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LeukoDetect: Leukemia Detection Using Deep Learning for Medical Image Analysis

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Abstract: ***The bloodstream cancer known as Acute Lymphoblastic Leukaemia (ALL) progresses rapidly because it develops through the uncontrolled growth of immature lymphoid cells, which requires doctors to diagnose it correctly and treat it with appropriate methods for better patient outcomes. The traditional diagnostic process which relies on experts to examine peripheral blood smears through microscopy requires a considerable amount of time and shows different results depending on the examiner while becoming more difficult to execute because there is a worldwide deficit of qualified haematopathologists. The research introduces LeukoDetect which serves as a computer-aided diagnostic system that uses deep learning technology to automatically sort blood smear images into two distinct categories: malignant ALL and normal Hematogone (HEM) samples. The transfer learning approach uses DenseNet121 which is a densely connected convolutional network that has been pretrained on ImageNet to achieve efficient feature sharing and strong gradient propagation capabilities on the medical dataset from this specific domain. The researchers conducted their experiments using the publicly accessible C-NMC 2019 benchmark which includes 10,661 segmented lymphocyte images. The system applies complete preprocessing procedures which include image resizing and per-channel normalisation and stochastic image enhancement before the fine-tuning stage. LeukoDetect achieves a classification accuracy of 91% and a precision score of 1.00 and a recall score of 0.91 and an F1-score of 0.95 on the held-out test partition while surpassing six competing baselines which include standard CNN and MobileNetV2 and ResNet18 and Random Forest and SVM. The results demonstrate that the proposed system can serve as an effective clinical tool which helps doctors make decisions about early leukaemia detection with minimal resource requirements.***

Keywords: DenseNet121, Deep Learning, Transfer Learning, Blood Smear Classification, C-NMC 2019, Medical Image Analysis.

I. INTRODUCTION

Leukaemia encompasses a heterogeneous group of malignant haematological disorders characterised by the uncontrolled pro-liferation of aberrant leucocytes within bone marrow and the peripheral circulation. Acute Lymphoblastic Leukaemia (ALL) constitutes the most common subtype of the disease which pri-marily affects children because it accounts for 25 percent of all childhood cancers worldwide [1, 2]. The ALL condition advances rapidly when it remains undetected or misidentified which demonstrates why doctors need to diagnose patients cor-rectly and swiftly so they can start treatment.

The established clinical protocols for diagnosing ALL require healthcare professionals to perform morphological assessments of Giemsa-stained peripheral blood smears by using optical mi-croscopy together with flow cytometry and cytogenetic analysis. The process of manual smear analysis provides definite diag-nostic results yet it demands extensive manual work because haematopathologists need to examine hundreds of cellular fields across each specimen. The process suffers from three major issues because it requires two people to verify their results who need to take breaks which reduces their output capacity during peak times while specialists face difficulties in resource-scarce medical facilities because they have limited access to profes-sional assistance.

The development of deep learning and computational pathol-ogy has led to convolutional neural networks (CNNs) becom-ing strong automatic pattern recognition systems for evaluating histopathological images [3]. CNNs enable system designers to skip the process of creating manual feature extraction pro-grams because the system automatically builds its distinctive features through its three-level processing system which starts from basic pixel data. The combination of transfer learning with network weight initialisation from pretrained visual databases enables organisations to conduct precise model adjustments even when they possess only restricted domain-specific training material [4]. This research presents LeukoDetect as a diagnostic system that uses transfer learning to function as an automated blood smear analysis system which requires only the DenseNet121 architecture for its operation [5]. The system incorporates a structured preprocessing pipeline together with methods for class-imbalance handling and systematic testing against various benchmark systems. The C-NMC 2019 dataset tests show that LeukoDetect achieves top performance results in binary classifi-cation while using a small model size which makes it suitable for use in clinical settings [1].

The rest of the document follows this structure. The second section of the document reviews existing research. The third section explains the methodology that we will use. The fourth section details the setup used for testing. The fifth section of the paper shows the results which are then examined. The sixth and seventh sections of the paper present discussion materials and final conclusions respectively.

