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MULTIPLE BLOOD CANCER PREDICTION FROM CELL IMAGES USING DEEP LEARNING TECHNIQUE

M. Nirmala[1]* and C. Karunya[2]

[1]Assistant Professor, Department of Computer Applications.

[2]Student, Department of Computer Applications.

[1,2]Hindusthan College of Engineering and Technology.

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***Corresponding Author**
M. Nirmala
Assistant Professor, Department of Computer Applications.

ABSTRACT

The traditional method of diagnosing blood problems relies on the physical acuity of the hematologist and is time-consuming, error-prone, and has limitations. To facilitate clinical decision-making, an automated optical image processing system is needed. The objective of deep learning blood cell classification is to build a machine learning system that can correctly classify different blood cell types from digital images of blood samples. The project makes use of deep learning techniques, which have been shown to outperform traditional machine learning algorithms in a wide range of computer vision applications. The project aims to improve the quality of blood cell images and build a deep learning model for categorizing blood cells using convolutional neural networks (CNN). It has been shown that the deep learning architecture CNN excels at categorization tasks involving images. Training a deep learning model: The project's objective is to train the CNN model using a big dataset of images of tagged blood cells. During training, the back propagation technique is utilized to modify the weights and biases of the network's neurons, enabling the model to correctly classify different types of blood cells. Evaluation of the deep learning model: The project's goal is to evaluate how well the trained CNN model performed on a different dataset of images of blood cells. F1-score, recall, accuracy, and precision are components of evaluation measures. The project's goal is to develop a method for classifying blood cells and make it accessible as a web or mobile application so that medical personnel may do so more accurately and efficiently. The major objective of the project is to develop a system that will

assist physicians in appropriately diagnosing and treating blood-related diseases. Deep learning is used to categorize blood cells.

1. INTRODUCTION

White blood cells (WBC) known as "blasts," which are immature and irregularly shaped, are produced abnormally during the course of leukemia, a type of malignancy. Leukemia is a condition that affects the bone marrow and blood and is related to white blood cells (WBC). Leukemia treatment and patient survival are greatly aided by an early, reliable, and safe diagnosis. Typically, a blood smear under a microscope is used to diagnose by examining the white blood cells. To identify various diseases, numerous machine learning methods have been created. The conventional approach to diagnosing blood issues is time-consuming, prone to error, and has certain limits because it depends on the hematologist's physical dexterity. An automated optical image processing system is necessary to assist clinical decision-making. In the course of leukemia, a kind of cancer, aberrant white blood cell (WBC) production results in "blasts," immature and atypically shaped white blood cells (WBC). White blood cells (WBC) are involved in the disorder known as leukemia, which can affect the bone marrow and/or blood. A quick, accurate, and secure diagnosis of leukemia is very helpful for both patient survival and therapy. White blood cells are typically examined on a blood smear under a microscope to get a diagnosis. Many machine learning techniques have been developed to detect different diseases.

Deep learning, which is currently all the rage, has established strong roots in numerous companies that are making investments in areas like artificial intelligence, big data, and analytics. Google, for instance, uses deep learning in its speech and picture recognition algorithms, whereas Netflix and Amazon use it to comprehend user behavior. Deep learning uses artificial neural networks, which are created to mimic how humans think and learn, whereas machine learning uses simpler principles. The biological neurons, which are only brain cells, make up a neural network. Deep learning models are quite useful in resolving the dimensionality issue since they are able to focus on the accurate features by themselves with just a little programming assistance. Particularly when there are many inputs and outputs, deep learning methods are used.

Similar to how the human brain is made up of neurons, neural networks are layers of nodes. Individual layer nodes are linked to neigh boring layer nodes. The number of layers in the network determines how deep it is considered to be. In the human brain, a single neuron takes

in hundreds of impulses from other neurons. Signals go between nodes and assign matching weights in an artificial neural network. A node's influence on the nodes in the layer beneath it will be stronger if it has a larger weight. The weighted inputs are combined to create an output in the final layer. Because deep learning systems handle a lot of data and perform several intricate mathematical computations, they demand strong hardware. But even with such sophisticated hardware, training a neural network can take days or even weeks.

Information is fed into deep learning systems as massive data sets since they need a lot of information to get correct findings. Artificial neural networks are able to classify data while processing it using the responses to a series of binary yes or false questions involving extremely difficult mathematical calculations. This advances one step thanks to deep learning. Because deep neural networks are used in deep learning, these features are automatically discovered, whereas in machine learning, these features had to be manually defined.

2. LITERATURE SURVEY

Deep residual learning is used by Siddharth Bhatia et al. (2019)[1] to identify lung cancer. They compare the performance of classifiers like Random forest and XGBoost to determine the chance of predicting cancerous CT images. The authors achieve the highest accuracy of 84% when they mix the two classifiers. The limitation of this model is its less precision Suren Makaju et al. (2018)[2] ranked cancer detection strategies based on their efficacy and chose the most effective strategy to improve its accuracy.

