



# Improving Malaria Detection Using L1 Regularization Neural Network


**Ghazala Hcini**

(Faculty of Sciences and Technology of Sidi Bouzid, University of Kairouan, Kairouan, Tunisia  
 <https://orcid.org/0000-0003-3571-417X>, [hcinihazala@fstbsz.u-kairouan.tn](mailto:hcinihazala@fstbsz.u-kairouan.tn))

**Imen Jdey**

(Faculty of Sciences and Technology of Sidi Bouzid, University of Kairouan, Kairouan, Tunisia  
 <https://orcid.org/0000-0001-7937-941X>, [imen.jdey@fstbsz.u-kairouan.tn](mailto:imen.jdey@fstbsz.u-kairouan.tn))

**Hela Ltifi**

(Faculty of Sciences and Technology of Sidi Bouzid, University of Kairouan, Kairouan, Tunisia  
 <https://orcid.org/0000-0003-3953-1135>, [hela.ltifi@fstbsz.u-kairouan.tn](mailto:hela.ltifi@fstbsz.u-kairouan.tn))

**Abstract:** Malaria is a huge public health concern around the world. The conventional method of diagnosing malaria is for qualified technicians to visually examine blood smears for parasite-infected red blood cells under a microscope. This procedure is ineffective. It takes time and requires the expertise of a skilled specialist. The diagnosis is dependent on the individual performing the examination's experience and understanding. This article offers a new and robust deep learning model for automatically classifying malaria cells as infected or uninfected. This approach is based on a convolutional neural network (CNN). It improved by the regularization method on a publicly available dataset which contains 27, 558 cell images with equal instances of parasitized and uninfected cells from the National Institute of health. The performance of our proposed model is 99.70% of accuracy and 0.0476 loss value.

**Keywords:** Malaria Parasite Detection, Deep Learning, Convolutional Neural Network, Binary classification, L1 Regularization, Overfitting, Accuracy, Loss

**Categories:** E, H, J, L, M

**DOI:** 10.3897/jucs.81681

## 1 Introduction

Malaria is a deadly epidemic disease caused by Plasmodium parasites [Andtaner, 21] [Sivaramakrishnan, 17] [Alqudah, 20] [Umer, 20]. This parasite has a complex intra-erythrocytic life cycle that moves through various stages of development while consuming the hemoglobin of the red blood cells (RBC).

After decades of huge decreases in malaria cases and deaths worldwide, progress toward malaria control and elimination had stalled prior to the COVID-19 pandemic [Awassa, 22], and malaria cases and deaths began to rise in 2020 (table 1).

Issue	The influence of COVID-19
Malaria	<ul style="list-style-type: none"> <li data-bbox="655 383 1259 443">– In 2020, there will be 14 million more instances than in 2019.</li> <li data-bbox="655 465 1259 622">– During the pandemic, disturbances in the provision of malaria prevention, diagnosis, and treatment resulted in 69,000 additional deaths; 47000/69,000 malaria deaths were connected to disruptions in the provision of malaria prevention, diagnosis, and treatment.</li> </ul>
Foreign and local financing/resources	COVID-19 reaction was diverted and rerouted

Table 1: COVID-19 repercussions [Chanda-Kapata, 22]

Malaria infection can be detected early, allowing professionals to administer suitable medication in a timely way. Although numerous innovative approaches for malaria diagnosis are available, the gold standard and most commonly used diagnostic technique for malaria is manual microscopy examination of peripheral blood smears [Jdey, 22]. Microscopy is a gold standard technique and well-established approach for diagnosing malaria. However, without technical skill, it is possible that the outcome would be poor. It is based on finger pricking blood that is placed onto a slide to create thin and thick blood films. After staining with Giemsa stain, the oil slides are examined using a compound microscope with an x100 lens using immersion oil slides. It is a sensitive and informative diagnostic tool that can detect 5–10 parasites per l of blood with good technical ability. In microscopy, all of the Plasmodium species and stages may be distinguished. Expert microscopists can detect any morphological changes in the parasites on blood film due to recent drug therapy. The number of parasites in a single RBC may also be easily quantified; such investigations are required to elaborate hyperparasitaemia. It is a low-cost diagnostic procedure. The cost of each slide examination is expected to be between 30 and 40 Pakistani rupees. It gives permanent proof of the analytic discovery (blood films). But it is a time-consuming [Almezhghwi, 21] and labor-intensive procedure that typically takes one hour from the moment blood is drawn to the final outcome [Bandyopadhyay, 17]. Microscopy is impossible without technical skills and adequate reagents. Microscopic discovery hazards become an untrustworthy instrument in these conditions, wasting valuable resources for questionable results. Because microscopy results are frequently delayed in reaching the clinician, pharmaceutical decisions are frequently made without the benefit of lab results. Rapid Diagnostic Test [Slater, 22] is based on the detection of malaria parasite antigens in RBCs by an immunochromatographic method. Immunochromatographic Technique is another name for RDT (ICT). It is based on the interaction between antigen and antibody. It is a highly good and sensitive diagnostic tool for field diagnostics. Malaria diagnosis has improved as a result of the widespread use of rapid diagnostic tests (RDTs).

However, the effectiveness of this strategy is limited by the ability of a skilled microscopist. The accuracy of a malaria microscopy diagnosis depends on the pathologist's expertise of the disease [Yang, 19]. This technique is time-consuming and inaccurate due

to subjectivity, resulting in erroneous and inconsistent outcomes [Pattanaik, 20]. This could lead to an inaccurate diagnosis and treatment. Even the patient's life may be lost [Dong, 19]. Previous research has demonstrated that a computer assisted system's degree of agreement as a decision support system can be crucial to a faster and more reliable diagnosis. It can serve as a baseline and a standardized technique of determining the severity of the disease's infection [Pan, 18]. The most cost-effective diagnostic method is a Computer Aided Diagnosis (CAD) based approach with digital microscopy and advanced image processing techniques combined with an intelligent system. Pathologists and hematologists will benefit from such deep learning technologies. These will cut down on the time it takes to observe, analyze, and infer, as well as provide a second, unbiased, and consistent view [Bandyopadhyay, 17]. The application of deep learning is used in the medical domain for its performance [Mazurowski, 19]. Deep learning is a kind of the well-known multilayer neural network that learns complex data representations [Abdou, 22], often known as features, automatically [Abubakar, 21].

Despite the fact that deep learning models have been successfully employed, developing an adequate deep learning model is a difficult undertaking due to the dynamic nature and variability of real-world situations and data. Furthermore, deep learning models are frequently seen as "black-box" devices, obstructing the standardization of deep learning research and applications [Sarker, 21]. For image classification tasks, state-of-the-art computer-aided diagnostic tools based on data-driven deep learning algorithms like convolutional neural network (CNN) have emerged as the architecture of choice. However, because of their sensitivity to training data variations, CNNs have a high variance and may overfit [Rajaraman, 19]. To assist human specialists in making the accurate diagnosis and to eliminate the requirement for manual evaluation, we focused on automatic malaria identification using a new architecture based on convolutional neural network improving by regularization technique to avoid the overfitting problem.

