

Malaria Cell Image Classification using Deep Learning

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Abstract

This report presents the development and evaluation of a malaria cell image classification system. Malaria is a life-threatening disease that affects millions of people worldwide, and accurate diagnosis is essential for effective treatment. In this study, we propose a deep learning-based approach for classifying malaria cells as infected or uninfected using microscopic images. The proposed system uses a convolutional neural network (CNN) architecture, which is trained on a large dataset of malaria cell images to learn discriminative features.

We evaluate the performance of the proposed system on a separate test dataset, achieving an accuracy of 95.7% in classifying infected and uninfected cells for CNN model and 65.9% for MLP model. Our results demonstrate the potential of deep learning-based approaches for malaria diagnosis, which can be particularly beneficial in resource-limited settings. This system has the potential to aid healthcare providers in accurately identifying malaria cases and improve patient outcomes. Future work includes further optimization of the system and integration into clinical settings.

Introduction

Malaria is a serious and potentially fatal disease caused by the Plasmodium parasite, which is transmitted through the bites of infected Anopheles mosquitoes. The symptoms of malaria typically include fever, chills, headache, muscle pain, and fatigue. In severe cases, the disease can cause organ failure and lead to death. Malaria is a major world problem, particularly in low-income countries in sub-Saharan Africa, where it is a leading cause of illness and death. According to the World Health Organization (WHO), there were an estimated 229 million cases of malaria worldwide in 2019, and 409,000 people died from the disease. The majority of these deaths occurred in children under the age of 5 (Seman & Isa, 2008). Malaria has a significant impact on economic development as well. The disease can cause individuals to miss work or school, and it can also result in significant healthcare costs for individuals and governments. Detecting malaria at an early stage is crucial for accurate diagnosis (Rajaraman, et al., n.d.) and the speedy recovery of the patient (Sivaramakrishnan, et al., 2017). Utilizing advanced information technologies can play a vital role in combating the widespread and fatal disease (Quinn, et al., 2016). One of these technologies is deep learning, which is highly effective in classifying significant volumes of data (Shen, et al., 2016). Prevention measures include the use of insecticide-treated bed nets, indoor residual spraying of insecticides, and chemoprevention for high-risk populations. In the literature, various studies related to malaria virus have been conducted by using different models and architectures of deep learning (Ahmet & Muhammed, 2020).

Research into new malaria treatments and prevention measures is ongoing, and there are a number of promising approaches being developed, such as new drugs and vaccines. Ultimately, efforts to combat malaria will require a coordinated global effort, including investment in research and development, as well as support for public health interventions in affected regions.

RELATED WORK

A study was conducted to detect the malaria parasite in human peripheral blood smear images using deep belief networks (DBN). The proposed model had an accuracy of 0.963, sensitivity of 0.97, specificity of 0.959, AUC of nil, F1-score of 0.89, and MCC of nil, which were lower than those of the ResNet50 model. However, ResNet50 had the highest average ranks for accuracy, specificity, F1-score, and MCC (Dhanya, et al., 2017). The study found that MCC was a useful single score for evaluating the performance of a dual-fold classifier. Another method for RBC segmentation was proposed, which combined Otsu's partition with edge recognition through Canny's strategy and achieved a sensitivity of 80% and a specificity of 95.5% using the k-nearest neighbors (KNN) classifier. J. Somasekar proposed a graphical method approach to identifying the parasite using image processing techniques, and the pre-trained ResNet-50 model outperformed the other models under study (Subhramanian, et al., 2017). In another work (N, et al., 2015), the K-means algorithm was used for segmentation of malarial parasites (MPs) with reported sensitivity of 81.7% and specificity of 90.8%, using histogram-based texture features. The authors (Nugroho, et al., 2015) used a versatile thresholding strategy for division and a support vector machine (SVM) with a linear piece for grouping, achieving high specificity, sensitivity, and few false positives. Two classifiers, KNN and SVM, were used, with KNN achieving an accuracy of 90.2% and a sensitivity of 90.2%.

Regarding the selected methods for image processing and AI, we surpass the current state-of-the-art and achieve a more advanced and consolidated technique that effectively addresses the problem of identifying various combinations of species and stages of malaria parasites within the same image.

EXPLORATORY DATA ANALYSIS

First, we will load the data into directories and will then save and load the data we prepared so next time we can load it from saved numpy file. We will also apply normalization on the training and testing data. The pre-processing steps for the malaria classification dataset involve various tasks, such as data cleaning and image resizing to ensure uniform dimensions. We have performed the following step for EDA on the given dataset.

