

CLASSIFICATION OF MALARIA DISEASES USING CONVOLUTIONAL NEURAL NETWORK

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ABSTRACT :

The goal of this project is to develop a system for the accurate classification of malaria diseases using Convolutional Neural Networks (CNNs) and VGG models. Malaria is a life-threatening disease caused by parasites transmitted to humans through the bites of infected mosquitoes. Early detection and accurate diagnosis are critical in the treatment of the disease. To achieve this goal, we propose the use of image-based diagnosis using CNNs and VGG models. These models have proven to be highly effective in image recognition and classification tasks. We will use a large dataset of malaria images to train our models, and evaluate their performance using various metrics such as accuracy, precision, recall, and F1 score. The proposed system will have several benefits, including improved accuracy and efficiency in malaria diagnosis, reduced workload for medical professionals, and increased access to reliable diagnosis in lowresource settings. The system can also be extended to other medical imaging applications, and can serve as a basis for further research in the field of deep learning for medical diagnosis. Overall, the successful implementation of this project will contribute significantly to the fight against malaria, which remains a major global health challenge.

Keywords : VGG(Visual Geometry Group), CNN(Convolutional Neural Network), LSTM(Long short-term memory), Deep Learning.

I INTRODUCTION

Malaria, a life-threatening disease caused by Plasmodium parasites transmitted through the bites of infected mosquitoes, remains a persistent global health challenge, particularly in regions with limited access to healthcare resources. With an estimated 229 million cases and over 400,000 deaths reported annually, malaria disproportionately affects vulnerable populations, including children under five and pregnant women. Despite concerted efforts to control and eliminate the disease, significant barriers to effective diagnosis persist, hindering timely treatment and prevention efforts. Conventional diagnostic methods for malaria, such as microscopy of blood smear samples, require skilled personnel and specialized equipment, often unavailable in remote or resource-constrained areas. Furthermore, manual microscopy is labor-intensive, time-consuming, and prone to human error, leading to diagnostic inaccuracies and delays in patient care. As a result, many individuals at risk of malaria do not receive prompt and accurate diagnoses, exacerbating

the burden of the disease and impeding progress towards its control and eradication. In recent years, advances in artificial intelligence and machine learning, particularly deep learning techniques, have revolutionized various fields, including medical imaging and diagnostics. Deep learning algorithms, particularly convolutional neural networks (CNNs), have demonstrated remarkable capabilities in image classification tasks, outperforming traditional methods in accuracy and efficiency. Leveraging these advancements, there is a growing interest in developing automated diagnostic tools for malaria that can overcome the limitations of conventional microscopy and improve access to timely and accurate diagnosis, especially in resource-constrained settings. This work seeks to address the challenges associated with malaria diagnosis by harnessing the power of deep learning approaches to automate the classification of malaria-infected red blood cells from those that are uninfected. By developing a robust and reliable classification model capable of accurately identifying malaria parasites in blood smear images, we aim to enhance the accessibility and effectiveness of malaria diagnosis, particularly in underserved

communities where the disease burden is most profound. Through this endeavor, we aspire to contribute to the global efforts to combat malaria and improve health outcomes for affected populations.

II. LITERATURE SURVEY

1. Detection of Malaria Disease Using Image Processing and Machine Learning.

Author: Md. Maruf Hasan, Sabiha Islam, Ashim Dey, Annesha Das Year:2022.

In this study, the researchers aimed to develop a computer-aided method for the automatic detection of malaria parasites using image processing and machine learning algorithms. They utilized a dataset comprising 27,558 cell images, encompassing both uninfected and parasitized blood cells. Handcrafted features were extracted from red blood cell images, and six machine learning models—Ad boost, K-Nearest Neighbor, Decision Tree, Random Forest, Support Vector Machine, and Multinomial Naive Bayes—were implemented to classify the cells. We consider the problem of planning the ISS cosmonaut training with different objectives. A pre-defined set of minimum qualification

levels should be distributed between the crew members with minimum training time differences, training expenses or a maximum of the training level with a limitation of the budget. First, a description of the cosmonaut training process is given. Then four models are considered for the volume planning problem. The objective of the first model is to minimize the differences between the total time of the preparation of all crew members, the objective of the second one is to minimize the training expenses with a limitation of the training level, and the objective of the third one is to maximize the training level with a limited budget. The fourth model considers the problem as an n -partition problem. Then two models are considered for the calendar planning problem. For the volume planning problem, two algorithms are presented. The first one is a heuristic with a complexity of (n) operations.

