JEEMECS (Journal of Electrical Engineering, Mechatronic and Computer Science ISSN 2614-4859
Vol. 8, No. 2, August 2025, pp. 85-90

Detection of Acute Lymphoblastic Leukemia Using SMMT and Watershed with DenseNet121 Classification

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Keywords
Acute Lymphoblastic Leukemia
Segmentation
Watershed
SMMT
DenseNet121

ABSTRACT

Acute Lymphoblastic Leukemia (ALL) is a type of blood cancer that commonly affects children and requires early detection to improve treatment success. This study proposes a method for ALL detection based on microscopic images of white blood cells using a deep learning approach. The research stages include data preprocessing with augmentation and the Self-Dual Multiscale Morphological Toggle (SMMT) method, segmentation using the Watershed method to separate the cell nucleus and cytoplasm, and classification using the DenseNet121 architecture. The dataset used consists of four classes of blood cells and is processed to be balanced before being trained on the model. The evaluation was carried out based on three batch-size testing scenarios to measure the effect of configuration on model performance. The results showed that the combination of SMMT and Watershed segmentation methods improved the quality of visual image features, while classification using DenseNet121 provided high accuracy with the best results at batch size 8, reaching 97%. This study proves that the combination of segmentation and deep learning techniques effectively detects ALL and can be further developed for automatic diagnostic systems.

1. Introduction

Blood cells play a crucial role in the human body, especially in oxygen transport, nutrient distribution, and the defense system against infection. Blood cells are categorized into three main types: red blood cells (erythrocytes), white blood cells (leukocytes), and thrombocytes (platelets). Among these, white blood cells function as key components of the immune system and are further classified into five subtypes, distinguished by the presence or absence of cytoplasmic granules. [1]. Leukocytes are produced in the spinal cord and several glands of the body, but excessive production can cause serious disorders such as leukemia [2]. Leukemia is a condition when the body produces abnormal white blood cells in excessive amounts, thus inhibiting the normal function of healthy blood cells [3]. This disease is divided into several types, one of which is Acute Lymphoblastic Leukemia (ALL), are the most common type of leukemia in children. According to WHO data, in 2020 there were 437,033 cases of leukemia worldwide with a death toll in the last five years reaching 1.1 million cases and making it one of the highest causes of death from cancer worldwide, with Asia contributing almost 50% of cases. In Indonesia, cases of ALL in children are estimated to reach 4.32% per 100,000 children with a mortality rate of $0.44 - 5.3\%$ per 100,000 children [4]. Therefore, early detection is an important step in increasing the success of treatment.

One approach to detecting leukemia is digital image analysis for the segmentation and classification of infected white blood cells. Previous research by [5] used Local Adaptive Thresholding and morphological operations to improve the readability of ancient manuscripts. This method is more effective than global thresholding in reducing noise during text segmentation, with dilation as an image quality enhancer. Evaluation using PSNR showed a maximum result of $34.107\ dB$ indicating good image quality.

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Another study by [6] developed an automatic system to detect white blood cells from unstained microscopic images. Segmentation using modified Watershed, with preprocessing such as Euclidean distance transform, Otsu Thresholding, erosion, and dilation. As a result, the detection accuracy reached 65.42% on unstained images and 94.82% on stained images, indicating the effectiveness of this method in improving the accuracy of white blood cell detection.

Further research by [7] examined breast cancer classification using DenseNet121 with statistical and texture feature extraction. With segmentation as the initial stage to reduce noise, this model achieved an accuracy of 98.87% and a precision of 99.45%. These results prove that segmentation before classification can improve model performance and demonstrate the superiority of DenseNet121 in producing high accuracy.

Based on this, this study proposes the application of the SMMT and Watershed methods for the segmentation of microscopic images of white blood cells infected with ALL, which are then classified using DenseNet121. The purpose of this study is to improve the accuracy of early detection of ALL through a combination of deep learning-based segmentation and classification methods. The output produced includes segmentation results and classification models with accuracy evaluations that can be used as a reference in developing a digital image-based leukemia detection system.