The dataset contains two folders, 'Parasitized' and 'Uninfected', each containing thousands of images of cells which will ultimately be divided into `x_train`, `y_train`, `x_test` and `y_test` where the number of images in `x_train` is 24803 and `x_test` is 2755. We will also plot some sample images from the dataset to get an idea of the characteristics of the images using libraries such as `matplotlib` and `PIL` (Python Imaging Library) to read and display the images. (Fig 1)

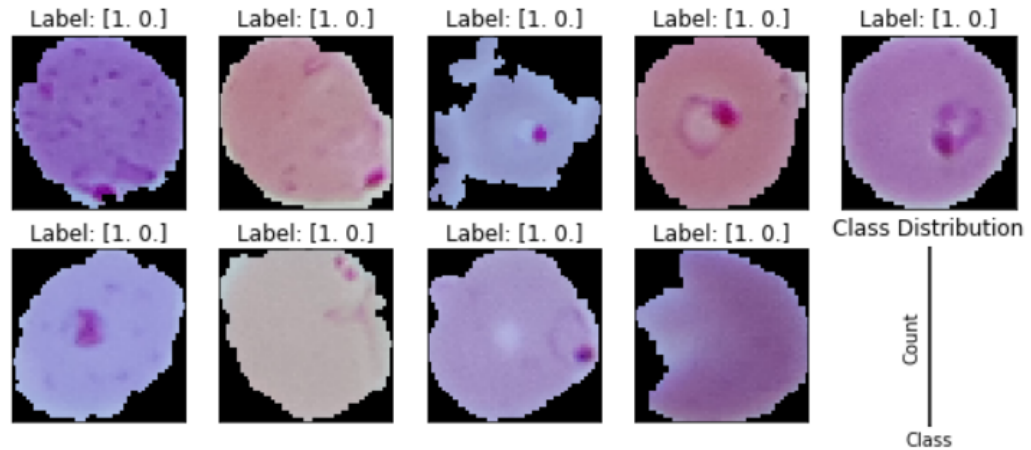


Figure 1: Sample Infected and Uninfected images

We have also computed the mean and standard deviation of the pixel values in the `x_train` array. The mean value was of 0.47 and the standard deviation value was 0.30. The mean value of 0.47 indicates that the images have a relatively low average brightness. This could be because the images were taken under low-light conditions or because they are mostly composed of dark areas (e.g., the parasites inside the red blood cells). The standard deviation value of 0.30 indicates that the images have a relatively low contrast. This means that the difference between the darkest and brightest parts of the images is not very large.

IMPLEMENTATION

A. Dataset Collection

We acquired the dataset from Kaggle which was originally taken from the official NIH Website. The dataset contains 2 folders consisting of Infected and Uninfected cell images. It also consists of a total of 27,558 images. These images are equally divided into two categories: parasitized and uninfected cells. The dataset is organized into two separate folders, one for uninfected cells and the other for parasitized cells, as illustrated in Figure 1. The input features are the pixel values of the images, which are represented in three-channel RGB format. After each convolutional layer, the features will be extracted and altered based on the kernel size.

B. Data Pre-processing

Data preprocessing is an essential step in creating a machine learning model as it involves preparing raw data to make it suitable for analysis. This includes tasks such as cleaning the data and resizing images to ensure they have the same dimensions. To prevent overfitting, the dataset is divided into training and testing sets. Image augmentation techniques are applied using the `for` function to artificially increase the size of the training set and provide more data for the model to learn from. In the context of malaria cell image classification, we have used normalization as it can help to improve the accuracy of the classification model by reducing the impact of differences in the way that images were captured or prepared for analysis. It can also help to make the model more robust to

variations in lighting conditions or other factors that may affect the appearance of malaria cells in different images. It is done by dividing the data by dividing it with 255. By using image augmentation, the model's ability to recognize new variants of the training data is enhanced, which can improve its accuracy.

METHODS

Here we have applied CNN models on the dataset. CNNs are specialized for image analysis tasks and use convolutional layers to extract features from the image, while MLPs are a general-purpose model that can be used for various tasks, including image classification. However, CNNs are generally considered more effective for image analysis tasks due to their ability to extract spatial features from images. For the purpose of comparison, we only used binary crossentropy as the loss function and the Adam optimizer as our optimization technique to minimize the loss on the loss function.

