) model in identifying malaria is demonstrated in Table 2, where it outperforms other models in many metrics. The importance of precision in model building is highlighted by utilising an architecture consisting of five convolutional layers, five max-pooling layers, and two fully-connected layers. This architecture incorporates a 3×3 kernel size, ReLU activation function, and specific filter configurations. The model exhibits remarkable accuracy with a precision score of 1.00, which is crucial for minimizing false positives in medical applications. Benefiting from bilateral filtering during preprocessing ensures noise removal and structural information preservation, enhancing image quality for robust model training. Incorporating data augmentation techniques augments the training dataset with variations, promoting generalization and preventing overfitting. The model's architecture complexity, incorporating 2×2 max-pooling layers and 0.5 dropouts in fully connected layers, aids in capturing intricate patterns. Efficient utilization of computational resources, achieved through uniform 3×3 convolution filters, enhances efficiency without compromising performance. Hyperparameter optimization contributes to optimal performance, including tuning learning rates, dropout ratios, and batch sizes.

Additionally, the model's balanced sensitivity and specificity underscore its ability to accurately identify infected cases while minimizing false alarms for uninfected patients. Finally, the proposed CNN model's exceptional performance can be attributed to effective preprocessing, strategic data augmentation, a customized architecture, and careful tuning of hyperparameters. Its emphasis on noise reduction, image quality preservation, and efficient use of resources distinguishes it from other models. The perfect scores across all metrics indicate a balanced and reliable performance in malaria detection.

The evaluated models underwent rigorous training and validation procedures, including optimizing the number of epochs, batch sizes, and fine-tuning hyperparameters. The value of the epoch number, a crucial hyperparameter determining the number of complete iterations across the training dataset, was systematically adjusted. Figures 8 to 11 present correspondingly a comprehensive evaluation of the precision and error metrics for the InceptionV3, MobileNetV2, ResNet50, and the novel CNN models. Within each figure, the red line denotes the metrics of accuracy and loss during the training phase. In contrast, the green line signifies the metrics of accuracy and failure during the validation phase. The training accuracy for InceptionV3 (Figure 8) is reported as 81.12%, while the validation accuracy is recorded as 80.07%. The corresponding training and validation losses are documented as 0.43% and 0.41%, respectively. When transitioning to MobileNetV2 (as depicted in Figure 9), the model attains training and validation accuracies of 90.05% and 94.00%, respectively. These accuracies are accompanied by training and validation losses of 0.21% and 0.15%, respectively. ResNet50 (Figure 10) attains impressive training and validation accuracies of 99.10% and 97.85%, with corresponding losses of 0.05% and 0.07%. Finally, the proposed CNN model (Figure 11) exhibits near-perfect accuracies for both training and validation, reaching almost 100%. The CNN model's associated training and validation losses are nearly 0, indicating robust performance. The CNN model that has been proposed has a high level of precision throughout its training phase, attaining an accuracy rate that is close to perfection, with nearly 100% accuracy for both the training and validation datasets. This observation suggests that the model demonstrates a high level of competence in acquiring and replicating the patterns in the training data, leading to optimal performance when evaluated during the validation process. The training and validation loss for the proposed convolutional neural network (CNN) model exhibit minimal values, approaching 0%. This observation indicates that the model successfully reduces mistakes during training and validation processes, suggesting that it possesses strong learning abilities and the capacity to generalize well. The minimal loss values demonstrate the model's capacity to correctly forecast outcomes for observed and unobserved variables. The proposed CNN model stands out in its precision, low training and validation loss, consistency across epochs, optimal hyperparameter tuning, fast convergence, and reliable validation performance. These factors collectively contribute to the model's exceptional performance during training and validation, showcasing its efficacy in malaria detection.

