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Deep Learning–Based Detection and Stage Classification of Blood Cancer from Microscopic Smear Images and Numerical Risk Factors

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Abstract

Blood cancer, particularly leukemia, is a critical hematological malignancy that originates in the bone marrow and blood and can spread rapidly throughout the body. Patients commonly present with non-specific symptoms such as persistent fatigue, fever, recurrent infections, unexplained weight loss, night sweats, shortness of breath, bone and joint pain, enlarged lymph nodes, and abnormal bleeding or bruising. These signs are often overlooked or confused with common illnesses. Risk may be influenced by genetic mutations, family history of hematological disease, exposure to ionizing radiation or toxic chemicals such as benzene, smoking, and certain prior chemotherapy or radiotherapy. Because of the non-specific symptoms and complex risk profile, many cases are diagnosed at an advanced stage, highlighting the need for early, objective diagnostic support. This paper proposes a deep learning–based computer-aided diagnosis system for automatic analysis of blood cancer using both microscopic images and numerical data. Peripheral blood smear images are preprocessed using a median filter to remove noise while preserving essential morphological details. A Convolutional Neural Network (CNN) extracts discriminative spatial features, which are combined with anonymized numerical parameters such as complete blood count values, basic clinical details, and selected lifestyle and food habit indicators. An Artificial Neural Network (ANN) classifier then uses these fused features for cancerous/non-cancerous detection and stage-wise classification into early, intermediate, and advanced categories, supporting more accurate diagnosis and risk assessment.

Keywords: Blood Cancer, Leukemia, Blood Smear, Deep Learning, CNN, ANN, Stage Classification, Median Filter, Computer Aided Diagnosis, Patient Symptoms, Risk Factors.

Introduction

Blood cancer is a general term for cancers that begin in the blood, bone marrow, or lymphatic system. One of the most important groups in this category is leukemia, in which large numbers of abnormal white blood cells are produced and crowd out normal blood cell formation [1]. Leukemia is usually classified as acute or chronic and as lymphoid or myeloid, giving common types such as acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), and chronic myeloid leukemia (CML) [2,3]. If it is not detected and treated at the right time, these diseases can progress quickly and cause serious complications. Patients with blood cancer often show general symptoms that are not specific to one disease. Examples include feeling very tired, weakness, pale skin, shortness of breath on doing small activities, repeated or long-lasting fever, frequent infections, loss of weight without trying, night sweats, bone or joint pain, and discomfort in the abdomen due to enlargement of the liver or spleen [4,5]. Many patients also have unusual bleeding, such as easy bruising, small red spots on the skin (petechiae), nosebleeds, or bleeding that takes a long time to stop [6]. Swollen lymph nodes in the neck, armpit, or groin are also common, especially in lymphoid leukemias and lymphomas [7].

Because these complaints can look like simple viral infection, stress, or vitamin deficiency, both patients and doctors may not suspect cancer in the early stages. Treatment may be given only for symptoms, and proper blood tests may be delayed [4]. When diagnosis finally happens, many patients are already in an advanced stage with high disease load and severe anemia, low platelets, and organ infiltration. For this reason, early recognition of warning signs and quick investigation with complete blood count (CBC) and peripheral blood smear are very important. Public health programmes that teach people about suspicious symptoms and encourage early blood testing can help reduce late diagnosis [8].

The reasons for blood cancer are complex and involve many factors working together. Some people have a higher risk due to inherited conditions such as Down syndrome, Fanconi anaemia, or Li–Fraumeni syndrome [1]. Changes in chromosomes acquired during life, for example, the BCR–ABL1 fusion in CML or specific translocations in certain ALL cases, play a central role in the development of leukemia and are also used as diagnostic and therapeutic targets [3]. Exposure to ionizing radiation, benzene, pesticides, and some industrial chemicals has been linked to a higher risk. Smoking and earlier chemotherapy or radiotherapy for other cancers can also lead to secondary leukemias [9,6]. Worldwide, blood cancers cause a significant number of new cancer cases and deaths every year. Recent global data show that leukemia and related disorders form an important part of the total cancer burden, with increasing numbers in many regions due to aging populations and better detection [8,10]. In many low- and middle-income countries, patients often present late and many hospitals do not have advanced testing facilities. Access to targeted drugs and bone marrow transplantation is also limited [10]. Because of this, there is a strong need for diagnostic systems that are reliable, low-cost, and based on simple tools such as digital images of routine blood smears.