2) Malaria Parasite Classification Using Machine Learning Techniques.

Author: S. Regina Lourdhu Sugnathi¹ , B. Janani² Year: 2021.

The study focuses on binary classification using machine learning algorithms such as Convolutional Neural Network (CNN),

Support Vector Machines (SVM), Random Forest (RF), Decision Tree (DT), and ensemble techniques. These algorithms are trained on a dataset containing images of infected blood cells to predict the Plasmodium species with high accuracy. Comparative analysis is conducted to determine the model with the highest accuracy.

3. Machine Learning Strategies for Malaria Risk Prediction based on Text-based Clinical Information.

Author: PRABHAT SAHU, Pragati Priyadarshini, Tripathy, Yasaswi Das, Suvendu Pradhan Year: 2023.

This research proposes a malaria risk prediction model based on machine learning techniques utilizing clinical data from malaria-endemic regions. The dataset includes demographic information, clinical symptoms, laboratory test results, and treatment history. Five machine learning classification models, namely logistic regression, GaussianNB, decision tree, extra tree, and random forest, are employed to build and evaluate prediction models. Feature selection approaches are utilized to identify relevant characteristics for malaria risk prediction.

4. Automatic identification of malaria and other red blood cell inclusions using convolutional neural networks.

Author: Angel Molina a, José Rodellar b, Laura Boldú a, Andrea Acevedo a b, Santiago Alférez c, Anna Merino a Year: 2021.

The study utilized digital images of 53 peripheral blood smears, from which 6415 images of red blood cells were segmented using thresholding and watershed transformation techniques. These images were then used to train a VGG-16 architecture using transfer learning. An independent test set of 23 smears was used to evaluate the model's performance in classifying malaria parasites and other red blood cell inclusions.

III SYSTEM ANALYSIS

EXISTING SYSTEM

For the detection of malaria-infected red blood cells, they integrated a Convolutional Long Short-Term Memory as well as Convolutional Bidirectional Long Short-Term Memory architecture in this system. Although the model's performance during testing was inadequate, it was accurate throughout training.

Limitations of Existing system

- Potential over fitting due to the model's inadequate performance during testing despite accurate training.
- Increased computational complexity and resource requirements associated with integrating ConvLSTM and ConvBiLSTM architectures.
- Reduced interpretability of model decisions due to the complex dynamics of recurrent and bidirectional layers in ConvLSTM and ConvBiLSTM

PROPOSED SYSTEM

In the suggested model, VGG19 is used to identify red blood cells that have been infected with malaria. Advanced CNN VGG19 has layers that have already been trained and has a strong comprehension of the characteristics of a picture in terms of shape, color, and structure. The extremely deep VGG19 has been trained on a massive amount of different images for challenging classification tasks.

Proposed system Advantages:

- Leveraging VGG19's pre-trained layers exploits its comprehensive

understanding of image characteristics, facilitating effective capture of complex features relevant to malaria-infected red blood cells.

- VGG19's extensive training on diverse datasets ensures it learns intricate patterns and variations across different image types, enhancing its robustness and adaptability in recognizing malaria-infected red blood cells among challenging classification tasks.
- The deep architecture of VGG19 enables hierarchical feature extraction, extracting both low-level and high-level features crucial for accurate classification, thereby enhancing its discriminative power in identifying malaria-infected red blood cells.

IV IMPLEMENTATION

Architecture:

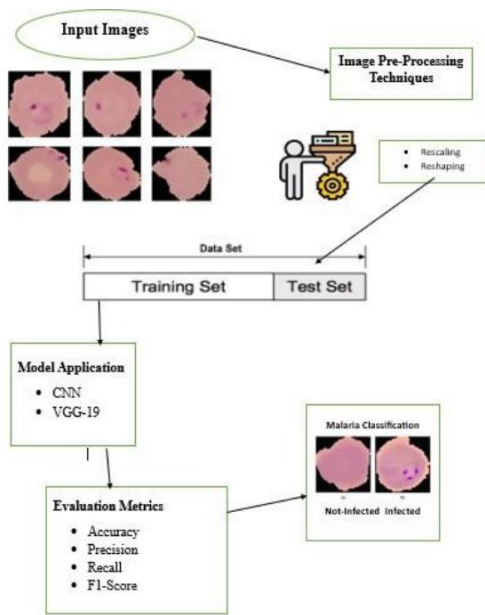


Fig-1. Architectures of the system model

1. Data Collection and Preprocessing:

- Acquire a comprehensive dataset of red blood cell images, including both parasitized (infected) and uninfected cells. Publicly available datasets such as the Malaria Cell Images Dataset can be used.