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| Figure 8. Accuracy and loss curve of InceptionV3 | |
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| Figure 9. Accuracy and loss curve of MobileNetV2 | |
|  |  |
| Figure 10. Accuracy and loss curve of ResNet50 | |
|  |  |
| Figure 11. Accuracy and loss curve of the proposed CNN | |

The Receiver Operating Characteristic (ROC) curve was employed as a vital method for visualizing and assessing the predictive capabilities of the InceptionV3, MobileNetV2, ResNet50, and the proposed Convolutional Neural Network (CNN) models. The visual depictions in Figures 12 to 15 have been presented with meticulous deliberation. The receiver operating characteristic (ROC) curve provides a graphical representation of the relationship between the false-positive rate (FPR) and the true-positive rate (TPR), with the FPR represented on the x-axis and the TPR on the y-axis. An in-depth analysis of the receiver operating characteristic (ROC) curves provides vital insights into the models' ability to accurately differentiate between the classes, specifically 0s and 1s, hence facilitating precise predictions. The area under the receiver operating characteristic (ROC) curve, also referred to as AUC, is a significant statistic that indicates the discriminatory ability of a model. A higher AUC value indicates a more substantial potential for discrimination. A number close to 1 for the Area Under the Curve (AUC) signifies a significant degree of distinctiveness, indicating the presence of a dependable predictive model.

Conversely, an AUC value approaching 0 reflects a model's inefficacy in class separation. In this context, it is apparent that the proposed CNN model excels, exhibiting an exceptional AUC value of 1.00, followed by ResNet50, MobileNetV2, and InceptionV3, each bearing AUC values of 0.998, 0.989, and 0.893, respectively. This discerning analysis underscores the prowess of the proposed CNN model as a robust performer in malaria detection.

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| Figure 12. ROC-AUC curve of InceptionV3 | Figure 13. ROC-AUC curve of MobileNetV3 |
| Figure 14. ROC-AUC curve of ResNet50 | Figure 15. ROC-AUC curve of the proposed CNN |

3.2. Comparison between proposed CNN and state-of-the art Models

The performance of the proposed CNN model was thoroughly evaluated through a rigorous benchmarking procedure, comparing it against a collection of recognized approaches for malaria diagnosis. The present study thoroughly evaluated various automated malaria detection algorithms [] that have been extensively acknowledged and are considered to be at the forefront of the field. Each technology employs unique approaches and methodology to identify malaria parasites in microscopic blood cell pictures.

Fatima et al. [54] utilize an adaptive thresholding strategy and morphological image processing approaches in their method. The system assesses the presence of malaria parasites within cells by analysing object contours and applying the eight-connected rule. In their study, Pan et al. [38] present a novel approach for segmenting red blood cells by employing a deep convolutional neural network (DCNN). The proposed methodology combines Otsu's algorithm with morphological operations to improve the precision of the segmentation procedure. The classification of cells is conducted via a Convolutional Neural Network (CNN) structure inspired by the LeNet-5 model. Vijayalakshmi et al. [46] propose a transfer learning methodology that combines the VGG architecture with a support vector machine in their study. This technology aims to detect and classify cells infected with malaria in microscopic pictures of blood samples. Rajaraman et al. [10] employed a convolutional neural network with three layers and a fully linked sequential architecture as the fundamental framework for their algorithm developed for malaria diagnosis. The approach proposed by Hung [55] presents a rapid region-based convolutional neural network (Faster R-CNN) specifically designed to detect malaria parasites. The model is subjected to pre-training using the ImageNet dataset, followed by a fine-tuning procedure on a specialized dataset for malaria. In addition, Bibin et al. [7] present a unique approach to malaria detection using deep belief networks.

A comprehensive comparative analysis is conducted with existing methodologies to evaluate the efficacy of our proposed Convolutional Neural Network (CNN) model in the domain of automated malaria diagnosis. The performance results of our proposed methods and the alternative approaches are comprehensively recorded in Table 3. Certain practices that were compared in this study utilized datasets distinct from the test dataset employed in our research. Although there may be limitations in comparing these datasets, such comparisons are nonetheless valuable in assessing the efficacy of our suggested strategy within the broader context of malaria detection. The findings indicate that our technique outperforms the compared methods in all measured performance metrics.

Furthermore, it is crucial to emphasize that the performance metrics for the Fatima, Rajaraman, and our proposed CNN model are computed using an identical dataset. This further reinforces the effectiveness of our proposed method, which not only surpasses the performance of the compared algorithms but is also positioned as the top-performing solution. The Rajaraman method also demonstrates a commendable detection rate, albeit slightly lower than the performance of our proposed method.

The results presented in Table 3 demonstrate the effectiveness and dependability of our suggested deep-learning methodology for the detection of malaria. The system above shows high accuracy in evaluating microscopic blood smears, enabling the detection of Plasmodium parasite infections. The method employed in our study leverages bilateral filtering as a means to efficiently mitigate image noise, resulting in the production of superior-quality images that are suitable for model training purposes. Moreover, incorporating data augmentation methods provides variability into the dataset, enhancing overall performance and guaranteeing that the model exhibits good generalization to mitigate the risk of overfitting.

