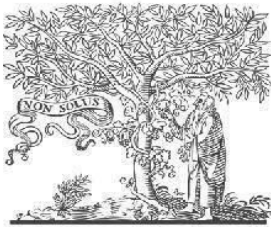


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MALARIA DISEASES USING CONVOLUTIONAL NEURAL NETWORK

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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 low resource 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: Convolutional Neural Networks (CNNs), VGG, Deep learning algorithms,

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. RELATED WORK

Detection of Malaria Disease Using Image Processing and Machine Learning

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

Introduction: Malaria remains a significant global health challenge, causing millions of deaths annually. Traditional laboratory diagnosis methods involve examining blood smears under a microscope, a process prone to errors and subjectivity. To address these challenges, researchers are increasingly turning to computer-aided methods leveraging image processing and machine learning techniques for automated malaria detection.

Methodology: 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—Adaboost, K-Nearest Neighbor, Decision Tree, Random Forest, Support Vector Machine, and Multinomial Naive Bayes—were implemented to classify the cells.

Malaria Parasite Classification Using Machine Learning Techniques

Author: S. Regina Lourdhu Sugnathi¹, B. Janani²

Introduction: Malaria, a disease caused by protozoan parasites transmitted through mosquito bites, poses a significant global health threat. Manual microscopic examination and Rapid Diagnostic Tests are common detection techniques but are prone to human errors. Early detection is crucial in reducing fatality rates, and identifying the type of Plasmodium species can aid in vaccine development. This research aims to use machine learning models to classify Plasmodium species accurately, improving detection efficiency.

Methodology: 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.

Findings: The results indicate that machine learning algorithms, particularly the Convolutional Neural Network (CNN), are effective in classifying Plasmodium species. CNN outperforms other models, demonstrating the highest accuracy in species classification. The automatic learning of features by CNN surpasses feature extraction methods, contributing to its superior performance.

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

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

Introduction: Malaria, a life-threatening disease transmitted through mosquito bites, poses a significant global health challenge, particularly impacting vulnerable populations such as infants, children, and pregnant women. Despite efforts to control malaria, the 2020 World Malaria Report indicated a concerning increase in cases and deaths compared to the previous year, highlighting the urgency of effective management strategies. Traditional diagnostic methods are often time-consuming and require trained personnel, underscoring the need for innovative approaches to improve early detection and treatment. Machine learning techniques offer a promising solution by leveraging clinical information to predict and classify malaria risk.

Methodology: 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

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

Alferez c, Anna Merino a

Introduction: Malaria remains a significant global health challenge, responsible for thousands of deaths annually. While machine learning techniques have been utilized for malaria diagnosis, existing approaches have not addressed the presence of other elements that may interfere with accurate recognition of malaria. In this study, the authors propose a novel deep learning model using convolutional neural networks (CNNs) capable of differentiating malaria-infected red blood cells from normal erythrocytes as well as erythrocytes with other types of inclusions.

Methodology: 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. METHODOLOGY

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 overfitting.

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 split is used. Initialize the VGG19 model with pre-trained weights on a large dataset (e.g., ImageNet) 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 overfitting, adjusting hyperparameters 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 hyperparameters 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.

Explore additional avenues for research, such as incorporating domain-specific knowledge or integrating with other diagnostic tools to enhance malaria diagnosis further.

IV. ALGORITHMS

Convolutional Neural Networks:

Convolutional Neural Networks (CNNs) stand as a groundbreaking class of deep learning neural networks, particularly revolutionizing the field of image recognition. Widely employed in tasks such as image classification, CNNs operate subtly in the background, powering applications ranging from Facebook's photo tagging to the intricate algorithms of self-driving cars. Their versatility extends across diverse domains, from healthcare to security, showcasing their speed and efficiency.

The architecture of a classic CNN involves a sequence of operations: Input -> Convolution -> ReLU -> Convolution -> ReLU -> Pooling -> ReLU -> Convolution -> ReLU -> Pooling -> Fully Connected

CNNs uniquely convolve learned features with input data, particularly excelling in processing 2D images. Unlike many other image classification algorithms, CNNs require minimal preprocessing, allowing them to learn filters autonomously rather than relying on handcrafted ones.

Inspired by biological processes and rooted in the research of Hubel and Wiesel from the 1960s, CNNs mimic the organization of the visual cortex in mammals. They function with input, output, and hidden layers, which typically include convolutional layers, ReLU layers, pooling layers, and fully connected layers.

In essence:

- ❖ Convolutional layers apply a convolution operation to the input, passing information to the next layer.

- ❖ Pooling combines the outputs of neuron clusters into a single neuron in the subsequent layer.
- ❖ Fully connected layers link every neuron in one layer to every neuron in the next, forming a comprehensive network.

CNNs excel in feature extraction from images, eliminating the need for manual feature extraction. The features are learned during the network's training on image sets. This intrinsic learning process makes CNNs highly accurate for computer vision tasks, as they progress through tens or hundreds of hidden layers, increasing the complexity of learned features.

