

RESEARCH ARTICLE

OPEN ACCESS

EFFICIENT ACUTE LYMPHOBLASTIC LEUKEMIA CLASSIFICATION USING GLCM AND HSV FEATURES WITH RESERVOIR COMPUTING ON TALEQANI HOSPITAL DATASET

Michael Angello Qadosy Riyadi^{*1}, Sulthonika Mahfudz Al Mujahidin², Nur Alifia Rustan³
A'isyah Belqis Febi Aulia⁴, Muhammad Adib Kamali⁵,
Farah Zakiyah Rahmanti⁶ and Khodijah Amiroh⁷

^{1, 2, 3, 4, 5, 6, 7}Department of Information Technology, Telkom University, Surabaya Campus, Surabaya, Indonesia.

¹<https://orcid.org/0009-0003-0853-0989>, ²<https://orcid.org/0009-0000-5873-1082>, ³<https://orcid.org/0009-0006-8714-5684>
⁴<https://orcid.org/0009-0007-0786-1443>, ⁵<https://orcid.org/0000-0002-1013-4358>, ⁶<https://orcid.org/0000-0003-1827-5857>,
⁷<https://orcid.org/0000-0001-9498-0553>

E-mail: *michaelangelo@student.telkomuniversity.ac.id, sulthonikamahfudzam@student.telkomuniversity.ac.id,
nralifalrs@student.telkomuniversity.ac.id, aisyahbelqis@student.telkomuniversity.ac.id, adibmkamali@telkomuniversity.ac.id,
farahzakiyah@telkomuniversity.ac.id, dijaamirah@telkomuniversity.ac.id

ARTICLE INFO

Article History

Received on: March 02, 2026
Reviewed on: April 02, 2026
Accepted on: May 01, 2026
Published on: July 31, 2026

Keywords:

Acute Lymphoblastic Leukemia,
Echo State Network,
Next-Generation Reservoir
Computing,
Feature Extraction,
Resource-Limited Clinical
Settings.

ABSTRACT

Detection of Acute Lymphoblastic Leukemia (ALL) from peripheral blood smear (PBS) images poses a major challenge in clinical diagnostics owing to intricate morphological variations and constrained computational resources in many healthcare facilities. This study proposes an efficient classification framework using Echo State Network (ESN) and Next-Generation Reservoir Computing (NG-RC), applied to a dataset of 3,256 PBS images from 89 patients. Feature extraction via Gray Level Co-occurrence Matrix (GLCM) and HSV histograms, combined with 10-fold cross-validation, yielded robust results. NG-RC achieved superior performance over ESN, with an average accuracy of 0.9917, precision of 0.9918, recall of 0.9917, F1-score of 0.9917, ROC-AUC of 0.9989, and remarkably low execution time of 1.88 seconds on CPU-only hardware. In additional benchmarking, NG-RC demonstrated competitive accuracy against high-end deep learning models trained on NVIDIA A100 GPU—DenseNet201 (accuracy 0.9978, execution time 176.5 s) and ResNet18 (accuracy 0.9966, execution time 54.6 s)—while outperforming most literature methods (e.g., YOLOv4 at 0.9600, Modified DCNN at 0.9769) and offering orders-of-magnitude faster inference without GPU dependency. These findings position NG-RC as a lightweight, resource-efficient alternative to deep learning, enabling reliable, rapid ALL detection in computer-aided diagnosis systems for resource-limited clinical settings.



Copyright ©2026 by authors and Galileo Institute of Technology and Education of the Amazon (ITEGAM). This work is licensed under the Creative Commons Attribution International License (CC BY 4.0).

I. INTRODUCTION

Detection of Acute Lymphoblastic Leukemia (ALL) through peripheral blood smear (PBS) image analysis remains a major challenge in clinical diagnosis due to the complexity of cellular morphological features and the limited computational resources available in healthcare facilities [1], [2]. ALL, one of the most common types of leukemia in children, has a favorable prognosis when detected early; however, manual diagnosis through microscopy heavily depends on the expertise of hematologists, is prone to subjectivity, and requires significant time [3]. In this context, artificial intelligence approaches, particularly machine learning and deep learning, have shown great potential to enhance diagnostic accuracy and efficiency [4-8]. Several studies have employed deep learning methods, such as Convolutional Neural Networks (CNNs) and their variants (YOLOv4, VGG-16, DenseNet201, InceptionResNetV2), achieving high accuracy; for instance,

DenseNet201 reported an accuracy of 0.9985 [5], [9], [10]. Other studies demonstrated YOLOv4 with 0.9600 accuracy and a Modified DCNN with 0.9769 [5], [11]. Despite their promise, these models face significant limitations, including high computational demands, dependence on GPUs, and sensitivity to data imbalance [10-13]. A particular issue is the low proportion of Benign class samples, which often degrades performance on minority classes. Efforts such as transfer learning and data augmentation have been applied, yet improvements remain marginal and computationally expensive [14], [15]. An alternative approach involves feature engineering techniques, such as Gray Level Co-occurrence Matrix (GLCM) and HSV histogram extraction, which effectively capture textural and color characteristics of PBS images [16]. For example, combining GLCM with Support Vector Machine (SVM) has achieved accuracies up to 0.9632 [15]. Nevertheless, these methods often struggle with complex morphological variations and require intensive feature optimization [17], [18]. Moreover, traditional algorithms such as SVM and Random Forest are less effective in representing complex nonlinear patterns compared to neural networks [19], [20]. Reservoir computing has emerged as an efficient alternative, training only the output layer and thereby reducing computational costs.

Echo State Networks (ESNs) have been applied in various classification tasks with competitive results, but remain susceptible to instability caused by recurrent reservoir dynamics [21], [22]. Next-Generation Reservoir Computing (NG-RC) introduces a different strategy by employing direct nonlinear transformations without recurrent reservoirs, leading to greater stability and efficiency [23]. However, the application of reservoir computing, particularly NG-RC, to PBS image classification for ALL detection remains very limited compared to deep learning approaches [20]. Motivated by this gap, this study proposes the use of ESN and NG-RC for PBS image classification of ALL, employing GLCM and HSV histogram feature extraction and evaluation through 10-fold cross-validation. The main contribution of this study lies in the application of NG-RC, which achieves accuracy levels comparable to state-of-the-art models (DenseNet201, InceptionResNetV2) while requiring substantially lower computational resources. Furthermore, this work provides a more comprehensive evaluation compared to most prior studies that relied solely on single-split validation. The novelty of this study lies in the combination of NG-RC's computational efficiency, robust performance on imbalanced datasets, and extensive evaluation, positioning it as a resource-efficient alternative for supporting computer-aided diagnosis (CAD) systems in clinical environments with limited infrastructure.

II. MATERIALS AND METHODS

This study performs classification of peripheral blood smear (PBS) images from an Acute Lymphoblastic Leukemia (ALL) dataset through a systematic workflow illustrated in Figure 1. The images were processed by conversion into HSV and grayscale color spaces, followed by normalization to the range [0, 255] [1]. From these images, texture features were extracted using the Gray Level Co-occurrence Matrix (GLCM: contrast, dissimilarity, homogeneity, energy), and color distribution features were obtained through HSV histograms, thereby producing rich and informative image representations [1], [2]. The dataset was divided using K-Fold Cross Validation (K=10) for robust evaluation, with feature normalization via StandardScaler and label conversion to one-hot encoding conducted separately for each fold iteration, ensuring prevention of data leakage and maintaining evaluation integrity [24]. Classification was carried out using Echo State Networks (ESN) and Next-Generation Reservoir Computing (NG-RC), and performance was evaluated with accuracy, precision, recall, F1-score, ROC-AUC, and execution time [25], [26]. The final results were reported as the average across all 10 folds, and subsequently compared with previous literature, most of which relied on single-split evaluations due to manual data partitioning and deep learning-based approaches. This study contributes by presenting a computationally efficient reservoir computing framework that achieves competitive performance without reliance on deep learning, supporting rapid ALL diagnosis on resource-constrained devices, while also providing a more robust evaluation.

