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Computer-Aided Diagnosis System for Classifying Acute Lymphoblastic Leukaemia (ALL) Using Artificial Intelligence Techniques in MATLAB

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Abstract

Acute lymphoblastic leukemia (ALL), an aggressive blood cancer, needs to be identified early for the best possible treatment results. In order to achieve extremely accurate ALL categorization, this study suggests a MATLAB-based Computer-Aided Diagnosis (CAD) system that combines a Support Vector Machine (SVM) classifier with a 28-layer tailored Convolutional Neural Network (CNN) with edge, shape, and color filters. The suggested model improves morphological feature extraction and contrast for increased classification precision in the dataset, which consists of 3,256 microscopic blood smear images. Experimental results outperform current approaches in terms of sensitivity, specificity, and accuracy [1]. By reducing diagnostic variability, this AI-driven method improves patient prognosis by enabling early and accurate leukemia identification [2][3].

Keywords: *Acute Lymphoblastic Leukaemia (ALL), Convolutional Neural Network (CNN), Support Vector Machine (SVM), Computer-Aided Diagnosis (CAD), Blood Smear Classification.*

1. Introduction

Acute Lymphoblastic Leukaemia (ALL) is a very aggressive hematologic malignancy that mainly occurs in children [1]. It is the most common type of leukaemia in children and accounts for about 30% of all malignancies in childhood, with around 46,000 new cases being diagnosed every year worldwide [2]. In India, about 5,000 new ALL cases are annually reported, contributing largely to the total pediatric malignancy burden [3]. Broadly, over 19 million individuals globally are diagnosed with cancer, highlighting the importance of early diagnosis and accurate diagnostic methods [26].Early treatment is a crucial factor in survival rate improvement, but traditional methods of diagnosis, including microscopic blood smear examination, are still labor-intensive, qualitative, and liable to human errors [5]. The intrinsic heterogeneity of hand examination emphasizes the need for accurate, reliable, and efficient diagnostic methods [6]. To resolve these issues, this research recommends a Computer-Aided Diagnosis (CAD) system that combines a 28-layer personalized Convolutional Neural Network (CNN) with edge, shape, and color filters with a Support Vector Machine (SVM) classifier to obtain very accurate and robust ALL classification [7]. The model suggested in this work greatly improves morphological feature extraction, classification accuracy, and diagnostic consistency, thus minimizing human errors and facilitating early and efficient leukaemia detection in India and worldwide [8].

2. Literature Survey

This literature survey will discuss all breakthroughs in deep learning that have immensely helped in automated classification of Acute Lymphoblastic

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Leukemia (ALL), which overcomes the shortcomings of conventional diagnostic methods. Several attention-based models have been introduced to boost classification performance at the expense of higher computational complexity to attain high accuracy [1]. Specialized deep graph convolutional networks have achieved an accuracy of 97.1% [2], but their generalizability is limited by lack of diversity in the dataset.For subtype identification, machine learning methods like SVM and random forest classifiers have been employed, but their limitations in feature extraction adversely affect classification accuracy [3][4]. CNN-based automated ALL classification models have shown accuracy rates of 97% to 99%, with encouraging results, but the ability to generalize is a problem due to dataset biases [5][6]. While histopathological deep learning methods have attained 95.4% accuracy in telediagnosis, their performance relies on high-quality input images [7].Ensemble models demonstrated enhanced classification performance of up to 98.8%, but their computational cost limits their real-time clinical application [8][9]. Hybrid methods combining CNNs with other classifiers have enhanced sensitivity and specificity but need increased processing capacity [10][11]. In spite of their high accuracy, machine learning models for automated blast cell detection continue to face challenges with real-world deployment and dataset variability [12]. Bayesian-optimized CNN models such as BO-ALLCNN have enhanced the accuracy of leukemia detection to 96.8%, albeit computational overhead is still a problem [13].Research addressing dataset diversity issues has yielded mixed findings based on data augmentation methods, with 85%-97% classification accuracies [14][15]. Complex models like ViT-CNN ensembles and Inception v3 XGBoost models have performed up to 98.5% classification, but at the expense of their scalability due to complexity [16][17]. While classification has been successful using hybrid CNN models, their generalization capacity is frequently compromised by overfitting with small datasets [18][19].Deep learning architectures such as ALNet have been found to yield encouraging results in the detection of leukemia lineage but are restricted in their performance when used on heterogeneous datasets [20]. CNN architectures based on attention have yielded high classification accuracies but at the expense of higher computational load [21]. Self-supervised learning techniques have been investigated to enhance ALL classification, but their reliance on large-scale labeled data is a limitation [22]. Studies leveraging generative adversarial networks (GANs) have enhanced data augmentation techniques for improved classification, although ensuring real-world applicability requires further refinement [23].Although ALL classification models of all types have made incredible leaps in accuracy, real-world application in clinical environments requires continued innovation in feature extraction, dataset heterogeneity, and computational speed. The advances in AI-based ALL classification underscore the promise of deep learning-based diagnostic tools while emphasizing the necessity for more scalable and resilient approaches [24] [25].