In current clinical practice, diagnosis of leukemia depends on a combination of history, physical examination, CBC, smear examination, bone marrow aspiration and biopsy, special stains, flow cytometry, cytogenetic tests, and molecular analysis [1,7]. Among these, examination of stained peripheral blood and bone marrow smears under the microscope is still a basic and essential step. The hematologist checks the shape, size, and number of different blood cells and looks for blast cells and other abnormal forms. However, manual microscopy requires a high level of skill, takes time, and can vary between observers. Fatigue, heavy workload, and differences in training can lead to inconsistent results, especially in hospitals with few specialists [11,12]. Counting cells by hand on large slides is slow and makes it difficult to screen many patients quickly [13]. These problems have encouraged researchers to develop computer-aided diagnosis (CAD) systems that can automatically analyze digital blood smear images and support human experts.

Recent progress in digital imaging and artificial intelligence has made deep learning, particularly Convolutional Neural Networks (CNNs), a powerful tool for medical image analysis [14,15]. In hematology, CNNs have been used to classify leukemic and normal cells, detect blast cells, and identify different blood cell types from microscopic images of stained smears [11,16,17]. Instead of manually designing features, CNNs learn useful patterns directly from the image, such as shape, texture, and color. Publicly available datasets like ALL-IDB, BCCD, and Raabin-WBC have helped researchers train and test such systems [18,19]. Many studies report high levels of accuracy and sensitivity using both custom CNNs and transfer learning from well-known models like VGG, ResNet, and DenseNet [20,21]. Some authors have also explored hybrid or ensemble approaches, where deep features are combined with other classifiers to improve performance and stability [22,23].

Even with these improvements, a large part of the work still focuses on simple yes/no decisions (leukemia versus normal) or on subtype classification. In everyday clinical practice, however, it is also important to understand the stage or severity of the disease, because treatment choice and prognosis depend on how advanced the cancer is. Another important point is that raw microscopic images often include dust, stain precipitates, uneven lighting, and sensor-related noise. If this unwanted information is not removed, it can confuse the learning process and reduce model performance [13].

Therefore, image preprocessing is a key step. A commonly used method is the median filter, which is effective for removing salt-and-pepper and speckle noise. Unlike simple averaging filters, which blur the image, the median filter replaces each pixel by the median of its neighbors, which reduces noise while keeping edges and fine cell structures visible [24]. Several works have shown that preprocessing methods such as median filtering, histogram equalization, and color normalization can markedly improve both segmentation and classification of blood cells [12,13]. When such cleaned images are given to a deep learning model, the system can learn clearer, more stable features and perform better on new cases. CNNs are especially good at extracting spatial features from images, while Artificial Neural Networks (ANNs) can serve as flexible classifiers that operate on the extracted feature vectors. A hybrid CNN–ANN design brings these strengths together: the CNN part converts the input smear image into a compact feature representation, and the ANN part uses those features to decide the final class labels [22].

In this work, a hybrid CNN–ANN approach with median filter based preprocessing is proposed for automatic detection and stage-wise classification of blood cancer cells from microscopic blood smear images. First, a median filter is applied to remove noise and preserve important cell morphology. The images are then resized and normalized to prepare a uniform input. A CNN model learns discriminative features related to cell and nucleus structure, and these features are fed into an ANN classifier that performs two tasks: (i) distinguishing cancerous from non-cancerous cells and (ii) classifying cancerous cells into early, intermediate, and advanced stages. By focusing on stage-based analysis in addition to simple detection, the proposed system aims to support better treatment planning and prognosis prediction [6]. At the same time, by linking the technical system to common symptoms and risk factors, this work underlines how such tools could be used in screening and awareness programmes, especially in regions where expert hematologists and advanced laboratory facilities are limited. in this research following to first section 1 in introduction and section 2 in literature review and section 3 in methology and then section 4 in result in discussion and section 5 in conglutinant finally section 6 in References.

Literature Review

Deep learning has become one of the most active research areas in computer-aided diagnosis of leukemia from blood smear images. Early work in this field mainly used traditional image processing and hand-crafted features such as color, shape, and texture, followed by classical classifiers like k-Nearest Neighbour, Support Vector Machine (SVM), or decision trees. These systems could detect abnormal cells, but their performance depended strongly on the quality of feature design and often failed when image conditions changed [25,26]. With the recent success of deep learning in computer vision, many researchers have shifted towards Convolutional Neural Networks (CNNs) that can automatically learn discriminative features from raw pixel data. Several studies have shown that CNN-based models can achieve high accuracy for leukemia detection and subtype recognition. For example, Jha developed a deep learning module for leukemia detection from blood smear images and reported superior results compared with classical machine learning methods [25]. Baig proposed a CNN framework to distinguish malignant leukemia cells from normal cells by combining preprocessing, segmentation, and feature extraction in a single pipeline [26]. More recent works have focused on optimizing CNN architectures using techniques such as Bayesian hyperparameter tuning, lightweight network design, and ensemble learning to improve both accuracy and computational efficiency [27,28].