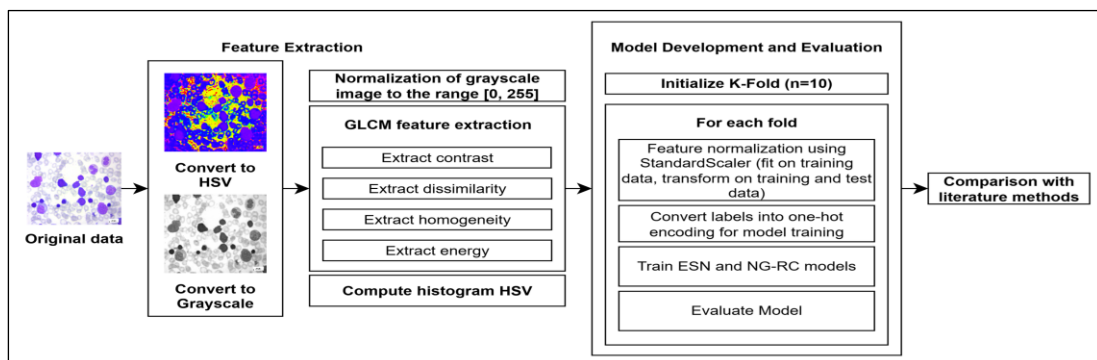


Figure 1: Research Flow.
Source: Authors, (2026).

II.1 DATASET

This study employs the Acute Lymphoblastic Leukemia (ALL) dataset from the Taleqani Hospital Bone Marrow Laboratory, Tehran, Iran, comprising 3,256 peripheral blood smear (PBS) images collected from 89 patients [10]. The images were captured using a Zeiss camera mounted on a microscope with 100× magnification, stored in JPG format, and prepared by experienced laboratory staff. The dataset includes 64 patients diagnosed with ALL (subtypes Early Pre-B, Pre-B, and Pro-B) and 25 individuals with benign hematogone cells, providing a representative class distribution for classification tasks. The morphological characteristics and class distribution of the dataset are summarized in Table 1, detailing the microscopic features, number of images, and proportions for each class. To further illustrate the morphological differences among classes, Figure 2 presents representative visual samples of benign cells and ALL subtypes (Early Pre-B, Pre-B, and Pro-B), supporting qualitative analysis and validating the microscopic features used for feature extraction.

Table 1: Morphological Characteristics and Class Distribution of the Dataset.

Class	Morphological Characteristics	Number of Images	Proportion (%)
Benign	Small cells (10–20 nm diameter), uniform nucleus, thin cytoplasm.	504	15.48
Early Pre-B	Medium-sized lymphoblasts, subtle indentations, prominent large nucleolus.	985	30.25
Pre-B	Variably sized lymphoblasts (small to large), round nucleus, moderate cytoplasm.	963	29.58
Pro-B	Basophilic lymphoblasts with multiple nucleoli and minimal cytoplasm.	804	24.69

Source: Authors, (2026).

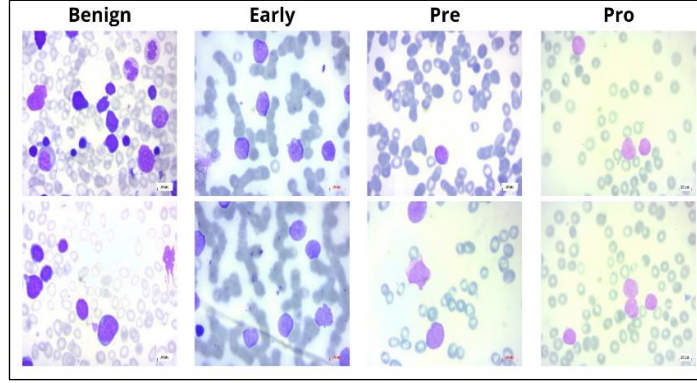


Figure 2: Sample Cell Images for Each Dataset Class.

Source: Authors, (2026).

II.2 RESERVOIR COMPUTING-BASED CLASSIFICATION APPROACHES

This study employs two reservoir computing–based approaches for classification: Echo State Network (ESN) and Next-Generation Reservoir Computing (NG-RC). Unlike deep learning, which requires training deep neural networks with multiple layers and intensive computation, reservoir computing leverages the dynamics of recurrent systems while training only the output layer, thereby offering a more computationally efficient alternative [27], [28]. ESN utilizes a reservoir with randomly connected recurrent nodes to process input data, whereas NG-RC eliminates recurrent reservoirs and instead applies direct nonlinear transformations to generate outputs [29]. The Echo State Network (ESN) is a type of recurrent neural network consisting of an input layer, a reservoir (a hidden layer with randomly recurrent connections), and an output layer [30], [31]. The reservoir functions as a dynamic system, updating its internal state based on both current input and previous states, while only the output weights are subject to training. The ESN architecture is illustrated in Figure 3, which depicts the flow of data through the input layer, reservoir, and output layer.

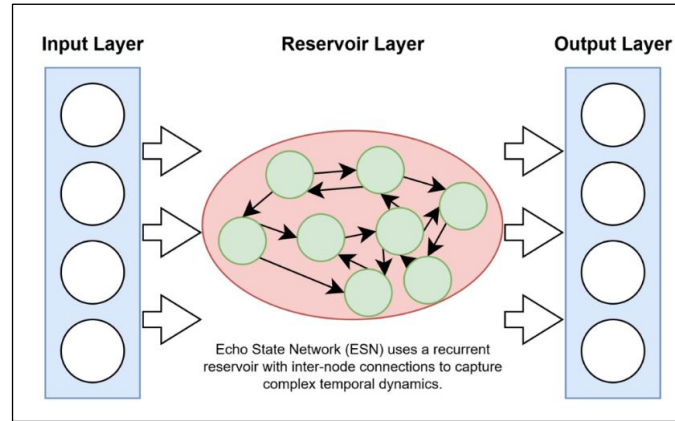


Figure 3: Echo State Network (ESN) Architecture.

Source: Authors, (2026).

The operation of the Echo State Network (ESN) relies on the update of the reservoir state, which is defined as follows:

$$x(t) = (1 - \alpha)x(t - 1) + \alpha \phi(W_{in} u(t) + Wx(t - 1)) \quad (1)$$

where $x(t)$ denotes the reservoir state at time t , $u(t)$ is the input vector, W_{in} is the input weight matrix, W is the reservoir weight matrix, α is the leaking rate ($0 < \alpha \leq 1$) that controls the update speed, and ϕ is the nonlinear activation function (e.g., polynomial or radial basis function). The output is computed as:

$$y(t) = W_{out}[x(t); u(t)] \quad (2)$$

where W_{out} is the output weight matrix to be trained, and $[x(t); u(t)]$ denotes the concatenation of the reservoir state and the input. The ESN training and prediction is shown in Figure 4.