Sajja T, Devarapalli R, et al. (2019)[3] explored the use of Google-Net to identify lung cancer. 60% of all neurons were deployed in the drop-out layers, resulting in a simpler and sparse network. The model needs to be tested with different dropout rates to see if it performs more accurately.

Tae-WooKim et al.[4] created a decision tree on occupational lung cancer, recording 153 instances between 1992 and 2007. The objective parameter was age, sex, years of smoking, histology, industry size, delay, working hours, and exposure to independent variables. The CART model was used as an indicator for word associated cellular breakdown in the lungs, but it is not definitive.

H. Azzawi et al.[5] proposed a GEP model to predict microarray data on lung cancer in 2016. Reliability tests showed that the GEP model with less features outperformed other models when precision, sensitivity, specialty, and region under the recipient functional property curve were taken into account. The GEP paradigm offered a more effective solution to lung cancer diagnosis.

Ali I et al.[6] developed and validated a reinforcement learning model based on deep artificial neural networks for early detection of lung nodules in thoracic CT images. The dataset used to train the model is the LIDC/IDRI database hosted by the lung nodule analysis (LUNA) challenge. The results show promise in solving the major issue of false positives in CT screening of lung nodules, and may help to save unnecessary follow-up tests and expenditures.

Masud et al[7] mentioned Cancer is the second leading cause of death globally, with lung and colon variants being the most common and deadliest. AI can be used to automate cancer diagnosis, allowing medical professionals to assess more cases in less time and cost. This paper proposes a classification framework to differentiate among five types of lung and colon tissues, with a maximum of 96.33% accuracy.

Tatdow Pansombut et. Al used a CNN classifier[8] to test the viability of a deep learning strategy for identifying lymphocytes and ALL subtypes for WHO classification. They also used MLP Classifier and Random Forest Technique.

Leukemia is a form of blood cancer that affects the body's ability to fight infection. Manual counting of cells from a peripheral blood smear or bone marrow aspiration is time consuming and prone to human errors. Automated techniques have been introduced which are faster, reliable and cheaper than manual methods. This paper focuses on how image processing techniques[9] can be used to identify Acute Lymphoblastic Leukemia (ALL) from the peripheral blood smear images.

M. Akter Hossain et. Al[10] studied Acute Lymphocytic Leukemia (ALL) to detect abnormal blood components prevalent in cancer patients. They selected 14 features to prepare the dataset before determining four essential attributes that are important in determining a Leukemia patient.

Salah HT et. Al[11] conducted an automated search of 58 papers to examine the use of Machine Learning in diagnosing Leukemia, with 22 studies included.

Litjens et. Al[12] proposed "deep learning" as a method for improving the fairness and efficiency of histopathology slide analysis. They found that all slides containing micro and macro-metastases of prostate and breast cancer can be recognized automatically without extra immunohistochemical markers or human involvement, but slides containing benign and normal tissues cannot. The paper concluded that deep learning has enormous promise for improving prostate cancer detection and classification.

3. RESEARCH METHODOLOGY

The proposed work uses a computer vision system in this project to identify blood cancer diseases and provide diagnosis data. It includes steps for features extraction and classification that make use of the Convolutional neural network method and the Grey level co-occurrence matrix. Convolutional Neural Network (CNN) architecture is suggested in order to distinguish between images of normal and diseased blood cells. Utilizing CNN offers several benefits, including the capacity to extract features that are superior to traditional statistical features and the potential to shorten processing time by allowing us to bypass most pre-processing steps. The sequence steps to be followed for detecting multiple types of blood cancer cell images using deep learning methodology are depicted in the **Figure 1.**