The following is a breakdown of the paper's structure. Section 2 discusses deep learning and Convolutional Neural Networks, as well as the problem of overfitting and the many regularization strategies that can be used to solve it. Section 3 includes a list of similar works as well as their limitations. The dataset and our suggested model are discussed in section 4, and the experimental results and comments are discussed in section 5. Section 6 finishes the work by outlining potential next directions.

## 2 Background of the study

### 2.1 Deep Learning

Automated malaria screening, which employs machine learning techniques such as deep learning, has the potential to be a useful diagnostic tool. Deep learning is a subfield of machine learning. It was inspired by the human brain's information processing mechanisms [Hcini, 21] [Madad, 20]. It is a kind of the well-known multilayer neural network that learns complex data representations, often known as features, automatically [Nakasi, 20]. This motivates scientists to extract discriminative features with the least amount of human labor and field knowledge possible [Alzubaidi, 21]. A trained network's qualities are vital for real-world applications. The first is its objectivity, which refers to the absence of impacts from human comments' subjective nature. The second is its consistency, which means that the trained network should annotate similar characteristics in the same way every time. The third factor is its validity, which refers to the accuracy of the network output. In practice, when the amount of training data is minimal, objectivity, dependability,

and validity are sometimes difficult to attain [Pelt, 20]. Deep learning usually necessitates a large number of training sets. Because annotated training images are substantially more difficult to collect due to expert knowledge requirements and privacy issues, medical applications have been among the slowest to use deep learning [Poostchi, 18]. This technology has recently increased the efficiency and accuracy of macroscopic computer vision tasks dramatically [Voulodimos, 18]. As a result, microscopic image analysis has received a lot of interest. Convolutional Neural Networks, a type of deep learning, have shown to be extremely useful in image recognition, classification, and categorization [Chauhan, 18] [Erickson, 17].

### What are the benefits of deep learning?

Several performance characteristics may provide an answer to this question [Alzubaidi, 21]:

- Universal Learning Approach: DL is sometimes referred to as universal learning since it can perform in nearly all application fields.
- Robustness: In general, DL approaches do not require precisely constructed features. Instead, the optimum traits are learned in an automatic manner that is relevant to the task at hand. Robustness to the input data's normal changes is achieved.
- Generalization: The same DL technique can be used for different data kinds or applications, a method known as transfer learning (TL). It's also a good method to use when there isn't enough data.

## 2.2 Convolutional Neural Network

A Convolutional Neural Network (CNN) [Jlassi, 21] is made up of numerous layers, each of which performs a different function [Joshi, 20]. A CNN has convolutional layers, ReLU layers, pooling layers and Fully connected layer (figure 1). A convolutional neural network works by extracting features from images. This eliminates the need for manual feature extraction.

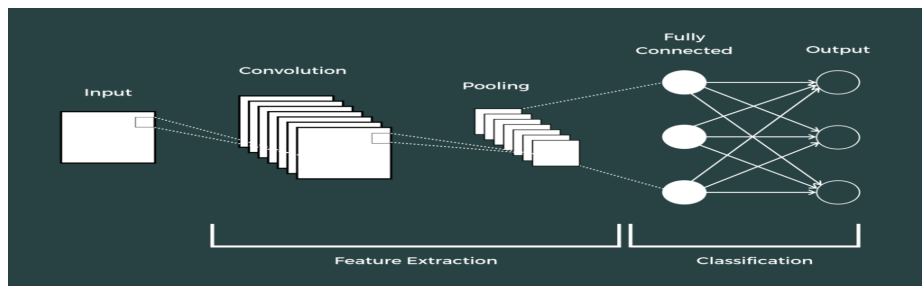


Figure 1: The basic block diagram of convolutional neural network

### 2.2.1 Convolutional Layer

The convolutional layer is the most important component in CNN design. It is made up of a set of convolutional filters (so-called kernels) [Yamashita, 18]. It contains a set of filters (or kernels) whose parameters must be learned during the course of the training. The filters are frequently smaller in size than the actual image. Each filter builds an activation map by converging with the image.

### 2.2.2 Pooling Layer

In most cases, a pooling layer is incorporated between two convolutional layers. By down sampling the representation, the pooling layer minimizes the number of parameters and computations. The maximum or average pooling function can be used. Max pooling is often utilized because it is more effective [Ke, 18].

### 2.2.3 Activation Function

The primary role of all sorts of activation functions in all types of neural networks is to map the input to the output. The weighted summation of the neuron input, as well as its bias, is used to determine the input value (if present). This means that the activation function creates the corresponding output after deciding whether or not to fire a neuron in response to a specific input [Alheejawi, 20].

### 2.2.4 Fully Connected Layer

This layer is usually found near the end of each CNN architecture. The so-called Fully Connected (FC) technique connects each neuron in this layer to all neurons in the previous layer. It's used as a CNN classifier.

### 2.2.5 Loss Functions

The anticipated error created across the training samples in the CNN model is calculated using some loss functions in the output layer. The difference between the actual and expected output is revealed by this inaccuracy. The CNN learning procedure will then be used to optimize it.

The Cross-Entropy Loss Function is a regularly used metric for assessing the performance of CNN models [Alzubaidi, 21]. The cross-entropy loss function's mathematical representation is (1):

$$H(p, y) = - \sum_i y_i \log(p_i) \text{ where } i \in [1, N] \quad (1)$$

CNNs are useful in fields where the shape of an item is crucial, such as image analysis, particularly in the medical sector's investigation of malignancies and body ailments, and video analysis [Luca, 22]. By stacking a series of operations such as convolution, pooling, and mapping of non-linear activation functions, convolutional neural networks extract high-level semantic information layer by layer from the input layer of raw data [Alam, 21]. Image classification is a complicated process that relies on a number of factors. Some of the presented strategies of image commands are addressed in the next section. The emphasis will be on cutting-edge classification approaches for improving characterization accuracy.

### 2.3 CNN's regularization

Overfitting is the most common problem with CNN models when it comes to achieving well-behaved generalization [Alzubaidi, 21]. An overfitting problem is indicated by a high variance in model performance. The difference between training and validation accuracy reveals how much overfitting has occurred figure 2.

