

Design a New Algorithm to Identify White Blood Cells for Classification Leukemic Blood Image using CNN

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Abstract: *Image processing and deep learning techniques are employed in this research to locate and classify White Blood Cells (WBCs) based on their respective categories. The aim is to enhance efficiency and alleviate the burden on doctors, as traditional manual counting methods are tedious, monotonous, and subject to potential subjectivity. The dataset for normal blood samples is obtained from the laboratory in the biotechnology department, while the datasets used for training in the Convolutional Neural Network (CNN) are sourced from the Leukocyte Images for Segmentation and Classification (LISC) website. White Blood Cells (WBCs), also known as leukocytes or leucocytes, are immune system cells responsible for defending the body against infectious diseases and foreign substances. They play a crucial role in fighting infections by attacking bacteria, viruses, and other microorganisms that invade the body. All leukocytes are derived from multipotent cells called hematopoietic stem cells. The lifespan of WBCs in the human body is approximately three to four days. In order to extract the nucleus of a white blood cell image, segmentation techniques are necessary. Once the WBCs are classified, they are counted and compared to the standard range of WBC types found in human blood samples. This enables the prediction of normal and abnormal blood samples based on the availability of different types of WBCs. The utilization of image processing and deep learning techniques in this research enables the automated detection and classification of WBCs. By training a Convolutional Neural Network (CNN) using datasets from the LISC website, the model can accurately classify WBCs based on their categories. This eliminates the need for manual counting methods, which are not only time-consuming but also prone to subjectivity. By employing this approach, the researchers aim to improve the efficiency of WBC analysis and reduce the workload on doctors. The automated classification and counting of WBCs provide a reliable method for predicting normal and abnormal blood samples based on the composition of different types of WBCs. Overall, this research contributes to the development of advanced techniques in the field of hematology and brings about significant improvements in the analysis of blood samples.*

Keywords: Magnetic Resonance Imaging (MRI), Convolutional Neural Network (CNN), Blood Cells, etc.

I. INTRODUCTION

Infections, leukemia, and specific types of cancers can be identified based on the classification results and white blood cell count. Microscopic examination of blood plays a crucial role in diagnosing various health conditions. The results obtained from a differential blood count inspection can provide valuable insights into hematological pathologies. Currently, skilled operators perform the traditional method of manual blood cell counting using a microscope. This process is laborious and time-consuming. Moreover, the accuracy and classification of cells may vary depending on the operators' expertise and experience. Therefore, the development of an automated system for differential blood cell counting has become necessary. Several approaches have been proposed recently to implement automated white blood cell recognition systems using image processing techniques. The performance of an automatic white blood cell classification system greatly relies on a robust segmentation algorithm to accurately separate white blood cells from the background. In our research, we extract three types of characteristics from the segmented cell regions. These characteristics serve as input for three distinct neural networks designed for the classification of the five types of white

blood cells. By leveraging these features and employing neural networks, we aim to achieve accurate classification results

II. RELATED WORK

Experimental results show that this method works successfully in the segmentation of colour smear microscopic images by Kroegel et al (2014). In their work, a novel white blood cell (WBC) segmentation scheme using scale-space filtering and watershed clustering is proposed. In this scheme, nucleus and cytoplasm, the two components of WBC, are extracted respectively using different methods. First, a sub-image containing WBC is separated from the cell image.

Experiments demonstrate that the proposed scheme performs really well, and HSV space is more appropriate than RGB space in WBC segmentation due to its low correlation, as given by Jiang et al (2016). Image processing techniques involve five basic components, which are image acquisition, image preprocessing, image segmentation, image postprocessing, and image analysis. The most critical step in image processing is the segmentation of the image. In this, they review some of the general segmentation methods that have found application in classification in biomedical image processing, especially in blood cell image processing.

O. Ryabchykov, A. Ramoji (2014) presented a fast segmentation scheme for automatic differential counting of white blood cells. The segmentation procedure consists of three phases. First, a novel simple algorithm is proposed for the localization of white blood cells. The algorithm is based on a priori information about blood smear images.

Dorini et al (2007) found out that cell segmentation is a challenging problem due to both the complex nature of the cells and the uncertainty present in video microscopy. Manual methods for this purpose are onerous, imprecise, and highly subjective, thus requiring automated methods that perform this task in an objective and efficient way.

T. Rosyadi, A. Arif, Nopriadi et al (2006) presented a fast white blood cell (WBC) image segmentation scheme implemented by an online trained neural network. A pre-selecting technique, based on the mean shift algorithm and uniform sampling, is utilized as an initialization tool to largely reduce the training set while preserving the most valuable distribution information.

