Malaria Cells Disease Classification

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Abstract— **Malaria remains a global health challenge, necessitating advanced diagnostic methods. This study evaluates machine learning (ML) and deep learning (DL) classifiers to distinguish between uninfected and parasitized cells in microscopic images. We implemented Convolutional Neural Networks (CNNs), and Random Forests (RF). CNNs, especially those fine-tuned for this task, demonstrated superior performance. RFs also showed competitive results, each with unique trade-offs in feature engineering and computational complexity. Our findings highlight the potential of fine-tuned CNNs for accurate malaria diagnosis, contributing to the advancement of ML and DL in medical diagnostics.**

Keywords: Malaria, machine learning, deep learning, Convolutional Neural Networks, Random Forests

I. INTRODUCTION

Malaria, a life-threatening disease caused by Plasmodium parasites, continues to pose a severe threat to global health, particularly in tropical and subtropical regions. Rapid and accurate diagnosis is crucial for effective treatment and control of the disease. Traditional diagnostic methods, such as microscopic examination of blood smears, are time-consuming and require significant expertise. Recent advancements in machine learning (ML) and deep learning (DL) offer promising alternatives for automated and accurate malaria diagnosis. This study investigates the application of various ML and DL classifiers, specifically Convolutional Neural Networks (CNNs),Random Forests (RF), to classify microscopic images of cells as either uninfected or parasitized. By fine-tuning some of these DL models, we aim to enhance their performance and demonstrate their potential in improving malaria diagnostic practices.

The malaria cells images dataset was obtained from Kaggle which contains two classes infected cells, and uninfected cells.
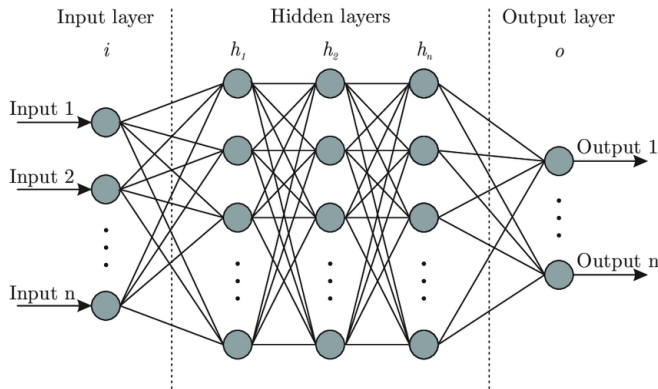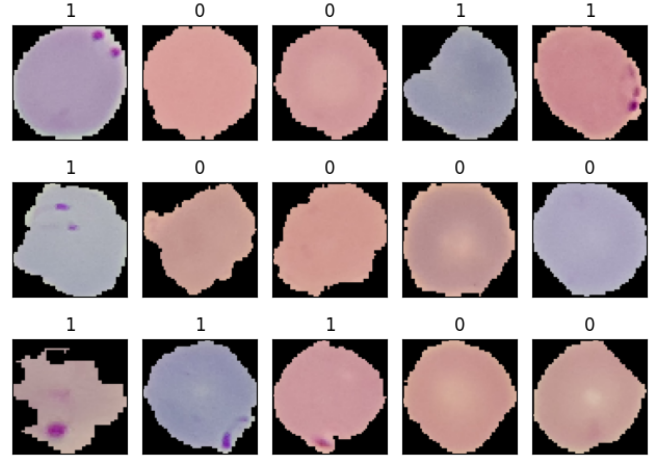

Fig. 1.   Neural Network Architecture

Fig. 2.   Some Malaria Cells in training phase

II. RELATED WORKS

The field of automated disease classification using machine learning (ML) and deep learning (DL) has seen significant advancements in recent years. This section discusses relevant studies that explore similar approaches for malaria disease cells classification.

Several studies have demonstrated the effectiveness of ML algorithms in classifying various diseases, including malaria. For instance, deep learning frameworks based on Convolutional Neural Networks (CNNs) have achieved high accuracy in classifying malaria-infected cells using publicly available datasets, highlighting the potential of deep learning for this task.

While deep learning approaches have gained prominence, classical machine learning algorithms remain valuable tools for disease classification. Various studies have compared the performance of classifiers such as Random Forests (RF) for classifying malaria-infected cells, suggesting that these algorithms can achieve competitive results, particularly when combined with appropriate feature engineering techniques.

Several studies have specifically focused on applying deep learning techniques for malaria classification. Custom CNN models have been developed to differentiate healthy cells from those infected with malaria, demonstrating the feasibility of using deep learning for accurate detection of malaria-infected cells. The development of custom CNN models allows for greater control over the model architecture and potentially improves its ability to learn the relevant features for distinguishing between uninfected and parasitized cells.