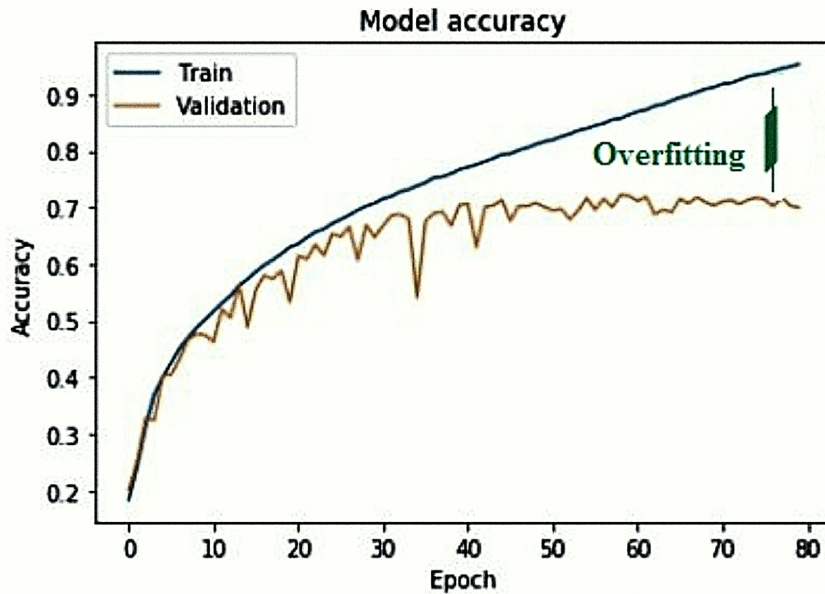


Figure 2: Overfitting on a model

Dropout, data Augmentation, cross-validation, and regularization techniques such as L1 and L2 are all alternatives for avoiding overfitting and improving model performance. The regularization method piqued our interest. It plays an important role in fine tuning the predictor design [Jaiswal, 18]. Reducing the number of features makes sense if overfitting occurs because a model is overly complex. If we do not know which characteristics to eliminate from our model, regularization methods like Lasso and L1 can help. Regularization imposes a "penalty" on the input parameters with the largest coefficients, lowering the variance of the model [ElSayed, 21].

Regularization is a technique for addressing the problem of overfitting [Jung, 18] by inserting fewer rules into the model. Regularization adds a cost term for adding more features and tries to reduce the weights of many features in the model to zero or extremely tiny values. The L1 and L2 regularizations are named after the L1 and L2 norms of a vector  $w$ . Here's a crash course in norms:

1 norm (also known as L1 norm):

$$\|W\|_1 = |w_1| + |w_2| + \dots + |w_N| \quad (2)$$

2 norm (also known as L2 norm or Euclidean norm):

$$\|W\|_2 = (|w_1|^2 + |w_2|^2 + \dots + |w_N|^2)^{1/2} \quad (3)$$

p-norm:

$$\|W\|_p = (|w_1|^p + |w_2|^p + \dots + |w_N|^p)^{1/p} \quad (4)$$

Loss function with no regularization:

$$\text{loss} = \text{Error}(Y, \hat{Y}) \quad (5)$$

Loss function with L1 regularization:

$$\text{loss} = \text{Error}(Y, \hat{Y}) + \lambda \sum_{i=1}^N |w_i| \quad (6)$$

Apart from having to minimize the error between the true  $Y$  and the predicted  $\hat{Y}$ , the regularization terms are 'constraints' that an optimization method must 'adhere to' when reducing the loss function.

A strategy of selecting the regularization parameter for the l1 regularization problem is also developed. In terms of damage detection, the current l1 regularization method outperforms the traditional l2 regularization method [Hou, 18].

### 3 Related Works

There has been a lot of research on medical diagnosis of malaria and other disorders in the literature, as well as a lot of reports on classification accuracy (table 2). In this study, we will evaluate methodologies to determine which is the most effective. It is recommended that these strategies be compared to public datasets rather than private datasets acquired from clinics and hospitals.

Masud, Mehedi, et al [Masud, 20] proposed a CNN model composed of four convolutional blocks and two fully connected dense layers, applied to classify 27,558 segmented cell images, the given segmented cell images have a resolution of  $224 \times 224 \times 3$  pixels. The trainable parameters of their proposed model have a relatively smaller size (409 K) compared to other complex models, its simplicity will be the first step while dealing with the problem of overfitting.

Alqudah, A. M., & Qazan, S. [Alqudah, 20] proposed a new CNN model using transfer learning to classify red blood cells into two classes infected and Uninfected.

Rahman, A., et al [Rahman, 19] employed a deep convolutional neural network to improve malaria identification using patches segmented from microscopic images of red blood cell smears. The accuracy and loss evaluation metrics, as well as 5-fold cross validation, were utilized to compare and identify the best performing architecture.

Sinha, Shruti, et al [Sinha, 21] in his paper proposed a deep learning approach. This model uses two different components of CNN (Sequential and ResNet). Indeed, the difference between the two architectures is that ResNet uses more hidden layers rather than sequential ones. Applied on a dataset which contains 27,558 cell images with 80% for training and 20% for testing.

Sandhya, Y. et al [Sandhya, 20] proposed an automated system based on deep learning the Convolutional Neural Network following these steps; Image Processing used to get the quality image then the application of CNN algorithm which contains the following layers; Convolution layer, Pooling layer, ReLU layer and Fully connected layer. This model applied to classify 27,558 images with 30\*30 pixels.

Maqsood, Asma, et al [Maqsood, 21] offered a customized CNN model (5 convolutional layers, 5 max-pooling layers, and 2 fully-connected layers) that beats all deep learning models currently available. Data preprocessing, feature extraction, and classification are the three aspects of the suggested method.

Elangovan, P. et al [Elangovan, 21] proposed a CNN model with four convolutional layers (C1, C2, C3, C4), two max pooling layers (P1, P2), and one fully connected layer (FC), using thin smear blood images to detect malaria parasites. Pre-processing, feature extraction, and classification are all stages of the proposed technique.

Magotra, V., et al [Magotra, 22] have constructed a CNN model with six convolutional layers and filter sizes ranging from 16 to 128 layers, as well as six max-pooling layers and the "ReLU" as an activation function. The model is trained on various data variations for epochs ranging from 5 to 14 with a callback applied.

Alharbi, A. H., et al [Alharbi, 22] built a CNN model that examines the blood sample to detect parasitized or uninfected cells to eliminate model inconsistencies and improve robustness and generalization. To obtain features, decrease computations, and update features, it is separated into four fully linked layers and is based on the convolution layer, the pooling layer, and the average pooling step.

Mishra, S. [Mishra, 21] intended to create a method that would aid in the quick and accurate identification of malaria, lowering fatality rates and eventually leading to a malaria-free environment. To automate the detection of the parasite in thin blood smear images, deep learning techniques such as transfer learning and snapshot ensemble were used. A bespoke model with a total of 13 layers is created from scratch, using three convolutional layers with 32, 64, and 128 filter units, two max-pooling layers, and a Global Average Pooling layer. With Batch Normalization, each convolutional unit is ReLU enabled. The input is convolved using filters of size (3x3) with padding set to 'same.' The pool window of the Max Pool layers is (2x2). A dense layer with one unit and sigmoid activation makes up the final classification layer. To test the efficiency of transfer learning in the malaria classification issue, pre-trained models such as 'DenseNet121', 'EfficientNet-B0', 'Inception-v3', 'InceptionResNetV2', 'ResNet50V2', and 'Xception' were used. The feature extractors were chosen as the last layer before the final classification layer, and the model was trained for 50 epochs with an early stopping patience level of 7.