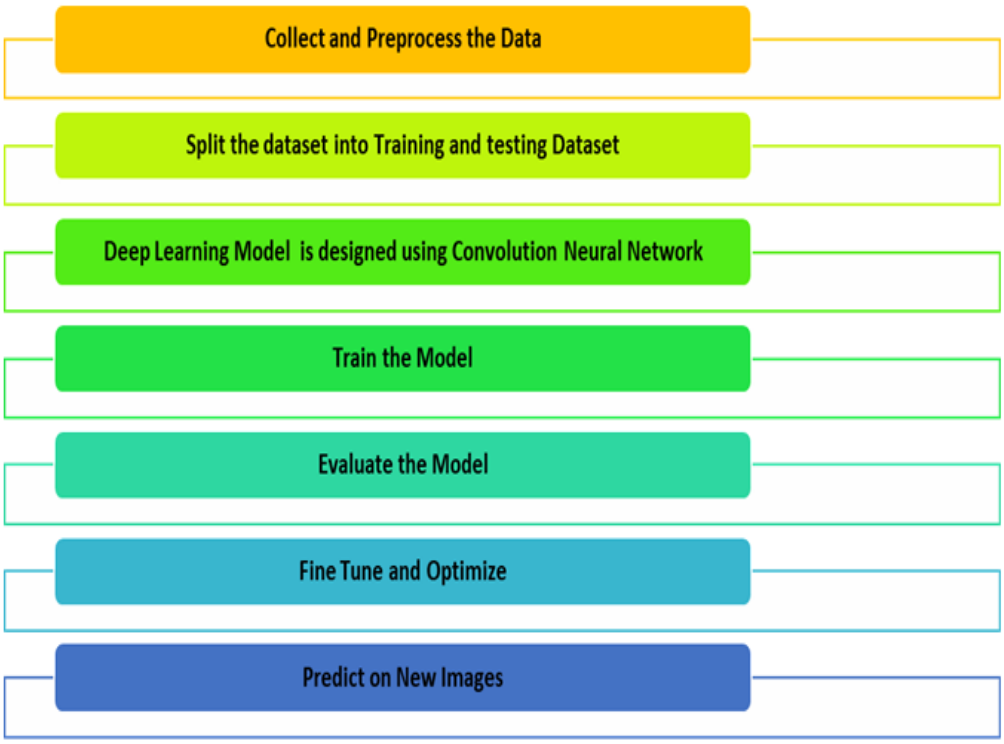

Figure 1: Deep learning sequence steps.

Convolution neural network algorithm

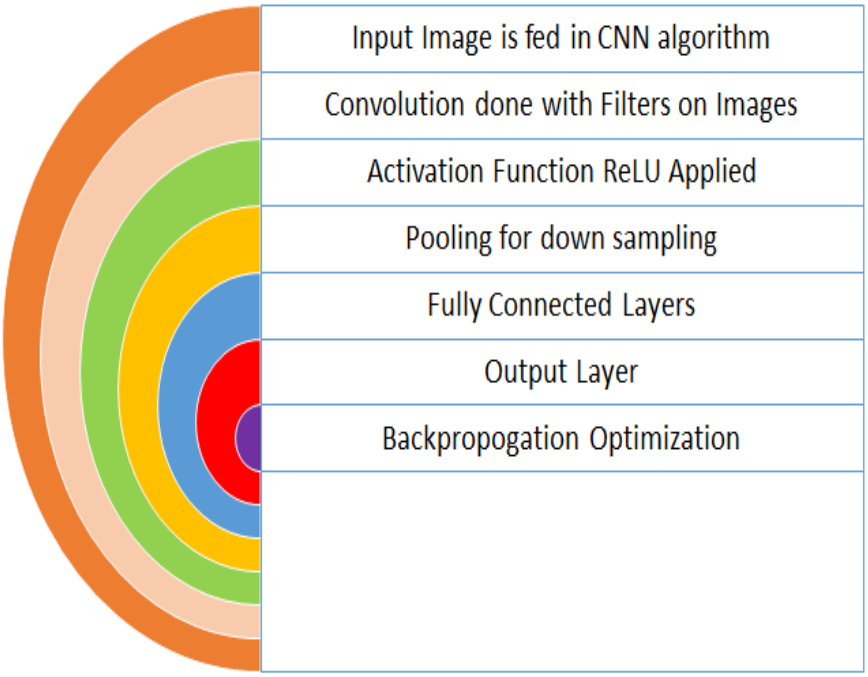

Figure 2: CNN Steps.

The CNN algorithm receives the input image. In the Convolution step, a group of teachable filters are convolved with the input image. The result of the convolution operation is then sent through a non-linear activation function, such as the Rectified Linear Unit (ReLU), to introduce non-linearity into the model.Using a pooling technique, such as maximum or average pooling, the output of the activation function is down sampled during this stage. After a number of convolutional and pooling layers, the output is flattened and fed into a series of fully connected layers. Back propagation is a technique used by the optimizer to change the model's weights and lower the loss function. The above operations are depicted in **Figure 2.**

Cancer is brought on by unchecked abnormal cell growth and development. In a healthy organism, cells grow, mature, carry out the function for which they were created, and finally perish. To maintain good cellular function and replace worn-out cells, the body periodically creates new ones. Cells may develop and multiply in an unpredictable and uncontrolled manner. The improper development of cells could prevent them from working as intended. Cells might not decompose as they ought to. One of these events, or a combination of them, may occur as cells develop into cancer. Leukemia is a malignancy of the blood-forming cells in the bone marrow. These disordered, immature cells are accumulated throughout the body's

organs and circulation. They cannot carry out the functions that blood cells ordinarily do. To determine the presence of leukemia and its type, hematologists look at the appearance and histology of the cells in a blood smear. Acute and chronic leukemia's are the two types. Acute leukemia patients have rapidly rising levels of defective leukemic cells in their blood. Typically, a bone marrow analysis will reveal high leukemic cell counts and low levels of normal white blood cells. Fatigue, bruising propensity, and recurring infections are common symptoms in people with acute leukemia, whereas chronic leukemia usually develops over time. Leukemic cells perform their designated functions normally in the early stages of the illness, but as the condition worsens, they suffer significant impairment. Initial diagnoses are made on the basis of abnormal blood test findings and the patients' reports of being exhausted and nauseated. If left untreated, leukemia cells will eventually exceed healthy blood cells, impairing systemic function. Both acute and chronic leukemia are further divided into subgroups based on the cell types involved. This second classification establishes whether the leukemia is lymphoid or myeloid in origin. Myeloid leukemia cells clump together to produce myeloid 'sarcomas,' extra medullary myeloid tumors, granulocytic sarcomas, or chloromas, in contrast to lymphoid leukemia cells, which group together to induce lymph node enlargement.