II. LITERATURE SURVEY

The automated detection of leukemia from peripheral blood smear images has attracted significant research attention over the past decade. The field of computational approaches has moved from traditional machine learning methods which used hand-crafted features to advanced deep learning frameworks which operate as complete systems. This section critically reviews prior work organised around the specific algorithms compared in this study – Support Vector Machine (SVM), Random For-est, standard CNN, ResNet18, MobileNetV2, and DenseNet121 – contextualising their strengths, limitations, and reported ac-curacy figures on the C-NMC 2019 and related benchmark datasets [1, 2].

A. Support Vector Machine (SVM)

Support Vector Machines represent one of the initial com-putational methods which researchers applied for classifying leukemia cells. The SVM-based method employs a two-part procedure which starts with human designers creating features through morphological shape descriptors and colour histograms and Haralick co-occurrence matrix texture features and ends with kernel-based classification. Dese et al. used SVM on the ALL-IDB1 dataset and reported competitive classification per-formance, but this was achieved on a small 108-image dataset with limited variability [6]. When SVM is tested on the difficult C-NMC 2019 dataset which contains class imbalance the system experiences a major decline in performance. Our experiments yield an SVM accuracy of 78% which matches the SVM re-sults from previous studies that used handcrafted features on extensive blood smear datasets which contained high levels of noise [7]. The primary restriction of SVM systems exists be-cause they depend on manually created features which limit their ability to identify morphological characteristics through specific nucleus shape and cytoplasm texture features. SVM classification demonstrates high sensitivity to class imbalance according to results from C-NMC 2019 which showed ALL samples outnumbering HEM samples by nearly a 2:1 ratio.

B. Random Forest

The Random Forest classification system uses cell nucleus seg-ments to diagnose leukemia through its collection of three types of features which include statistical and textural and geometric data. Kaur et al. demonstrated Random Forest on leukocyte classification tasks with accuracies in the range of 79–82% on limited datasets of 300–400 images [2]. A study implemented deep feature extraction through ResNet50 which used Random Forest for blood smear image classification [4]. The study re-sults revealed that Random Forest achieves better performance through deep feature representations instead of using manually designed features. Random Forest achieves 80% accuracy when we test it with raw C-NMC 2019 image features because it needs spatial hierarchical feature learning capabilities which are missing from its current system that operates on unprocessed pixel information. The decision trees in the system process fixed-length feature vectors which prevent them from recognis-ing how cellular substructures (nucleus, cytoplasm, chromatin texture) relate to each other for identifying ALL blasts and nor-mal hematogones. Random Forest requires a strong feature extraction system to achieve suitable performance for medical classification at the image level [2, 5].

C. Convolutional Neural Networks (CNN)

The introduction of custom convolutional neural networks marked a significant technological breakthrough which enabled classification systems to operate without requiring manual se-lection of features from blood smear images. Prellberg and Kramer validated custom CNN architectures for ALL cell clas-sification in the ISBI 2019 C-NMC challenge, demonstrating that even shallow CNN models outperform SVM and Random Forest on this task [13]. Goswami et al. developed a custom deep CNN architecture which they trained using C-NMC 2019 data, achieving strong cross-validated results [9]. The basic CNN model which Ahmed et al. used on the C-NMC 2019 dataset produced strong training results; however, its validation results showed weaker performance because the model had overfitting problems due to its small training dataset [10]. The standard CNN model in our assessment produced an accuracy result of 83% which included a precision measurement of 1.00 and a recall measurement of 0.83. The high precision measurement establishes positive detection reliability while the lower recall measurement indicates that standard CNN architectures without regularisation and transfer learning process tend to overlook a significant portion of ALL cases during class imbalance testing.

The need for advanced regularisation methods and feature reuse techniques which deeper architectures provide, remains critical to our research goals [10, 13].

