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Research Article

Evaluating Thresholding-Based Segmentation and Humoment Feature Extraction in Acute Lymphoblastic Leukemia Classification using Gaussian Naive Bayes

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Abstract:
This study, titled "Evaluating Thresholding-Based Segmentation and HuMoment Feature Extraction in Acute Lymphoblastic Leukemia Classification using Gaussian Naive Bayes," investigates the application of image processing and machine learning techniques in the classification of Acute Lymphoblastic Leukemia (ALL). Utilizing a dataset of microscopic blood smear images, the research focuses on the efficacy of thresholding-based segmentation and Hu moment feature extraction in distinguishing between benign and malignant cases of ALL. Gaussian Naive Bayes, known for its simplicity and effectiveness, is employed as the classification algorithm. The study adopts a 5-fold cross-validation approach to evaluate the model's performance, with particular emphasis on metrics such as accuracy, precision, recall, and F1-score. Results indicate a high precision rate across all folds, averaging approximately 84.13%, while exhibiting variability in accuracy, recall, and F1-scores. These findings suggest that while the model is effective in identifying malignant cases, further refinements are necessary for improving overall accuracy and consistency. This research contributes to the field of medical image analysis by demonstrating the potential of combining simple yet efficient techniques for the automated diagnosis of hepatological diseases. It highlights the importance of integrating image processing with machine learning to enhance diagnostic accuracy in medical applications.

Keywords: Acute Lymphoblastic Leukemia, Gaussian Naive Bayes, Hu Moment Feature Extraction, Image Segmentation, Thresholding, Machine Learning, Medical Image Analysis.

Dataset link: https://www.kaggle.com/datasets/mehradaria/leukemia/

1. Introduction

Acute Lymphoblastic Leukemia (ALL) is a critical hematological malignancy marked by the proliferation of immature lymphocytes. In recent years, advancements in digital image processing and machine learning have opened new avenues for medical diagnostics, particularly in hematological malignancies. The microscopic examination of blood smears plays a pivotal role in the diagnosis of ALL. However, manual examination is time-consuming and susceptible to human error, necessitating the need for automated, accurate, and efficient diagnostic techniques. In this context, the integration of image processing techniques for feature extraction and machine learning algorithms for classification emerges as a promising approach for the automated diagnosis of ALL.

The primary challenge in the automated analysis of microscopic images for leukemia detection lies in accurately segmenting cells from complex backgrounds and extracting distinctive features that aid in effective classification. Traditional methods often struggle with the variability in cell shapes and overlapping cells, leading to inaccuracies in subsequent classification steps. This study aims to address these challenges by applying thresholding-based segmentation and Hu moment feature extraction. The efficiency of these methods, however, has yet to be thoroughly evaluated in the context of ALL classification, particularly using Gaussian Naive Bayes, a simple yet potent classifier.

The primary objective of this research is to evaluate the effectiveness of thresholding-based segmentation and Hu moment feature extraction in the classification of ALL using the Gaussian Naive Bayes classifier. We aim to investigate the robustness of this combined approach in handling variations in cell morphology and the complexities of blood smear images. Further, the study seeks to determine the optimal parameters for segmentation and feature extraction to maximize the classification accuracy.

This research revolves around key questions: Can thresholding-based segmentation effectively isolate leukocytes from complex backgrounds in blood smear images? How well do Hu moment features represent the morphological characteristics of leukocytes for the purpose of leukemia classification? We hypothesize that the combination of thresholding-based segmentation and Hu moment feature extraction, when applied to Gaussian Naive Bayes classification, will yield high accuracy, precision, recall, and F1-score [1], [2] in distinguishing between benign and malignant leukocytes.

The scope of this research is confined to the evaluation of thresholding-based segmentation, Hu moment feature extraction, and Gaussian Naive Bayes classification in the context of ALL. The study utilizes a specific dataset of blood smear images, and the findings are contingent on the characteristics of this dataset. While the research aims to provide a comprehensive evaluation, it is limited by the inherent assumptions of the Gaussian Naive Bayes model and the singular focus on Hu moments for feature extraction. Additionally, the variability in imaging conditions and sample preparation techniques across different datasets may impact the generalizability of the results.