4. EXPERIMENTAL SETUP

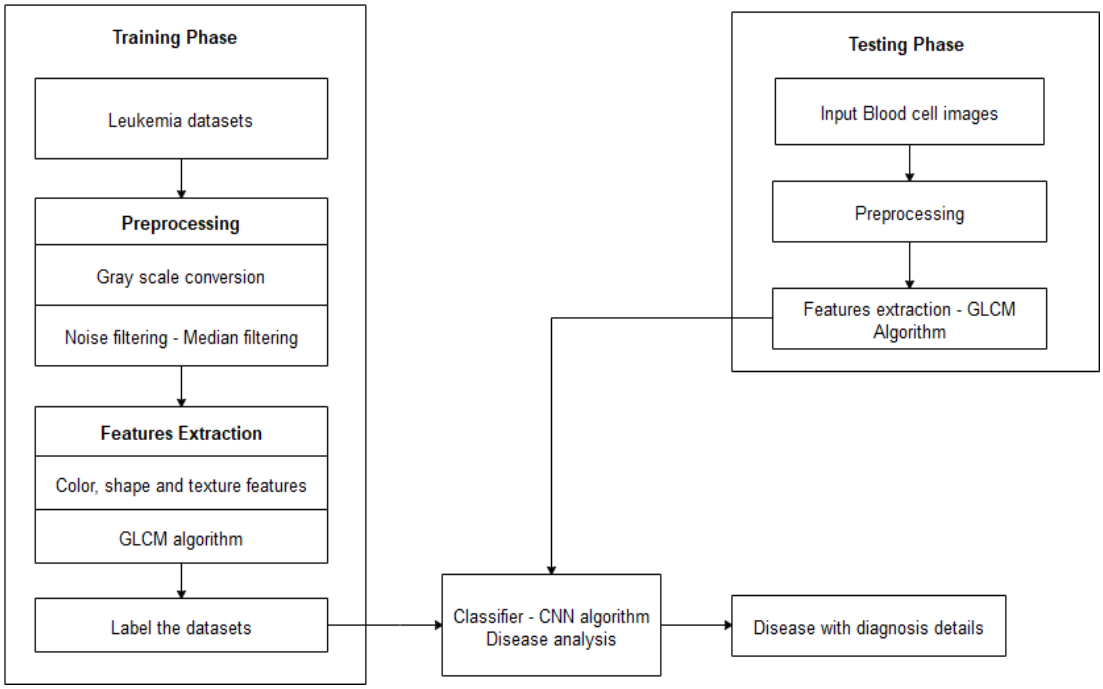

Figure 3: System architecture.

Upload microscopic images

Alterations in the morphology of blood cells and other cell traits might result from any pollution in the human body. The microscopic blood cell pictures are examined for signs of pollutants inside the body with the expectation of illnesses and outliers. With the right cell segmentation, illness detection becomes more accurate and active. The microscopic inspection of blood cells is an essential step in the pathological investigation. It places a strong emphasis on examining the correct disease after precise localization and then an order of anomalies, which is essential for understanding various ailments, developing therapies, and evaluating the effectiveness of those treatments. Clinicians can utilize white blood cell (WBC) counting and nucleus characterization to identify different diseases or stages of a specific disease. This module allows us to upload blood cell images for analysis of the blood cancer disease. Images can be of any size and type. The four types of classification carried out in this proposed work are ['EOSINOPHIL', 'LYMPHOCYTE', 'MONOCYTE', 'NEUTROPHIL'] classes

Median value for noise prediction

Images need to be processed before they can be used for model training and inference. This includes, but is not limited to, changes in colour, size, and orientation. Model preprocessing may also reduce the amount of time needed for model training and accelerate model inference. If the input photos are exceptionally large, reducing their size will dramatically speed up model training time without significantly compromising model performance. The RGB image will be converted to a range of grey intensities by using this module's grey scale conversion. Colour changes are an example of a picture modification that can be applied to all images (train and test) or modified at random in training, similar to augmentations. Grey scaling often entails giving all images a colour shift. Colour images are saved as red, green, and blue values while grayscale images are merely preserved as a range from black to white. Digital photos always contain noise during the stages of picture collection, coding, transmission, and processing. Virtually all image processing systems employ the traditional method of filtering image data. Filters are used to achieve this. They lessen noise by preserving the photos' details. The selection is influenced by the type of data and filter behavior. The Mean filter, a simple sliding window, replaces the center value with the Median of all the pixel values in the window. Though it is frequently square, the window or kernel can have any shape.