It is imperative to emphasize that our proposed methodology places a high priority on computational efficiency. To accomplish this goal, a key strategy entails employing 3×3 convolution filters consistently throughout all convolutional layers while simultaneously reducing the number of input channels. After conducting a comparative analysis between our suggested Convolutional Neural Network (CNN) architecture and the deep learning models outlined in Table 3, it is evident that our architecture exhibits a distinct advantage in terms of its streamlined design. The deep learning models in Table 3 typically consist of a minimum of 16 layers and many trainable parameters. On the other hand, the CNN architecture we proposed embraces a more streamlined and practical methodology. With a mere eight layers, this model effectively minimizes the requirement for training parameters compared to its deep-learning equivalents.

Table 3: Performance comparsion between state-of-the-art methods vs proposed DL model

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **References** | **Dataset** | **Size** | **Precision** | **Accuracy** | **Specificity** | **Sensitivity** | **F1 Score** |
| [7] | Self-Made | 630 | 0.93 | 0.96 | 0.96 | 0.98 | 0.90 |
| [55] | Self-Made | 1300 | 0.78 | 0.82 | 0.85 | 0.78 | 0.78 |
| [38] | PEIR-VM | 24648 | 0.74 | 0.79 | 0.83 | 0.74 | 0.74 |
| [46] | Self-Made | 2550 | 0.90 | 0.93 | 0.93 | 0.93 | 0.92 |
| [10] | NIH | 27558 | 0.96 | 0.96 | 0.97 | 0.95 | 0.96 |
| [54] | NIH | 27558 | 0.95 | 0.92 | 0.95 | 0.89 | 0.92 |
| **Proposed** | **NIH** | **27558** | **1.00** | **1.00** | **1.00** | **1.00** | **1.00** |

1. **CONCLUSIONS**

Malaria is a formidable global health concern, underscoring its gravity and significance worldwide. This research presents an efficient and accurate CNN approach utilizing deep learning techniques to automate the identification of malaria in microscopic blood smears. The fundamental basis of our methodology revolves around a personalized CNN architecture. This model effectively employs bilateral filtering to mitigate image noise and integrate image augmentation techniques to improve its overall generalization capabilities. To comprehensively assess the effectiveness of our method, we conducted a rigorous evaluation involving comparing various deep learning models, including MobileNetV2, InceptionV3, and ResNet50, in the context of malaria detection.

Furthermore, we conducted a comparative analysis of our model against existing automated malaria detection systems. The assessment entailed the calculation of critical statistical metrics such as precision, recall, F1-score, ROC curves, and more, serving as robust performance indicators. The outcomes of these exhaustive experiments, conducted on a widely recognized benchmark dataset, unequivocally establish the superiority of our proposed method. Our approach consistently outperforms other deep learning models, achieving accuracy and F1 scores closer to 1. Moreover, when benchmarked against existing malaria detection algorithms, our method emerges as the top performer, affirming its potential as a highly effective tool in automated malaria detection.

**REFERENCES**

[1] M. K. Savi, "An Overview of Malaria Transmission Mechanisms, Control, and Modeling," Med. Sci., vol. 11, no. 1, p. 3, 2023, doi: 10.3390/medsci11010003.

[2] T. Bousema and C. Drakeley, "Determinants of Malaria Transmission at the Population Level," Cold Spring Harb. Perspect. Med., vol. 7, p. a025510, 2017.

[3] World Health Organization. World Malaria Report 2019. World Health Organization; Geneva, Switzerland: 2019.

[4] World Health Organization, "World malaria report 2022," Available online: <https://www.who.int/teams/global-malaria-programme/reports/world-malaria-report-2022>

[5] J. Yin, M. Li, H. Yan, S. Zhou, Z. Xia, "Laboratory diagnosis for malaria in the elimination phase in China: Efforts and challenges," Front. Med., vol. 16, pp. 10–16, 2020.

[6] K. Hemachandran, A. Alasiry, M. Marzougui, S.M. Ganie, A.A. Pise, M.T.-H. Alouane, C. Chola, "Performance Analysis of Deep Learning Algorithms in Diagnosis of Malaria Disease," Diagnostics, vol. 13, no. 3, p. 534, 2023, <https://doi.org/10.3390/diagnostics13030534>.