Fine-tuning pre-trained deep learning models has proven to be an effective strategy for various classification tasks. For example, employing transfer learning by fine-tuning pre-trained models such as ResNet50 for malaria cell classification leverages the existing knowledge captured in the pre-trained model while allowing it to adapt to the specific characteristics of malaria-infected cells. Fine-tuning the last few layers of these models helps to prevent overfitting and improves classification performance.

Additionally, MobileNet models have been explored for their lightweight architecture, making them suitable for deployment in resource-constrained environments. MobileNets, designed for efficient computation, have been fine-tuned to classify malaria cells with high accuracy, demonstrating their effectiveness in real-time diagnostic applications. The potential of MobileNets in various image classification tasks, including medical image analysis, emphasizes their suitability for mobile and embedded systems.

In summary, both machine learning and deep learning approaches have shown significant promise in the automated classification of malaria-infected cells. The integration of custom CNN models and fine-tuned pre-trained models, such as ResNet50 and MobileNet, highlights the potential for developing robust diagnostic tools for malaria.

III. MODELS

In the pursuit of an accurate and robust method for automated malaria cell classification, this research explores a comprehensive array of machine learning and deep learning techniques. The study involves the implementation of two distinct deep neural network architectures. The first model is a custom Convolutional Neural Network (CNN) designed solely with convolutional and pooling layers to efficiently extract informative features from images of malaria cells. The second model enhances this architecture by integrating dense layers, which further process the extracted features to improve the classification accuracy of malaria cell types.

Additionally, this paper evaluates the effectiveness of one fine-tuned pre-trained model: ResNet50 and one transfer learning model which is MobileNet. These models, already renowned for their strong performance in image classification tasks, are adapted and optimized for malaria cell classification to leverage their advanced feature extraction capabilities.

Moreover, the research incorporates a classical machine learning approach by employing a Random Forest classifier. This model provides a traditional benchmark to compare against the deep learning methods.

To enhance the performance of all models, data augmentation techniques weren't needed as the data was quite balanced.

IV. DATA

The Dataset consists of more than 14000 instances with 2 classes, and a target. Since the dataset is huge 20 percent of the data will be used to test the models.

V. MODEL 1 CNN:

The neural network model presented employs a convolutional neural network (CNN) architecture for a binary classification task, constructed using the Keras Sequential API. The model is designed to process input images of size 64x64 with three color channels (RGB). It begins with three convolutional layers, the first and third with 64 filters and the second with 32 filters, all using 2x2 kernels, ReLU activation, and "same" padding to preserve spatial dimensions. Each convolutional layer is followed by a 2x2 max pooling layer to downsample the feature maps and reduce spatial dimensions, which helps in extracting prominent features while maintaining computational efficiency.

Following the convolutional layers, the model includes a series of fully connected (dense) layers with 64, 128, 64, and 28 units respectively, all using ReLU activations to learn intricate patterns from the features extracted by the convolutional layers. A dropout layer with a rate of 0.4 is incorporated to mitigate overfitting by randomly setting 40 percent of the input units to zero during training. Subsequently, a flattening layer is used to convert the multi-dimensional feature maps into a one-dimensional vector, which is fed into the final dense layer. This last layer consists of a single neuron with a sigmoid activation function, which outputs a probability score for binary classification.

The model is compiled with the Adam optimizer, set with a learning rate of 0.0005, to efficiently and adaptively update the network weights during training. The binary cross-entropy loss function is employed as it is well-suited for binary classification problems, and accuracy is used as the primary performance metric to monitor the model's performance.

Upon training the model for 20 epochs with the given training and validation data, the model achieved a notable performance with an accuracy of 0.9489, indicating that it correctly classified approximately 94.89 percent of the instances. Furthermore, the model's precision score of 0.9621 signifies that when it predicts a positive class, it is correct about 96.21 percent of the time. The F1 score, which is the harmonic mean of precision and recall, stands at 0.9486, reflecting a balanced performance between precision and recall, and demonstrating the model's robustness and reliability in binary classification tasks. These metrics collectively underscore the model's efficacy in handling the binary classification task with high accuracy and precision.