Fuhad, K. M., et al [Fuhad, 20] proposed an architecture based on auto encoders. The suggested encoder is made up of three Convolutional layers, each followed by a Max-pooling layer. The kernel size is defined as (3 × 3) with the same padding and 1-pixel stride in each layer for executing the convolutional process. The first convolutional layer's kernel number was set to 16, while the second and third layers were set to 8 and 4, respectively. Four deconvolutional layers and three upsampling layers make up the decoder. The kernel size for all Deconvolutional layers is 3 × 3 with the same padding and the number of kernels is 4, 8, 16, and 3 accordingly. Deconvolutional layers are the



polar opposite of convolutional layers; instead of mapping  $3 \times 3$  features into 1 pixel, Deconvolutional layers map 1 pixel to a vector of  $3 \times 3$  features. To induce non-linearity, the hidden units were activated with the ReLU activation function. To recreate the input image from the latent representation, up-sampling with window size  $2 \times 2$  was used.

Qanbar, M. M., et al [Qanbar, 19] created a deep learning approach for the classification and diagnosis of malaria called the Residual Attention Network (RAN), which used a deep learning Convolutional Neural Network (CNN) technique with previously classified datasets. The RAN model outperformed other algorithm types in terms of image processing and classification. The training simulation results for the RAN model indicated a classification accuracy rate of 95.79%. Only 83.30% classification accuracy was obtained using the Support Vector Machine (SVM). The table 2 includes references to all of these works.

Study	Approach	Accuracy	Research Gap
[Masud, 20]	CNN	97.30%	The model does not converge effectively, and there is a considerable variation in loss and accuracy between the training and validation outcomes. Furthermore, as the training advances towards the finish, the values of loss and accuracy show a lot of variation. This implies that the model has not been properly trained and is possibly overfitting to the training data.
[Alqudah, 20]	CNN	98.85%	It is about a model (VGG-19) that is more powerful than the suggested model with 99.32% correctness in the comparison analysis [Rajaraman, 19].
[Rahman, 19]	CNN, VGG16, CNNEx-SVM	97.77%	Overfitting can be evident as the model advances through training, and the loss begins to increase.
[Sinha, 21]	ResNet/Sequential	96.78%/96%	Overfitting is evident from the curve results.
[Sandhya, 20]	CNN	96%	The performance of the proposed system was not compared with other deep learning models.
[Maqsood, 21]	CNN	96.82%	There is still room for improvement. They are simply concerned with the time.
[Elangovan, 21]	CNN	97.8%	Only pre-trained networks were used to compare the suggested model.
[Magotra, 22]	CNN	96%	As a performance metric, only accuracy was used.

[Alharbi, 22]	CNN	97%	The curves reveal that it is overfitting after 25 epochs.
[Mishra, 21]	CNN	99.37%	<ul style="list-style-type: none"> <li>– Only pre-trained networks were used to compare the suggested model.</li> <li>– Loss has a very high value</li> </ul>
[Fuhad, 20]	CNN based on auto encoders	99.23%	Since 2006, a comparison has been conducted with older works.
[Qanbar, 19]	Residual Attention Network	95.79%	The proposed system's performance was not compared to that of other cutting-edge deep learning or machine learning models.

Table 2: Representative work about deep learning models for malaria classification [2019-2022] applied on dataset of 27, 558 cell images

## 4 Dataset and Proposed Model

### 4.1 Data Collection

For this work, the used data set was collected from the National Institute of Health (NIH), which contains 27,588 images of parasitized and uninfected cells (figure 3). The distribution of these two classes is as follows 13,794 images by each class. As we have an equal distribution of cell images, we do not have to deal with the issues that come with unbalanced data, therefore it is less likely to be skewed towards one class. Collecting publicly available protozoan parasite datasets is critical for training models and determining their overfitting, resilience, and generalization.

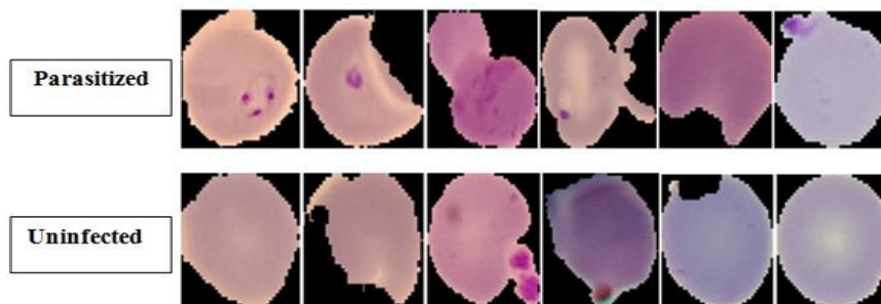


Figure 3: Sample images from NIH dataset: Parasitized and Uninfected

## **4.2 Data Preprocessing**

After data collection, the next step was data preprocessing. The essential step to reduce the impact of variations in intensity and clean up noise. We resize all the images into 64\*64 dimensions. For the data in this stage, we represent parasitized images as 1 and uninfected images as 0.

## **4.3 Data Splitting**

In this step, we divide the data into two different parts (80, 20), i.e. 80% of the data used for training and the remaining 20% data used for testing. 80% of the features are set aside for training, while the remaining 20% are used to test the developed classification algorithm. To generalize successfully, machine-learning algorithms require a large number of data samples to learn from, which is why a large fraction of the features are assigned to training [Jdey, 12]. The testing split was used to assess the models' final prediction accuracy. Then, we applied the CNN algorithm for classifying the data.

## **4.4 Building a model**

A deep learning system uses data from task-related inputs and outputs to create software that can automatically distinguish them. We will not cover deep learning models in this study, but we will show the framework we utilized to complete it. A pretrained model based on convolutional neural network (CNN). Early studies in the study of biological vision influenced convolutional neural networks (CNNs). It used to overcome the shortcomings of manual feature extraction.

The three major types of layers utilized to build the CNN architecture are convolutional layers, pooling layers, and fully connected layers. In comparison to classic neural networks, CNNs can extract features without sacrificing much of the input's spatial correlations. Each layer is made up of neurons with programmable weights and biases. For the deep learning network used, after we have completed the steps outlined below data collection, data preprocessing and data splitting. Two convolution layers, two pooling layers, a flatten layer, and three dense layers are included in the suggested model. The figure 7 depicts the successive layers and summarizes their nodes. The shapes of the matrices processed at each successive point are described by the terms 'input' and 'output'. The information about the training parameters can be found in the table above (table 3).