Basically, segmentation of the image divides the whole image into some unique disjoint regions. The fact that the segmented image should retain maximum useful information and discard unwanted information makes the whole process critical, as published by Robiyanti et al (2018).

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III. PROPOSED METHODOLOGY

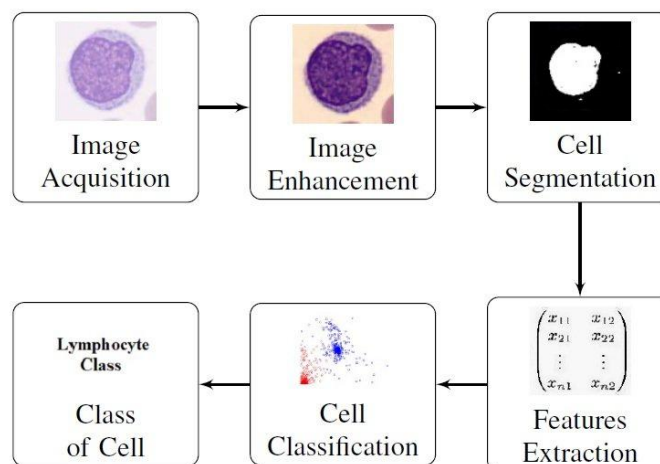


Figure 3.1 Process of cell segmentation

The main task of the segmentation is to extract the objects from an image. During segmentation, the size and shape of the nucleus should be maintained. Many segmentation algorithms have been developed for various applications. To overcome from the problem of image shaping, it may use the classification of CNN. This study gives a technique for WBC detection based on Convolutional Neural Network (CNN). This proposed method effectively works for WBC detection, and effectively reduces the computational time and preserve the shapes and edges of the image. The main objective is to segment the WBC from the blood smear image to detect an immature cell.

- Segmentation divides an image into its constituent regions or objects
- Segmentation of images is a difficult task in image processing. It is still under research
- Segmentation allows to extract objects in images.
- Segmentation is unsupervised learning.
- Model based object extraction, e.g., template matching, is supervised learning.

3.1 WBC CLASSIFICATION

Several researchers have already proposed features to distinguish leukocytes. Ramesh et al. (2012) classified leukocytes based on cytoplasmic and nuclear characteristics. Hematologists study cell shape, size, color, and texture in combination with core features. When selecting features, it is important to consider the rules and heuristics used by hematology professionals. Pathologists traditionally report that normal white blood cells fall into five classes: monocytes, lymphocytes, neutrophils, eosinophils, and basophils.

In addition, the ratio of nuclear to cell areas, nuclear "rectangularity" (the ratio of the perimeter of the narrowest circumscribing rectangle to the perimeter of the nucleus), cell "circularity" (the ratio of the perimeter of the narrowest circumscribing circle to the cell perimeter), the number of lobes in the nucleus, the area of the cytoplasm, and the average grayscale intensity were calculated. The system was evaluated using 10-fold cross-validation.

We compared the performance using different classifiers, including nearest neighbor classifiers, feedforward neural networks, radial basis function neural networks, and parallel classifiers built with feedforward neural networks. In this method, a preliminary classification of leukocytes based on the number and feature set of intranuclear lobes (uni- or multi-lobed) is proposed to achieve a better classification rate for each leukocyte subtype.