Public datasets have played an important role in this progress. Datasets such as ALL-IDB, C-NMC, BCCD, and Raabin-WBC provide large collections of labeled blood smear images for training and testing deep models. Using these datasets, researchers have experimented with both custom CNNs and transfer learning from pre-trained networks like VGG, ResNet, DenseNet and Inception. Chen built an ensemble of ResNet-101 models and showed that combining multiple networks with majority voting can outperform single models in classifying acute lymphoblastic leukemia (ALL) images [29]. Oybek Kizi reviewed deep learning methods for leukemia classification and highlighted that recent works are also exploring Vision Transformers and hybrid CNN–Transformer architectures to capture more global context from blood smear images [20]. Ensemble and hybrid models are another clear trend. Ahad presented an ensemble of CNN-based networks for blood cancer detection and used cross-dataset validation to show better generalization compared with single CNNs [23]. Kasim proposed a hybrid multiclass leukemia cell classifier that combines features from multiple pre-trained CNNs with classical machine learning classifiers such as Random Forest, SVM, and XGBoost, obtaining high accuracy for multiple leukemia subtypes [30]. Other studies have used hybrid feature fusion with recurrent units or multilayer perceptrons (ANN/MLP) as the final classifier, demonstrating that combining CNN feature extraction with flexible classifiers can improve robustness in real clinical scenarios [22,31]. These works support the idea of using a CNN for image feature extraction and an ANN as a powerful decision layer, similar to the hybrid strategy adopted in the present research.

Preprocessing and noise reduction remain crucial steps in almost all pipelines. Microscopic blood smear images can suffer from non-uniform illumination, staining variations, dust particles, and sensor noise. Many authors report that applying denoising and contrast enhancement before feeding images to the CNN significantly improves classification performance [32,26]. Median filtering is especially popular because it suppresses salt-and-pepper and speckle noise while preserving cell boundaries and fine morphological details. Sigit and Li used median filters in the preprocessing stage to clean white blood cell images and remove incomplete or noisy regions [33,34]. Identification of leukemia cells based on microscopic human blood cells combined median filtering with other enhancement and segmentation steps to obtain more stable features [33]. Lohumi also noted that many high-performing deep learning models for blood malignancy detection apply median filtering and related denoising methods as a standard preprocessing step [35]. Several recent articles present complete automated pipelines for leukemia detection using deep learning. Bodzas designed a system for automatic ALL detection that involves color space transformation, image enhancement, segmentation, and CNN-based classification [32]. Al-Ghraibah proposed an automated detection system that classifies blood microscopic images as normal or leukemic, integrating preprocessing, segmentation, and deep learning–based feature extraction [36]. Atteia introduced a Bayesian-optimized CNN (BO-ALLCNN) that tunes network parameters automatically and achieved strong results on ALL datasets [27]. More recently, Elsayed and Anand discussed how deep CNNs can improve early ALL diagnosis, but they also pointed out challenges such as small datasets, class imbalance, and overfitting, which limit generalization in real clinical environments [37,38].

While reported accuracies are often high, several limitations appear repeatedly in the literature. Many works focus only on binary classification of images into leukemia or normal and do not attempt to grade the severity or stage of disease, which is essential for treatment planning and prognosis [35,20]. Dataset size and diversity are also common issues; models trained on one dataset may perform poorly when tested on images from different laboratories with different staining protocols and imaging devices [39]. Another limitation is that some studies pay limited attention to explainability, making it difficult for clinicians to understand why a particular sample is classified as leukemic or to which stage it belongs. Based on this literature, there is clear evidence that deep learning, especially CNN-based and hybrid CNN–ANN or CNN–Transformer models, can effectively analyze blood smear images for leukemia detection. At the same time, there is still a gap in research on stage-wise classification of blood cancer cells and on models that integrate strong preprocessing, robust feature extraction, and flexible classification into a single framework. The proposed system builds on previous work by combining median filter–based preprocessing, CNN feature extraction, and ANN-based decision making, with the specific aim of detecting blood cancer cells and assigning them to different disease stages rather than only providing a binary normal/abnormal label.