Cell features extraction

Image parameters are extracted as part of the feature extraction process in order to explain the microscopically features of leukemia and make a diagnosis based on these features. Medical experts make use of leukemia features. The selection of features is greatly influenced by the chosen diagnosis strategy. For instance, asymmetry and colored network are the features of the contour rule and pattern analysis, respectively. The features evaluation of leukemia diagnosis is particularly difficult visually because to the complexity of the information included in photographs and the requirement that only experienced medical professionals be able to analyze them. The selection of features is a crucial step before categorization. Its objective is to reduce the number of feature descriptors that are extracted, hence reducing the computational expense of classification. This reduction is nonetheless important because eliminating duplication could weaken the power of discrimination. This module includes features for colour and texture. Both the textural characteristics and the statistical features are included in the recovered HSV colour features.

Lesion segmentation

Several neural network algorithms are used to classify images of leukemia cells. Convolutional neural networks are currently employed in sickness prediction. Max is used with the fully linked convolutional layers to represent the CNN feed-forward neural network. It makes use of spatial local correlation by reinforcing the local connection patterns between the neurons in the adjacent layers. Max pooling layers mimic and replace the intricate features of the simple cells and convolutional layers in human visual brain. To frame a full CNN, numerous pairs of convolutional layers and layers with maximum pooling are used. It is successfully shown that CNN has a hierarchical structure by carefully studying observable representations. The appearance of objects that belong to distinct classes and have diverse shapes is the fundamental challenge with such visual tasks. The hyper-spectral data is represented by a 2D curve with thousands of spectral channels. Each class curve has a unique visual shape that distinguishes it from other classes (such as gravel and self-blocking bricks), making it difficult for the human eye to discriminate between relative classes. CNNs can solve complex problems and outperform humans by using spectral properties. This capability spurs scientists to investigate the possibility of classifying blood cells using CNNs. Depending on how the network was trained, the convolutional layers and max pooling layers of the CNN are implemented in different ways.

Reporting disease

Microscopic image analysis plays a significant role in both the first leukemia screening and the accurate diagnosis of leukemia. Because the current conventional approaches partially rely on manual examination, which is time-consuming and highly dependent on the expertise of domain specialists, automated leukemia diagnosis gives up new opportunities to minimise human intervention and provide more accurate clinical information. The categorization process is the system's final stage. The likelihood of true positives was independently evaluated for each segment once the structure was examined. Cancer illnesses are grouped using the convolutional neural network algorithm. Thus, the suggested technique more accurately addresses the irregular borders separation in blood image classification. Finally, predict the various blood cancer types based on the outcomes of blood cell segmentation. Details concerning the diseases' diagnoses should also be included.

5. EXPERIMENTED RESULTS AND DISCUSSIONS

The blood cell classification is carried out in 3 phases. Image uploading, Training images and testing images. The UI interface screen shot of Blood Cell classification is depicted in Figure 4 and the image uploading screenshot is depicted in Figure 5.

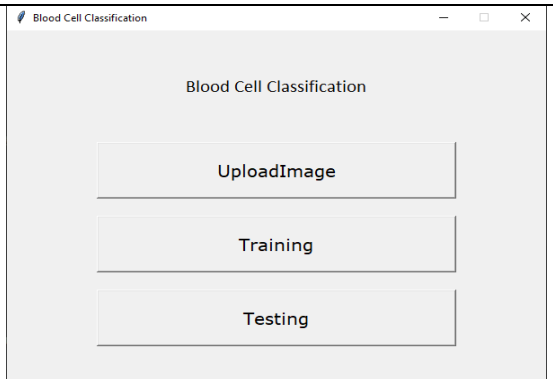

Figure 4: Blood Cell Classification UI Interface.

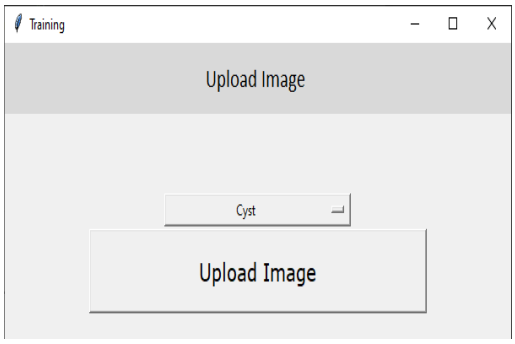

Figure 5: Image uploading.

The Image selection process of the Training Phase is depicted in **Figure 6**.