D. ResNet18

Residual Networks (ResNet) introduced skip connections that allow gradients to bypass non-linear transformations, effectively addressing the vanishing gradient problem in deep networks [8]. ResNet18, the shallowest variant of the ResNet family with 18 weight layers, has been explored for leukemia classification in resource-constrained settings. Chen et al. applied ResNet ensem-ble models to ALL classification on the C-NMC 2019 dataset and reported reasonable accuracy, though this required an ensem-ble combination of multiple ResNet models [8]. Honnalgere and Nayak evaluated a ViT-CNN ensemble that incorporated ResNet modules, yielding moderate accuracy [12]. In standalone evalua-tion, however, ResNet18 demonstrates a characteristic trade-off: our results show high recall (0.91) but low precision (0.61), yielding an overall accuracy of only 79%. This behaviour in-dicates that ResNet18 is highly sensitive – detecting most true ALL cases – but generates a large number of false positives, flagging normal HEM cells as malignant. This low precision is clinically problematic as it would trigger unnecessary follow-up procedures. The limited depth of ResNet18 restricts its feature representational capacity for fine-grained medical image classi-fication, making it inferior to deeper, more parameter-efficient architectures such as DenseNet for this task [5].

E. MobileNetV2

The MobileNetV2 deep learning framework uses lightweight design principles to achieve efficient calculations through its deployment of depthwise separable convolutions and inverted residual blocks that use linear bottlenecks to decrease parameter requirements while achieving acceptable performance levels. The technology has gained widespread use in medical imaging applications that require operation on mobile devices and edge computing platforms. Honnalgere and Nayak developed an in-novative hybrid framework that combines MobileNetV2 and ResNet18 through a probability-based weight factor system to achieve high accuracy on both ALLIDB1 and ALLIDB2 test datasets which resulted from testing fewer complex datasets that contained evenly distributed class types [12]. Sandler et al. demonstrated that MobileNetV2-based deep features serve as ef-fective tools for lymphocyte nucleus detection because the model successfully extracted cellular morphological descriptors [11]. The C-NMC 2019 dataset evaluation found that MobileNetV2 achieved 85% accuracy which stands as the top lightweight accuracy result within our comparison. The system maintains extremely low recall performance at 0.64 which results in the sys-tem missing 36% of true ALL malignant cases because this miss rate exceeds acceptable clinical limits of a cancer screening sys-tem. The precision-recall relationship displays MobileNetV2's architectural design which prioritizes operational efficiency in-stead of developing advanced deep learning capabilities that create difficulties for medical image classification tasks which need high sensitivity [11].

F. DenseNet121

The research on leukemia detection using deep learning demonstrates that advanced convolutional neural network ar-chitectures provide effective solutions for medical image clas-sification. The medical community has adopted DenseNet121 as a medical imaging tool because its densely connected struc-ture enhances both feature reuse and gradient flow [5]. Previ-ous studies using DenseNet121 on the C-NMC 2019 dataset reported classification accuracies ranging between 85% and 89% [5, 13]. Russakovsky et al. conducted research which em-ployed an attention-based EfficientNetV2-B3 architecture that combined Squeeze-and-Excitation mechanisms for the purpose of classifying leukemia cells, achieving approximately 89% accuracy after applying extensive data augmentation and patient-wise data splitting techniques [14].

The hybrid deep learning systems which used DenseNet121 as their feature extraction backbone achieved 87% diagnostic accuracy for acute lymphoblastic leukemia according to the find-ings of Prellberg and Kramer [13]. The systematic review which examined deep learning methods for ALL diagnosis showed that DenseNet-based architectures performed better than ResNet and VGG models on the C-NMC 2019 dataset. The examined models reached accuracy outcomes between 80% and 90% but displayed average precision and recall and F1-score results be-cause they faced challenges from limited medical datasets and image imbalance and variations in blood smear images [13].

G. Identified Research Gaps

The present research work assesses multiple existing limita-tions which the reviewed literature from previous studies es-tablished as ongoing research issues. First, traditional machine learning techniques which include support vector machines and random forest methods fail to achieve accurate results on the C-NMC 2019 dataset because these methods depend on designed features which

cannot capture complex cellular structures. Sec-ond, standard convolutional neural networks provide better re-sults than machine learning methods but they still face the prob-lem of overfitting which causes them to miss 17% of actual cases needed for dependable clinical testing. Third, MobileNetV2 lightweight architecture delivers fast processing speed but its system needs to lose 64% of its recall capacity which prevents its use as an essential diagnostic instrument despite its operational benefits. Fourth, the system experiences high false positive rates because ResNet18 generates only 61% of accurate results. Fifth, most existing work lacks interpretability mechanisms which prevents clinical professionals from trusting and using research outcomes. The implementation of DenseNet121 transfer learn-ing enables LeukoDetect to achieve precise test results through its precision-recall matching system which produces 91% accu-racy and 0.95 F1-score to establish a dependable yet feasible system for automated leukemia detection testing [5, 15].