This study contributes to the field of medical image analysis by providing an in-depth evaluation of thresholding and Hu moment feature extraction in leukemia classification, a domain where such a combination has not been extensively explored. The findings will offer valuable insights into the applicability of simple yet effective machine learning techniques in medical diagnostics, potentially paving the way for more efficient and accurate automated diagnostic tools. Additionally, the research underscores the importance of integrating image processing and machine learning in addressing complex challenges in medical image analysis, particularly in hepatological studies.

2. Method

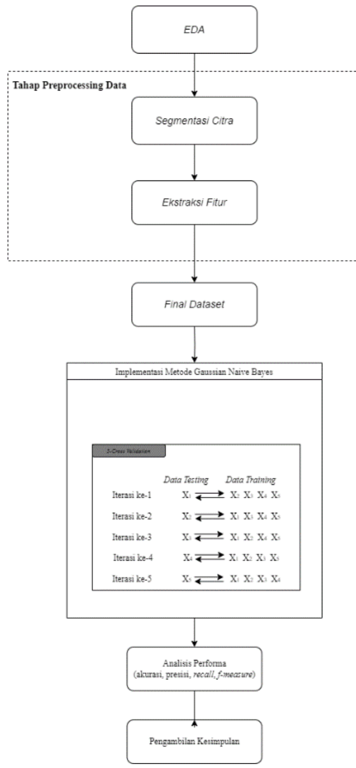

Figure 1: Gaussian Naïve Bayes Evaluation Workflow

This study adopts a quantitative research design, focusing on the application and evaluation of image processing and machine learning techniques for the classification of Acute Lymphoblastic Leukemia (ALL). The research involves several key stages: dataset collection, image segmentation using thresholding, feature extraction using Hu moments, classification using Gaussian Naive Bayes, and performance evaluation through cross-validation. Each stage is methodically designed to contribute to the overall objective of assessing the efficacy of these combined techniques in leukemia classification. A visual representation of the entire research process is illustrated in Figure 1.

Sample or Data Selection:

The dataset consists of microscopic blood smear images, labeled as either benign or malignant (ALL). These images are sourced from a publicly accessible medical database, ensuring a diverse representation of cases. The selection criteria include image quality, resolution, and the presence of distinguishable leukocytes. The dataset is split into a training set and a testing set, with the training set used for model development and the testing set reserved for model evaluation.

Tools and Technology Used:

The study utilizes Python for data processing and analysis, leveraging libraries such as OpenCV for image processing, NumPy for numerical operations, and scikit-learn for machine learning tasks. The thresholding and feature extraction processes are implemented using OpenCV, while scikit-learn provides the necessary functions for Gaussian Naive Bayes classification and cross-validation.

Data Collection Process:

The dataset is collated from the selected database, ensuring adherence to ethical guidelines and data quality standards. Each image undergoes a pre-processing phase to enhance contrast and reduce noise, facilitating better segmentation and feature extraction.

Image Segmentation using Thresholding

Thresholding is applied to segment leukocytes from the background [3]–[7]. The Otsu's method is used for threshold selection, which computes an optimal threshold value (T) that maximizes the between-class variance. The formula for basic thresholding is given by Equation (1):

$$\sigma_B^2(T) = \omega_0(T)\omega_1(T)[\mu_0(T) - \mu_1(T)]^2 \tag{1}$$

Where ω_0 and ω_1 are the probabilities of the two classes separated by the threshold T, μ_0 and μ_1 are the class means. In Figure 2 and 3 the results of image segmentation using Thresholding features on the dataset are shown.