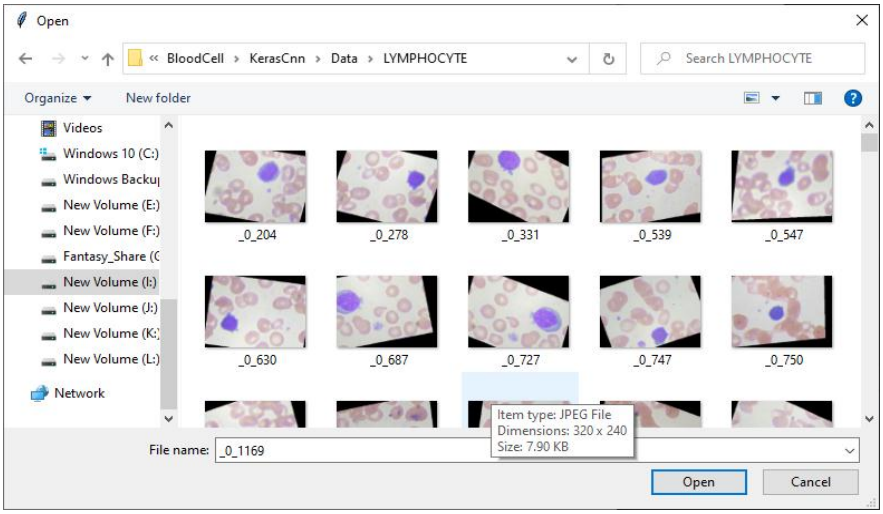

Figure 6: Image selection.

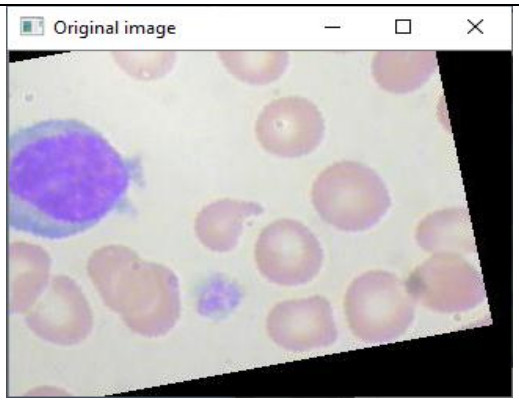

Figure 7: Original uploaded image – training phase.

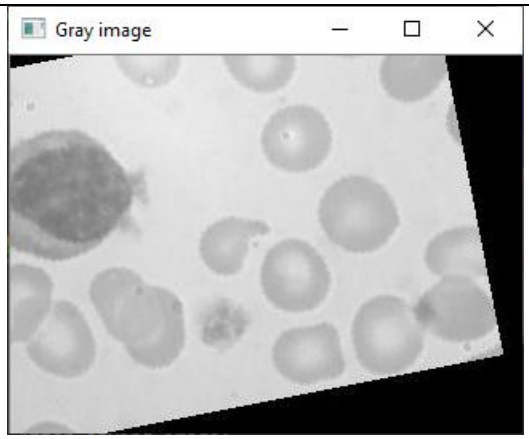

Figure 8: Gray scale converted image.

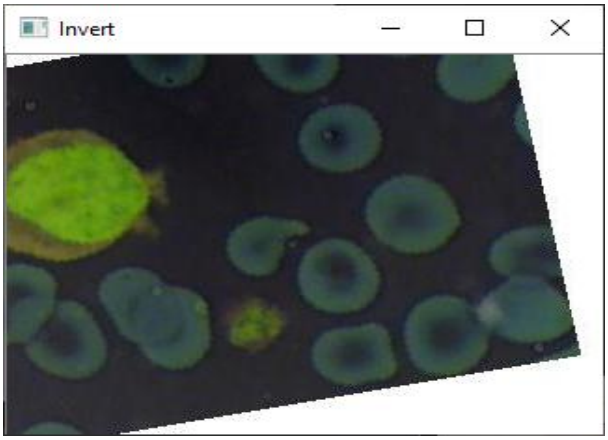

Figure 9: Inverted image.

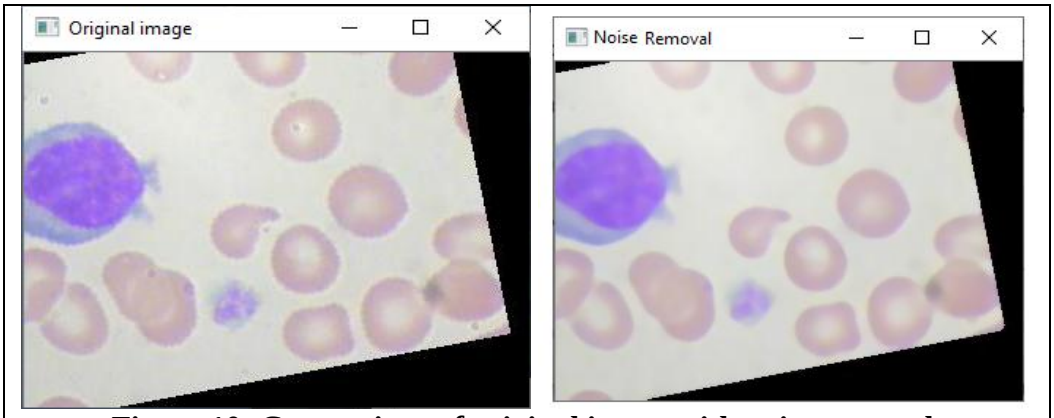

Figure 10: Comparison of original image with noise removal.