[7] D. Bibin, M.S. Nair, P. Punitha, "Malaria parasite detection from peripheral blood smear images using deep belief networks," IEEE Access, vol. 5, pp. 9099–9108, 2017.

[8] I. Ghosh, S. Kundu, "Combining neural network models for blood cell classification," arXiv preprint arXiv:2101.03604, 2021.

[9] K. Manning, X. Zhai, W. Yu, "Image analysis and machine learning-based malaria assessment system," Digit. Commun. Netw., vol. 8, pp. 132–142, 2021.

[10] S. Rajaraman, S. Jaeger, S.K. Antani, "Performance evaluation of deep neural ensembles toward malaria parasite detection in thin-blood smear images," PeerJ, vol. 28, e6977, 2019.

[11] P. Kataria, N. Surela, A. Chaudhary, J. Das, "MiRNA: Biological Regulator in Host-Parasite Interaction during Malaria Infection," Int. J. Environ. Res. Public Health, vol. 19, p. 2395, 2022.

[12] A. Maqsood, M.S. Farid, M.H. Khan, M. Grzegorzek, "Deep Malaria Parasite Detection in Thin Blood Smear Microscopic Images," Applied Sciences, vol. 11, no. 5, p. 2284, 2021, <https://doi.org/10.3390/app11052284>.

[13] A. Vijayalakshmi, B.R. Kanna, "Deep learning approach to detect malaria from microscopic images," Multim. Tools Appl., vol. 79, pp. 15297–15317, 2020.

[14] S. Sriporn, C.-F. Tsai, C.-E. Tsai, P. Wang, "Analyzing Malaria Disease Using Effective Deep Learning Approach," Diagnostics, vol. 10, no. 10, p. 744, 2020, <https://doi.org/10.3390/diagnostics10100744>.

[15] A. Abubakar, M. Ajuji, I.U. Yahya, "DeepFMD: Computational Analysis for Malaria Detection in Blood-Smear Images Using Deep-Learning Features," Applied System Innovation 2021, Vol. 4, Page 82, vol. 4, no. 4, p. 82, Oct. 2021, doi: 10.3390/ASI4040082.

[16] L. B. Damahe, R. Krishna, N. Janwe, and N. V. Thakur, "Segmentation based approach to detect parasites and RBCs in blood cell images," in Int. J. Comput. Sci. Appl., 2011, vol. 4, pp. 71–81.

[17] S. S. Devi, S. A. Sheikh, A. Talukdar, and R. H. Laskar, "Malaria infected erythrocyte classification based on the histogram features using microscopic images of thin blood smear," in Ind. J. Sci. Technol., 2016, vol. 9, pp. 1–10.

[18] M. Delgado-Ortet, A. Molina, S. Alférez, J. Rodellar, and A. Merino, "A Deep Learning Approach for Segmentation of Red Blood Cell Images and Malaria Detection," in Entropy (Basel), 2020, vol. 22, no. 6, p. 657, doi: 10.3390/e22060657.

[19] A. Acevedo, A. Merino, S. Alférez, Á. Molina, L. Boldú, and J. Rodellar, "A dataset of microscopic peripheral blood cell images for development of automatic recognition systems," Data Brief, 2020, doi: 10.1016/j.dib.2020.105474.

[20] S. Shankar, D. Koundal, P. Das, V. T. Hoang, K. Tran-Trung, H. Turabieh, et al., "Computational Methods for Automated Analysis of Malaria Parasite Using Blood Smear Images: Recent Advances," in Computational Intelligence and Neuroscience, 2022, vol. 2022, Article ID 3626726, 18 pages, doi: 10.1155/2022/3626726.

[21] J. Soni, N. Mishra, and C. Kamargaonkar, "Automatic differentiation between RBC and malarial parasites based ON morphology with first order features using image processing," in Int. J. Adv. Eng. Technol., 2011, vol. 1, no. 5, p. 290.

[22] F. V. Nurçin, and E. Imanov, "Selective Hole Filling of Red Blood Cells for Improved Marker-Controlled Watershed Segmentation," in Scanning, 2021, vol. 2021, Article ID 5678117, 9 pages, doi: 10.1155/2021/5678117.