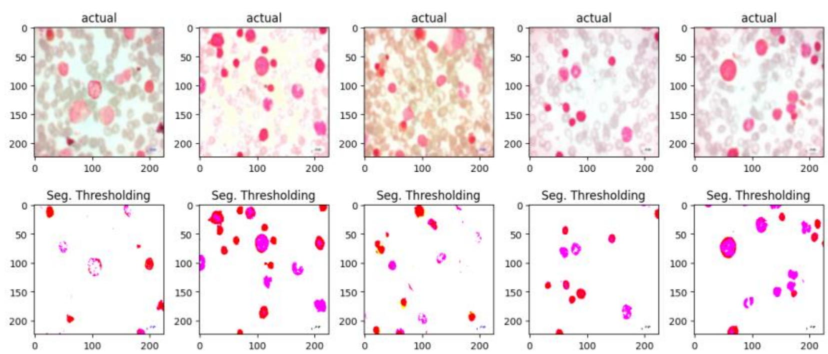

Figure 2: Thresholding Edge Detection Results for Healthy Class

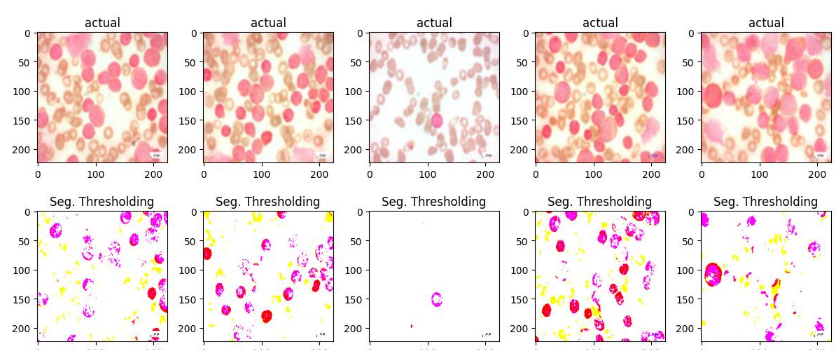

Figure 3: Thresholding Edge Detection Results for Bacterial Pneumonia Class

Feature Extraction using Hu Moments

Hu moments were extracted from the segmented images. Hu moments are a set of seven moment invariants derived from image moments, providing a basis for shape description[8], [9]. The Hu moments are defined as Equation (2):

$$\phi_1 = n_{20} + n_{02}$$
$$\phi_2 = (n_{20} + n_{02})^2 + 4n_{11}^2 \quad (2)$$

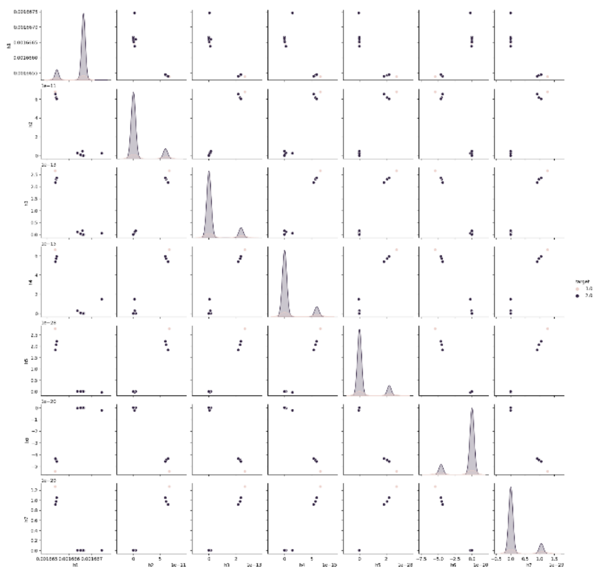

Figure 4: Scatter Plot Visualization of Extracted Hu Moments Features

Model Training and Testing

The Gaussian Naive Bayes classifier is employed, based on the assumption that the features follow a Gaussian distribution [10]–[14]. The probability of a class given a feature vector x is calculated using Bayes' theorem can be represented as Equation (3) [15]:

$$P(C_k|x) = \frac{P(C_k)P(x|C_k}{P(x)} \quad (3)$$

Performance Evaluation

5-fold cross-validation is used for model evaluation [16]–[18]. In each fold, the dataset is divided into five parts, using each part once as the test set while the remaining parts form the training set. This method ensures that every sample contributes to both training and testing, providing a comprehensive evaluation of the model's performance. The formulas for these metrics are as follow Equation (4) [19]–[21]:

$$\text{Accuracy} = \frac{\text{Number of Correct Predictions}}{\text{Total Number of Predictions}}$$

$$\text{Precision} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}} \quad (4)$$

$$\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}$$

$$F1 = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

3. Result and Discussion

The study evaluated the performance of the Gaussian Naive Bayes classifier in identifying Acute Lymphoblastic Leukemia (ALL) using thresholding-based segmentation and Hu moment feature extraction. The results, derived from 5-fold cross-validation, reveal notable variations in the classifier's performance across different folds.

Visualization of the Results

The detailed results are presented in Table 1 and visualized in Figure 5 for a clearer understanding and comparison of the metrics across different iterations.

Table 1: Performance Metrics Across 5-Fold Cross-Validation for the Gaussian Naïve Bayes Algorithm

K-n	Performa			
	Akurasi	***Presisi***	***Recall***	***F-Measure***
K-1	60.58%	73.26%	60.58%	65.50%
K-2	62.52%	74.30%	62.52%	67.08%
K-3	90.32%	91.32%	90.32%	88.39%
K-4	90.63%	91.31%	90.63%	88.94%
K-5	89.25%	90.46%	89.25%	86.67%
$\sum \boldsymbol{Avg}$	78.66%	84.13%	78.66%	79.32%

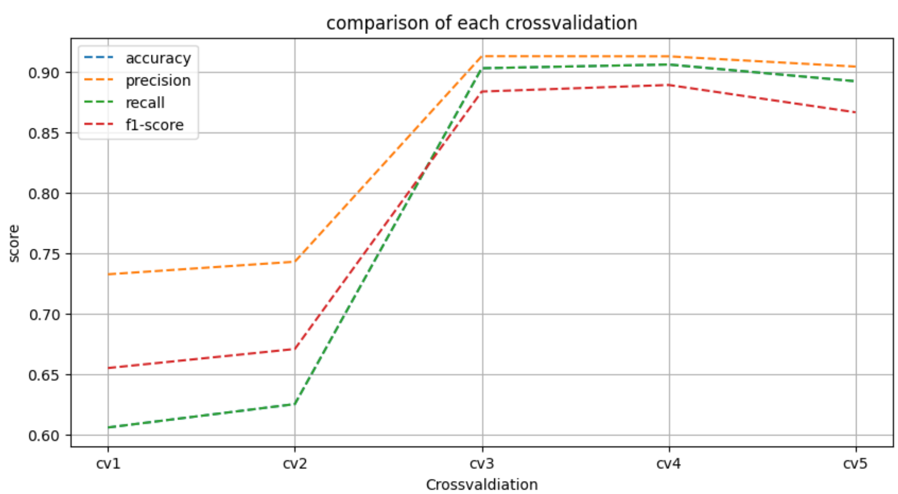

Figure 5: Visualization of Performance Metrics Across 5-Fold Cross-Validation for Gaussian Naïve Bayes Algorithm

These results could be visualized using a line graph or a bar chart to depict the variation across different folds.

Interpretation of the Results

The Gaussian Naive Bayes classifier demonstrated an average accuracy and recall of approximately 78.66%, while precision averaged at a higher 84.13%, and the average F1-score was around 79.32%. The variation in performance metrics across different folds indicates sensitivity to specific data subsets, suggesting potential inconsistencies in the dataset or the feature extraction process. The high precision suggests that the classifier is effective in correctly identifying malignant cases when it predicts them as such. However, the lower accuracy and recall in some folds indicate potential challenges in generalizing the model across varied data samples.