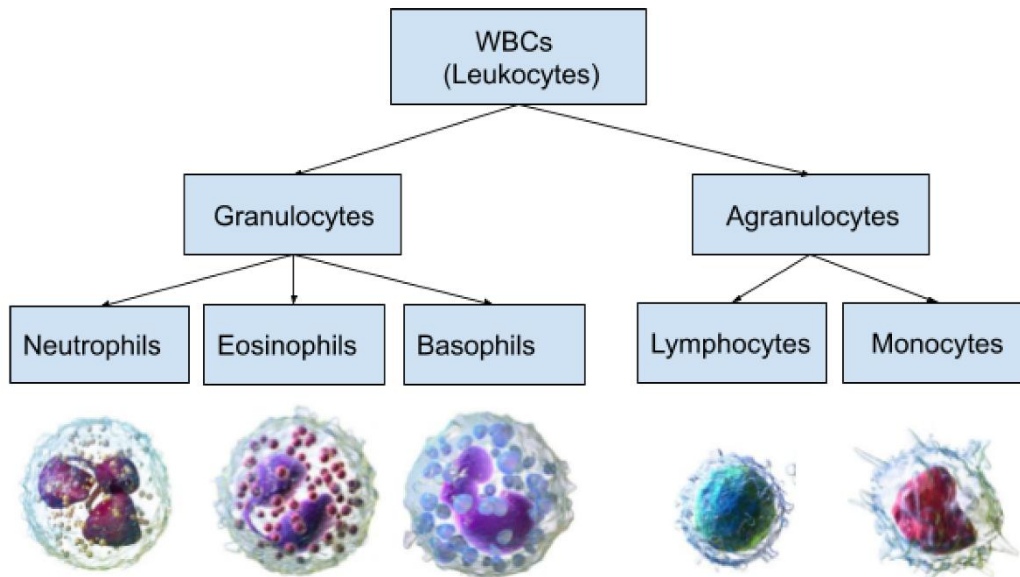


Figure 3.2 WBC Classifications

The several types of features such as intensity and colour-based features, texture-based features, and shape-based features are utilized for a robust representation of WBCs. Classification methods used in this work include k-Nearest Neighbors, Learning Vector Quantization, MultiLayer Perceptron, and Support Vector Machine. Then they evaluated the binary images of the cytoplasm and nucleus to characterize the feature set. The standard set of features like area,

perimeter, convex areas, solidity, major axis length, orientation, filled area, eccentricity were separately evaluated for the nucleus and the cytoplasm.

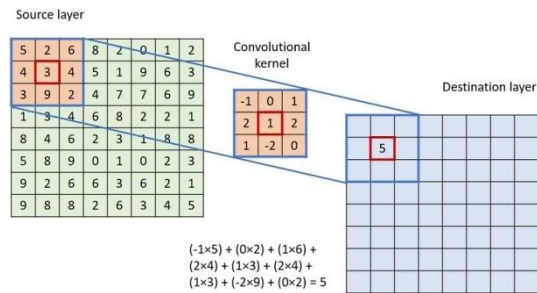
IV. CONVOLUTIONAL NEURAL NETWORK (CNN)

Convolutional Neural Networks (CNN) is also known as CNNs or ConvNets. They are categories of a neural network that are very effective in the computer vision tasks like image recognition and classification. CNN's are feed-forward neural networks that are used to analyze image data by processing it in the grid-like topology. An image data can be represented digitally as a matrix of pixel values. The series of pixels arranged in a grid-like manner represents pixel values about the color and intensity of the color for each pixel. After seeing the particular image, the human brain processes information related to the image. Each neuron in the brain works as an individual receptive field connected with other neurons to cover the whole visual area. Similarly, each neuron in the CNN is process data only in the receptive field. The layers of the CNN architectures arranged in a manner that processes simple information like lines and curves first. With the CNNs, it is possible to provide sight to the computer. The major four operations that exist in the CNNs are as follows:

- Convolution operation
- Non-Linearity
- Pooling
- Fully Connected layers or Classification

4.1 Convolution Operation

One of the basic building blocks of CNN is the convolution layer. The convolution layers carry the main portion of the computational load. This layer does the dot product between the matrix of learnable parameters known as the kernel and matrix with a limited receptive field. The height and width of the kernel will be spatially small. However, the depth of the kernel extends up to three RGB channels of the input image. While performing the forward pass, the kernel slides through the image's height and width, which is responsible for the image representation of a particular receptive region (Smeda, K., 2019).



4.2 Non-Linearity

To achieve the non-linearity in the CNN network, Rectified Linear Unit (ReLU) activation function is used. ReLU stands for a rectified linear unit. Once the feature set is obtained in the next step, they are forwarded to the ReLU layer (Smeda, K., 2019). It operates on each and every element of the feature set and set the value of all negative pixels to zero. It is represented in Figure 4.2.

4.3 Pooling Layer

Like the convolutional layer, the pooling layer is used to reduce the spatial size of the convolved features obtained after convolution operation. Applying pooling on the obtained features reduces the computational power required for data processing using dimensionality reduction. Moreover, it helps in effective

4.4 Fully Connected Layers or Classification

The fully connected layer is a typical multi-layer perceptron that uses softmax as an activation function in the output layer. The neurons in the fully connected layer are fully connected with the neurons in the preceding and succeeding

layer. For the input RGB image, the output of the convolutional and pooling layer delivers the high-level features. Based on the training dataset provided to the network, the fully connected layer utilizes these features for input classification into different classes (Smeda, K., 2019). Also, fully connected layers are usually used for learning a non-linear combination of the features obtained from the previous layers. The working of fully connected layers is described in Figure 4.4.