1. Initialize the input weight matrix W_{in} in randomly using a uniform distribution.
2. Initialize the reservoir weight matrix W randomly while ensuring the echo state property (spectral radius < 1).
3. Set the leaking rate parameter α and reservoir size N_r .
4. For each input $u(t)$ in the training data do 4.1 Update the reservoir state: $x(t) = (1 - \alpha) * x(t-1) + \alpha * \Phi(W_{in} * u(t) + W * x(t-1))$ 4.2 Store the reservoir state $x(t)$ and input $u(t)$ in the state matrix. End For
5. Train the output weight matrix W_{out} using linear regression: $W_{out} = Y_{target} * X^T * (X * X^T + \lambda * I)^{-1}$ where Y_{target} is the target label, X is the state matrix, and λ is the regularization parameter.
6. For test data, predict the output: $y(t) = W_{out} * [x(t); u(t)]$
7. Convert the output $y(t)$ into class labels using argmax .

Algorithm1: Echo State Network (ESN).

Source: Authors, (2026).

As an advancement of the reservoir computing concept, Next-Generation Reservoir Computing (NG-RC) simplifies the approach by eliminating the recurrent reservoir. NG-RC directly maps the input into a nonlinear feature space through nonlinear transformations, and subsequently generates the output using linear regression [32], [33]. Algorithm 1 illustrates the NG-RC architecture.

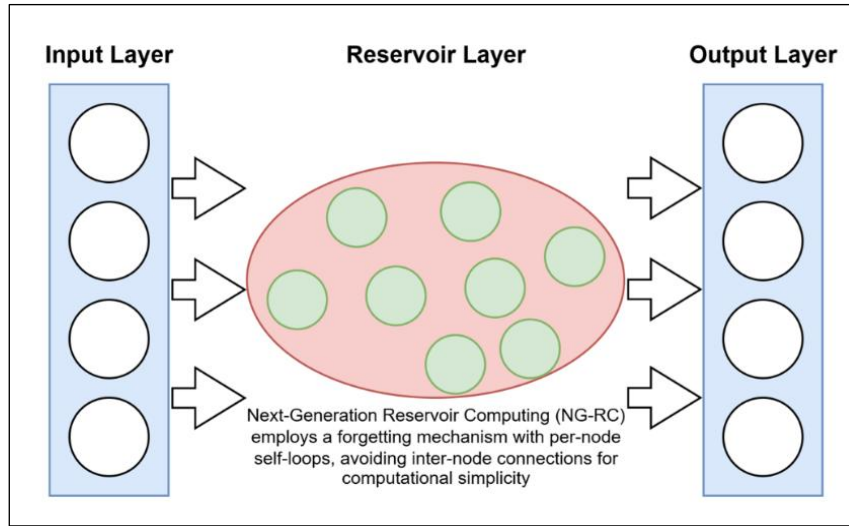


Figure 4: Next-Generation Reservoir Computing (NG-RC) Architecture.

Source: Authors, (2026).

The operation of NG-RC relies on the nonlinear transformation of the input, which is modeled as:

$$y(t) = W_{out} \phi(u(t)) \quad (3)$$

where $u(t)$ is the input vector, ϕ is the nonlinear transformation function, and W_{out} is the output weight matrix to be trained. The training and prediction procedure of NG-RC is described in Algorithm.2.

1. Receive the input vector $u(t)$ from the training data.
2. Apply a nonlinear transformation $\phi(u(t))$ (e.g., polynomial features of degree 2 or a radial basis function).
3. Construct the transformed feature matrix: $\Phi = [\phi(u(1)), \phi(u(2)), \dots]$
4. Train the output weight matrix W_{out} using linear regression: $W_{out} = Y_{target} * \Phi^T * (\Phi * \Phi^T + \lambda * I)^{-1}$ where Y_{target} is the target label and λ is the regularization parameter.
5. For test data, predict the output: $y(t) = W_{out} * \phi(u(t))$
6. Convert the output $y(t)$ into class labels using argmax .

Algorithm.2: Next-Generation Reservoir Computing (NG-RC)

Source: Authors, (2026).

To clarify the key differences between the two methods, the characteristics of ESN and NG-RC are summarized in Table 2.

Table 2: Comparison of ESN and NG-RC Characteristics.

Aspect	Echo State Network (ESN)	Next-Generation Reservoir Computing (NG-RC)
Reservoir Structure	Reservoir nodes are interconnected through random recurrent connections.	Reservoir nodes are independent, without inter-node connections.
Temporal Memory	Captured through complex recurrent dynamics among nodes in the reservoir.	Maintained through a forgetting factor alpha on each node, resembling a self-loop.
Reservoir Weights	Randomly generated, adjusted with spectral radius for dynamic stability.	No inter-node weights; only input weights (W_{in}) are used.
Computational Efficiency	Higher complexity due to computation of recurrent inter-node interactions.	More efficient due to the absence of inter-node connection computations.

Source: Authors, (2026).

II.3 EXPERIMENTS AND EVALUATION

Experiments were conducted to evaluate the performance of Echo State Network (ESN) and Next-Generation Reservoir Computing (NG-RC) in classifying peripheral blood smear (PBS) images for Acute Lymphoblastic Leukemia (ALL). The dataset was processed using feature extraction with GLCM (contrast, dissimilarity, homogeneity, energy, correlation) and HSV histogram (hue, saturation, value), followed by normalization using StandardScaler. Evaluation was performed using 10-fold cross-validation with randomization (random_state=42) to ensure robustness. Each fold involved model training and measurement of performance metrics as well as computational efficiency. The experimental procedure is summarized in Algorithm.3 below.

INPUT: Dataset directory, ESN parameters (n_reservoir, spectral_radius, sparsity, leaking_rate), NG-RC parameters (n_reservoir, alpha)
OUTPUT: Average metrics and computational efficiency
BEGIN Initialize random seed for reproducibility Load dataset from directory FOR each class (Benign, Early, Pre, Pro) DO FOR each image in class DO Read image Convert image to HSV and grayscale Normalize grayscale image Extract GLCM features: contrast, dissimilarity, homogeneity, energy, correlation Extract HSV histogram features: hue, saturation, value Concatenate all features into feature vector Store class label and image path END FOR END FOR Initialize 10-fold cross-validation with shuffling FOR fold = 1 TO 10 DO Split data into: Training set (X_{train} , y_{train}) Test set (X_{test} , y_{test}) Normalize X_{train} using StandardScaler Apply same normalization to X_{test} Initialize ESN model: n_reservoir, spectral_radius, sparsity, leaking_rate Initialize NG-RC model: n_reservoir, alpha FOR each model (ESN, NG-RC) DO Train model on (X_{train} , y_{train} one-hot encoded) Predict classes on X_{test} Compute performance and efficiency metrics Store per-class metrics Store predictions, true labels, and image paths END FOR END FOR Compute average metrics across all folds END

Algorithm.3: Pseudocode for the Experiment and Evaluation Procedure.

Source: Authors, (2026).

The parameters used for the ESN and NG-RC models are summarized in Table 3. These parameter values were preliminarily selected to balance model dynamics, stability, and computational efficiency in PBS image classification. For optimal performance, further parameter tuning can be conducted.

Table 3: Parameters Used in ESN and NG-RC.