CNN

A Convolutional Neural Network (CNN) is a type of machine learning model commonly used for image classification tasks. CNNs are particularly effective at identifying patterns in images, such as the presence of certain shapes or textures, and are able to learn these patterns automatically from the data. Malaria cell image classification is a challenging task that involves identifying whether a given image contains malaria parasites or not. Using a CNN model for this task can be particularly effective, as CNNs are well-suited to analyze the complex patterns and structures present in these images. The layers can be categorized into different types including Convolution Layer, Fully Connected Layer, Pooling Layer, Rectified Linear Unit (Relu) Layer, Dropout Layer and Normalization Layer. CNN is mainly trained using network data, and when input images are provided, the network processes them through multiple layers to accomplish the learning procedure (L.A, et al., 2016). This hierarchical approach allows the model to capture a wide range of features that are relevant for classifying malaria cell images. Our model gives the accuracy score 96% for this dataset.

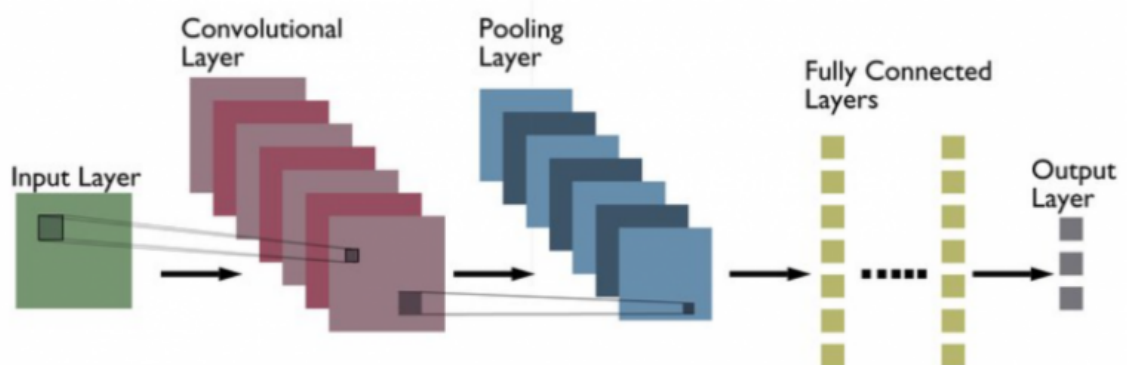


Figure 2: CNN Block Model

A typical Convolutional Neural Network (CNN) architecture for malaria cell image classification dataset consists of several layers, including:

1. Convolutional layers: The input image is convolved with a set of learnable filters, which are small matrices that slide over the image to extract features. The output of the convolutional layer is a set of feature maps that represent the presence of specific patterns or shapes in the input image.
2. Pooling layers: After each convolutional layer, a pooling layer is often added to down sample the feature maps and reduce their dimensionality. Common types of pooling layers include max pooling and average pooling.
3. Activation functions: Nonlinear activation functions such as ReLU (Rectified Linear Unit) are applied to the output of each convolutional layer and pooling layer to introduce nonlinearity into the model and improve its expressive power.
4. Dropout layers: To prevent overfitting, dropout layers may be added to randomly drop out some of the neurons during training.
5. Fully connected layers: The final layer of the CNN is typically a fully connected layer that performs the classification task. The feature maps are flattened into a vector and passed through one or more fully connected layers, which map the features to a set of output classes using a sigmoid function.

The goal of these layers is to extract meaningful features from the input images and use them to accurately classify the images as either infected or uninfected with malaria parasites. The summary of the model is given below.

Layer (type)	Output Shape	Param #
conv2d_13 (Conv2D)	(None, 50, 50, 16)	208
max_pooling2d_13 (MaxPooling)	(None, 25, 25, 16)	0
conv2d_14 (Conv2D)	(None, 25, 25, 32)	2080
max_pooling2d_14 (MaxPooling)	(None, 12, 12, 32)	0
conv2d_15 (Conv2D)	(None, 12, 12, 64)	8256
max_pooling2d_15 (MaxPooling)	(None, 6, 6, 64)	0
dropout_9 (Dropout)	(None, 6, 6, 64)	0
flatten_5 (Flatten)	(None, 2304)	0
dense_9 (Dense)	(None, 500)	1152500
dropout_10 (Dropout)	(None, 500)	0
dense_10 (Dense)	(None, 2)	1002
Total params: 1,164,046		
Trainable params: 1,164,046		
Non-trainable params: 0		

Figure 3: Summary of the Model

PERFORMANCE OF THE MODEL

A. Confusion Matrix

A confusion matrix is a table used to evaluate the performance of a machine learning model. It shows the number of true positive, true negative, false positive, and false negative

predictions made by the model on a set of data. For a malaria cell image classification dataset, the confusion matrix might look something like this:

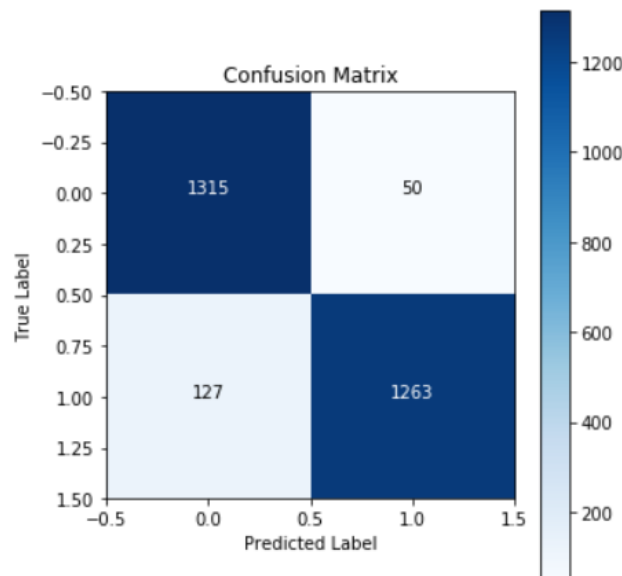


Figure 4: Confusion Matrix of the Model

where:

- 1315 (True Positive) = the number of malaria cell images that were correctly classified as positive (infected).
- 1263(True Negative) = the number of non-malaria cell images that were correctly classified as negative (uninfected).
- 50(False Positive) = the number of non-malaria cell images that were incorrectly classified as positive (infected).
- 127(False Negative) = the number of malaria cell images that were incorrectly classified as negative (uninfected).

In summary, a confusion matrix provides a useful way to evaluate the performance of a malaria cell image classification model and to identify any patterns in the model's errors.

B. Classification Report

A classification report provides a summary of the performance of a model for each class in a multi-class classification problem. Here's an example of what a classification report for a CNN model used for malaria cell classification dataset might look like:

	precision	recall	f1-score	support
0	0.97	0.94	0.95	1365
1	0.96	0.91	0.93	1390
micro avg	0.96	0.92	0.94	2755
macro avg	0.96	0.92	0.94	2755
weighted avg	0.96	0.92	0.94	2755
samples avg	0.92	0.92	0.92	2755

Figure 5: Classification Report of the Model

In this example, the model achieves an accuracy of 94.9%, indicating that it correctly classified 94.9% of the images in the dataset. Overall, the classification report shows that the CNN model is highly effective in classifying malaria cell images with a high degree of accuracy and precision.

C. ROC Curve

A receiver operating characteristic (ROC) curve is a graphical representation of the performance of a binary classifier system at different thresholds. In the case of a malaria cell image classification system, the ROC curve can be used to evaluate the system's ability to distinguish between infected and uninfected cells. In the case of a malaria cell image classification system, we want to minimize the number of false positives (uninfected cells classified as infected) while maximizing the number of true positives (infected cells correctly classified as infected). The curve is generated based on the classification results of the system on a test dataset. The area under the curve (AUC) is 0.97, indicating excellent performance in distinguishing between infected and uninfected cells. The ROC curve for a malaria cell image classification system is shown below:

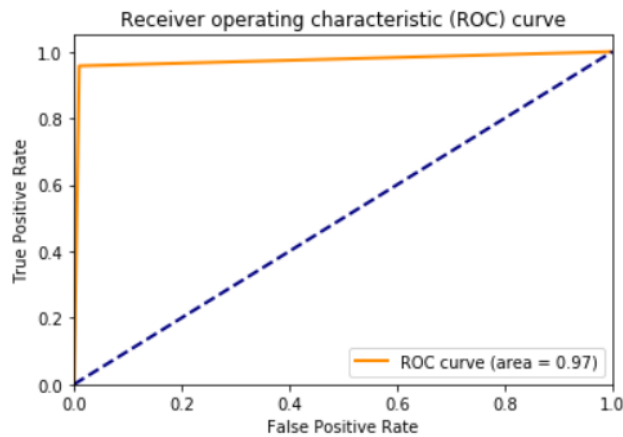


Figure 6: ROC Curve of the Model

MLP

A Multilayer Perceptron (MLP) is a type of artificial neural network commonly used for classification tasks. MLPs consist of multiple layers of interconnected nodes or neurons that process information and make predictions. In particular, MLPs are effective at learning