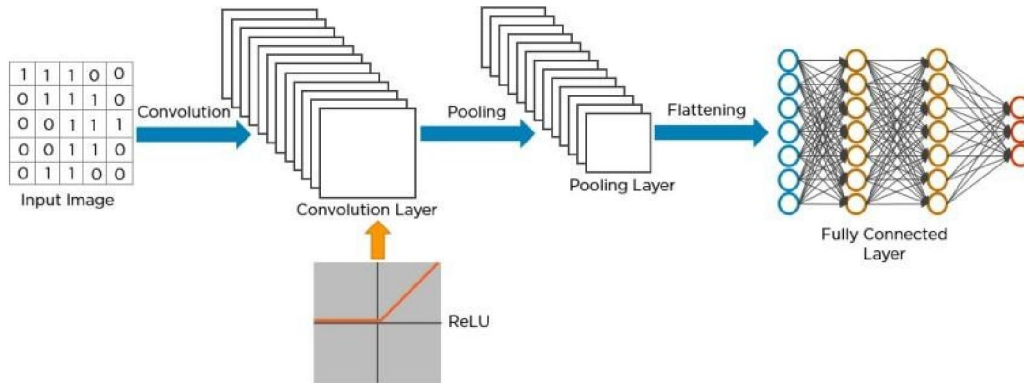


Figure 4.4 Fully Connected Layers for Classification

V. RESULTS AND OUTPUT

White blood cells play a crucial role in the body's defense against infections, and an elevated count of white blood cells may indicate inflammation, infection, or stress in a patient. However, a proper diagnosis requires a comprehensive understanding of the white blood cells present in a blood smear. In a normal peripheral blood sample, there are five main types of white blood cells, each with their typical proportion: neutrophils (40–78%), lymphocytes (25–33%), monocytes (2–8%), eosinophils (1–4%), and basophil granulocytes (0–2%). Additionally, plasma cells are present in small numbers ranging from 0.2% to 2.8%.

