AI DRIVEN BLOOD CELL ANALYSIS FOR MALARIA ANDBLOOD CANCER SCREENING

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Abstract - Malaria and blood Cancer is one of the deadliest diseases cross the globe. This is caused by the bite of female Anopheles mosquito that transmits the Plasmodium parasites. Some current malaria detection techniques include manual microscopic examination and RDT. These approaches are vulnerable to human mistakes. Early detection of malaria can help in reducing the death rates across the globe.Deep Learning can emerge as a highly beneficial solution in the diagnosis of disease. This model gives a faster and cheaper method for detecting plasmodium parasites. It Was Designed to Identify Malaria Parasites and Cancerous Cell Presence in Blood Using Images of Blood Samples which got Tested with Giemsa-stain. Convolutional neural networks (CNNs) are then trained on these extracted features to accurately classify blood cell images into disease positive or disease-negative categories. The CNN detects malaria parasites in microscopic images by classifying them into parasitized and healthy cells, enabling the detection of malaria parasites. The proposed model consists of three convolutional layers and fully connected layers each. The neural network presented is a cascade of several convolutional layers having multiple filters present in layers, which yields the exceptionally good accuracy as per the available resources. The experiment results demonstrate a significant improvement in malaria parasite and blood cancer recognition. Compared to traditional manual microscopy, the proposed system is more accurate and faster. Finally, this study demonstrates the need to provide robust and efficient solutions by leveraging state-of-the-art technologies to combat malaria and blood cancer.

Keywords : Deep Learning, CNN, Image analysis , InceptionresnetV2

1.INTRODUCTION

Malaria a mosquito-borne infectious disease caused by Plasmodium parasites, and cancer a complex group of diseases characterized by abnormal cell growth. Malaria and blood cancer, two globally prevalent diseases, pose significant challenges to healthcare systems worldwide due to their complex diagnostic requirements and potential life-threatening consequences if left undetected. However, the advent of AIdriven blood cell classification techniques offers a promising solution to these challenges by leveraging advanced algorithms to automate and enhance the diagnostic process. For malaria screening these featuresmay include the identification of Plasmodium parasites byanalyzing the pigmentations. while for cancer screening, features such as irregular cell shapes and sizes are crucial. In pathology labs, the blood samples are collected and the diagnosis of malaria infection is done by identifying the parasites in blood slides through a microscope by the experts. A chemical process is used in the detection of malaria parasites called Giemsa staining. In this process, the parasite in the blood sample is recognized and detected. In staining, the red blood cells (RBC)and Plasmodium parasites are colored. In the detection of plasmodium parasites, stained objects are required. To avoid false results, these stained objects are analyzed further to determine whether they are parasitized or healthy. As per the WHO protocol, there are various techniques used in the detection of malaria that involve an intensive examination. In manual testing, the clinician needs to observe 5000 cells at 100X magnification and exhausting. To make the diagnosis faster polymerase chain reaction (PCR) and rapid diagnostic test (RDT) came into consideration. These analyses are fast but less accurate. Detection of parasites from Giemsa blood samples needs trained and experienced technicians. By digitizing the process, the time consumed for screening reduces. Thishelps in improving the consistency in diagnosis.

2.BODY OF THE PAPER

2.1 LITERATURE REVIEW

Leukocytes, produced in the bone , make percent of all blood cells. Uncontrolled growth of these white blood cells leads to the birth of blood cancer. Out of the three different types of cancers, the proposed study provides a robust mechanism for the classification of Acute Lymphoblastic Leukemia and Multiple Myeloma using the SN-AM dataset. Acute lymphoblastic leukemia (ALL) is a type of cancer where the bone marrow forms too many lymphocytes. On the other hand, Multiple myeloma (MM), a different kind of cancer, causes cancer cells to accumulate in the bone marrow rather than releasing them into the bloodstream. Therefore, they crowd out and prevent the production of healthy blood cells. Conventionally, the process was carried out manually by a skilled professional in a considerable amount of time. The proposed model eradicates the probability of errors in the manual process by employing deep learning techniques, namely convolutional neural networks. The model, trained on cells' images, first pre-processes the images and extracts the best features. This is followed by training the model with the optimized Dense Convolutional neural network framework (termed DCNN here) and finally predicting the type of cancer present in the cells. The model was able to reproduce all the measurement correctly while it recollected the samples exactly 94 times out of 100. The overall accuracy was recorded to be 97.2%, which is better than the conventional machine learning methods like Support Vector Machine 7(SVMs), Decision Trees, Random Forests, Naive Bayes, etc.