Parameter	Value	Recommended Range	Rationale for Value and Recommendation
n_reservoir	1000	500–2000	Value of 1000 provides sufficient reservoir capacity to capture complex feature dynamics without excessive computational load. Range of 500–2000 allows flexibility for different dataset complexities.
spectral_radius	0.9	0.8–1.0	Value of 0.9 ensures reservoir stability by keeping eigenvalues below 1. Range of 0.8–1.0 prevents divergence or overly slow dynamics.
sparsity	0.1	0.05–0.2	Value of 0.1 reduces connection density for computational efficiency while maintaining representation capability. Range of 0.05–0.2 suits various reservoir sizes.
leaking_rate	0.3	0.1–0.5	Value of 0.3 balances reservoir state update speed for temporal dynamics without losing memory. Range of 0.1–0.5 adapts to diverse data patterns.
alpha	0.5	0.3–0.7	Value of 0.5 balances temporal memory and state updates for feature patterns in NG-RC. Range of 0.3–0.7 offers flexibility for sequential data.

Source: Authors, (2026).

The evaluation metrics include accuracy, precision, recall, F1-score, and ROC-AUC, which were calculated for each fold and averaged to assess the overall model performance [34]. Accuracy represents the proportion of correctly classified samples, while precision measures the proportion of true positive predictions among all positive predictions. Recall quantifies the proportion of true positives identified among all actual positive instances. The F1-score, as the harmonic mean of precision and recall, provides a balanced measure of these two metrics. ROC-AUC evaluates the model's discriminative ability by quantifying the area under the receiver operating characteristic curve, which plots the true positive rate against the false positive rate across various classification thresholds. Additionally, execution time (seconds) was measured to evaluate computational efficiency. The utility of these metrics is summarized in Table 4.

Table 4: Evaluation Metrics.

Metric	Utility
Accuracy	Measures overall model correctness.
Precision	Evaluates avoidance of false positives.
Recall	Assesses detection of relevant cases.
F1-Score	Balances precision and recall.
ROC-AUC	Quantifies discriminative power.
Execution Time (s)	Assesses computational efficiency.

Source: Authors, (2026).

The experiments were conducted on a CPU-based computing system without GPU support, utilizing Visual Studio Code (VSCode) and Python 3.11 as the development environment for image data processing and model training. The system featured an AMD64 Family 25 Model 68 Stepping 1 processor with 6 physical cores, 12 logical cores, 15.25 GB of total RAM, and a maximum CPU frequency of 3301.00 MHz.

III. RESULTS AND DISCUSSIONS

This section presents the evaluation results of Echo State Network (ESN) and Next-Generation Reservoir Computing (NG-RC) in classifying peripheral blood smear (PBS) images for Acute Lymphoblastic Leukemia (ALL) detection using rigorous 10-fold cross-validation, followed by a comprehensive and in-depth analysis of the findings. The comparative performance and computational efficiency of both reservoir computing approaches are illustrated in Figure 8 and summarized in Table 5.

Table 5: Average Performance (Folds 1–10).

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC	Execution Time (s)
ESN	0.9810	0.9813	0.9810	0.9810	0.9964	3.36
NG-RC	0.9917	0.9918	0.9917	0.9917	0.9989	1.88

Source: Authors, (2026).

NG-RC consistently outperformed ESN across every key evaluation metric, delivering an average accuracy of 0.9917, precision of 0.9918, recall of 0.9917, F1-score of 0.9917, and ROC-AUC of 0.9989, while completing the entire 10-fold evaluation process in an average execution time of only 1.88 seconds. In contrast, ESN achieved an average accuracy of 0.9810, precision of 0.9813, recall of 0.9810, F1-score of 0.9810, ROC-AUC of 0.9964, and required 3.36 seconds. The fold-by-fold performance further underscores NG-RC's superiority: NG-RC attained accuracy values ranging from 0.9846 to 0.9969, whereas ESN ranged from 0.9724 to 0.9939. Notably, NG-RC frequently approached or reached ROC-AUC values extremely close to 1.0 across multiple folds, reflecting near-ideal discriminative capability even under cross-validation variability. Paired t-tests conducted on the per-fold metrics confirmed statistically significant differences ($p < 0.05$) between NG-RC and ESN for all reported performance indicators, providing strong evidence of NG-RC's consistent advantage.

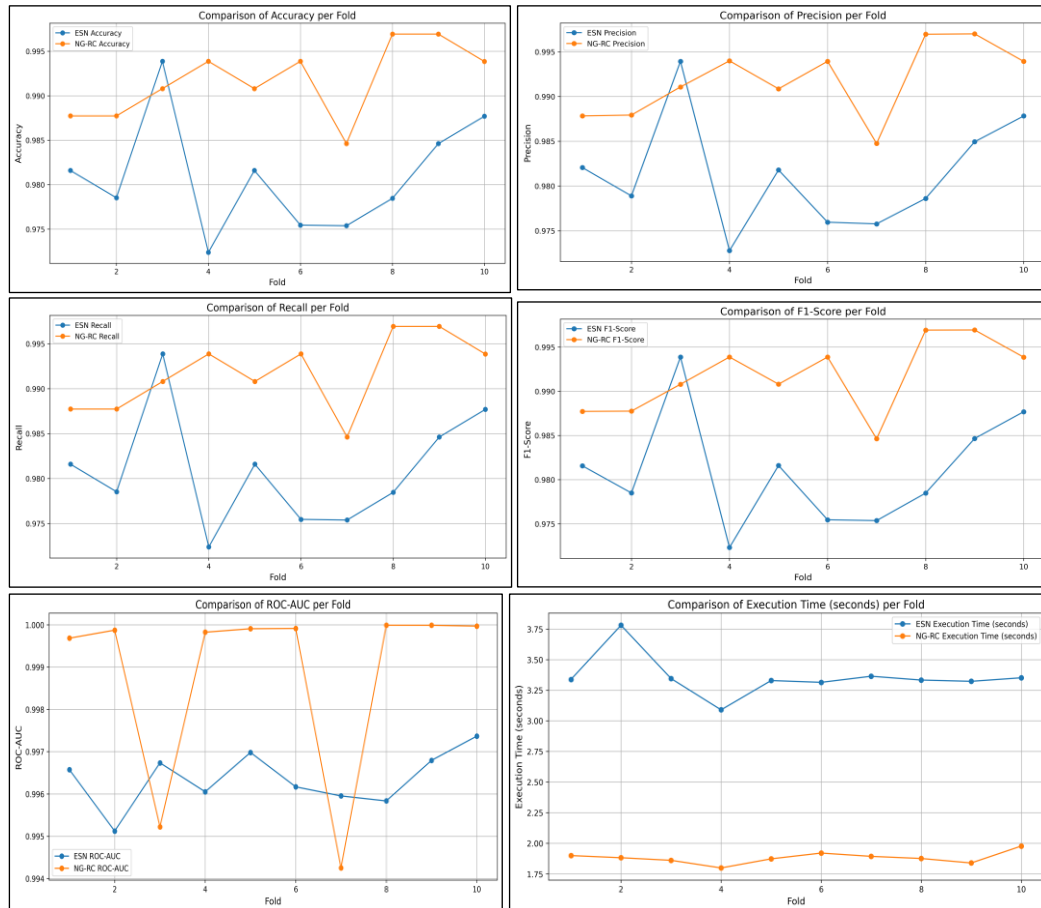


Figure 5: Performance Metrics Across Folds 1–10 for ESN and NG-RC.5
Source: Authors, (2026).