Parameter	Description	Range
Input image size	It specifies the image's height and width in pixels.	64*64
Batch size	The number of training samples used in a single epoch.	64
Epoch	It specifies how many passes the model makes over the full training dataset.	5, 100
Optimizer	In the field of neural networks, Adam is one of the most widely used step-size techniques. Adaptive Moments inspired the name [Haji, 21].	Adam
Activation function	In a neural network, an activation function specifies how the weighted sum of the input is turned into an output from a node or nodes in a layer.	Sigmoid, ReLU

Table 3: Training parameters

#### 4.5 CNN with L1 regularization

Our goal is to build a sparse convolutional neural network that performs as well as or better than existing models. Matrix multiplication is used to change the output dimension of a network, and this can be a problem because it can lead to weight redundancy. To reduce this, theoretical and practical approaches must be developed to help with the process. During optimization, the L1 regularization algorithm imposes penalties on layer parameters or layer activity. Regularizing the 'weights' and 'bias' of the three "dense layers" will result in a more accurate model. The loss function that the network optimizes includes the total of all penalties. Because L1 regularization offers sparse solutions, it is the favored method when there are many features. Even so, the computational advantage is advantageous because it is possible to avoid features with zeroes coefficients. The L1 regularization, in this situation, can help with feature selection by removing unimportant features. Different facets of the dense layer are regularized:

- *kernel\_regularizer*: to apply penalty on the layer's kernel weights
- *bias\_regularizer*: to apply penalty on the layer's bias
- *activity\_regularizer*: to apply a penalty on the layer's output

Weight regularization offers a method to lessen the convolutional neural network model's overfitting to the training data and enhance the model's performance on new data. We added a weight regularization to the "dense layers". This is achieved by setting the *kernel\_regularizer* argument. The total absolute values of all the weights in the model make up L1 regularization.

$$\text{loss} = \text{Error}(Y, \hat{Y}) + \lambda \sum_{i=1}^N |w_i|$$

We are calculating the sum of the absolute value of all of the weights. These weights can be either positive or negative, and they can vary greatly in terms of what they measure. We sum up all the weights and multiply them by a value called alpha which you should tell "how much effect you want L1 alpha to have". It tries to shrink the error as much as possible if when you add the sum of the weights to that error it will shrink those weights because that's just an additive property of the weights so it's trying to shrink the weights. The workflow for image classification is displayed in the following figure 4.

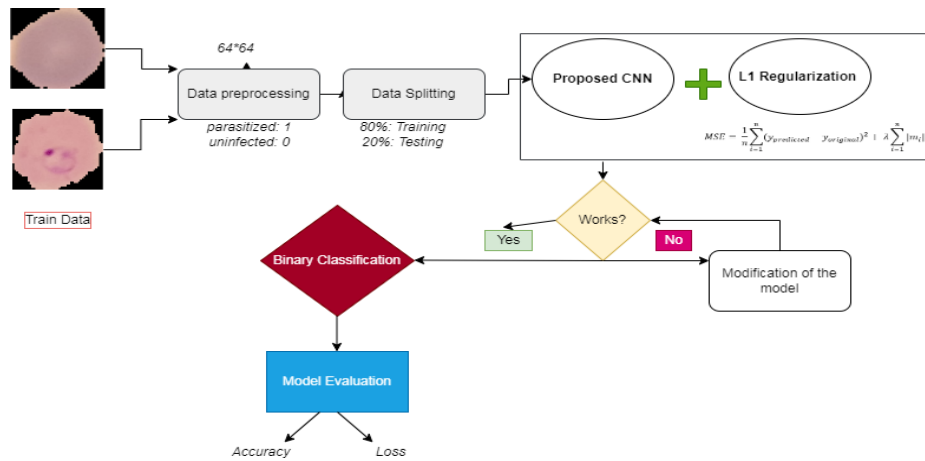


Figure 4: Image classification workflow

## 5 Results and Discussion

### 5.1 Results

Experiments are carried out on the malaria cell images dataset which contains 27,588 images of parasitized and uninfected cells. We evaluate our proposed architecture on accuracy for 5 epochs (figure 5). The training takes 1min23s to give the final result on the ‘Malaria dataset’.

The results of this metric are shown in table 4 below before and after improving with regularization technique to reduce loss rate.

Epoch	Loss: Before	Loss: After	Accuracy: Before	Accuracy: After
1	0.9132	0.8603	0.5643	0.5841
2	0.3973	0.3940	0.8607	0.8680
3	0.1929	0.21397	0.9690	0.9641
4	0.0999	0.1076	0.9930	0.9885
5	<b>0.0537</b>	<b>0.0476</b>	<b>0.9970</b>	<b>0.9970</b>

Table 4: Results of our proposed architecture for 5 epochs before and after applying regularization technique

Figure 5 shows performance curves. It is based on the graphical curve plotting the relationship between Accuracy and loss.

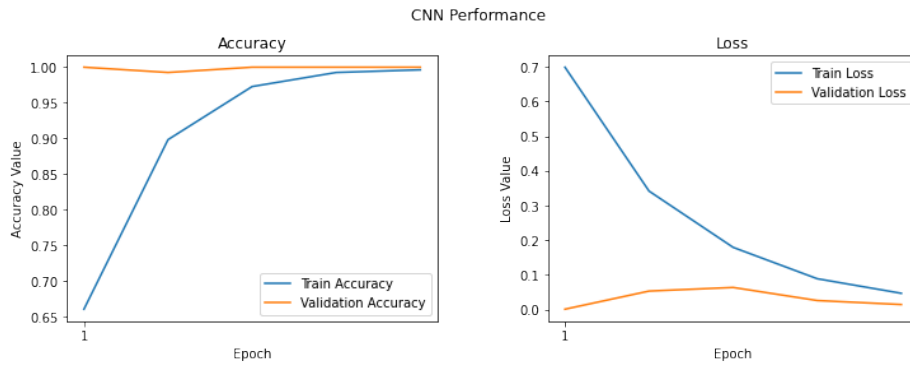


Figure 5: Proposed model experimental result evaluation for 5 epochs

We tried to fit our model to the dataset, and after spending some time fine-tuning the parameters, we found the best number of epochs (5 epochs). We also attempted to put the model through its paces throughout 100 epochs (figure 6).