2. The Proposed Method/Algorithm

2.1. Flowchart of Research Methods

Based on the flowchart on Fig. 1,

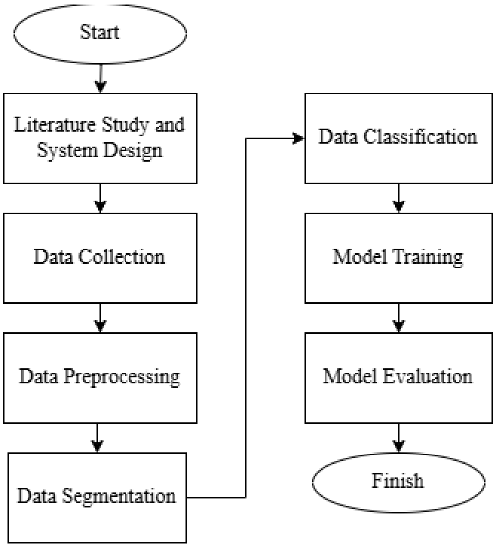

Fig. 1. Flowchart of research method

The research begins with image acquisition of cytological samples, followed by preprocessing steps like resizing and enhancement. Segmentation is applied using SMMT, Local Adaptive Thresholding, and Watershed methods to isolate regions of interest. The segmented images are then classified using DenseNet121 to predict the severity of Acute Lymphoblastic Leukemia (ALL), a malignancy of the bone marrow characterized by abnormal white blood cell production [8]. ALL can affect both children and adults, with symptoms including fatigue, bleeding, and infection, also diagnosis is typically established through a combination of blood examinations, bone marrow biopsy procedures, and cytogenetic evaluations. Treatment involves chemotherapy, targeted therapy, and bone marrow transplantation [9]. An image is mathematically described as a two-dimensional function of light intensity [10], with digital images represented as matrices of pixels [12]. These images can be color (RGB), grayscale, or binary, each with specific intensity representations [13]. Image processing techniques include quality enhancement, feature extraction, and segmentation [14], with the final goal being recognition and interpretation of image features [15].

Mathematical Morphology analyzes geometric structures in images [16], using operations such as erosion, dilation, opening, and closing to manipulate object shapes and remove noise [17].

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ISSN 2614-4859

Watershed segmentation views the image as a 3D surface, with boundaries created where pixel intensity values differ, allowing for accurate object separation. Convolutional Neural Networks (CNN) are deep learning architectures designed for visual data processing [19], efficiently extracting features from images for classification [20]. DenseNet, a deep-learning model, connects each layer to every other layer, enhancing feature propagation and addressing the vanishing gradient problem [22].

3. Method

This section outlines the detailed methods used to classify Acute Lymphoblastic Leukemia (ALL) severity levels. The research process includes data preprocessing, segmentation, and classification with DenseNet121. Each step is carefully selected to optimize feature extraction and improve classification performance.

3.1. Data Preprocessing

Before proceeding to the SMMT segmentation stage, the dataset undergoes several initial processes. The initial stage involves evaluating class distribution within the dataset, as imbalanced data can result in overfitting, where a condition in which the model demonstrates high accuracy on training data but fails to generalize effectively to unseen test data. To address this, data augmentation is applied to ensure that each class is represented by 1000 images. Following this, the dataset is split into three parts: training, validation, and testing data, to facilitate the proper evaluation of the model's performance. Self-Dual Multiscale Morphological Toggle (SMMT) is utilized to enhance critical features within the image, particularly the nucleus, which plays a crucial role in medical image analysis. The process begins with adjusting the brightness of the image to improve the contrast between the object of interest and the surrounding background. This is followed by morphological operations, namely dilation, which serves to emphasize object boundaries and erosion, which helps to eliminate background noise and unwanted artifacts. By combining these steps, SMMT enhances the visibility of important structures while suppressing irrelevant details. The main objective of applying SMMT in this study is to minimize the leaking effect during segmentation, ensuring that only the intended regions are accurately extracted without including neighboring areas or external objects. This preprocessing step is critical to ensure better performance in the subsequent segmentation and classification stages.

3.2. Data Segmentation

In this research, image segmentation is carried out using the Watershed algorithm, which interprets the image as a topographic map, where high-intensity (bright) pixels are viewed as peaks and low-intensity (dark) pixels are treated as valleys. The segmentation mimics the process of water gradually filling the valleys; when two bodies of water meet, virtual walls are built to separate them, resulting in the clear delineation of object boundaries, particularly between the nucleus and the cytoplasm. To further enhance the segmentation outcome, additional morphological operations are applied. Flood fill is used to fill empty regions within segmented areas, ensuring that internal gaps do not interfere with object continuity. Furthermore, closing operations are implemented to unite disconnected parts of the objects, strengthening the integrity of the segmented regions. Through this combination of Watershed and morphological enhancement, the segmentation results become more accurate, reducing noise and improving boundary clarity, which is essential for reliable feature extraction in subsequent classification stages.