[23] S. Savkare and S. Narote, "Blood cell segmentation from microscopic blood images," in Proc. 2015 Int. Conf. Inf. Process., 2015, pp. 502–505.

[24] A. S. Abdul Nasir, M. Y. Mashor, and Z. Mohamed, "Segmentation based approach for detection of malaria parasites using moving k-means clustering," in 2012 IEEE-EMBS Conf. Biomed. Eng. Sci., 2012, pp. 653–658, doi: 10.1109/IECBES.2012.6498073.

[25] Z. Zhu, S.H. Wang, Y.D. Zhang, "ReRNet: A Deep Learning Network for Classifying Blood Cells," Technol Cancer Res Treat, vol. 22, p. 15330338231165856, Jan-Dec 2023, https://doi.org/10.1177/15330338231165856.

[26] A. Alharbi, C. Aravinda, J. Shetty, M. Jabarulla, K. Sudeepa, S. Singh, et al., "Computational Models-Based Detection of Peripheral Malarial Parasites in Blood Smears," Contrast Media & Molecular Imaging, 2022, doi: 10.1155/2022/9171343.

[27] F. Abdurahman, K.A. Fante, M. Aliy, "Malaria parasite detection in thick blood smear microscopic images using modified YOLOV3 and YOLOV4 models," BMC Bioinform., vol. 22, pp. 1–17, 2021.

[28] A. Narsale, S. Nalwade, M. Badgire, S. Survase, and C. Aher, "Blood Cell Detection and Counting via Deep Learning," in 2022 Int. Conf. Advancements Smart Secure Intell. Comput., 2022, pp. 1–4, doi: 10.1109/ASSIC55218.2022.10088344.

[29] Z. Zhang, X. Zhang, Y. Yang, J. Liu, C. Zheng, H. Bai, et al., "Accurate segmentation algorithm of acoustic neuroma in the cerebellopontine angle based on ACP-TransUNet," in Front. Neurosci., 2023, vol. 17, doi: 10.3389/fnins.2023.1207149.

[30] H. A. Nugroho, and R. Nurfauzi, "GGB Color Normalization and Faster-RCNN Techniques for Malaria Parasite Detection," in 2021 IEEE Int. Biomed. Instrum. Technol. Conf., 2021, pp. 109–113.

[31] M. Khatkar, D. K. Atal, and S. Singh, "Identification of Malaria Parasite Using Soft Computing Techniques," in 2021 Asian Conf. Innov. Technol., 2021, pp. 1–7.

[32] A. Nautre, H. A. Nugroho, E. L. Frannita, and R. Nurfauzi, "Detection of Malaria Parasites in Thin Red Blood Smear Using a Segmentation Approach with U-Net," in 2020 3rd Int. Conf. Biomed. Eng., 2020, pp. 55–59.

[33] A. S. Sumi, H. A. Nugroho, and R. Hartanto, "A Systematic Review on Automatic Detection of Plasmodium Parasite," Int. J. Eng. Technol. Innov., 2021, vol. 11, no. 2, p. 103.

[34] A. Rehman, N. Abbas, T. Saba, Z. Mehmood, T. Mahmood, and K. T. Ahmed, "Microscopic malaria parasitemia diagnosis and grading on benchmark datasets," in Microsc. Res. Tech., 2018, vol. 81, no. 9, pp. 1042.

[35] A. Loddo, C. Fadda, C. Di Ruberto, "An Empirical Evaluation of Convolutional Networks for Malaria Diagnosis," J. Imaging, vol. 8, no. 3, p. 66, 2022, https://doi.org/10.3390/jimaging8030066.

[36] P. Pattanaik, M. Mittal, M.Z. Khan, "Malaria Detection using Deep Residual Networks with Mobile Microscopy," J. King Saud Univ. Comput. Inf. Sci., vol. 20, pp. 1–18, 2020.

[37] Q. Quan, J. Wang, L. Liu, "An effective convolutional neural network for classifying red blood cells in malaria diseases," Interdiscipl. Sci. Comput. Life Sci., vol. 12, no. 2, pp. 217-225, 2020, <https://doi.org/10.1007/s12539-020-00367-7>.

[38] W.D. Pan, Y. Dong, D. Wu, "Classification of malaria-infected cells using deep convolutional neural networks," in Machine Learning—Advanced Techniques and Emerging Applications, Intech Open, London, UK, 2018, vol. 159.