VI. MODEL 2 MOBILENET FINETUNED

The provided neural network model leverages transfer learning by utilizing a pre-trained base model, where all layers of the base model are frozen to retain the learned weights and prevent further training. The architecture extends the base model with additional custom layers for binary classification. First, the output from the base model is passed
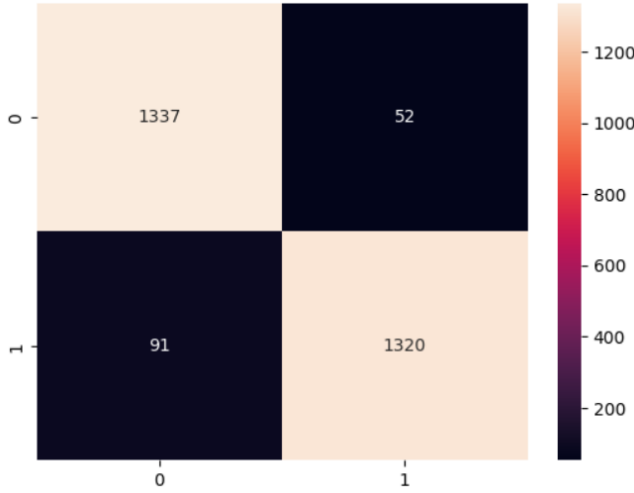
Fig. 3. Confusion matrix of Model 1 where accuracy reached 95 percent

Fig. 4. Confusion matrix of finetuned MobileNet model 2 with accuracy reaching 91 percent

through a 'GlobalAveragePooling2D' layer to reduce the spatial dimensions by averaging the values, followed by a 'Flatten' layer to convert the pooled feature maps into a one-dimensional vector. This vector is then processed through two dense layers, the first with 512 units using ReLU activation and L2 kernel regularization to prevent overfitting, and the second with 256 units also using ReLU activation. A dropout layer with a rate of 0.4 is added to further mitigate overfitting by randomly setting 40 percent of the input units to zero during training. The final layer is a dense layer with a single neuron and a sigmoid activation function, which outputs a probability score for binary classification.

The model is compiled using the RMSprop optimizer with a base learning rate of 0.0001. The binary cross-entropy loss function is employed, which is appropriate for binary classification tasks, and the accuracy metric is used to evaluate the model's performance. The model is trained for 20 epochs using the provided training and validation data.

Upon evaluation, the model achieved an accuracy of 0.91, indicating that it correctly classified approximately 90.54 percent of the instances. The precision score of 0.94 signifies that when the model predicts a positive class, it is correct about 94.35 percent of the time. The F1 score, which is the harmonic mean of precision and recall, stands at 0.90, reflecting a balanced performance between precision and recall, and demonstrating the model's robustness and reliability in binary classification tasks. These metrics collectively underscore the model's efficacy in handling the binary classification task with high accuracy and precision.

VII. CONCLUSION

In this study, we explored a comprehensive approach to classify malaria disease cells using a combination of machine learning (ML) and deep learning (DL) models. Our investigation encompassed custom convolutional neural networks (CNNs), classical ML algorithms like Random Forests (RF), as well as fine-tuned pre-trained DL models and transfer learning such as ResNet50 and MobileNet.
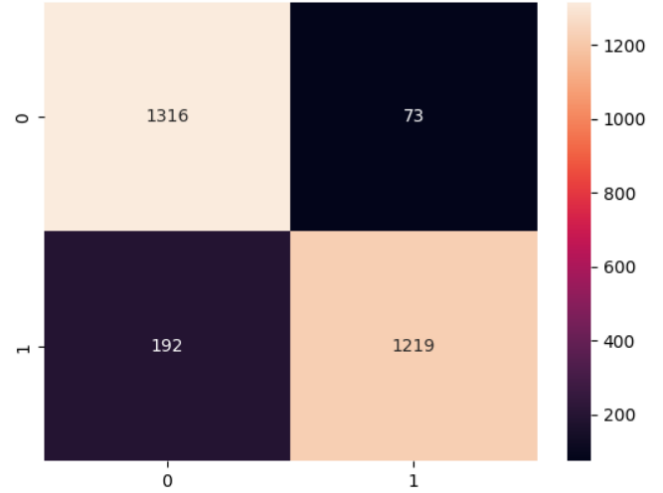
Through rigorous experimentation and evaluation, we demonstrated the efficacy of these models in accurately distinguishing between uninfected and parasitized cells in microscopic images. Our results underscored the versatility and robustness of DL models, particularly when fine-tuned for specific classification tasks. Additionally, classical ML algorithms proved to be valuable tools, especially when combined with appropriate feature engineering techniques.

Furthermore, the integration of custom CNNs and fine-tuned pre-trained models showcased the potential for developing advanced diagnostic tools for malaria. By leveraging the strengths of various ML and DL techniques, we aimed to contribute to the advancement of automated malaria diagnosis, facilitating faster and more accurate detection of the disease.

Overall, this study highlights the importance of interdisciplinary approaches in medical diagnostics, where innovative machine learning techniques can play a crucial role in combating infectious diseases like malaria. Our findings pave the way for future research and development efforts aimed at improving healthcare outcomes through the application of cutting-edge technologies.

References are important to the reader; therefore, each citation must be complete and correct. If at all possible, references should be commonly available publications.