- Preprocess the images to ensure uniformity and enhance model performance. This may involve resizing the images, normalization, and augmentation techniques to increase the diversity of the dataset and prevent over fitting.

2. Model Selection and Architecture Design:

- Choose an appropriate deep learning architecture for the task. In this case, a Convolutional-Recurrent Neural Network (CRNN) based on the VGG19 architecture is proposed.

- VGG19 is a convolutional neural network known for its simplicity and effectiveness. The addition of recurrent layers allows the model to capture temporal dependencies in the image data.

3. Model Training:

- Split the dataset into training, validation, and testing sets. Typically, an 80-10-10 splits used.

- Initialize the VGG19 model with pre-trained weights on a large dataset (e.g., Image Net) to leverage learned features.

- Fine-tune the model on the malaria-infected red blood cell dataset using transfer learning. Freeze the convolutional layers and train only the recurrent layers along with the classifier.

- Utilize appropriate optimization techniques such as stochastic gradient descent (SGD) or Adam optimizer with a suitable learning rate schedule.

- Monitor the model's performance on the validation set to prevent over fitting, adjusting hyper parameters as necessary

4. Model Evaluation:

- Evaluate the trained model on the independent testing set to assess its performance accurately.
- Calculate metrics such as accuracy, precision, recall, F1-score, and ROC-AUC to quantify the model's performance in detecting malaria-infected red blood cells.
- Visualize the model's predictions and compare them with ground truth labels to identify any areas of improvement or potential biases.

5. Model Optimization and Fine-Tuning:

- Fine-tune the model architecture and hyper parameters based on the evaluation results to improve performance further.
- Experiment with different recurrent architectures, regularization techniques, and optimization algorithms to optimize the model's performance.
- Consider ensemble methods or model stacking to combine multiple models for improved accuracy and robustness.

6. Deployment and Future Work:

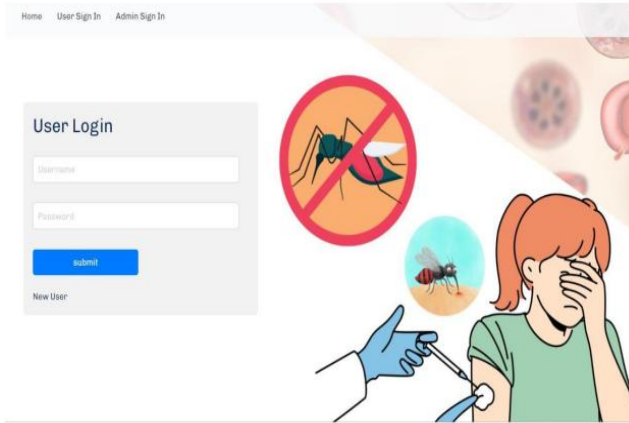
- Once satisfied with the model's performance, deploy it for real-world applications, possibly in collaboration with healthcare professionals.
- Monitor the model's performance in the field and gather feedback for iterative improvements.

V RESULT AND DISCUSSION

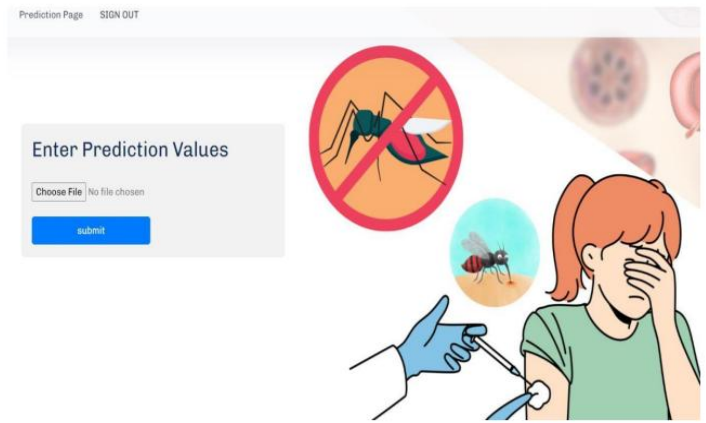
Home page:



Login page:



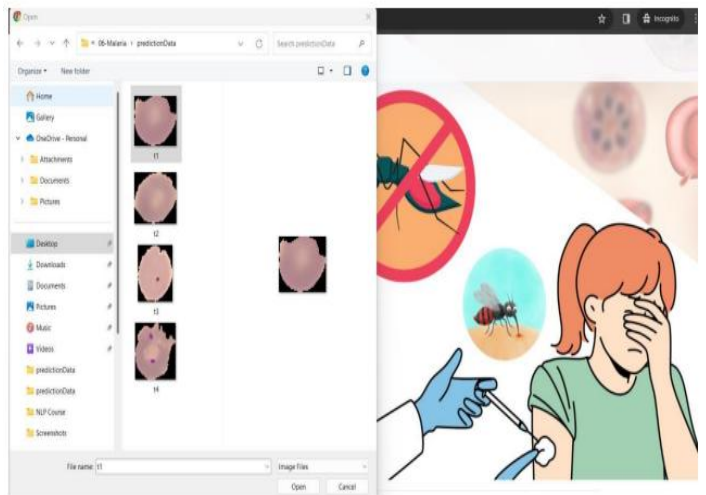
Prediction page:



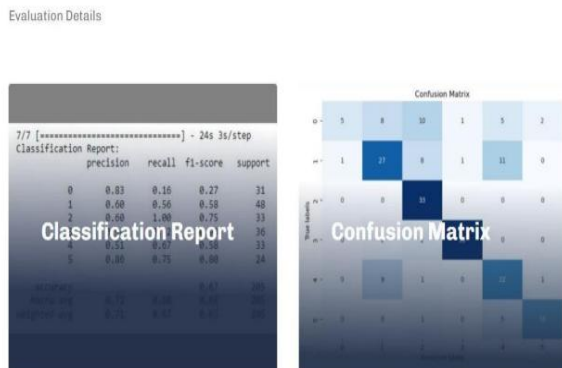
Load image:



Model performance:



Output results:



Input data:

VI CONCLUSION

In conclusion, this study demonstrates the potential of deep learning techniques, specifically advanced Convolutional Neural Networks (CNNs) AS 96% and VGG19 as 93%, in effectively classifying malaria-infected red blood cells from uninfected ones. Malaria, a disease caused by the Plasmodium parasite transmitted through mosquito bites, remains a significant global health concern, necessitating accurate and timely diagnosis for effective management. Traditionally, the detection of malaria-infected red blood cells relies on microbiological analysis through microscopy, followed by manual interpretation by specialists. However, this process can be labor-intensive and subject to interpretation biases. By leveraging deep learning approaches in the computer vision domain, this study proposes a framework that automates the detection process, offering the potential for improved efficiency and accuracy. The utilization of a publicly available dataset containing parasitized and uninfected red blood cell images facilitates the training and testing of the proposed model. The results of this work indicate that the developed method outperforms traditional microscopy-based

approaches in the detection of malaria-infected red blood cells. This suggests that deep learning-based systems have the potential to revolutionize malaria diagnosis by offering a faster, more objective, and scalable solution.

FUTURE ENHANCEMENT

- **Data Augmentation Techniques:** Integrating advanced data augmentation techniques can help improve the robustness and generalization capabilities of the CNN model. Techniques such as rotation, translation, scaling, flipping, and adding noise to the images can help the model learn more diverse features and reduce over fitting.
- **Transfer Learning:** Leveraging transfer learning from pre-trained models can be beneficial, especially if there's a scarcity of labeled data for malaria classification. Fine-tuning pre-trained VGG models on malaria datasets can expedite the training process and potentially enhance the model's performance.
- **Architectural Modifications:** Exploring modifications to the VGG architecture or using more advanced CNN architectures can be fruitful. Architectures like ResNet, Inception, or Efficient Net have demonstrated superior performance in various image classification tasks and may

offer better results compared to the original VGG architecture.

- **Ensemble Methods:** Combining predictions from multiple CNN models using ensemble methods such as averaging or stacking can often lead to improved performance compared to individual models. Building an ensemble of VGG-based models or combining VGG with other architectures can potentially enhance classification accuracy.

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