Decoding the Layers of Convolutional Neural Networks (CNN)

Convolutional Layer: Unveiling Essential Features

At the core of a CNN lies the pivotal convolutional layer, meticulously crafted to unearth intricate features from input images. Executing the convolution operation with the aid of a feature detector and map, this layer delicately applies a filter pixel by pixel through matrix multiplication. This strategic approach mirrors human perception, where recognition involves identifying features like hats, dresses, or tattoos rather than scrutinizing each pixel. By enabling the model to spotlight critical features, the convolutional layer kickstarts the image detection journey.

ReLU Layer: Elevating Non-Linearity

Infusing non-linearity into the network, the Rectified Linear Unit (ReLU) layer emerges as a crucial enhancement to the convolution layer. By applying an activation function to feature maps, ReLU enriches the model's

capacity to grasp the intrinsic non-linear essence of images. The expulsion of negative values and the introduction of non-linear elements, exemplified by ReLU, empower the network to learn real-world data more adeptly. This amplifies training speed without compromising the accuracy of generalization.

Pooling: Embracing Spatial Diversity

A pivotal phase, pooling ensures the network avoids fixating on specific features in exact locations, shades, or orientations. Instead, it embraces spatial diversity and flexibility, empowering the CNN to identify objects across diverse conditions. The progressive reduction in input representation size achieved by pooling facilitates object detection, irrespective of factors like location, size, or orientation. Furthermore, pooling contributes to overfitting control by minimizing required parameters and computational load, ensuring the network's adaptability.

Flattening: Streamlining for Advanced Processing

The straightforward yet indispensable flattening process transforms the pooled feature map into a sequential column of numbers, constructing an extended vector. This sequential representation assumes the role of the input layer for an artificial neural network, laying the foundation for subsequent processing stages.

Fully Connected Layer: Harmonizing Features for Precision

Introducing an artificial neural network into the CNN framework, the fully connected layer harmonizes features into enriched attributes, elevating class predictions. This stage involves meticulous error calculation,

backpropagation, and fine-tuning of weights and feature detectors to optimize overall model performance. The iterative refinement process empowers the network to continually train on data, enhancing its predictive capabilities. The fully connected layer stands as a pivotal orchestrator, amalgamating features and attributes to yield more accurate class predictions, signifying the zenith of the intricate architecture embedded within the CNN.

VGG19

VGG19 is a specific variant of the VGG (Visual Geometry Group) network architecture. It was introduced as part of the VGG project by the Visual Geometry Group at the University of Oxford. VGG19 is renowned for its deep structure and its effectiveness in image classification tasks.

The "19" in VGG19 refers to the total number of layers in the network, including convolutional layers, pooling layers, and fully connected layers. Specifically, VGG19 consists of 16 convolutional layers and 3 fully connected layers. Here's a breakdown of the key components of the VGG19 architecture:

1.Input Layer: Accepts input images of a fixed size, typically 224x224 pixels.

2.Convolutional Layers: VGG19 consists of 16 convolutional layers, each followed by a rectified linear unit (ReLU) activation function. These convolutional layers use small 3x3 filters with a stride of 1 and same padding, allowing the network to learn rich feature representations at different spatial scales.

3.Pooling Layers: After every two convolutional layers, VGG19 includes maxpooling layers with a 2x2 filter size and

a stride of 2. These pooling layers help reduce the spatial dimensions of the feature maps while retaining the most salient features.

4.Fully Connected Layers: The final layers of VGG19 consist of three fully connected layers, which take the flattened feature maps from the last convolutional layer as input. The fully connected layers progressively reduce the dimensionality of the feature representations, culminating in an output layer with softmax activation for classification.

5.Output Layer: The output layer of VGG19 produces a probability distribution over the classes in the dataset, typically using softmax activation for multi-class classification tasks.

One notable aspect of VGG19 is its uniform architecture, where all convolutional layers have the same filter size (3x3) and same padding, and all pooling layers have the same filter size (2x2) and stride. This simplicity contributes to its ease of understanding and implementation.

While VGG19 achieved remarkable performance on benchmark datasets like ImageNet, its main drawbacks include its large number of parameters, which can make training and inference computationally expensive. Nevertheless, VGG19 remains a significant milestone in the development of deep learning architectures and continues to be used as a baseline for comparison in various computer vision tasks.

V.RESULTS AND DISCUSSION

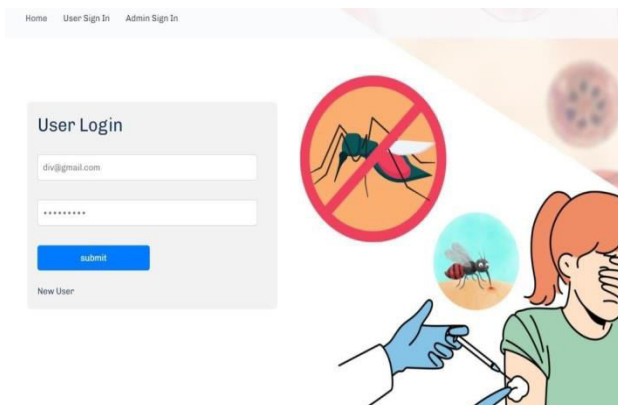


Fig 1,User Login

Data Preprocessing

In this project we are using Image Preprocessing by using Computer Vision.