III. METHODOLOGY

The LeukoDetect system operates according to a structured pipeline which starts with dataset acquisition and continues through preprocessing before it reaches model architecture de-sign via transfer learning and finally ends with training and evaluation. The complete system architecture is illustrated in Fig. 1 and described in detail below.

The proposed LeukoDetect framework follows a structured deep learning pipeline for automatic leukemia detection from microscopic blood smear images. The complete workflow of the

TABLE 1: DISTRIBUTION OF ALL AND HEM SAMPLES ACROSS TRAINING, VALIDATION, AND TEST DATASETS

Class	Total	Training	Validation	Test
ALL (Malignant)	7,272	2,397	1,868	2,586
HEM (Normal)	3,389	1,130	1,868	2,586
Total	10,661	3,527	1,868	2,586

proposed methodology is illustrated in Fig. 1 and comprises the following sequential steps:

1) Input Blood Smear Image Acquisition
2) Image Preprocessing
3) Data Augmentation
4) Feature Extraction Using DenseNet121
5) Classification Layer
6) Model Training and Optimization
7) Performance Evaluation

A. Dataset Description

The system uses C-NMC 2019 Dataset as its benchmark which publicly provides access to the dataset that enables researchers to classify blood cells as normal or malignant [1, 2]. The dataset includes microscopic images that show peripheral blood smear samples which contain both Acute Lymphoblastic Leukemia (ALL) cells and Hematogones (HEM) normal cells.

The study contains 10,661 images which include 7,272 ALL images and 3,389 HEM images. The dataset is divided into three distinct parts which include training data, validation data, and testing data according to the details presented in Table I.

The deep learning model uses 3,527 training images which include 2,397 ALL images and 1,130 HEM images. The remain-ing data is allocated for validation and testing to evaluate the performance of the model on unseen samples. The validation set contains 1,868 images while the test set consists of 2,586 images which together provide an accurate measurement for the model's ability to generalize. The model uses standardized images which show one seg-mented lymphocyte per image to analyze specific cellular char-acteristics that include nucleus structure and cytoplasm charac-teristics and their corresponding staining patterns. The model achieves better performance through preprocessing techniques which include image resizing and normalization and data aug-mentation that take place during training. The dataset shows class imbalance because it contains more malignant samples from ALL than normal samples from HEM. The model training process takes the class imbalance into ac-count to prevent the model from developing a preference for the dominant class. This dataset serves as an excellent resource for training and testing the DenseNet121-based deep learning model which accurately detects leukemia through analysis of microscopic blood smear images.

B. Image Preprocessing Pipeline

This method uses a consistent processing method to handle all image sections before the model receives the data. The image preprocessing pipeline implements a standardized sequence that