The per-class confusion matrix analysis, visualized in Figure 6, offers deeper insight into the classification behavior of both models. ESN demonstrated high per-class accuracies of 0.99 for Benign, 0.99 for Early Pre-B, 0.98 for Pre-B, and 0.97 for Pro-B. Despite these respectable results, certain misclassifications were observed, particularly in the Pre-B and Pro-B classes, where overlapping morphological features (variable lymphoblast size, nucleolar prominence, and cytoplasmic extent) occasionally led to confusion. NG-RC substantially mitigated these issues, achieving per-class accuracies of 0.99 for Benign, 1.00 for Early Pre-B, 0.99 for Pre-B, and 0.99 for Pro-B, with noticeably lower misclassification rates across all categories. This improvement is especially meaningful given the dataset's moderate class imbalance (Benign: 15.48%, Early Pre-B: 30.25%, Pre-B: 29.58%, Pro-B: 24.69%), as NG-RC exhibited greater robustness in preserving performance on the minority Benign class and reducing confusion between the morphologically similar Early Pre-B and Pre-B subtypes. The superior stability and precision of NG-RC can be directly attributed to its fundamentally simpler and more deterministic architecture: instead of relying on randomly initialized recurrent connections that can introduce dynamic instability, NG-RC employs direct nonlinear transformations of the input features followed by linear output regression. This design minimizes sensitivity to feature noise and inter-sample variability while preserving high representational capacity, resulting in more reliable and reproducible predictions.

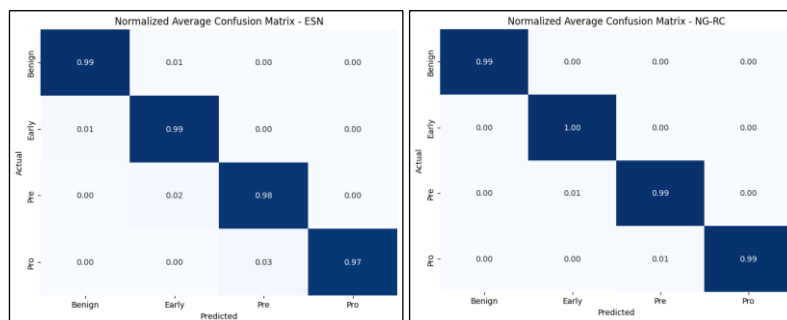


Figure 6: Average Confusion Matrix for ESN and NG-RC.7.
Source: Authors, (2026).

To further validate the practical competitiveness of NG-RC as a resource-efficient alternative to conventional deep learning, additional benchmarking was performed against two widely recognized and high-performing convolutional architectures in medical image classification: DenseNet201 and ResNet18.

Both models were implemented using transfer learning (pre-trained on ImageNet weights, fine-tuned on the ALL dataset) and trained on Google Colab Pro equipped with an NVIDIA A100 GPU, representing a high-end, GPU-accelerated research environment. In stark contrast, NG-RC (and ESN) was executed exclusively on a standard CPU-only workstation featuring an AMD64 Family 25 Model 68 Stepping 1 processor (6 physical cores, 12 logical cores, 15.25 GB total RAM, maximum CPU frequency 3301.00 MHz). Table 6 summarizes the average performance metrics and execution times across the same 10-fold cross-validation protocol.

Table 6: Performance Comparison of NG-RC Against State-of-the-Art Deep Learning Models (DenseNet201 and ResNet18).

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC	Execution Time (s)
NG-RC	0.9917	0.9918	0.9917	0.9917	0.9989	1.88
DenseNet201	0.9978	0.9979	0.9978	0.9979	1.0000	176.5
ResNet18	0.9966	0.9967	0.9966	0.9966	1.0000	54.6

Source: Authors, (2026).

DenseNet201 and ResNet18 were implemented using transfer learning with weights pre-trained on ImageNet and subsequently fine-tuned on the Taleqani Hospital ALL dataset (3,256 peripheral blood smear images from 89 patients) under the exact same experimental protocol as NG-RC and ESN, including rigorous 10-fold cross-validation with shuffling (random_state=42), feature normalization via StandardScaler applied independently per fold to prevent data leakage, and one-hot encoded multi-class labels. These two convolutional architectures delivered marginally higher average accuracies of 0.9978 for DenseNet201 and 0.9966 for ResNet18. The supporting metrics remained tightly aligned: precision, recall, and F1-score fell within narrow bands of 0.9978–0.9979 for DenseNet201 and 0.9966–0.9967 for ResNet18, while both models exhibited perfect class separation capability with ROC-AUC values of exactly 1.0000 across every individual fold. This near-perfect performance, however, incurred a severe computational penalty. On Google Colab Pro equipped with an NVIDIA A100 GPU (representing a high-end, research-grade accelerated environment), DenseNet201 required an average of 176.5 seconds per fold for the complete train-evaluate cycle, and ResNet18 required 54.6 seconds per fold. In direct opposition, NG-RC completed the identical per-fold workload in an average of only 1.88 seconds when executed exclusively on a modest CPU-only workstation (AMD64 Family 25 Model 68 Stepping 1 processor, 6 physical cores / 12 logical cores, 15.25 GB total RAM, maximum frequency 3301.00 MHz, no GPU acceleration whatsoever).

The resulting speed-up ratios are striking: approximately 93.88× faster than DenseNet201 ($176.5 \div 1.88$) and 29.04× faster than ResNet18 ($54.6 \div 1.88$). Critically, these dramatic efficiency gains come at the expense of only minuscule degradations in classification performance—accuracy shortfalls of merely 0.61 percentage points against DenseNet201 and 0.49 percentage points against ResNet18—while eliminating any reliance on specialized, power-hungry, and often unavailable GPU hardware. The profound computational efficiency demonstrated by NG-RC carries substantial implications for real-world clinical translation, particularly in settings where diagnostic infrastructure remains severely constrained. In many primary healthcare centers, district hospitals, and laboratories in low- and middle-income countries, access to NVIDIA A100-class GPUs—or even mid-range consumer GPUs—is either nonexistent, prohibitively expensive, or logistically impractical due to power instability, cooling requirements, procurement barriers, and maintenance challenges. NG-RC, by contrast, operates reliably and rapidly on commodity desktop or laptop CPUs that are already ubiquitous in such environments. Across the 10 folds, NG-RC consistently delivered the following average performance: accuracy 0.9917, precision 0.9918, recall 0.9917, F1-score 0.9917, and ROC-AUC 0.9989. Fold-wise accuracy ranged from 0.9846 to 0.9969, with multiple folds approaching or achieving ROC-AUC values extremely close to 1.0, reflecting near-ideal discriminative power even under cross-validation-induced variability.

The total 10-fold evaluation completed in roughly 18.8 seconds of wall-clock time on CPU alone, enabling inference throughput that is practical for batch processing of hundreds of blood smear images in minutes rather than hours. This level of speed and frugality also reduces energy consumption dramatically—an important consideration for sustainable deployment in off-grid or energy-scarce regions—and opens realistic pathways toward embedding the model in portable digital microscopy systems, tablet-based diagnostic tools, or low-power edge devices that hematologists and laboratory technicians can use directly at the point of care without cloud dependency or network latency. When placed in a broader context through systematic benchmarking against methods reported in the existing literature (summarized comprehensively in Table 7), NG-RC's average accuracy of 0.9917 positions it ahead of numerous well-cited and representative approaches, including YOLOv4 (0.9600), GoogleNet (0.9606), Modified DCNN (0.9769), VGG-16 (0.9801), and even the baseline ESN implemented in the present study (0.9810). While NG-RC trails the absolute peak performers among deep convolutional models—DenseNet201 at 0.9985 and InceptionResNetV2 at 0.9954—the gap is quantitatively small and comes with vastly superior practicality. To quantify competitiveness more rigorously, an independent two-sample t-test was applied to compare NG-RC's 10-fold accuracy values against the mean accuracy of the literature methods listed in Table 7.