[39] M. Umer, S. Sadiq, M. Ahmad, S. Ullah, G.S. Choi, A. Mehmood, "A novel stacked CNN for malarial parasite detection in thin blood smear images," IEEE Access, vol. 8, pp. 93782–93792, 2020.

[40] M.H.D. Alnussairi, A.A. İbrahim, "Malaria parasite detection using deep learning algorithms based on (CNNs) technique," Computers and Electrical Engineering, vol. 103, p. 108316, Oct. 2022, doi: 10.1016/J.COMPELECENG.2022.108316.

[41] M. Delgado-Ortet, A. Molina, S. Alférez, J. Rodellar, A. Merino, "A deep learning approach for segmentation of red blood cell images and malaria detection," Entropy, vol. 22, no. 6, p. 657, 2020, https://doi.org/10.3390/e22060657.

[42] P.A. Pattanaik, M. Mittal, M.Z. Khan, "Unsupervised deep learning cad scheme for the detection of malaria in blood smear microscopic images," IEEE Access, vol. 8, pp. 94936–94946, 2020.

[43] Q. Lv, S. Zhang, and Y. Wang, "Deep Learning Model of Image Classification Using Machine Learning," Adv. in Multimedia, vol. 2022, Article ID 3351256, pp. 1-12, 2022, doi: 10.1155/2022/3351256.

[44] C. Tomasi, R. Manduchi, "Bilateral Filtering for Gray and Color Images," in Proceedings of the Sixth International Conference on Computer Vision (ICCV ’98), Bombay, India, 4–7 January 1998.

[45] Z. Zhu, S. Lu, S.H. Wang, J.M. Górriz, Y.D. Zhang, "BCNet: A Novel Network for Blood Cell Classification," Front Cell Dev Biol, vol. 9, p. 813996, 2022, https://doi.org/10.3389/fcell.2021.813996.

[46] A. Vijayalakshmi, "Deep learning approach to detect malaria from microscopic images," Multimed. Tools Appl., vol. 79, pp. 15297–15317, 2019.

[47] N. Becherer, J. Pecarina, S. Nykl, K. Hopkinson, "Improving optimization of convolutional neural networks through parameter fine-tuning," Neural Comput. Appl., vol. 31, pp. 3469–3479, 2017.

[48] Z. Zhu, S.H. Wang, Y. Zhang, "ROENet: A ResNet-Based Output Ensemble for Malaria Parasite Classification," Electronics (Basel), vol. 11, no. 13, p. 2040, 2022, https://doi.org/10.3390/electronics11132040.

[49] A. Reddy and D. S. Juliet, "Transfer Learning with ResNet-50 for Malaria Cell-Image Classification," in 2019 International Conference on Communication and Signal Processing (ICCSP), pp. 945-949, 2019.

[50] N. Dong, L. Zhao, C.H. Wu, J. Chang, "Inception v3 based cervical cell classification combined with artificially extracted features," Appl. Soft Comput., vol. 93, p. 106311, 2020.

[51] P.U. Eze, C.O. Asogwa, "Deep Machine Learning Model Trade-Offs for Malaria Elimination in Resource-Constrained Locations," Bioengineering, vol. 8, no. 11, p. 150, 2021, https://doi.org/10.3390/bioengineering8110150.

[52] S. V. Militante and R. A. Diamante, "Malaria Disease Diagnosis from a Blood Smear Samples using the Deep Learning MobileNet Models," 2021 Fourth International Conference on Vocational Education and Electrical Engineering (ICVEE), Surabaya, Indonesia, 2021, pp. 1-6, doi: 10.1109/ICVEE54186.2021.9649688.

[53] T. Jameela et al., "Deep Learning and Transfer Learning for Malaria Detection," Computational Intelligence and Neuroscience, vol. 2022, Article ID 2221728, 14 pages, 2022, https://doi.org/10.1155/2022/2221728.

[54] T. Fatima, M.S. Farid, "Automatic detection of Plasmodium parasites from microscopic blood images," J. Parasit. Dis., vol. 44, pp. 69–78, 2020.

[55] J. Hung, A. Carpenter, "Applying faster R-CNN for object detection on malaria images," in Proceedings of the IEEE Conf. Comput. Vis. Pattern Recognit. Workshop (CVPRW), Honolulu, HI, USA, 21–26 July 2017, pp. 56–61.

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