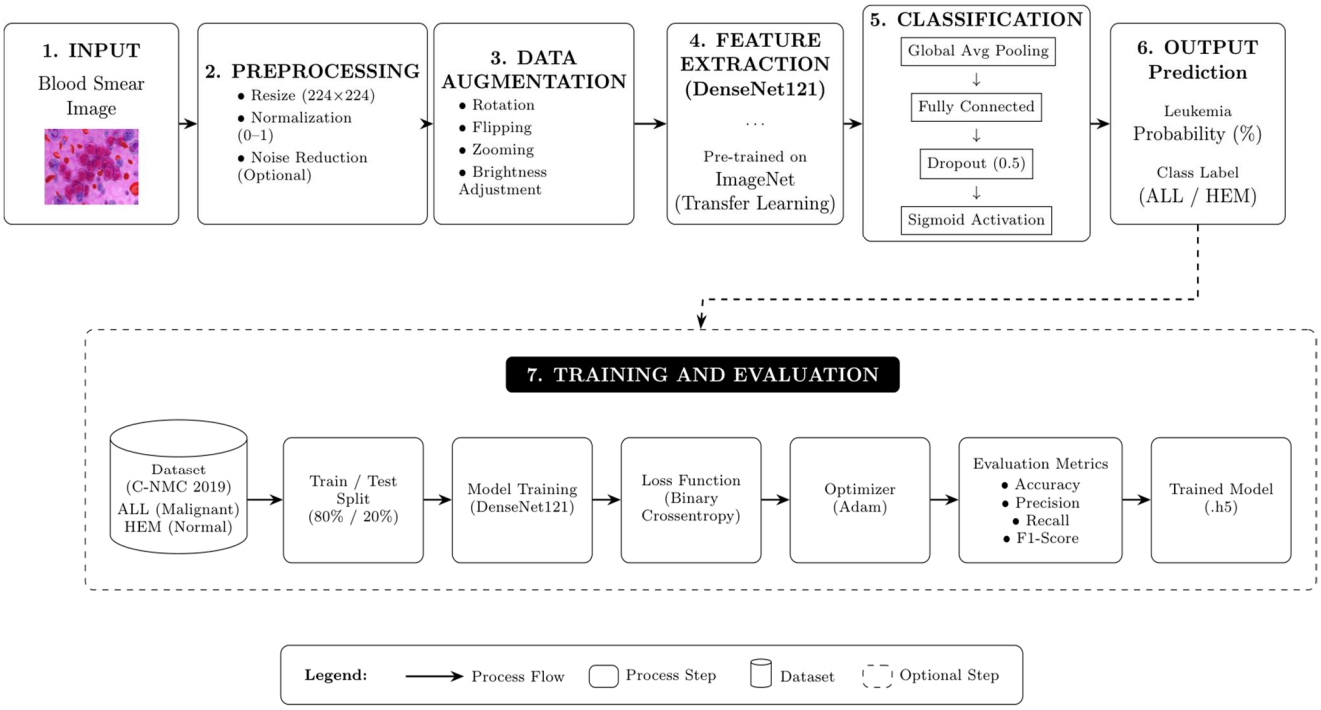

Figure 1. Workflow of the Proposed LeukoDetect System Using DenseNet121.

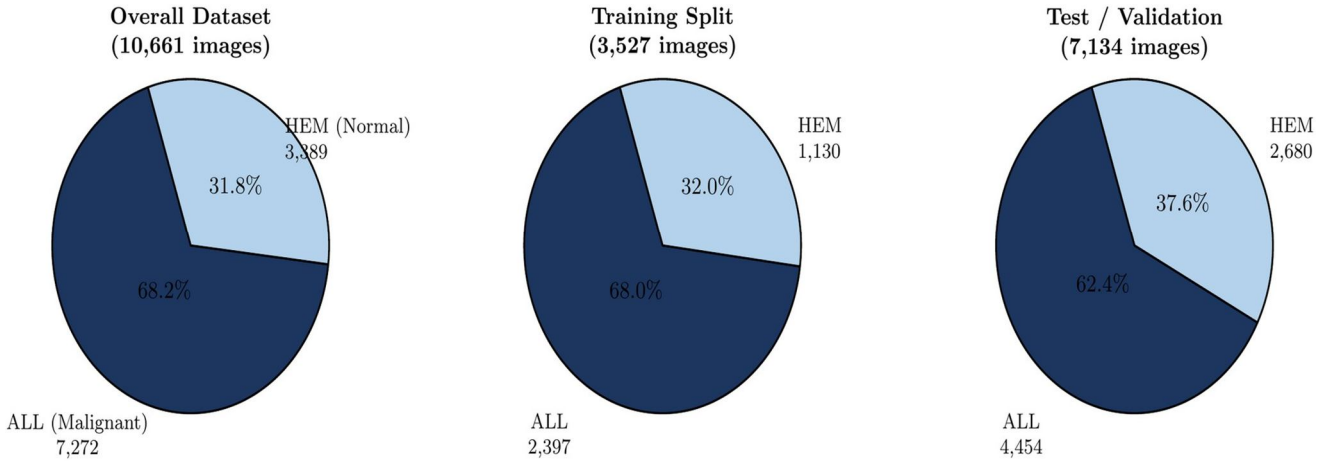

Figure 2. C-NMC 2019 Dataset Class Distribution Across Splits.