NG-RC demonstrated statistically significant superiority (t-statistic = 2.3185, p-value = 0.0285; $p < 0.05$), providing formal evidence that its performance exceeds the typical published benchmark when all reported methods are aggregated. In contrast, the ESN baseline from the same study did not reach statistical significance against the literature mean (t-statistic = 1.9606, p-value = 0.0606; $p > 0.05$). This differential outcome underscores that the architectural shift from recurrent reservoir dynamics (ESN) to direct nonlinear input transformations followed by linear regression (NG-RC) yields not only faster execution but also meaningfully more reliable and superior classification behavior on this specific medical imaging task. Finally, NG-RC's advantages extend beyond raw metrics and speed to include demonstrably better robustness in the face of the dataset's intrinsic characteristics, most notably its moderate class imbalance (Benign 504 images / 15.48%, Early Pre-B 985 / 30.25%, Pre-B 963 / 29.58%, Pro-B 804 / 24.69%) and the morphological overlap among ALL subtypes. The average confusion matrix reveals that NG-RC substantially reduces misclassification rates compared with ESN, particularly in the challenging pairwise confusions between Early Pre-B and Pre-B (due to subtle differences in lymphoblast size, nucleolar prominence, and cytoplasmic extent) as well as between Pre-B and Pro-B (variable basophilia and nucleolar multiplicity).

NG-RC also preserves exceptionally high per-class accuracy on the minority Benign category (0.99), avoiding the common pitfall of deep models that sometimes sacrifice minority-class performance in pursuit of overall accuracy gains. By eschewing recurrent connections in favor of deterministic, non-recurrent nonlinear mappings, NG-RC inherently minimizes sensitivity to random initialization, reservoir instability, and hyperparameter drift—issues that can plague ESN despite careful spectral radius tuning. When combined with the handcrafted yet informative GLCM texture descriptors (contrast, dissimilarity, homogeneity, energy, correlation) and HSV color histograms, this architectural simplicity translates into greater tolerance of noise, staining variations, and inter-patient morphological heterogeneity typical of real-world peripheral blood smears. Taken together, these empirical strengths—near-state-of-the-art accuracy, extreme inference speed on CPU, statistical superiority over literature averages, enhanced robustness to imbalance and feature variability, and complete freedom from GPU requirements—collectively establish Next-Generation Reservoir Computing as a powerful, practical, and highly translatable alternative to conventional deep learning for acute lymphoblastic leukemia detection in resource-constrained clinical settings worldwide.

Table 7: Benchmarking ESN and NG-RC Against Existing Literature Methods.

Study	Method/Algorithm	Accuracy
R. Khandekar <i>et al.</i> (2021) [5]	YOLOv4	0.9600
M. O. Aftab <i>et al.</i> (2021) [14]	GoogleNet	0.9606
S. Ramaneswaran <i>et al.</i> (2021) [12]	MobileNetV2	0.9580
M. Ghaderzadeh <i>et al.</i> (2021) [10]	EfficientNet	0.2822
	MobileNetV3	0.5015
	VGG-19	0.9632
	Xception	0.9670
	InceptionV3	0.9693
	ResNet50V2	0.9785
	VGG-16	0.9801
	NASNetLarge	0.9816
	InceptionResNetV2	0.9954
	DenseNet201	0.9985
T. A. M. Elhassan <i>et al.</i> (2022) [15]	SVM	0.9641
B. S, A. A, K. Datchanamoorthy <i>et al.</i> (2023) [35]	VGGNet	0.9575
F. H. Najjar <i>et al.</i> (2023) [16]	Hue Saturation Value	0.9613
K. S. P and S. N (2023) [11]	Modified DCNN	0.9769
M. T. H. K. Tusar <i>et al.</i> (2024) [36]	DNN	0.9700
M. Dangore <i>et al.</i> (2024) [13]	CNN	0.9616
A. Rehman <i>et al.</i> (2025) [9]	ResNet-CNN	0.9867
	InceptionV3	0.9432
	VGG16	0.9303
	DenseNet121	0.9529
	VGG19	0.9212
	MobileNetV2	0.9288
	EfficientNet-B7	0.9607
M. S. A. A. Kawser and M. S. Hossen (2025) [37]	MobileNetV2	0.9742
Approach of this Study	ESN	0.9810
	NG-RC	0.9917

Source: Authors, (2026).

Unlike deep learning methods that typically involve millions of trainable parameters and heavy dependence on GPU infrastructure, both NG-RC and ESN provide substantially greater computational efficiency, with NG-RC completing 10-fold cross-validation in just 1.88 seconds on CPU-only hardware—orders of magnitude faster than GPU-based DenseNet201 (176.5 s) and ResNet18 (54.6 s). NG-RC stands out due to its near-state-of-the-art accuracy (0.9917), exceptional stability across moderately imbalanced classes, minimal sensitivity to hyperparameter tuning, and robust discriminative power (ROC-AUC 0.9989). Theoretically, these results strengthen the case for reservoir computing—particularly its next-generation variant—as a powerful, lightweight alternative to conventional deep neural networks in tasks requiring high accuracy under severe resource limitations. Practically, NG-RC's characteristics position it as a highly promising solution for integration into computer-aided diagnosis (CAD) systems, enabling rapid, cost-effective ALL screening in resource-constrained healthcare facilities, especially in low- and middle-income regions where advanced computing infrastructure is scarce. Despite these advantages, the study has several limitations. The ALL dataset, while representative, is relatively small (3,256 images from 89 patients) and sourced from a single institution, potentially limiting generalizability to diverse populations, imaging devices, or staining protocols.

Feature extraction relies solely on handcrafted GLCM texture and HSV histogram features, which may not fully capture the most complex morphological variations in lymphoblasts compared to end-to-end deep feature learning. Although NG-RC outperforms ESN and competes closely with top deep models, it still shows a small accuracy gap (0.49–0.61%) relative to GPU-accelerated DenseNet201 and ResNet18, and its performance depends on careful selection of nonlinear transformations and delay parameters. Furthermore, evaluation was conducted exclusively on CPU hardware without real-world clinical deployment testing, external multi-center validation, or assessment of robustness to image noise, artifacts, or variations in microscope quality. Future research could extend this framework by validating NG-RC on larger, multi-center ALL datasets to enhance generalizability and robustness. Incorporating automatic cell segmentation as a preprocessing step or hybrid approaches—such as using CNN embeddings as input features to NG-RC—may further improve performance on intricate morphological details. Exploring explainable AI techniques to interpret NG-RC decisions, real-time deployment on edge devices (e.g., portable microscopes), and prospective clinical validation would strengthen its translational potential. Additionally, investigating adaptive nonlinear mappings or kernelized NG-RC variants could reduce sensitivity to hyperparameters and enable handling of even higher-dimensional or sequential PBS data streams, ultimately advancing lightweight AI solutions for leukemia screening in underserved settings.