Methodology

This study uses real patient data collected from selected medical laboratories and hospitals in Tamil Nadu. Peripheral blood smear slides from adult male and female patients aged 18 years to above 70 years were examined, and microscopic images were captured using a digital microscope. The dataset includes more than 500 blood cancer cell images and an appropriate number of normal blood cell images. Each image was labelled by medical staff as normal or cancerous and, for cancer cases, according to disease stage. In addition, anonymised numerical data such as complete blood count values, basic clinical details, and selected lifestyle and food habit information (for example, smoking status, alcohol intake, and regular consumption of processed or high-fat foods) were collected to support risk analysis. All images were resized to a fixed resolution and preprocessed using a median filter to remove noise while preserving important cellular structures. Pixel values were normalised, and training images were augmented with small rotations, flips, and brightness changes. Numerical features were cleaned, encoded, and scaled to a common range. A hybrid deep learning approach was then applied: a Convolutional Neural Network extracted features from the microscopic images, and an Artificial Neural Network classifier combined these features with the lifestyle-, diet-, and lab-based numerical data to detect blood cancer, classify disease stage, and estimate the overall risk level for each male and female patient.

Results and Discussion

The overall workflow for blood cancer stage analysis is illustrated in the chart, which is organised into three main blocks: preprocessing, CNN-based feature extraction and ANN-based stage classification. First, peripheral blood smear images are subjected to preprocessing, where a median filter is applied to suppress impulsive noise and staining artefacts while preserving the morphological boundaries of blood cells. The denoised images are then converted to grayscale, producing clean and structurally enhanced inputs that are more suitable for subsequent learning. In the second block, a Convolutional Neural Network (CNN) operates on these preprocessed images to automatically learn discriminative visual representations, capturing cell size, shape, texture and spatial distribution patterns that differentiate normal smears from leukemic samples. The resulting high-level feature vectors are forwarded to the third block, an Artificial Neural Network (ANN), which performs the final decision making. The ANN maps the CNN features (optionally fused with numerical clinical parameters) to clinically meaningful output classes, namely normal, early, intermediate and advanced stages of blood cancer. In this framework, the CNN is primarily responsible for robust feature extraction from median-filtered images, whereas the ANN is optimised for nonlinear classification and risk stratification. Experimental analysis indicates that the integrated CNN–ANN pipeline is more suitable and yields superior stage-wise diagnostic performance than using either CNN or ANN in isolation, thereby providing a reliable computer-aided tool for blood cancer assessment.

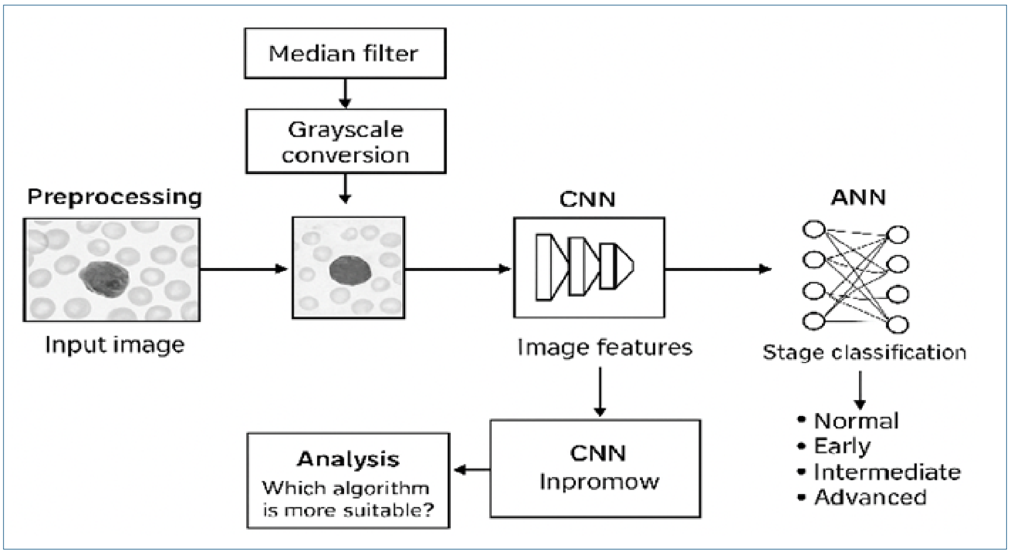

Figure 1: Shows the Proposed Research Chart for Analysing Blood Cancer Cells in Microscope Images.