3.3. Data Classification

The model is trained using pre-processed training data. The architecture used is DenseNet121, which connects each layer directly through Dense Blocks, allowing feature reuse and reducing the number of parameters. To manage the spatial data dimension, transition layers are applied using 1x1 convolutions and pooling to control the complexity of the model. In addition, bottleneck layers with 1x1 convolutions before 3x3 convolutions are used to optimize the number of parameters and computational efficiency. In the final stage, Global Average Pooling transforms the features into an average vector before the output layer, producing class probabilities for classification.

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4. Results and Discussion

Initially, the dataset is partitioned into three subsets, comprising 80% for training purposes, 10% for validation, and the remaining 10% for testing. The segmentation process begins with the adjustment of brightness and contrast to enhance the image, followed by converting it to grayscale to simplify the analysis of shape and texture. Gaussian Blur is then applied to smooth the image, reducing noise and intensity variations. Subsequently, dilation and erosion operations are performed, and the results are compared with the original image as part of the SMMT process. Depending on the differences between dilation, erosion, and the original image, pixels are selected accordingly. The watershed method is then applied to separate overlapping objects by calculating the Euclidean distance transformation, where each white pixel's distance to the nearest edge is computed, and the local peaks are identified as markers. The watershed algorithm utilizes these markers to partition the image into distinct regions by identifying the lowest contour boundaries between them, thereby producing well-separated objects. In the classification phase, DenseNet121 is utilized as a feature extractor with pre-trained weights from ImageNet through transfer learning, while the final fully connected layer is removed and adjusted for image classification. After feature extraction, global average pooling is used to summarize each feature map, reducing the risk of overfitting, followed by processing through a dense layer with 1024 neurons and a ReLU activation function. A 50% dropout is applied to further suppress overfitting, and the final layer uses softmax activation for multi-class classification. During initial training, the DenseNet121 weights are frozen to retain the features learned from ImageNet. The model is optimized using Adam, and sparse categorical crossentropy loss is employed for multi-class classification. To evaluate the model, tests with batch sizes of 4, 8, and 16 are conducted, with all scenarios using the same data split (80% training, 10% validation, 10% testing) and 30 epochs.

	precision	recall	f1-score	support
Benign	0.98	0.91	0.94	100
Early Pre-B	0.94	0.94	0.94	100
Pre-B	0.97	1.00	0.99	100
Pro-B	0.96	1.00	0.98	100
accuracy			0.96	400
macro avg	0.96	0.96	0.96	400
weighted avg	0.96	0.96	0.96	400

Fig. 2. Result Batch Size of 4

	precision	recall	f1-score	support
Benign	1.00	0.91	0.95	100
Early Pre-B	0.93	0.99	0.96	100
Pre-B	0.98	1.00	0.99	100
Pro-B	1.00	1.00	1.00	100
accuracy			0.97	400
macro avg	0.98	0.97	0.97	400
weighted avg	0.98	0.97	0.97	400

Fig. 3. Result Batch Size of 8

	precision	recall	f1-score	support
Benign	1.00	0.86	0.92	100
Early Pre-B	0.89	1.00	0.94	100
Pre-B	0.99	0.99	0.99	100
Pro-B	0.98	1.00	0.99	100
accuracy			0.96	400
macro avg	0.97	0.96	0.96	400
weighted avg	0.97	0.96	0.96	400

Fig. 4. Result Batch Size of 16

Based on Fig. 2, Fig. 3, and Fig. 4 the results indicate that batch size significantly impacts model performance. A batch size of 4 achieves an accuracy of 0.96, but the recall for the Benign class is only 0.91, suggesting some misclassification. With a batch size of 8, the accuracy increases to 0.97, and a perfect F1-score of 1.00 is achieved for the Pro-B class, with improved precision for the Benign class (1.00), indicating optimal performance. However, with a batch size of 16, while accuracy remains

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ISSN 2614-4859

high at 0.96, the recall for the Benign class drops to 0.86, highlighting that too large a batch size may reduce sensitivity to certain classes. Thus, batch size 8 provides the most consistent and optimal performance across all classes.

5. Conclusion

In this research, the impact of batch size variation on the performance of a leukemia cell type classification model was evaluated using the DenseNet121 architecture with microscopic images. The findings demonstrate that a batch size of 8 yields the most optimal and consistent results in comparison to batch sizes 4 and 16. Specifically, the model trained with a batch size of 8 achieved the highest accuracy of 0.97, accompanied by a very good F1-score across all classes. This batch size outperformed smaller and larger batch sizes, which were found to decrease sensitivity, especially for the Benign class. A batch size that is either too small or too large appears to affect the model's ability to differentiate subtle variations in certain classes, ultimately lowering its performance. Therefore, based on these results, batch size 8 is recommended as the ideal configuration for training the classification model in this context.

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