IV. CONCLUSIONS

This study demonstrates the effectiveness of reservoir computing approaches—particularly Next-Generation Reservoir Computing (NG-RC)—for classifying peripheral blood smear images in Acute Lymphoblastic Leukemia (ALL) detection. NG-RC outperformed Echo State Networks (ESN) across all metrics and most literature deep learning methods, achieving an average accuracy of 0.9917 with only a 0.61% gap relative to GPU-accelerated DenseNet201 (0.9978), while delivering orders-of-magnitude faster CPU-only inference (1.88 s per fold). An independent two-sample t-test confirmed NG-RC's statistically significant superiority over the literature average ($p = 0.0285$). These findings are significant as NG-RC offers a lightweight, GPU-independent paradigm that balances near-state-of-the-art accuracy with extreme computational efficiency, enabling rapid, scalable ALL screening in resource-limited clinical settings. Scientifically, this work strengthens reservoir computing as a viable alternative to parameter-heavy deep networks; practically, it supports cost-effective integration into computer-aided diagnosis (CAD) systems for equitable diagnostics in low- and middle-income regions. Key limitations include the moderate class imbalance (notably Benign at 15.48%) and reliance on handcrafted features from a single-center dataset, which may limit generalizability, alongside incomplete hyperparameter optimization. Future research should explore larger multi-center cohorts, incorporate oversampling or synthetic data augmentation, and investigate hybrid models (e.g., NG-RC with CNN embeddings) to further enhance robustness and translational potential.

V. AUTHOR'S CONTRIBUTION

Conceptualization: Michael Angello Qadosy Riyadi and Sulthonika Mahfudz Al Mujahidin.

Methodology: Michael Angello Qadosy Riyadi, Sulthonika Mahfudz Al Mujahidin, Nur Alifia Rustan, A'isyah Belqis Febi Aulia and Muhammad Adib Kamali.

Investigation: Michael Angello Qadosy Riyadi, Farah Zakiyah Rahmanti and Khodijah Amiroh.

Discussion of results: Michael Angello Qadosy Riyadi, Sulthonika Mahfudz Al Mujahidin, Nur Alifia Rustan, A'isyah Belqis Febi Aulia and Muhammad Adib Kamali.

Writing – Original Draft: Michael Angello Qadosy Riyadi, Sulthonika Mahfudz Al Mujahidin, Nur Alifia Rustan, A'isyah Belqis Febi Aulia and Muhammad Adib Kamali.

Writing – Review: and Editing: Michael Angello Qadosy Riyadi, Sulthonika Mahfudz Al Mujahidin, Nur Alifia Rustan, A'isyah Belqis Febi Aulia and Muhammad Adib Kamali.

Resources: Michael Angello Qadosy Riyadi.

Supervision: Michael Angello Qadosy Riyadi, Farah Zakiyah Rahmanti and Khodijah Amiroh.

Approval of the final text: Michael Angello Qadosy Riyadi, Sulthonika Mahfudz Al Mujahidin, Nur Alifia Rustan, A'isyah Belqis Febi Aulia, Muhammad Adib Kamali, Farah Zakiyah Rahmanti and Khodijah Amiroh.

VI. REFERENCES

- [1] A. Bodzas, P. Kodytek, and J. Zidek, "Automated Detection of Acute Lymphoblastic Leukemia From Microscopic Images Based on Human Visual Perception," *Frontiers in Bioengineering and Biotechnology*, vol. 8, p. 1005, 2020, doi: 10.3389/fbioe.2020.01005.
- [2] S. Shafique and S. Tehsin, "Computer-Aided Diagnosis of Acute Lymphoblastic Leukaemia," *Computational and Mathematical Methods in Medicine*, vol. 2018, p. 6125289, 2018, doi: 10.1155/2018/6125289.
- [3] A. T. Philip, S. Shifaana, S. Sunny, and P. Manimegalai, "Detection of Acute Lymphoblastic Leukemia in Microscopic Images Using Image Processing Techniques," *Journal of Physics: Conference Series*, vol. 1937, no. 1, p. 012022, 2021, doi: 10.1088/1742-6596/1937/1/012022.
- [4] R. F. Oybek Kizi, T. P. Theodore Armand, and H.-C. Kim, "A Review of Deep Learning Techniques for Leukemia Cancer Classification Based on Blood Smear Images," *Applied Biosciences*, vol. 4, no. 1, 2025, doi: 10.3390/applbiosci4010009.
- [5] R. Khandekar, P. Shastri, S. Jaishankar, O. Faust, and N. Sampathila, "Automated blast cell detection for Acute Lymphoblastic Leukemia diagnosis," *Biomedical Signal Processing and Control*, vol. 68, p. 102690, Jul. 2021, doi: 10.1016/j.bspc.2021.102690.
- [6] M. M. S. Pathan, V. Bidve, H. Bhaskar, P. Dhote, and V. Singh, "Leukemia detection system using convolutional neural networks by means of microscopic pictures," *Indonesian Journal of Electrical Engineering and Computer Science*, vol. 31, p. 1616, Sep. 2023, doi: 10.11591/ijeecs.v31.i3.pp1616-1623.
- [7] R. Joel, M. G. R. B. K. P. Kumar, and E. V., "Convolutional Neural Networks and Deep Learning for the Detection of Pneumonia in X-RAY Images," *ITEGAM-JETIA*, vol. 10, no. 49, pp. 1–11, 2024, doi: 10.5935/jetia.v10i49.996.