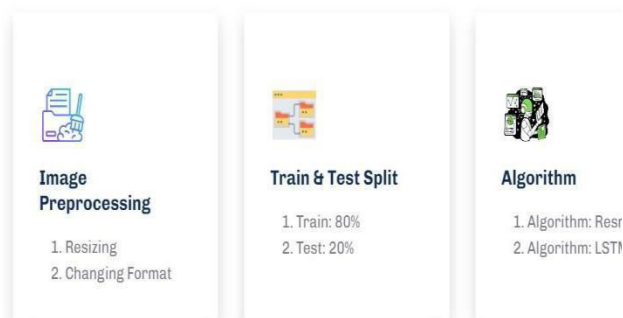


Fig 2,Data Processing

Model Performance

Evaluation Details



Fig 3,Model performance



Fig 4,Prediction Values

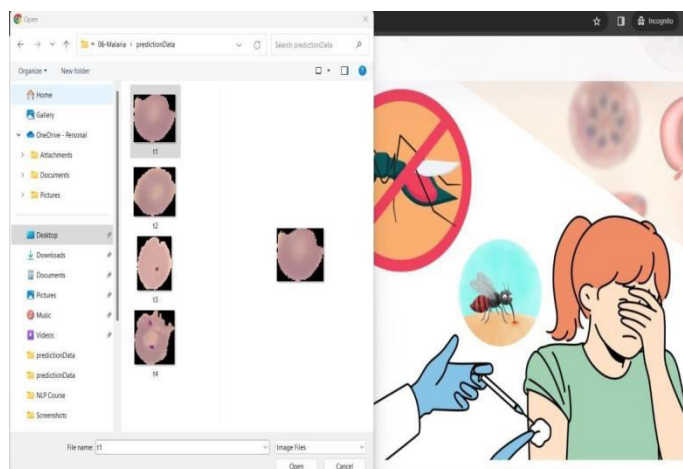


Fig 5,Prediction Data



Fig 6,Model Prediction Page

II. 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 ENHANCEMENTS:

Exploring modifications to the VGG architecture or using more advanced CNN architectures can be fruitful. Architectures like ResNet, Inception, or EfficientNet 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.

REFERENCES

- [1]Yuhang Dong¹, Zhuocheng Jiang¹, Hongda Shen¹, W. David Pan¹ Lance A. Williams², Vishnu V. B. Reddy², William H. Benjamin, Jr.², Allen W. Bryan, Jr.
- “Evaluations of Deep Convolutional Neural Networks for Automatic Identification of Malaria Infected Cells”, 2017
- [2]Zhaohui Liang, ¹ Andrew Powell,² Ilker Ersoy,³ Mahdieh Poostchi,⁴ Kamolrat Silamut,⁵ Kannappan Palaniappan,⁴ Peng Guo,⁶ Md Amir Hossain,⁷ Antani Sameer,⁸
- Richard James Maude,⁵ Jimmy Xiangji Huang, ¹ Stefan Jaeger,^{8*} George Thoma⁸ “CNNBased Image Analysis for Malaria Diagnosis”, IEEE International Conference on
- Bioinformatics and Biomedicine (BIBM), 2016

[3]Alif Bin Abdul Qayyum*, Tanveerul Islam and Md. Aynal Haque “Malaria Diagnosis with Dilated Convolutional Neural Network Based Image Analysis”, IEEE International Conference on Biomedical Engineering, Computer and Information Technology for Health

(BECITHCON), 2019

[4]Gautham Shekar, S. Revathy, Ediga Karthick Goud “Malaria Detection using Deep

Learning”, International Conference on Trends in Electronics and Informatics (ICOEI 2020), 2020

[5]Adedeji Olugboja, Zenghui Wang “MALARIA PARASITE DETECTION USING

DIFFERENT MACHINE LEARNING CLASSIFIER,International Conference on

Machine Learning and Cybernetics,2017

[6]] Satabdi Nayak, Sanidhya Kumar, Mahesh Jangid “Malaria Detection Using Multiple

Deep Learning Approaches”, International Conference on Intelligent Communication and Computational Techniques (ICCT) , 2019

[7]Roy, K., Sharmin, S. Mukta, R. B. M., & Sen, A. (2018). Detection of malaria parasite in giemsa blood sample using image processing. Int J ComputSciInfTechnol, 10, 55-65.

[8]Purwar, Y., Shah, S. L., Clarke, G., Almugairi, A., &Muehlenbachs, A. (2011). Automated and unsupervised detection of malarial parasites in microscopic images. Malaria journal, 10(1), 1-11[16] K. Kourtit, M. M. M. Pele, P. Nijkamp, and D. T. Pele, “Safe

citiesin the new urban world: A comparative cluster dynamics analysis through machine learning,” Sustain. Cities Soc., vol. 66, Mar. 2021,Art. no. 102665.