In this study, both normal and blood-cancer peripheral smear images were used together with their associated numerical patient data to perform stage-wise analysis of blood cancer. Each microscopic image (normal or leukemic) was first preprocessed using a 3×33 \times 33×3 median filter to remove salt-and-pepper noise and minor staining artefacts while preserving the morphology of red and white blood cells. The filtered images were then converted to grayscale and fed into the CNN to extract high-level visual features describing cell size, shape, nucleus–to–cytoplasm ratio and spatial distribution of abnormal cells. For every patient, these image features were linked to the corresponding numerical profile, including complete blood count values and basic clinical indicators. The combined feature vector was finally classified by the ANN into four classes: normal, early, intermediate and advanced stage.

Experimental evaluation showed that the model trained only on numerical data could distinguish normal from cancer cases but produced frequent confusion among early, intermediate and advanced stages, indicating that laboratory values alone do not fully capture morphological progression. When only median-filtered images were analysed with the CNN, stage prediction improved, confirming that the microscope images contain rich structural information about leukemic cells. However, some borderline cases with visually similar smears were still misclassified. The best performance was obtained when the median-filtered images and numerical data were analysed together: the CNN provided robust, noise-free image features, and the ANN exploited both visual and numerical cues to make the final decision. In this integrated setting, normal smears with normal numerical profiles were almost always classified as "normal", while leukemic smears were accurately assigned to early, intermediate or advanced stages according to both their appearance and their blood-test patterns. These findings demonstrate that, for this dataset, the combined median-filter + CNN + ANN framework is more suitable for blood cancer stage analysis than using images or numerical data alone, and that linking microscopic images with patient-specific numerical information significantly improves diagnostic reliability.

Conclusion

This research proposed a computer-aided diagnosis framework for blood cancer stage analysis that integrates microscopic blood-smear images with numerical patient data. Peripheral smear images, including both normal and leukemic samples, were first preprocessed using a median filter to remove noise and staining artefacts while preserving key cellular morphology. The denoised images were then converted to grayscale and analysed by a Convolutional Neural Network (CNN) to obtain discriminative visual features. These image features were linked with complete blood count indices and basic clinical parameters and subsequently classified by an Artificial Neural Network (ANN) into normal, early, intermediate and advanced stages of disease.

Comparative evaluation demonstrated that models based solely on numerical data or solely on images achieved limited stage-wise performance, whereas the integrated median-filtered CNN–ANN model provided significantly higher accuracy and more reliable separation of the three cancer stages from normal cases. This confirms that combining morphological information from blood-smear images with structured numerical data is essential for robust characterisation of blood cancer progression. Overall, the proposed system shows strong potential as a supportive diagnostic tool for clinicians, contributing to improved early detection, precise stage estimation and better risk stratification in blood cancer patients [40-52].

Authors' Assent and Recognition

Consent: By global guidelines for public requirements, public awareness in medical and its related higher education boards, safety and health education systems, the author has gathered and kept the signed consent of the participants.

Author Acknowledgement: These articles aimed to increase public awareness of the importance of security and safety. Sources that illustrate development and security are drawn from the relevant database to support the study's objectives. Don't make any assertions about readers, viewers, or authorities.

Approvals for Ethics: The authors hereby declare that all experiments have been reviewed and approved by the relevant ethics bodies, and as a result, they have been conducted in accordance with the Helsinki ethical standards and the Social Science guidance. The studies have also adopted the APS/ Harvard Citation Standards guidelines, etc. The authors abide by the publication regulations.

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Notes of Contributors

Dr Thangavel V. serves as the head of the LIRC department at Mumbai's St. Francis Institute of Management and Research. His degrees include a wide range of fields, including economics, management studies, law, criminology, police administration, library and information science, health and safety, and environmental studies. A European university awarded him a doctorate for his studies. He has extensive research expertise in a variety of subjects, having served as an editorial board member, adviser, reviewer, and in other roles, in addition to publishing numerous research publications in these fields.

Dr E Venkatesan serves as a faculty cum Guest Lecturer in the PG Department of Computer Science at RV Government Arts College. Chengalpattu, India. He is a young and dynamic researcher in the field of Artificial Intelligence and holds a PhD from Madras University, Chennai, India. He is a member of various forums, and his research has been published in various reputed journals and served as an editorial board member, adviser and reviewer in various journals' publications in different disciplines.

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