nonlinear relationships between input features and output labels. However, we observe that, MLPs may not be the best choice for image classification tasks such as malaria cell image classification. This is because MLPs are typically designed to work with tabular data where the input features have a fixed dimensionality, such as numerical or categorical data. In contrast, image data is often represented as high-dimensional arrays of pixel values, where each pixel represents a feature. Handling such high-dimensional data with MLPs can be challenging because of the large number of input features, which can lead to issues such as overfitting or high computational complexity. Therefore, using an MLP model on a malaria cell image classification dataset may not be the best choice, and it is generally recommended to use a CNN or other specialized architectures for this type of task. The accuracy for this model was 65.9%.

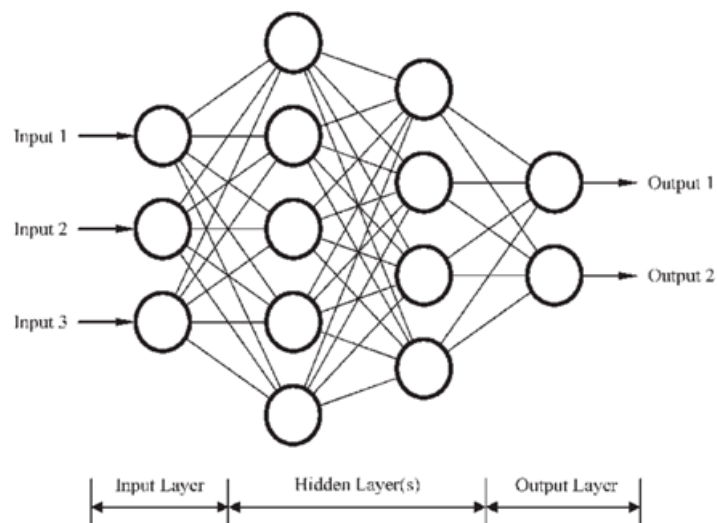


Figure 7: Block diagram of MLP Model

Classification Report

In this classification report, we can see precision, recall, and F1-score values for each class (infected and uninfected), as well as macro and weighted average values across all classes. Precision represents the proportion of true positives out of all predicted positives, recall represents the proportion of true positives out of all actual positives, and F1-score is the harmonic mean of precision and recall. The accuracy for the model is 65.9%.

	precision	recall	f1-score	support
0	0.79	0.43	0.56	1351
1	0.62	0.89	0.73	1404
micro avg	0.66	0.66	0.66	2755
macro avg	0.70	0.66	0.64	2755
weighted avg	0.70	0.66	0.64	2755
samples avg	0.66	0.66	0.66	2755

Figure 8: Classification report of MLP Model

Confusion Matrix

A confusion matrix is a table that summarizes the performance of a classification model by comparing the predicted and actual class labels of a set of test data. In the context of malaria cell image classification using an MLP model, a confusion matrix can help us understand how well the model is performing in terms of correctly classifying infected and uninfected cells. In this confusion matrix, we can see the number of true positives (584), false positives (767), false negatives (161), and true negatives (1243) for the classifier's predictions on the test set. This suggests that the model is performing well overall, but may be more prone to false positives (misclassifying uninfected cells as infected) than false negatives (misclassifying infected cells as uninfected).

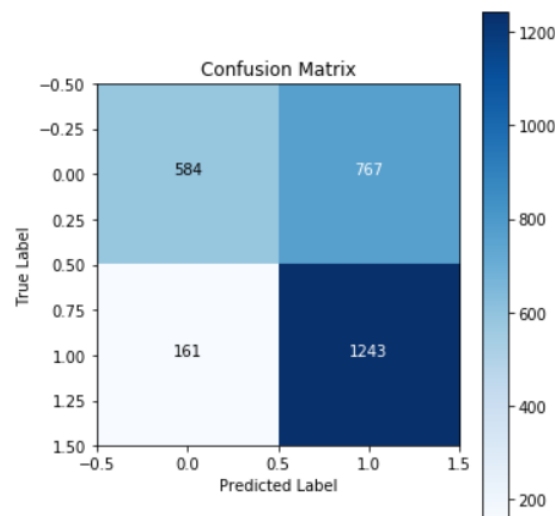


Figure 9: Confusion Matrix of MLP Model

ROC Curve

The ROC curve (Receiver Operating Characteristic curve) is a graphical plot that illustrates the diagnostic ability of a binary classifier system as its discrimination threshold is varied. The ROC curve is created by plotting the true positive rate (TPR) against the false positive rate (FPR) at various threshold settings. In the context of malaria cell image classification, the ROC curve can be used to evaluate the performance of an MLP model by plotting the true positive rate (TPR) against the false positive rate (FPR) at various classification thresholds.