Blood cancer (Leukemia) is one of the leading causes of death among humans. The pace of healing depends mainly on Carly detection and diagnosis of a disease. The main reason behind occurrence of Leukemia is when bone marrow produces a lot of abnormal white blood cells this happens. Microscopic study on images. is done by Hematologists who make of human blood samples, from which it leads to the requirement of following methods, which are microscopic color imaging, image segmentation, clustering and classification which allows easy identification of patients suffering from this disease. Microscopic imaging allows for various methods of detecting blood cancer in visible and immature white blood cells. Identifying Leukemia early and quickly greatly helps practitioners in providing appropriate treatment to patients. Initially to start with, Segmentation stage is achieved by segregating white blood cells from other blood components i.c. erythrocytes and platelets by using Statistical parameters such as mean, standard deviation. For diagnosing prediction of Leukemia geometrical features such as area, perimeter of the white blood cell nucleus's investigated. In the proposed methodology we make use of K-means, for identifying cancerous wingsand its early detection. Experimentation and results were found to he promising with the accuracy of 90% identification of the cancer cells.

Malaria is one of the deadliest disease across the globe. This is caused by the bite of female Anopheles mosquito that transmits the Plasmodium parasites. Some current malaria detection techniques include manual microscopic examination and RDT. These approaches are vulnerable to human mistakes. Early detection of malaria can help in reducing the death rates across the globe. Deep Learning can emerge as a highly beneficial solution in the diagnosis of disease. This model gives a faster an cheaper method for detecting plasmodium parasites. The custom convolutional neural network is primarily designed to distinguish between healthy and infected blood samples. The proposed model consists of three convolutional layers and fully connected layers each. The neural network presented is a cascade of several convolutional layers having multiple filters present in layers, which yields the exceptionally good accuracy as per the available resources. The model is trained and later several blood sample images are fed to test the accuracy of the designed system. The CNN classifier has performed exceptionally well under limited computational resources giving an accuracy of 95%. Blood smear sample analysis can also aid in the detection of certain other illneses and the application of deep learning models will help in the greater good of humankind

Plasmodium parasite is identified as amenable for spreading a disease named Malaria. Under the stodgy method, the blood splotch is first smeared on the slidescrutinized under the microscope, and parasites (which can cause malaria) in blood cells are detected. For beneficial parasite detection, image processing proves to be very much dominant. The reason for this is accuracy in the results. This research presents 9Malaria detection in blood smear images using supervised learning methods. This proposed method starts with the preprocessing in which images are resized and converted into grayscale. The thresholding technique is implemented to identify blobs for segmentation. For feature extraction, GoogLe Net is maneuvered, and the results of the classification show that this method has an accuracy of 95.8% for detecting malaria in blood smear image.

2.2 METHODOLOGY

The architecture for AI Driven blood cell analysis for malaria and blood cancer using deep learning typically involves a combination of convolutional neural networks (CNNs) and other deep learning techniques. Here is a high-level overview of the steps involved, Data Collection and Preprocessing: Blood samples are collected and processed to obtain high-resolution images of blood cells. Preprocessing techniques are applied to enhance the quality of the images and remove any noise or artifacts. Convolutional Neural Network (CNN) Architecture: Deep learning models, such as CNNs, are commonly used for image analysis tasks. The CNN architecture consists of multiple layers, including convolutional layers, pooling layers, and fully connected layers, to extract features from the blood cell images. Training and Validation: The CNN model is trained on a large dataset of labeled blood cell images to learn the patterns associated with malaria and blood cancer. The model is validated on a separate dataset to ensure its accuracy and generalization to new data. Feature Extraction: The trained CNN model extracts important features from the blood cell images, such as cell morphology, texture, and color, that are indicative of malaria or blood cancer. Classification and Diagnosis: The extracted features are used to classify blood cells as normal or abnormal, indicating the presence of malaria or blood cancer. The AI system provides a diagnosis based on the classification results. Decision Support System: The AI system includes a decision support 1819 system that assists healthcare professionals in interpreting the results and making informed decisions about patient diagnosis and treatment. Integration with Healthcare Systems: The AI-driven blood cell analysis system is integrated with existing healthcare systems to facilitate seamless workflow and access to patient data. This integration ensures efficient screening and diagnosis of malaria and blood cancer. Overall, the system design and architecture for AI-driven blood cell analysis for malaria and blood cancer screening using deep learning involve data collection, preprocessing, CNN architecture, training and validation, feature extraction, classification, a decision support system, and integration with healthcare systems to provide accurate and timely results for patient screening and diagnosis.