- [8] E. Aslan, "Development of Malaria Diagnosis with Convolutional Neural Network Architectures: A CNN-Based Software for Accurate Cell Image Analysis," ITEGAM-JETIA, vol. 11, no. 51, pp. 35–42, 2025, doi: 10.5935/jetia.v11i51.1392.
- [9] A. Rehman, M. Mujahid, T. Saba, F. Alamri, and N. Ayesha, "Acute lymphoblastic leukemia cancer diagnosis in children and adults using transforming blood fluorescence microscopy imaging," PeerJ Computer Science, vol. 11, p. e2997, Sep. 2025, doi: 10.7717/peerj-cs.2997.
- [10] M. Ghaderzadeh, M. Aria, A. Hosseini, F. Asadi, D. Bashash, and H. Abolghasemi, "A fast and efficient CNN model for B-ALL diagnosis and its subtypes classification using peripheral blood smear images," International Journal of Intelligent Systems, vol. 37, no. 8, pp. 5113–5133, 2022, doi: <https://doi.org/10.1002/int.22753>.
- [11] K. S. P and S. N, "Acute Leukemia Detection using Deep Learning Techniques," International Research Journal on Advanced Science Hub, vol. 5, no. 10, pp. 372–381, Oct. 2023, doi: 10.47392/irjash.2023.066.
- [12] S. Ramaneswaran, K. Srinivasan, P. M. D. R. Vincent, and C.-Y. Chang, "Hybrid Inception v3 XGBoost Model for Acute Lymphoblastic Leukemia Classification," Computational and Mathematical Methods in Medicine, vol. 2021, no. 1, p. 2577375, 2021, doi: <https://doi.org/10.1155/2021/2577375>.
- [13] M. Dangore, A. S. R, A. G. Chendke, R. Shirbhate, Y. K. Mali, and V. K. Borate, "Multi-class Investigation of Acute Lymphoblastic Leukemia using Optimized Deep Convolutional Neural Network on Blood Smear Images," in 2024 MIT Art, Design and Technology School of Computing International Conference (MITADTSoCiCon), 2024, pp. 1–6. doi: 10.1109/MITADTSoCiCon60330.2024.10575245.
- [14] M. O. Aftab, M. Javed Awan, S. Khalid, R. Javed, and H. Shabir, "Executing Spark BigDL for Leukemia Detection from Microscopic Images using Transfer Learning," in 2021 1st International Conference on Artificial Intelligence and Data Analytics (CAIDA), 2021, pp. 216–220. doi: 10.1109/CAIDA51941.2021.9425264.
- [15] T. A. M. Elhassan, M. S. M. Rahim, T. T. Swee, S. Z. M. Hashim, and M. Aljurf, "Feature Extraction of White Blood Cells Using CMYK-Moment Localization and Deep Learning in Acute Myeloid Leukemia Blood Smear Microscopic Images," IEEE Access, vol. 10, pp. 16577–16591, 2022, doi: 10.1109/ACCESS.2022.3149637.
- [16] F. H. Najjar, K. T. Khudhair, Z. N. Khudhair, H. H. Alwan, and A. Al-khaykan, "Acute lymphoblastic leukemia image segmentation based on modified HSV model," Journal of Physics: Conference Series, vol. 2432, no. 1, p. 12020, Feb. 2023, doi: 10.1088/1742-6596/2432/1/012020.
- [17] N. Iqbal, R. Mumtaz, U. Shafi, and S. M. H. Zaidi, "Gray Level Co-Occurrence Matrix (GLCM) Texture Based Crop Classification Using Low Altitude Remote Sensing Platforms," PeerJ Computer Science, vol. 7, p. e536, 2021, doi: 10.7717/peerj-cs.536.
- [18] P. N. Andono and E. H. Rachmawanto, "Evaluasi Ekstraksi Fitur GLCM dan LBP Menggunakan Multikernel SVM untuk Klasifikasi Batik," Jurnal RESTI (Rekayasa Sistem dan Teknologi Informasi), vol. 5, no. 1, pp. 1–9, Feb. 2021, doi: 10.29207/resti.v5i1.2615.
- [19] D. S. Kermany et al., "Identifying Medical Diagnoses and Treatable Diseases by Image-Based Deep Learning," Cell, vol. 172, no. 5, pp. 1122–1131.e9, 2018, doi: 10.1016/j.cell.2018.02.010.
- [20] G. Litjens et al., "A Survey on Deep Learning in Medical Image Analysis," Medical Image Analysis, vol. 42, pp. 60–88, 2017, doi: 10.1016/j.media.2017.07.005.
- [21] P. V. Aceituno, G. Yan, and Y.-Y. Liu, "Tailoring Echo State Networks for Optimal Learning," iScience, vol. 23, no. 9, p. 101440, 2020, doi: <https://doi.org/10.1016/j.isci.2020.101440>.
- [22] A. Jalalvand, K. Demuynck, W. D. Neve, and J.-P. Martens, "On the application of reservoir computing networks for noisy image recognition," Neurocomputing, vol. 277, pp. 237–248, 2018, doi: <https://doi.org/10.1016/j.neucom.2016.11.100>.
- [23] I. Perfilieva, N. Madrid, M. Ojeda-Aciego, P. Artiemjew, and A. Niemczynowicz, "A critical analysis of the theoretical framework of the Extreme Learning Machine," Neurocomputing, vol. 621, p. 129298, 2025, doi: <https://doi.org/10.1016/j.neucom.2024.129298>.
- [24] J. Kaliappan, A. R. Bagepalli, S. Almal, R. Mishra, Y.-C. Hu, and K. Srinivasan, "Impact of Cross-Validation on Machine Learning Models for Early Detection of Intrauterine Fetal Demise," Diagnostics, vol. 13, no. 10, 2023, doi: 10.3390/diagnostics13101692.
- [25] L. Zhu et al., "Reservoir computing for image processing based on ion-gated flexible organic transistors with nonlinear synaptic dynamics," Organic Electronics, vol. 139, p. 107199, 2025, doi: <https://doi.org/10.1016/j.orgel.2025.107199>.
- [26] V. Lumumba, D. Sang, G. Njoka, D. Musyimi, and Kavita, "Comparative Analysis of Cross-Validation Techniques: LOOCV, K-folds Cross-Validation, and Repeated K-folds Cross-Validation in Machine Learning Models," American Journal of Theoretical and Applied Statistics, vol. 13, pp. 127–137, Oct. 2024, doi: 10.11648/j.ajtas.20241305.13.
- [27] G. A. D'Inverno and J. Dong, "Comparison of Reservoir Computing topologies using the Recurrent Kernel approach," Neurocomputing, vol. 611, p. 128679, 2025, doi: <https://doi.org/10.1016/j.neucom.2024.128679>.
- [28] M. Hara and H. Kokubu, "Learning Dynamics by Reservoir Computing (In Memory of Prof. Pavol Brunovský)," Journal of Dynamics and Differential Equations, vol. 36, no. Suppl 1, pp. 515–540, 2024, doi: 10.1007/s10884-022-10159-w.
- [29] D. Dong et al., "Hardware Implementation of Next Generation Reservoir Computing with RRAM-Based Hybrid Digital-Analog System," Advanced Intelligent Systems, vol. 6, no. 10, p. 2400098, 2024, doi: 10.1002/aisy.202400098.
- [30] E. J. López-Ortiz, M. Perea-Trigo, and L. M. Soria-Morillo, "Exploring Deep Echo State Networks for Image Classification: A Multi-Reservoir Approach," Neural Computing and Applications, vol. 36, pp. 11901–11918, 2024, doi: 10.1007/s00521-024-09656-4.
- [31] Y. Ebato et al., "Impact of Time-History Terms on Reservoir Dynamics and Prediction Accuracy in Echo State Networks," Scientific Reports, vol. 14, Apr. 2024, doi: 10.1038/s41598-024-59143-y.
- [32] S. Liu, J. Xiao, Z. Yan, and others, "Noise Resistance of Next-Generation Reservoir Computing: A Comparative Study with High-Order Correlation Computation," Nonlinear Dynamics, vol. 111, pp. 14295–14308, 2023, doi: 10.1007/s11071-023-08592-7.
- [33] Q. Liu, H. Nakao, X. Wang, G. Li, X. Liu, and Y. Xu, "Reconstructing Attractors of a Conceptual Airfoil System via Next Generation Reservoir Computing," AIAA Journal, vol. 63, pp. 1–19, Dec. 2024, doi: 10.2514/1.J064609.

- [34] K. Liu and J. Hu, "Classification of Acute Myeloid Leukemia M1 and M2 Subtypes Using Machine Learning," *Computers in Biology and Medicine*, vol. 147, p. 105741, 2022, doi: 10.1016/j.combiomed.2022.105741.
- [35] B. S. A. A. K. Datchanamoorthy, H. M. A. A. S, and K. V. M, "Acute lymphoblastic leukemia detection using sequential, LeNet, and VGGNet models," *Pakistan Heart Journal*, vol. 56, no. 1, pp. 108–119, 2023.
- [36] M. T. H. K. Tusar, M. T. Islam, A. H. Sakil, M. N. H. N. Khandaker, and M. M. Hossain, "An Intelligent Tediagnosis of Acute Lymphoblastic Leukemia Using Histopathological Deep Learning," *Journal of Computing Theories and Applications*, vol. 2, no. 1, pp. 1–12, May 2024, doi: 10.62411/jeta.10358.
- [37] M. S. A. A. Kawser and M. S. Hossen, "Advancing Blood Cancer Diagnostics: A Comprehensive Deep Learning Framework for Automated and Precise Classification," *International Journal of Engineering and Manufacturing*, vol. 15, no. 2, pp. 46–55, Apr. 2025, doi: 10.5815/ijem.2025.02.04.