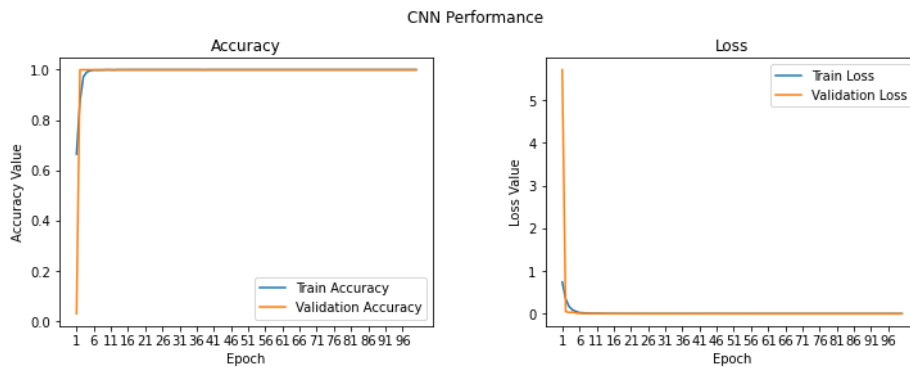


Figure 6: Proposed model experimental result evaluation for 100 epochs

### 5.2 Discussion

Many researches employed pre-trained CNN to extract characteristics before classification, whereas others used customized CNN. We compared the suggested CNN model's outcomes to state-of-the-art deep learning models published in the field, applied on the same dataset. This represents the highest accuracy our architecture can hope to achieve (figure 5).

In general, accuracy refers to the classifier's recognition rate. It is defined as the ratio of the sum of true positive (TP) and true negative (TN) values to the sum of TP, TN, FP, and FN values. Equation (7) shows the mathematical expression for accuracy:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (7)$$

We employ the L1 regularization technique to avoid the overfitting issue. Other works, such as [Oyewola, 22], make advantage of data augmentation. On the data from infected and uninfected malaria blood samples, they employed a data augmentation technique. Basic image transformations, such as rotation, translation, horizontal and vertical scale, random shear, and random reflection, were used to supplement the data. Random rotation, random translation, and horizontal and vertical scale were used as augmentations in this investigation. The images are rotated between  $20^\circ$  and  $20^\circ$  to the right or left along the axis. The rotation degree parameter is used to calculate rotation stability. Despite these encouraging outcomes, their strategy has a number of flaws. To begin with, all deep learning algorithms have a proclivity for overfitting the training dataset. Because the goal of deep learning models is to generalize successfully from training data to any data from the problem domain, CNN must make predictions on datasets it has never seen before. When a model tries to learn too many details from the training data while still allowing for noise, it is said to be overfitting. As a result, the model's performance on unidentified or test datasets is poor. In malaria screening utilizing image recognition, deep learning algorithms paired with reinforcement learning can produce an accuracy of 94.79%.

Another study that trained the ResNet model suggested by [Akgul, 22] using 5 K-Fold cross-validation. To assess the model's effectiveness and error rates, they employed a binary cross entropy loss function. The parameters and values used to train ResNet model structures are K-Fold (5), Mini Batch Size (64), Optimizer (Adamax), Loss Function (Binary Cross Entropy), and Classifier Activation (Sigmoid). The ResNet-50 model had the best success accuracy among the models addressed in the study, with a success rate of 94.09%, and a loss value of 0.2333 using the validation dataset.

<b>Model</b>	<b>Accuracy</b>	<b>Loss</b>
CNN [Maqsood, 21]	96.82%	Not mentioned
CNN [Elangovan, 21]	97.8%	Not mentioned
CNN [Alharbi, 22]	97%	Not mentioned
CNN [Magotra, 22]	96%	Not mentioned
Data Augmentation CNN [Oyewola, 22]	94.79%	Not mentioned
[Akgul, 22]	94.09%	0.2333
<b>Proposed model</b>	<b>99.70%</b>	<b>0.0476</b>

*Table 5: Performance comparison between CNN based deep learning models in literature on malaria dataset*

Based on the results presented in Table 5, we investigate the importance of CNN model in our classification task and we found it important step to include regularization method in training and evaluation of the proposed model. We must think about the data that has been provided to us for the project since it will help us decide which strategies to utilize. The collecting of labeled data has greatly expanded the scope of what we can accomplish with this project. Another factor to consider is the amount of time required for the chosen system's training and evaluation. The benefit that leads to a longer period of time must be significant. At this point, a sophisticated system isn't required; instead, simplifying is the goal. The amount of training data provided will be

the project's restriction. Because there are so many variables in cell size, shape, and rotation, training data is crucial. The project's major goal would be to create a reliable, generalizable system.

### 5.3 Advantages and limitations

The results reveal that our model may be used to detect malaria parasites in blood samples with a 99.70% accuracy for 5 epochs and 100% accuracy for 100 epochs. The major advantages of our custom CNN are less bandwidth requirement, easy implementation with limited memory. To some extent, the proposed scheme leads to faster learning and less computational load, as well as better overcoming challenges basically overfitting. We will look at how convolutions on images can help increase knowledge in this area that can be applied to other applications later, as well as the mutual information content of filters in classifiers that have been trained for different thresholds. As a result, control over deep Learning algorithms will be severely limited.

## 6 Conclusions and Future Work

Traditional methods have shown limited accuracy for malaria parasite detection. And even though some models have good accuracy results and perform well on training data, they perform badly when applied to new data "Overfitting". Therefore, our work proposed a new convolutional neural network architecture with L1 regularization technique to avoid the overfitting problem and to improve malarial classification from thin blood smear images. The layers have been fine-tuned to reduce complexity using a customized technique on a benchmark dataset like the one used in this study. The achieved results prove that with convolutional layers can extract different abstract level features for classification. This study proves that features extracted by CNN are better than hand-crafted features. The CNN model using regularization method outperformed than state-of-the-art deep learning methods. Experimental results of the proposed CNN model with 99.70% accuracy and loss value 0.0476.

By applying the proposed approach to different imaging modalities, we hope to enlarge the dataset. It's possible that the dataset contains parasites other than malaria. As a result, this is a constraint worth investigating in the future, in addition to detecting each parasite (i.e., *Plasmodium ovale*, *Plasmodium malariae*, *Plasmodium vivax*, and *Plasmodium falciparum*). As a result, it is critical to test the suggested technique on a multi-classification assignment. Also, while a private reservation is required in the medical setting, the usage of Block chain or the transition to federated learning must be considered.