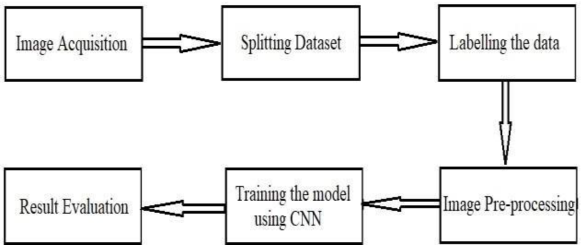


Fig 1 : Methodology

2.2.1 Data Acquisition:

The Blood cell images are acquired from Data Set Zip File from Open source National Library of Medicine , Kaggle.The dataset is used to train a model to classify blood cell images into categories such as and normal. Data can be sourced from medical imaging centers, hospitals, or public databases. These images are usually in DICOM (Digital Imaging and Communications in Medicine) format but might be converted to PNG or JPG for easier processing. Each image is labeled by medical professionals to indicate the type of cancer and malaria present or if the scan has healthy cells. Labels could be categorical (e.g., benign, malignant, none) or more detailed with specific types Carcinoma, Sarcoma, Leukemia, Lymphoma, Multiple Myeloma, Melanoma. The dataset might contain anywhere from 33808 images used in the project.

2.2.2 Preprocessing:

Raw blood cell images undergo preprocessing steps such as Segmentation, normalization, and resizing to ensure consistency and quality for subsequent analysis

2.2.3 Training Data:

Labeled datasets comprising blood cell images with corresponding annotations (e.g., healthy, malaria-infected, cancerous) are used to train the machine learning models
Training Dataset:
➢ Benign - 404 Images
➢ Cancer - 704 Images
➢ Early Maligant - 885 Images

2.2.4 Convolutional Neural Network (CNN) Architecture:

A Layers such as convolutional layers, pooling layers, and activation functions are used to extract relevant features from the input images, Also using algorithm InceptionResNetV2.

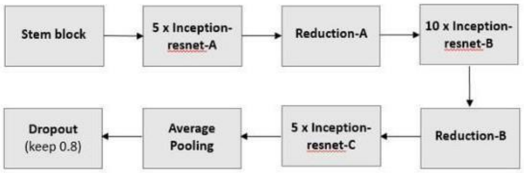


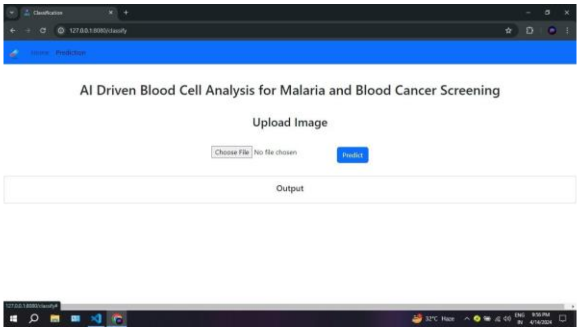
Fig 2 : InceptionResnetV2 Architecture

2.2.5 Validation:

The Trained Models undergoes rigorous Validation using Independent datasets toassess their performance metrics such as accuracy, sensitivity and specificity.

Testing Dataset
➢ Benign - 100 Images
➢ Cancer - 100 Images
➢ Early Maligant - 100 Images
➢ Parasitized - 1300 Images
➢ Pre Maligant - 100 Images
➢ Uninfected - 1300 Images
Total Training Images: 27808 Images
Total Testing Images: 3000 Images
Total validation Images: 3000 Images