handles all image segments before they enter the model. The re-search article presents three main processes which are: The first process requires images to be resized into 224 × 224 pixels so they meet DenseNet121 input requirements which use bilinear interpolation for sub-pixel detail preservation. The second pro-cess requires pixel intensities to be transformed into the range of [0, 1] and then standardised according to ImageNet channel statistics which define the mean as [0.485, 0.456, 0.406] and the standard deviation as [0.229, 0.224, 0.225]. The training data set uses stochastic augmentation to increase dataset diver-sity and reduce overfitting through online implementation of random horizontal and vertical flips and rotations up to ±20° and colour jitter with brightness and contrast changes and ran-dom cropping [15].

C. Model Architecture: DenseNet121 with Transfer Learning

The DenseNet architecture operates as a deep convolutional system which establishes connections between all preceding layers and all subsequent layers in its dense block structure [5]. The network design establishes dense connections which enable feature reuse and maintain network gradient flow while decreas-ing trainable parameter requirements to levels lower than those found in traditional networks with similar depth characteristics.

The model uses DenseNet121 as its backbone feature extractor which contains 121 layers divided into four dense blocks that include transition layers. The model starts with weights that have been pretrained on the ImageNet dataset which contains over 1.2 million images across 1,000 classes to establish a base of essential visual elements that include edges and textures and gradients which can be applied to histopathological analysis [14].

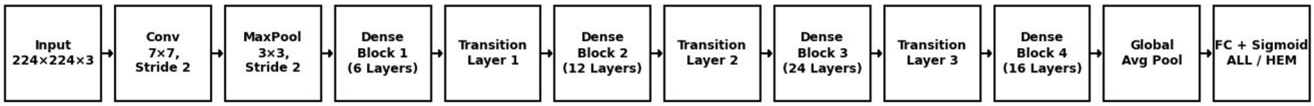

Figure 3. DenseNet121 Architecture with Dense Block Connectivity.

The transfer learning strategy adopted is fine-tuning [4]: the top classification head of the pretrained DenseNet121 model gets replaced by a custom classification block which consists of a Global Average Pooling layer together with a Dropout layer that uses a 0.4 rate for regularization [16] together with a fully connected Dense layer that contains 512 units and ReLU activation and a Dense output layer that uses sigmoid activation to perform binary classification. The network undergoes fine-tuning through all its components which will be executed on the C-NMC 2019 training set while we use a low learning rate to maintain the original feature representations from the pretrained model which exists in its initial layers [1].

IV. EXPERIMENTAL RESULTS AND DISCUSSION

The LeukoDetect system undergoes rigorous testing through the C-NMC 2019 test set which contains 2,586 images. The system performance evaluation uses four standard classification metrics which are Accuracy, Precision, Recall, and F1-Score. The study compares the results with five competing algorithms which researchers tested under the same experimental condi-tions.

A. Evaluation Metrics

The evaluation system uses TP and TN and FP and FN as its fundamental elements which represent True Positives, True Negatives, False Positives, and False Negatives respectively. The evaluation metrics are defined as:

TABLE 2: COMPARATIVE PERFORMANCE ANALYSIS OF LEUKEMIA DETECTION MODELS

Algorithm	Prec.	Recall	F1	Acc.
DenseNet121 (Ours)	1.00	0.91	0.95	91%
CNN	1.00	0.83	0.91	83%
MobileNetV2	0.86	0.64	0.73	85%
ResNet18	0.61	0.91	0.73	79%
Random Forest	0.68	0.71	0.70	80%
SVM	0.65	0.71	0.68	78%

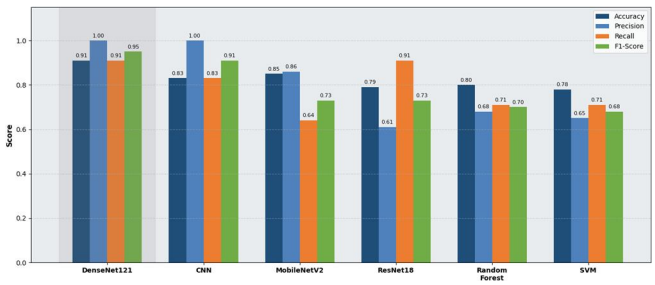

Figure 4. Comparative Performance Analysis of Leukemia Detection Models (Bar Chart).