### Data Availability Statement

The data underpinning the analysis reported in this paper are deposited at "Mendeley Data" at doi: 10.17632/y7z2vg7fmy.1." reference [HCINI, Ghazala (2022), "Malaria: cell images", Mendeley Data, V1, doi: 10.17632/y7z2vg7fmy.1]



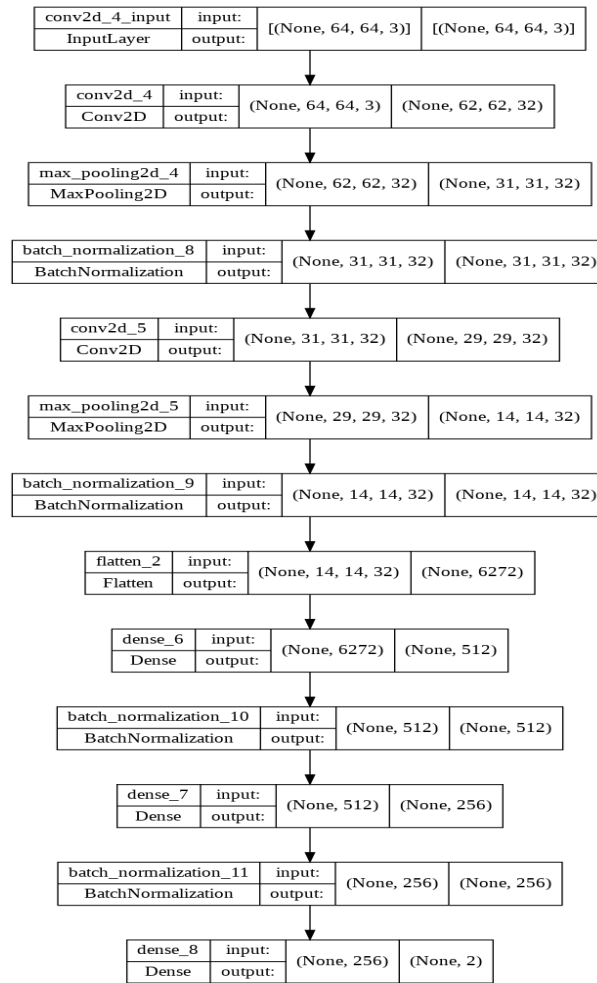


Figure 7: CNN model based on the Keras format

## References

- [Abdou, 22] Abdou, Mohamed A. "Literature review: Efficient deep neural networks techniques for medical image analysis." *Neural Computing and Applications* (2022): 1-22.
- [Abubakar, 21] Abubakar, Aliyu, Mohammed Ajuji, and Ibrahim Usman Yahya. "DeepFMD: Computational Analysis for Malaria Detection in Blood-Smear Images Using Deep-Learning Features." *Applied System Innovation* 4.4 (2021): 82.
- [Akgul, 22] AKGÜL, İsmail, and K. A. Y. A. Volkan. "CLASSIFICATION of CELLS INFECTED with the MALARIA PARASITE with RESNET ARCHITECTURES." *Journal of Scientific Reports-A* 048: 42-54.
- [Alam, 21] Alam, Muhammad, et al. "Convolutional neural network for the semantic segmentation of remote sensing images." *Mobile Networks and Applications* 26.1 (2021): 200-215.
- [Alharbi, 22] Alharbi, Amal H., et al. "Detection of Peripheral Malarial Parasites in Blood Smears Using Deep Learning Models." *Computational Intelligence and Neuroscience* 2022 (2022).
- [Alheejawi, 20] Alheejawi, Salah, et al. "Deep learning-based histopathological image analysis for automated detection and staging of melanoma." *Deep Learning Techniques for Biomedical and Health Informatics*. Academic Press, 2020. 237-265.
- [Almezhghwi, 21] Almezhghwi, Khaled. "Malaria Detection Using Convolutional Neural Network." *International Conference on Theory and Application of Soft Computing, Computing with Words and Perceptions*. Springer, Cham, 2021.
- [Alqudah, 20] Alqudah, Amin, Ali Mohammad Alqudah, and Shoroq Qazan. "Lightweight Deep Learning for Malaria Parasite Detection Using Cell-Image of Blood Smear Images." *Rev. d'Intelligence Artif.* 34.5 (2020): 571-576.
- [Alzubaidi, 21] Alzubaidi, Laith, et al. "Review of deep learning: Concepts, CNN architectures, challenges, applications, future directions." *Journal of big Data* 8.1 (2021): 1-74.
- [Andtaner, 21] andTaner Tuncer, Mohammed Mansur Abubakar. "Malaria Microscopic Cell Image Classification Using Custom-Built CNN Architecture." *International Journal of Signal Processing (IJSP)* 2.3 (2021).
- [Awassa, 22] Awassa, Lamia, et al. "Study of Different Deep Learning Methods for Coronavirus (COVID-19) Pandemic: Taxonomy, Survey and Insights." *Sensors* 22.5 (2022): 1890.
- [Bandyopadhyay, 17] Bandyopadhyay, S. K., S. Nag, and N. Basu. "Computer Aided Diagnosis Based Malarial Parasite Detection-A Review." *Int J Exp Clin Res: IJEACR*-113. DOI 10 (2017).
- [Chanda-Kapata, 22] Chanda-Kapata, Pascalina, et al. "Tuberculosis, HIV/AIDS and Malaria Health Services in sub-Saharan Africa—A Situation Analysis of the Disruptions and Impact of the COVID-19 Pandemic." *International Journal of Infectious Diseases* (2022).
- [Chauhan, 18] Chauhan, Nitin Kumar, and Krishna Singh. "A review on conventional machine learning vs deep learning." *2018 International conference on computing, power and communication technologies (GUCON)*. IEEE, 2018.
- [Dong, 19] Dong, Yuhang, W. David Pan, and Dongsheng Wu. "Impact of misclassification rates on compression efficiency of red blood cell images of malaria infection using deep learning." *Entropy* 21.11 (2019): 1062.
- [Elangovan, 21] Elangovan, Poonguzhali, and Malaya Kumar Nath. "A Novel Shallow ConvNet-18 for Malaria Parasite Detection in Thin Blood Smear Images." *SN Computer Science* 2.5 (2021): 1-11.
- [ElSayed, 21] ElSayed, Mahmoud Said, et al. "A novel hybrid model for intrusion detection systems in SDNs based on CNN and a new regularization technique." *Journal of Network and Computer Applications* 191 (2021): 103160.