2.2.6 Integration (Web Application):



AI Driven Blood Cell Analysis for Malaria and Blood Cancer Screening

Upload Image

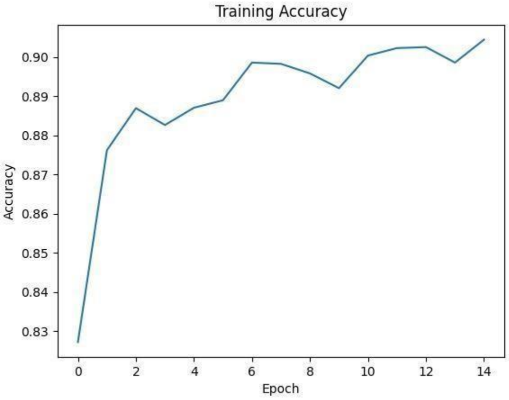
Output

Fig 3 : Web Application Interface

2.3 PERFORMANCE EVALUATION

EVALUATION METRICS:

The model was evaluated to generate different metrics using the test data by using a data generator to randomize the data, and the batch size taken was 100. The following metrics were obtained that are represented in table 1 given below, accuracy, recall, precision specificity. The saved model was used to evaluate the given metrics to create a scorecard where these metrics are shown for both training set and validation set.



Graph

METRIC TRAINING SCORE VALIDATION:

Training Accuracy: 90.45%
Testing Accuracy: 92.37%
Overall Accuracy: 91.41%
Precision: 0.92
Recall: 0.88
F1-score:0.90

3. CONCLUSION

The primary goal of this research focuses on development of automated medical imaging segmentation i.e. quick detection of Malaria and blood cancer.In medical imaging assistive segmentation by lab-technician prove to be very time consuming and resource intensive which might not be available in remote regions. So, this task of advanced automation techniques for malaria and blood cancer detection can be proved to be very beneficial in a substantial amount of cases. In order to overcome this obstacle, the primary algorithm used in this system was InceptionResNet, which helped in outlining the image and it was very close to the ground truth and it also gave highly accurate predictions in images. Different methods of progressive and innovative malaria and blood cancer detection approaches are discussed in this article. As a result, the target area is segmented, and the presence of the malaria and blood cancer may be determined using the approach provided here, allowing clinicians to detect the diseases easily during the period. The advantages of this approach are that it enhances the level of image segmentation and its spatial localization, and hence it performs better in comparison to other systems. It is faster to train and requires less time to calculate than different networks with less number of parameters. Further studies will include enhancing accuracy with a low rate of errorby employing various classifier algorithms. Further, this can be modified to be used to predict the survivability of patients having malaria and blood cancer. Future work may include using larger and varied datasets which will help to test in real-life scenarios and medical trials.

REFERENCES

1. Deepika Kumar, Nikita Jain, Aayush Khurana, Sweta Mittal “Automatic Detection of White Blood Cancer from Bone Marrow Microscopic Images using CNN” 2023.
2. Ranjitha P, Sudharshan Duth P “Detection of Blood Cancer – Leukemiausing K –means Algorithm” 2021.
3. Divyansh Sah, Khushbu Kawale, Masumi Shah, Santhosh Randive, Rahul Mapari “Malaria Parasite Detection Using Deep Learning” 2021.
4. Ilsa Rameen, Ayesha Shahadat, Mehwish Mehreen, Saqlain Razzaq, Muhammad Adeel Asghar, MuhammadJamil Khan “Leveraging Supervised Machine Learning Techniques for Identification of Malaria Cells using Blood Smears” 2021.
5. David J Foran, Dorin Comaniciu, Peter Meer, and Lauri A Good well. Computerassisted discrimination among malignant lymphomas and leukemia using immunophenotyping, intelligent image repositories, and telemicroscopy. IEEE Transactions on Information Technology in Biomedicine, 4(4):265-273, 2000.
5. Neslihan Bayramoglu, Juho Kannala, and Janne Heikkilä. Human epithe- lial type 2 cell classification with convolutionalneural networks. In 2015 IEEE 15th International Conference on Bioinformatics and Bioengineer- ing (BIBE), pages 1-6. IEEE, 2015.
6. TTP Thanh, Caleb Vununu, Sukhrob Atoev, Suk-Hwan Lee, and Ki-Ryong Kwon. Leukemia blood cell image

classification using convolutional neu- ral network. International Journal of Computer Theory and Engineering, 10(2):54-58, 2018.

7. Tomasz Markiewicz, Stanislaw Osowski, Bonenza Marianska, and Leszek Moszczynski. Automatic recognition of the blood cells of myelogenous leukemiausing svm. In Proceedings. 2005 IEEE.