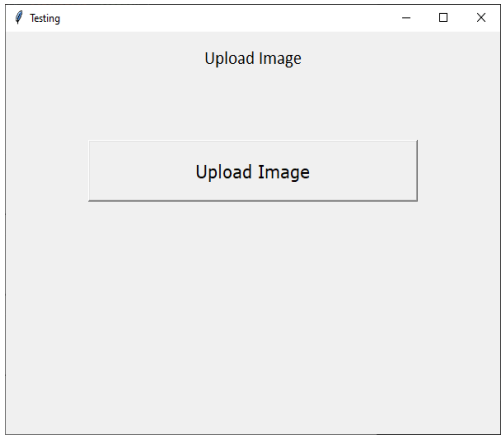

Figure 11: Testing User Interface

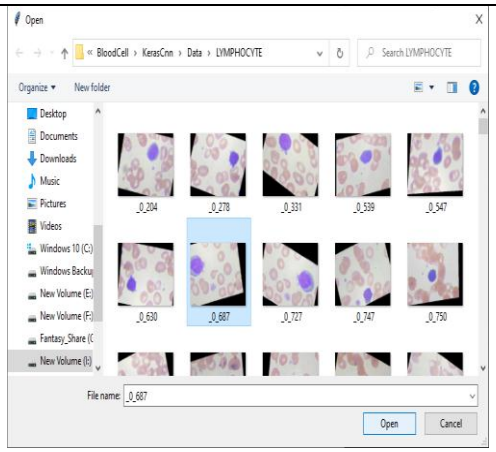

Figure 12: Original Uploaded Image – Testing Phase

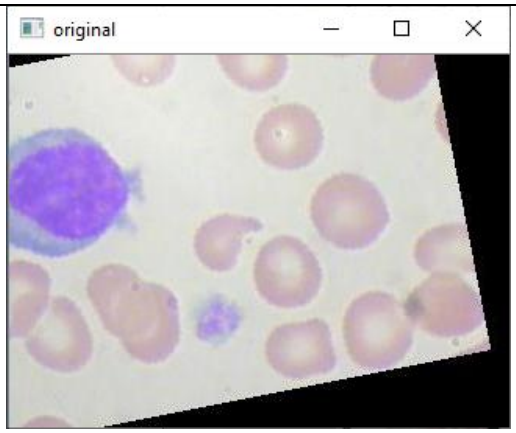

Figure 13: Original test image.

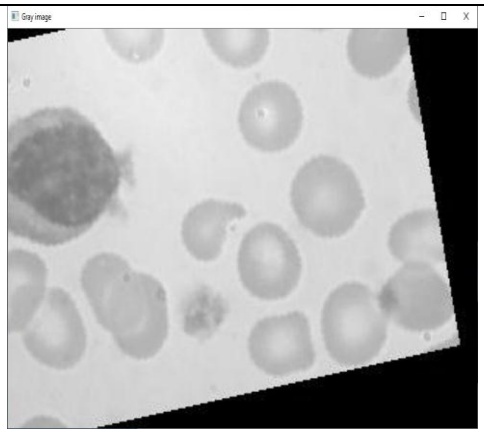

Figure 14: Gray scale test image.

Image Data Generator generates batches of augmented images with target size of 200x200 pixels and 32 classes. The classes are explicitly specified as ['EOSINOPHIL', 'LYMPHOCYTE', 'MONOCYTE', 'NEUTROPHIL']. The class_mode is set to 'categorical' since categorical labels are used. The Sequential class from Keras creates a sequential model with convolutional, max pooling, and fully connected layers. The model architecture is defined to have multiple convolutional layers with increasing number of filters and a dense

layer with softmax activation for multiclass classification. The model is compiled with the categorical cross-entropy loss function, RMSprop optimizer with a learning rate of 0.001, and accuracy as the evaluation metric. The model is trained using the fit_generator function, which takes the train_generator as input along with the number of steps per epoch and the number of epochs.

The training history is stored in the history variable. The trained model is saved as 'model.h5'. The accuracy and loss values from the training history are extracted. The training and validation accuracy curves are plotted using Matplotlib. The training and validation loss curves are also plotted in **Figure 15** and **Figure 16**. The saved model is loaded using tf.keras.models.load_model. An example test image is loaded using image.load_img. The image is preprocessed and expanded to match the model's input shape. The loaded model is used to predict the class of the test image. The predicted class is printed based on the highest probability and its respective output is shown in **Figure 17** and the precaution step for the disease is also included in the application and is depicted in **Figure 18**.

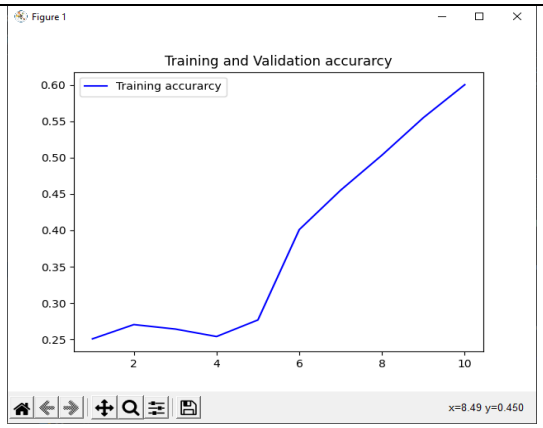

Figure 15: Training accuracy.