5.1 Classification of WBC :

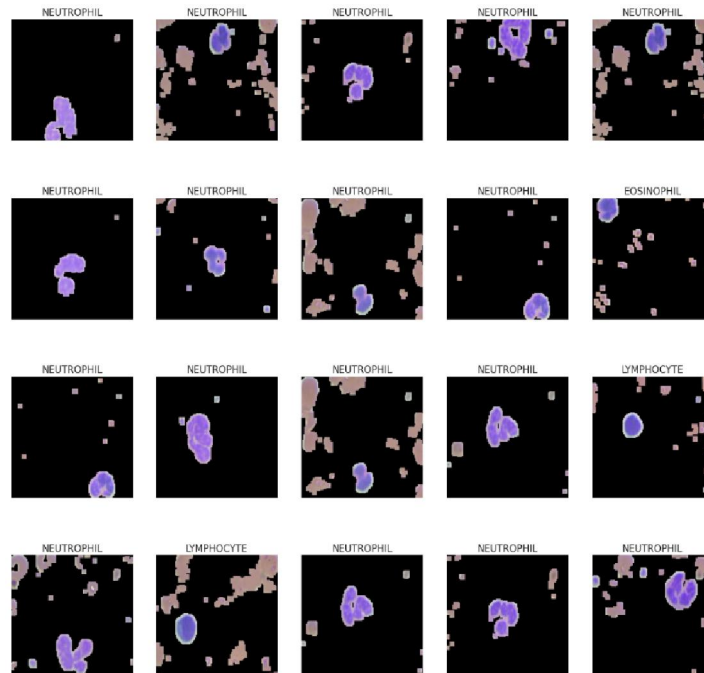


Figure 5.1 Blood Cells Classification Using CNN

5.2 Confusion Matrix :

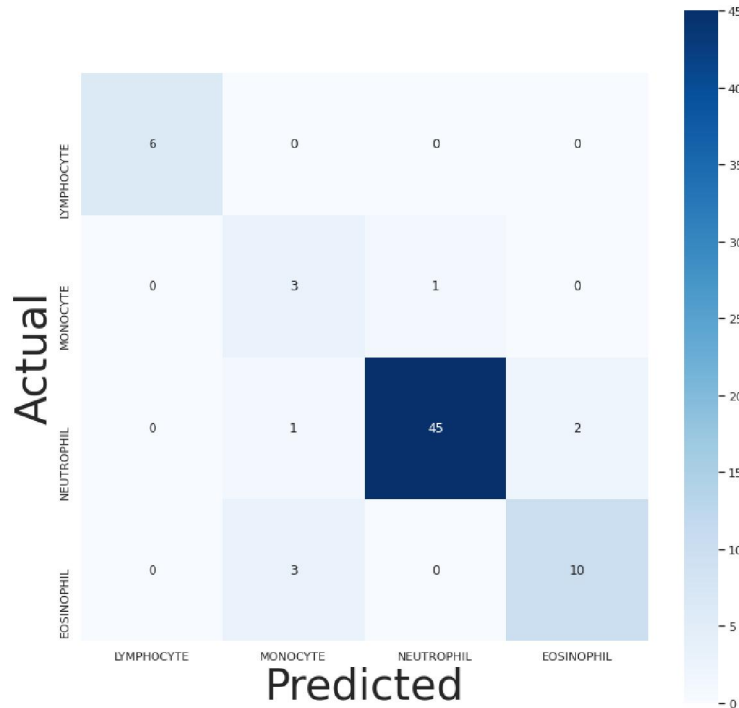


Figure 5.3 Confusion Matrix of actual and Predicted Blood Cells Classification Using CNN

5.3 Losses Vs Epochs and Accuracy Vs Epochs:

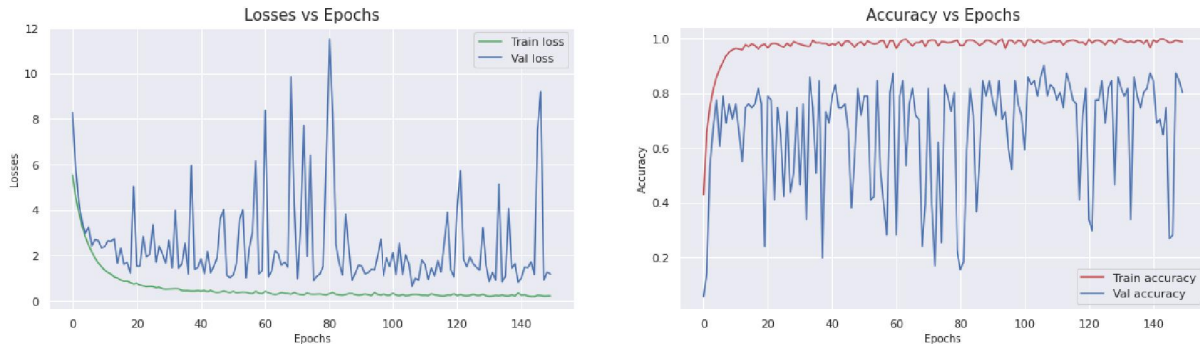


Figure 5.6 Various Graphs of Accuracy and Loss

VI. CONCLUSION

In conclusion, the design and implementation of a new algorithm for identifying white blood cells in leukemic blood images using Convolutional Neural Networks (CNN) hold significant promise for improving the accuracy and efficiency of classifying these cells. By leveraging the power of deep learning and image processing techniques, this algorithm offers a robust solution to automate the identification and classification of white blood cells, particularly in leukemic blood samples.

The utilization of CNN allows for the extraction of intricate features and patterns from the blood images, enabling accurate differentiation between different types of white blood cells. This approach eliminates the limitations and subjectivity associated with manual counting methods, providing a more objective and efficient alternative for hematologists and pathologists in diagnosing leukemia and other related blood disorders.

The algorithm's effectiveness lies in its ability to learn from a vast dataset of leukemic blood images, enabling it to recognize subtle variations in cell morphology and accurately classify different types of white blood cells. By

incorporating state-of-the-art image processing techniques and leveraging the power of deep learning, this algorithm offers a promising avenue for enhancing the diagnosis and treatment of leukemic patients.

Furthermore, the algorithm's automation of the identification and classification process significantly reduces the burden on medical professionals, allowing them to focus on other critical aspects of patient care. The speed and efficiency of the algorithm make it a valuable tool in supporting timely and accurate diagnoses, leading to improved patient outcomes and treatment decisions.

In summary, the design of a new algorithm utilizing CNN for the identification and classification of white blood cells in leukemic blood images represents a significant advancement in the field of hematological analysis. With its potential to enhance accuracy, efficiency, and objectivity, this algorithm holds great promise for assisting medical professionals in diagnosing and managing leukemia, ultimately contributing to improved patient care and outcomes.

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