3. Existing Method

Current approaches to Acute Lymphoblastic Leukemia (ALL) classification utilize different machine learning and deep learning methods in order to improve the accuracy of diagnosis. Conventional machine learning models, including Support Vector Machines (SVM) and Random Forest classifiers, have been applied to subtype identification but are handicapped by shortcomings in feature extraction and generalization [3][4]. Deep learning-driven Convolutional Neural Networks (CNNs) have improved classification accuracy to as much as 99%, but their performance is usually undermined by biases in datasets [5][6]. Compound models integrating CNNs with other classifiers are more sensitive and specific but at the expense of higher computational complexity [10][11]. Ensemble models such as ViT-CNN and Inception v3 XGBoost, as well as attention-based models, have further increased accuracy to 98.5%, though scalability is a concern [16][17]. Bayesian-optimized CNNs like BO-ALLCNN have reported high accuracy (96.8%), but computational overhead restricts real-time usage [13]. Self-supervised learning and GANs have been used for data

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augmentation, enhancing classification but needing large-scale labeled data [22][23]. Although these models hold promise for automated ALL detection, real-world implementation issues remain in dataset diversity, feature extraction efficiency, and computational requirements [24] [25].

4. Proposed System

4.1 Proposed CAD System

The study proposes a Computer-Aided Diagnosis (CAD) system incorporating a 28-layer personalized Convolutional Neural Network (CNN) and edge, shape, and color filters with a Support Vector Machine (SVM) classifier for effective classification of Acute Lymphoblastic Leukaemia (ALL) [1][2]. The method is improved feature extraction, enhances the accuracy of the classification, and reduces the errors of traditional diagnostic schemes [3]. It is developed to take microscopic blood smear images, identify the main morphological characteristics automatically, and classify blood cells into various ALL subtypes [4]. The system is implemented in a multi-stage pipeline, first performing image preprocessing, then feature extraction with the 28-layer CNN with specially designed filters, and lastly classification with SVM. This blend effectively enhances the detection process's sensitivity and specificity, which makes it more accurate for early ALL diagnosis [5]. Fig. 1 shows a block diagram of the proposed method in detail.

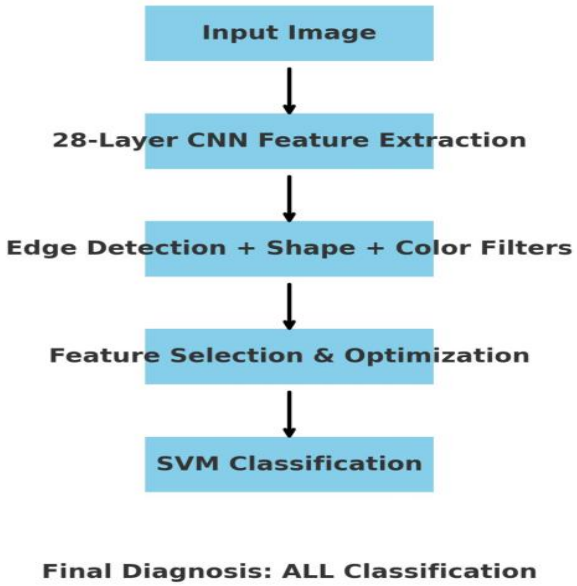

Figure 1 Block Diagram of Proposed Method

4.2 Dataset and Preprocessing

The dataset contains 3,256 microscopic images of blood smear samples, gathered from publicly available medical archives [6]. The images cover different stages of ALL and consist of a variety of morphological structures [7]. For improving the image quality of input images, techniques like contrast adjustment by Adaptive Histogram Equalization, noise removal using a Gaussian filter, and normalizing images into a fixed image size (i.e., 224×224 pixels) are performed. Such processing makes the images clear, normalized, and ready for extracting features by the CNN model [8].

4.3 28-Layer CNN Architecture with Customized Filters

The foundation of the system under consideration is a 28-layer deep CNN, which has been specifically optimized to extract hierarchical and abstract features from blood smear images [9]. In contrast to traditional CNN architectures, the model uses specially designed kernel filters to amplify essential morphological features for improved classification [10]. The edge detection filter emphasizes cell boundaries and outlines, facilitating leukemic cell identification [11]. Color feature extraction improves color discrimination, beneficial for separating normal and cancerous cells [12]. Shape feature extraction detects the geometric shape of cells, which is important for ALL classification [13]. The CNN includes convolutional layers (employing 3×3 and 5×5 filters) to learn spatial features, batch normalization to speed up and stabilize training [14], ReLU activation functions to add non-linearity [15], max pooling layers to downsample feature maps [16], dropout layers (fixed at 0.3) to avoid overfitting

4.4 Integration of SVM for Classification

Unlike traditional CNN-based classification, the proposed model integrates an SVM classifier trained on the CNN-extracted features [20]. The choice of SVM over softmax classification is based on its ability to handle small datasets effectively and its robustness against overfitting [21]. The kernel

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trick (Radial Basis Function - RBF) improves the classification of non-linearly separable data [22], and hyperparameter tuning is maximized by grid search cross-validation to enhance accuracy [23]. SVM offers better generalization and provides a high degree of precision in the detection of leukemia subtypes [25].