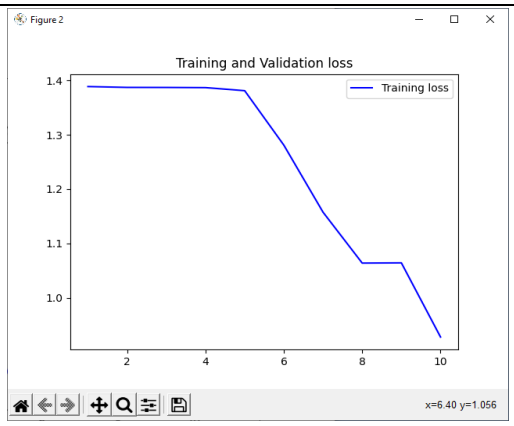

Figure 16: Training loss.

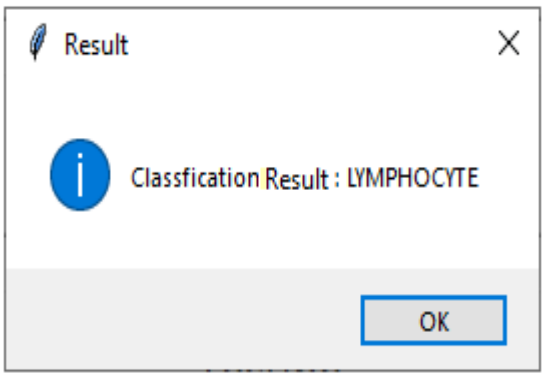

Figure 17: Classification result.

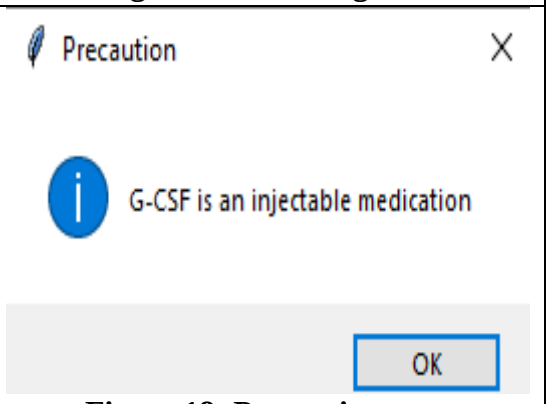

Figure 18: Precaution step.

6. CONCLUSION

The choice of the appropriate architecture for a given problem's solution is crucial because

some datasets may contain too many underlying deep features that call for sophisticated methods to extract their parameters, whereas other datasets do not call for such a complex process of laborious task undertaking to create a model or algorithm because they do not contain parameters that need to be pruned deeper. When developing a complicated structured solution for such relatively easy feature extraction necessary data, the intermediate values frequently get over-improved, which tampers with the originality or important parameters of the input taken into consideration. In this study, hematologists employ microscopic images of the cells to classify White Blood Cells into subgroups using Convolutional Neural Network techniques. This classification helps to identify cells and identify the type of illness a patient is suffering from. The outcomes of this experiment assist in more reliably identifying photographs when compared to machine learning techniques. The test set's accuracy rate was above 90%, which is a high level. As a result, when the model is trained with strong computational capabilities present, a perfect model can be developed and used in medical analysis and applications dealing with the number of white blood cells and sub types of white blood cells.

7. FUTURE ENCHANCEMENT

The whole study explains and compares the findings of various machine learning and in-depth learning implemented to cancer prognosis. Specifically, several trends related to those same kinds of machines techniques to be used, the kinds of training data to be incorporated, the kind of endpoint forecasts to be made, sorts of cancers being investigated, and the overall performance of cancer prediction or outcome methods have been identified. While the ANNs are common, it is clear that a broader variety of alternative learning approaches is also used to predict at least three different cancer types. ANNs continue to be prevalent. Furthermore, it is clear that machine training methods typically increase the efficiency or predictable accuracy of most prognostics, in particular when matched with conventional statistical or expert systems. Although most researches are usually excellently-designed and fairly validated, more focus is quite desirable for the planning and implementation of experiments, in particular with regard to quantity and quality of biological data. Improving the experimental design and the biological validation of several device classification systems would undoubtedly increase the general Quality, replicability and reproductivity of many systems. In total, we believe that the usage of the devices education & deep learning classificatory will probably be quite common in many clinical and hospital settings if the quality of study continues to improve. The assimilation of multifaceted heterogeneous data,

which can offer a promising tool for cancer infection and foresee the disease, also demonstrates the incorporation in the application of different analytical and classification methods. In future, by using the proposed framework, we would like to use other state of the art machine learning algorithms and extraction methods to allow more intensive comparative analysis.

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