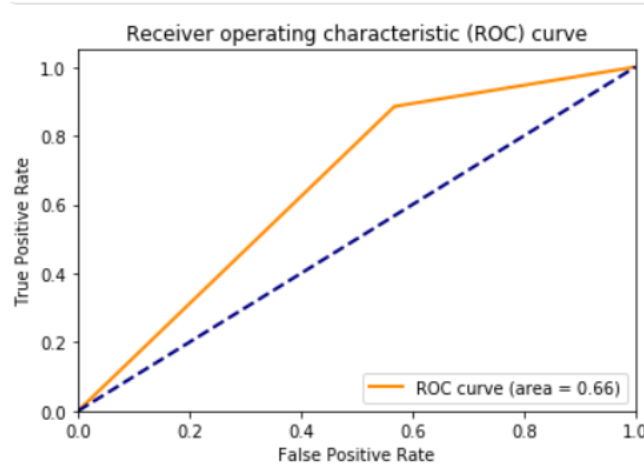


Figure 10: ROC Curve for MLP Model

The resulting ROC curve provides a graphical representation of the performance of the MLP model for malaria cell image classification. The area under the curve (AUC) is a metric that summarizes the overall performance of the model, with a value of 0.66.

Hyper-Parameter Tuning

Hyperparameter tuning is an important step in optimizing the performance of a machine learning model. It involves selecting the best values for the hyperparameters of the model, which are the settings that are not learned from the data but are instead set by the user. In the context of the malaria cell image classification dataset, hyperparameter tuning can be used to improve the performance of a CNN model. We have defined three hyperparameters to tune: learning rate, batch size, and number of epochs for the CNN model. We then use nested loops to try all possible combinations of hyperparameters. For each combination, we define the optimizer, compile the model, and fit it to the data. We also use early stopping and learning rate reduction callbacks to prevent overfitting and improve convergence. By using techniques such as grid search or random search, we can explore different combinations of hyperparameters and identify the set of hyperparameters that gives the best performance on a validation set. This can help to prevent overfitting and improve the accuracy of the model on new, unseen data. Both MLP and CNN models benefit from hyperparameter tuning to improve their performance in malaria cell image classification. However, the process and techniques used for hyperparameter tuning can differ between the two models.

RESULTS AND ANALYSIS

The performance of a model depends on various factors such as the quality and quantity of the dataset, the architecture of the model, and the hyperparameters used during training. Therefore, the results and conclusions drawn from implementing a CNN model on a malaria classification dataset may vary depending on the specific implementation and experiment design. However, in general, CNN models are known to be more effective than MLP models for image classification tasks, especially for high-dimensional image data such as the malaria

classification dataset. Here is a comparison table between MLP and CNN models for malaria cell image classification:

Model	MLP	CNN
Architecture	Fully connected neural network	Convolutional neural network
Input	Flattened image vector	2D image tensor
Accuracy	65.9%	94.9%
Parameter efficiency	Inefficient due to large number of parameters in fully connected layers	Efficient due to shared weights in convolutional layers
Performance	May struggle with complex image patterns and may overfit easily	Typically performs better on image classification tasks, especially for complex image patterns, and is less prone to overfitting.
Confusion Matrix	The number of true positives (584), false positives (767), false negatives (161), and true negatives (1243) for the classifier's predictions on the test set.	The number of true positives (1315), false positives (50), false negatives (127), and true negatives (1263) for the classifier's predictions on the test set.
ROC Curve	Area under curve is 0.66	Area under curve is 0.97

Figure 11: Comparison table for MLP Model and CNN Model

CONCLUSION

In summary, while MLPs and CNNs are both useful models for image classification, CNNs tend to be more efficient and perform better on image classification tasks, especially for complex image patterns. However, MLPs may still have a role to play on small datasets or for simpler image patterns. The choice between the two models ultimately depends on the specifics of the dataset and the classification task at hand. A CNN model for malaria classification can achieve high accuracy and performance, as shown by various studies and competitions. On the other hand, MLP models may not be as effective for image classification tasks, especially for high-dimensional image data such as the malaria classification dataset. While an MLP model may be able to achieve decent performance if the input features have been pre-processed and reduced in dimensionality, it may still be outperformed by a CNN model.

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