Discussion

The study's findings demonstrate the potential of thresholding-based segmentation and Hu moment feature extraction in leukemia classification. The Gaussian Naive Bayes classifier's performance, particularly in precision, indicates its suitability for this application. However, the variability across different folds points to the need for further optimization. The results align with previous studies that advocate for the integration of image processing and machine learning in medical diagnostics. The effectiveness of Hu moments in feature extraction, as evidenced by the precision scores, is consistent with their established robustness in shape-based image analysis.

The study's findings have significant implications for the development of automated diagnostic tools for ALL. The high precision of the model could potentially reduce the workload of medical professionals by accurately identifying malignant cases, though its variability calls for caution in direct clinical application. The research is limited by its reliance on a specific dataset and the inherent assumptions of the Gaussian Naive Bayes model. Additionally, the variability in the dataset, including differences in cell morphology and image quality, may have impacted the results.

Recommendations for Further Research

Further research should explore the integration of additional image processing techniques and alternative machine learning models to enhance accuracy and generalizability. Investigating the model's performance on a more diverse and larger dataset would be beneficial. Additionally, studies could focus on developing a more robust feature extraction method that can better handle the variability inherent in medical images.

4. Conclusion

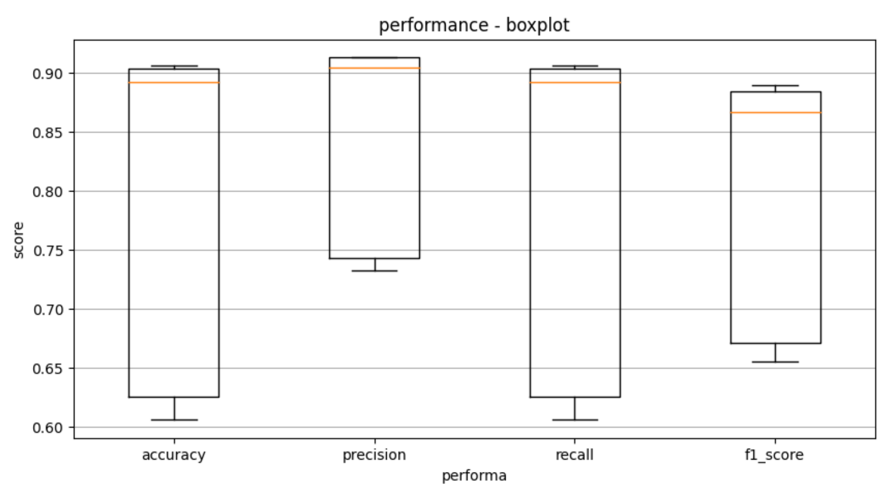

Figure 6: Boxplot of Performance Metrics Across 5-Fold Cross-Validation for Gaussian Naïve Bayes Algorithmky

The study's exploration into the utilization of thresholding-based segmentation and Hu moment feature extraction for the classification of Acute Lymphoblastic Leukemia (ALL) using the Gaussian Naive Bayes algorithm has yielded insightful results. The varied performance across different folds, with an average precision of approximately 84.13% and fluctuating accuracy, recall, and F1-scores, highlights both the potential and limitations of the approach. The consistently high precision across all folds demonstrates the model's effectiveness in correctly identifying malignant cases, addressing the initial hypothesis about the efficacy of these combined techniques. However, the variation in accuracy and recall points to a need for further refinement to enhance the model's consistency and generalizability. These findings contribute to the growing body of knowledge in medical image analysis, particularly in the automated classification of hematological malignancies, and highlight the importance of integrating image processing and machine learning techniques in medical diagnostics.

The research underscores the necessity for further investigation in this field. Future studies should focus on expanding the dataset to include a more diverse range of samples, exploring alternative machine learning models, and refining feature extraction methods to better handle the complexities of medical images. Additionally, the development of more sophisticated image preprocessing techniques could potentially improve the model's performance. In practical terms, these findings pave the way for more accurate and efficient diagnostic tools, which could significantly aid in the early detection and treatment of ALL, ultimately contributing to improved patient outcomes.

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