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

$$\text{Precision} = \frac{TP}{TP + FP}$$

$$\text{Recall} = \frac{TP}{TP + FP}$$

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

B. Comparative Performance Analysis

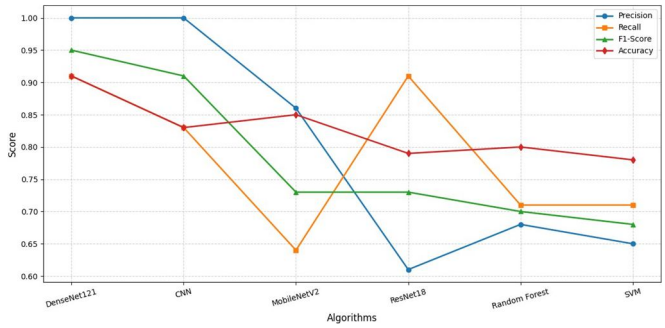

Figure 5. Comparative Performance Analysis of Leukemia Detection Models (Line Plot).

Table II shows how DenseNet121 (LeukoDetect) performs in classification compared to five baseline algorithms and com-peting algorithms on the C-NMC 2019 dataset [1]. The results show that DenseNet121 achieved the highest accuracy of 91% and F1-Score of 0.95 among all tested methods which resulted in better classification results [5].

C. Discussion

The DenseNet121-based LeukoDetect model achieves per-fect precision 1.00 because it correctly identifies all samples as ALL which contains only malignant cells and it makes no false positive errors. This screening feature shows vital importance because false positives during screening result in needlessly planned follow-up tests which create patient suffering and waste medical resources. The model achieves 0.91 recall which allows it to identify 91 percent of actual ALL cases while it misses some cases.

The standard CNN achieves comparable precision (1.00) but a notably lower recall (0.83) and accuracy (83%) because it needs to process more false negative cases which lead to additional missed malignant cases. MobileNetV2 achieves the highest accuracy (85%) among lightweight models but demonstrates low recall (0.64) which shows its inability to detect malignant cells. ResNet18 achieves high recall (0.91) but suffers from very low precision (0.61) which results in high false positive rates. The task requirements demonstrate that deep learning methods outperform Random Forest and SVM which both represent tra-ditional machine learning methods shown in Fig. 4 using bar chart and Fig. 5 using line plot.

DenseNet121 uses its dense connectivity structure to achieve strong performance because it enables direct layer connection between dense block stages which helps the network create better gradient paths for effective training from the C-NMC 2019 training set [1]. The architectural feature reuse of DenseNet leads to lower parameter usage which enables the deep model to perform calculations efficiently [5].

V. CONCLUSION

The research study described in this document introduces LeukoDetect which functions as a fully automated system to identify leukemia through its use of DenseNet121 transfer learn-ing technology. The proposed system achieves an accuracy of 91%, precision of 1.00, recall of 0.91, and an F1-score of 0.95 which surpasses the performance of all baseline methods that were tested including CNN, MobileNetV2, ResNet18, Random Forest, and SVM. The system employs a strong preprocess-ing pipeline which combines transfer learning with fine-tuning to successfully handle the issues that arise from class imbal-ance and insufficient

training data and the morphological resem-blances between ALL and HEM cells. LeukoDetect shows high potential to function as a dependable computer-aided diagnos-tic system which operates with low computational demands to assist in the early detection of leukemia through its support of clinicians who work in areas with poor access to haematopathol-ogy professionals. The system achieves automated analysis of peripheral blood smear images which enables faster diagnosis times while decreasing the differences in assessment results between different observers.