- [Erickson, 17] Erickson, Bradley J., et al. "Toolkits and libraries for deep learning." *Journal of digital imaging* 30.4 (2017): 400-405.
- [Fuhad, 20] Fuhad, KM Faizullah, et al. "Deep learning based automatic malaria parasite detection from blood smear and its smartphone based application." *Diagnostics* 10.5 (2020): 329.
- [Haji, 21] Haji, Saad Hikmat, and Adnan Mohsin Abdulazeez. "Comparison of optimization techniques based on gradient descent algorithm: A review." *PalArch's Journal of Archaeology of Egypt/Egyptology* 18.4 (2021): 2715-2743.
- [Hcini, 21] Hcini, G.; Jdey, I.; Heni, A.; Ltifi, H. Hyperparameter optimization in customized convolutional neural network for blood cells classification. *J. Theor. Appl. Inf. Technol.* 2021, 99, 5425–5435.
- [Hou, 18] Hou, Rongrong, Yong Xia, and Xiaoqing Zhou. "Structural damage detection based on l1 regularization using natural frequencies and mode shapes." *Structural Control and Health Monitoring* 25.3 (2018): e2107.
- [Jaiswal, 18] Jaiswal, Shruti, Ashish Mehta, and G. C. Nandi. "Investigation on the effect of L1 and L2 regularization on image features extracted using restricted boltzmann machine." 2018 Second International Conference on Intelligent Computing and Control Systems (ICICCS). IEEE, 2018.
- [Jdey, 22] Jdey, Imen, Ghazala Hcini, and Hela Ltifi. "Deep learning and machine learning for Malaria detection: overview, challenges and future directions." *arXiv preprint arXiv:2209.13292* (2022).
- [Jdey, 12] Jdey, Imen, et al. "The contribution of fusion techniques in the recognition systems of radar targets." (2012): 94-94.
- [Jlassi, 21] Jlassi, Sinda, Imen Jdey, and Hela Ltifi. "Bayesian Hyperparameter Optimization of Deep Neural Network Algorithms Based on Ant Colony Optimization." *International Conference on Document Analysis and Recognition*. Springer, Cham, 2021.
- [Joshi, 20] Joshi, Amogh Manoj, Ananta Kumar Das, and Subhasish Dhal. "Deep learning based approach for malaria detection in blood cell images." 2020 IEEE REGION 10 CONFERENCE (TENCON). IEEE, 2020.
- [Jung, 18] Jung, Jee-Weon, et al. "Avoiding speaker overfitting in end-to-end dnns using raw waveform for text-independent speaker verification." *extraction* 8.12 (2018): 23-24.
- [Ke, 18] Ke, Qihong, et al. "Computer vision for human-machine interaction." *Computer Vision for Assistive Healthcare*. Academic Press, 2018. 127-145.
- [Luca, 22] Luca, Andreea Roxana, et al. "Impact of quality, type and volume of data used by deep learning models in the analysis of medical images." *Informatics in Medicine Unlocked* (2022): 100911.
- [Madad, 20] Madad Zadeh, Sabrina, et al. "SurgAI: deep learning for computerized laparoscopic image understanding in gynaecology." *Surgical endoscopy* 34.12 (2020): 5377-5383.
- [Magotra, 22] Magotra, Varun, and Mukesh Kumar Rohil. "Malaria Diagnosis Using a Lightweight Deep Convolutional Neural Network." *International Journal of Telemedicine and Applications* 2022 (2022).
- [Maqsood, 21] Maqsood, Asma, et al. "Deep malaria parasite detection in thin blood smear microscopic images." *Applied Sciences* 11.5 (2021): 2284.
- [Masud, 20] Masud, Mehedi, et al. "Leveraging deep learning techniques for malaria parasite detection using mobile application." *Wireless Communications and Mobile Computing* 2020 (2020).
- [Mazurowski, 19] Mazurowski, Maciej A., et al. "Deep learning in radiology: An overview of the concepts and a survey of the state of the art with focus on MRI." *Journal of magnetic resonance imaging* 49.4 (2019): 939-954.

- [Mishra, 21] Mishra, Saurav. "Malaria Parasite Detection using Efficient Neural Ensembles." *Journal of Electronics, Electromedical Engineering, and Medical Informatics* 3.3 (2021): 119-133.
- [Nakasi, 20] Nakasi, Rose, et al. "A new approach for microscopic diagnosis of malaria parasites in thick blood smears using pre-trained deep learning models." *SN Applied Sciences* 2.7 (2020): 1-7.
- [Oyewola, 22] Oyewola, David Opeoluwa, et al. "A novel data augmentation convolutional neural network for detecting malaria parasite in blood smear images." *Applied Artificial Intelligence* (2022): 1-22.
- [Pan, 18] Pan, W. David, Yuhang Dong, and Dongsheng Wu. "Classification of malaria-infected cells using deep convolutional neural networks." *Machine learning: advanced techniques and emerging applications* 159 (2018).
- [Pattanaik, 20] Pattanaik, Priyadarshini Adyasha, Mohit Mittal, and Mohammad Zubair Khan. "Unsupervised deep learning cad scheme for the detection of malaria in blood smear microscopic images." *IEEE Access* 8 (2020): 94936-94946.
- [Pelt, 20] Pelt, Daniel M. "Deep Learning: Tackling the challenges of bioimage analysis." *Elife* 9 (2020): e64384.
- [Poostchi, 18] Poostchi, Mahdieh, et al. "Image analysis and machine learning for detecting malaria." *Translational Research* 194 (2018): 36-55.
- [Qanbar, 19] QANBAR, Mohanad Mohammed, and Sakir Tasdemir. "Detection of malaria diseases with residual attention network." *International Journal of Intelligent Systems and Applications in Engineering* 7.4 (2019): 238-244.
- [Rahman, 19] Rahman, Aimon, et al. "Improving malaria parasite detection from red blood cell using deep convolutional neural networks." *arXiv preprint arXiv:1907.10418* (2019).
- [Rajaraman, 19] Rajaraman, Sivaramakrishnan, et al. "Assessment of an ensemble of machine learning models toward abnormality detection in chest radiographs." *2019 41st Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC)*. IEEE, 2019.
- [Rajaraman, 19] Rajaraman, Sivaramakrishnan, Stefan Jaeger, and Sameer K. Antani. "Performance evaluation of deep neural ensembles toward malaria parasite detection in thin-blood smear images." *PeerJ* 7 (2019): e6977.
- [Sandhya, 20] Sandhya, Yamala, Prasanta Kumar Sahoo, and K. Eswaran. "Malaria Disease Detection Using Deep Learning Technique." *Int. J. Adv. Sci. Technol* 29 (2020): 7736-7745.
- [Sarker, 21] Sarker, Iqbal H. "Deep learning: a comprehensive overview on techniques, taxonomy, applications and research directions." *SN Computer Science* 2.6 (2021): 1-20.
- [Sinha, 21] Sinha, Shruti, et al. "Performance assessment of Deep Learning procedures on Malaria dataset." *Journal of Robotics and Control (JRC)* 2.1 (2021): 12-18.
- [Sivaramakrishnan, 17] Sivaramakrishnan, Rajaraman, Sameer Antani, and Stefan Jaeger. "Visualizing deep learning activations for improved malaria cell classification." *Medical informatics and healthcare*. PMLR, 2017.
- [Slater, 22] Slater, Lucinda, et al. "Current methods for the detection of Plasmodium parasite species infecting humans." *Current Research in Parasitology & Vector-Borne Diseases* (2022): 100086.
- [Umer, 20] Umer, Muhammad, et al. "A novel stacked CNN for malarial parasite detection in thin blood smear images." *IEEE Access* 8 (2020): 93782-93792.
- [Voulodimos, 18] Voulodimos, Athanasios, et al. "Deep learning for computer vision: A brief review." *Computational intelligence and neuroscience* 2018 (2018).
- [Yamashita, 18] Yamashita, Rikiya, et al. "Convolutional neural networks: an overview and application in radiology." *Insights into imaging* 9.4 (2018): 611-629.

[Yang, 19] Yang, Feng, et al. "Deep learning for smartphone-based malaria parasite detection in thick blood smears." *IEEE journal of biomedical and health informatics* 24.5 (2019): 1427-1438.