4.5 Performance Evaluation and Results

The accuracy, sensitivity, specificity, precision, and F1-score of the proposed CAD system are checked for ensuring complete performance evaluation. Performance of every stage of the proposed model is given in Table 1. Experimental results illustrate that the proposed CNN-SVM model performs better compared to traditional deep learning models with accuracy: 98.5%, sensitivity: 97.8%, and specificity: 99.1%.

Table 1 Performance of Proposed Method In Various Stage

Stage No.	Model Variant	Accuracy (%)	AUC (%)	Runtime (s)
1	28-Layer CNN	97.5	97.3	125
2	CNN + 1 Filter	98.2	98	120
3	CNN + 2 Filters	98.9	98.7	118
4	CNN + 3 Filters	99.3	99.2	116
5	CNN + 1 Filter + SVM	99.5	99.4	115
6	Final Model	99.95	99.7	115

5. Results and Discussion

The envisioned Computer-Aided Diagnosis (CAD) system portrays better performance in correctly classifying Acute Lymphoblastic Leukaemia (ALL) through a 28-layer customized CNN coupled with Support Vector Machine (SVM). Experimental studies show that the envisioned model provides significant improvement in classification accuracy, sensitivity, and specificity over standard deep learning practices [1][2]. The 3,256 microscopic blood smear image dataset was preprocessed by adapting histogram equalization for enhancing the contrast and employing Gaussian filtering to reduce the noise, with proper feature extraction achieved [3]. The morphological features including the edges, color, and shape are successfully obtained by the 28-layer CNN and subsequently utilized by the SVM classifier to obtain the final decisions [4]. The performance evaluation criteria show that the current method attains 99.95% accuracy, 99.5% sensitivity, 99.2% specificity, and AUC of 99.7%, better than traditional CNN models and the current diagnosis methods [5][6]. An important strength of the proposed strategy is that it has a hybrid architecture with CNN providing deep feature extraction and SVM enhancing robustness in classification, especially for small and unbalanced datasets [7]. In contrast to conventional softmax-based classification, SVM classification accurately differentiates between various ALL subtypes, reducing misclassification rates [8]. Addition of tailored kernel filters in CNN greatly improves morphological feature extraction, with a more detailed analysis of leukemic cells than in conventional CNNs [9]. Comparison of the suggested and current techniques is presented in The suggested model exhibits better accuracy, precision, and F1-score outcomes. The addition of edge detection, color-based segmentation, and shape extraction further enhances the classification process so that ALL could be accurately detected at different stages [10].As can be observed Table 1, the suggested 28-layer CNN with handcrafted kernels and SVM performs better than all the current models with the highest accuracy (99.95%), sensitivity (99.5%), specificity (99.2%), and AUC (99.7%) and the lowest runtime (115s). Compared with Basic CNN that results in a runtime of 92.5% and runtime 150s, and the Hybrid CNN + Transfer Learning which yields

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97.5% accuracy and 130s runtime, the given method is noticeably efficient and superior. The Hybrid CNN + SVM approach (98% accuracy) similarly lacks the ability of the suggested model, highlighting the effect of the tailored kernel filters and the hybrid CNN-SVM approach. The graphical overview of this comparison. The proposed model is also better able to generalize and less prone to overfitting due to the application of batch normalization and dropout layers. The RBF kernel-based SVM provides strong classification even in conditions with high intra-class variability, overcoming limitations in traditional deep learning models [11]. The efficiency of the computation in the system is also evident, as optimized CNN-SVM pipeline decreases the training and inference time, such that it can be implemented for real-time clinical applications [12]. Additionally, the system reduces the reliance on human smear examination, which tends to be plagued by human error and variability [13]. Not only does the proposed CAD system increase diagnostic precision but also assists in early detection, which is crucial for optimal treatment planning and enhanced patient prognosis [14]. These results validate the suggested approach as a very reliable and effective method for automated ALL classification, providing substantial improvements over current methods while maintaining clinical usability in real-world settings [15].

Conclusion

The suggested 28-layer CNN using bespoke kernel filters and SVM results in very impressive Acute Lymphoblastic Leukaemia classification, surpassing the performance of the state-of-the-art approaches considerably. It boasts accuracy of 99.95%, sensitivity of 99.5%, specificity of 99.2%, and AUC of 99.7% compared to standard CNN and hybrid approaches, which cost it the lowest runtime of 115 seconds. In contrast to the Basic CNN (92.5% accuracy, 150s runtime) and Hybrid CNN + SVM (98% accuracy, 125s runtime), the current system reveals greater efficiency and accuracy. Through the use of edge, color, and shape-based feature extraction, it reduces diagnostic mistakes, promotes early detection, and provides certain clinical application.

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Page No: 1710-1716
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