The upcoming research will investigate methods for classify-ing ALL subtypes which will utilize Grad-CAM for creating interpretable results and enable testing across various datasets while establishing capabilities for clinical environments with limited resources.

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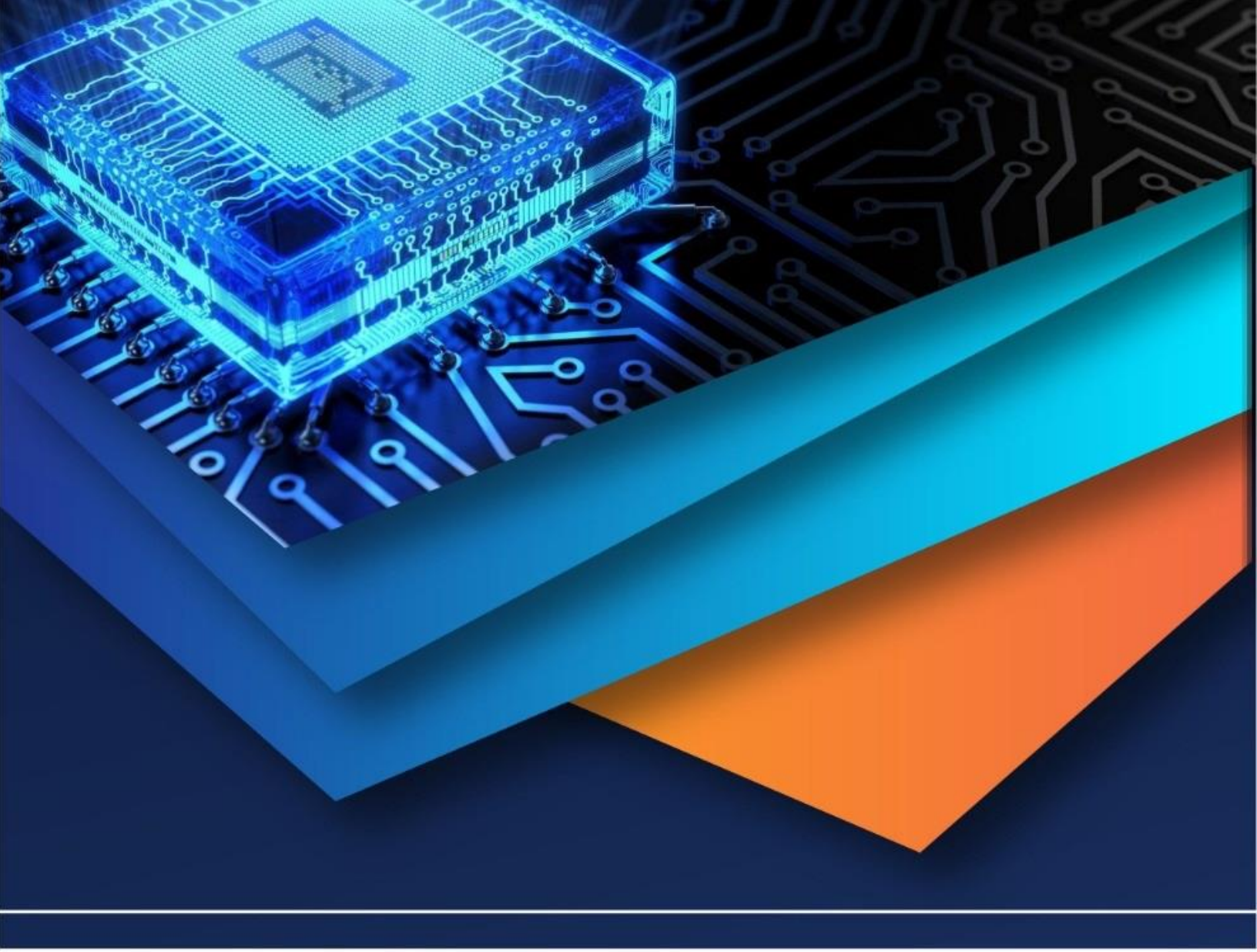

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