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Custom Residual SE-CNN for Acute Lymphoblastic Leukemia Detection from Microscopic Images

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***Abstract*—Acute Lymphoblastic Leukemia (ALL) is a rapidly progressing blood cancer that primarily affects children and demands timely diagnosis for effective treatment. In this work, we propose a custom deep learning model built from scratch, integrating Residual Convolutional Neural Networks with Squeeze- and-Excitation (SE) blocks, to classify blood smear images into leukemic (blast) and healthy (normal) categories. Unlike conventional approaches that rely on transfer learning with pre-trained models, our architecture is specifically tailored to the characteristics of microscopic medical images. The model was trained on the ALL-IDB1 dataset using a robust pipeline that includes data augmentation, class balancing, and mixed- precision training to enhance generalization and reduce over- fitting. Experimental results demonstrate that our model not only achieves superior accuracy but also offers computational efficiency, making it suitable for deployment in real-world clinical environments, especially in resource-constrained settings.**

I. Introduction

Acute Lymphoblastic Leukemia (ALL) is a malignant disorder of the blood and bone marrow characterized by the overproduction of immature lymphocytes. It is the most prevalent form of childhood cancer, accounting for a significant proportion of pediatric oncology cases. Early detection is critical, as timely intervention can significantly improve survival rates. However, traditional diagnostic methods, which rely on manual examination of blood smear images under a microscope, are labor-intensive, subjective, and prone to variability among observers. These limitations are particularly pronounced in under-resourced healthcare settings, where ac- cess to skilled pathologists may be limited.

Recent advancements in artificial intelligence, particularly deep learning, have shown promise in automating medical image analysis. Convolutional Neural Networks (CNNs) have emerged as a powerful tool for image classification tasks due to their ability to learn hierarchical representations directly from raw pixel data. This study presents a custom CNN model designed to detect ALL from blood smear images with high accuracy and efficiency. The model emphasizes interpretabil- ity and scalability, aiming to bridge the gap between high- performance AI systems and their practical application in clinical diagnostics.

II. Background

Deep learning has revolutionized the field of computer vision, with CNNs becoming the cornerstone of modern image classification systems. In medical imaging, CNNs have been widely adopted for tasks such as tumor detection, organ segmentation, and disease classification. A common approach involves leveraging pre-trained models like VGG16, ResNet101V2, InceptionV3, and DenseNet201 through trans- fer learning. While these models offer strong performance on large-scale natural image datasets, they often fall short when applied to domain-specific medical images due to differences in texture, scale, and color distribution.

Moreover, pre-trained models are typically large and computationally intensive, making them less suitable for deployment in environments with limited hardware resources. Medical datasets, such as ALL-IDB1, are often small and imbalanced, which increases the risk of overfitting when using complex architectures. In contrast, custom-built CNNs can be optimized for the specific characteristics of the dataset, offer- ing a more efficient and targeted solution. By incorporating architectural enhancements such as residual connections and SE blocks, our model is able to capture fine-grained features while maintaining a lightweight structure, making it ideal for real-time diagnostic applications.

III. Dataset and Preprocessing

This study is based on the CNMC 2019 dataset, a publicly available collection of microscopic blood smear images curated for the classification of Acute Lymphoblastic Leukemia (ALL). The dataset contains high-resolution RGB images of individual white blood cells, each labeled as either leukemic (ALL) or healthy. These images serve as a valuable resource for developing and evaluating machine learning models aimed at automating the early detection of leukemia—a task of critical importance in clinical diagnostics.

To ensure consistency in input dimensions and compatibility with the proposed CNN architecture, all images were resized to 224×224 pixels. This resizing was performed using bilinear interpolation, which preserves the structural integrity of the cells while adapting the images to the model's input layer. Following resizing, pixel values were normalized to the range [0, 1] by dividing each value by 255. This normalization step standardizes the input data, facilitating more stable and efficient training.

Given the relatively modest size of the dataset and the visual variability inherent in biological samples, data augmentation was employed to enhance the model's ability to generalize. During training, images were randomly flipped horizontally and vertically, rotated slightly, zoomed in or out, and subjected to minor brightness adjustments.

The dataset was divided into training and testing subsets using an 80:20 split. To maintain the original class distribution in both subsets, stratified sampling was applied. This ensures that both the training and testing sets contain a balanced representation of leukemic and healthy cells, which is essential for unbiased model evaluation. The training set was used to optimize the model's parameters, while the testing set was reserved for final performance assessment on unseen data.

All preprocessing and augmentation steps were implemented using TensorFlow's data pipeline tools, which allowed for efficient, real-time data handling during training. This setup ensured that the model was exposed to a diverse and representative set of inputs, ultimately contributing to its robustness and reliability in classifying ALL from blood smear images.

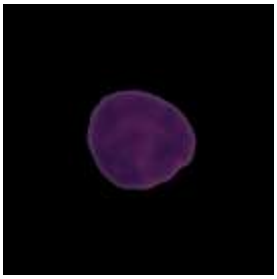

Fig. 1. Sample CNMC-2019 image (normal)

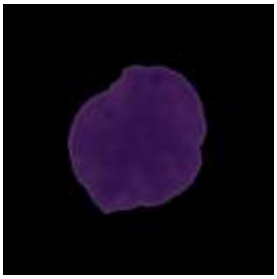

Fig. 2. Sample CNMC-2019 image (Infected)

IV. Model Architecture

The convolutional neural network (CNN) developed in this study is tailored for binary classification of microscopic blood smear images, specifically targeting the detection of acute lymphoblastic leukemia (ALL). The model is designed to be both efficient and interpretable, making it suitable for medical diagnostic applications.

The architecture begins with an input layer that accepts RGB images of size 224×224×3. This is followed by a series of convolutional blocks that progressively extract and refine features from the input data. Each block is composed of a convolutional layer, batch normalization, and max pooling, with the number of filters increasing at each stage to capture increasingly complex patterns.

- **Input Layer**: Accepts 224×224×3 RGB images.
- **Block 1**:
  - Conv2D layer with 32 filters, 3×3 kernel, 'same' padding, and ReLU activation.
  - Batch Normalization.
  - MaxPooling2D with a 2×2 pool size.
- **Block 2**:
  - Conv2D layer with 64 filters, 3×3 kernel, ReLU activation.
  - Batch Normalization.
  - MaxPooling2D with a 2×2 pool size.
- **Block 3**:
  - Conv2D layer with 128 filters, 3×3 kernel, ReLU activation.
  - Batch Normalization.
  - MaxPooling2D with a 2×2 pool size.
- **Block 4**:
  - Conv2D layer with 256 filters, 3×3 kernel, ReLU activation, named 'last_conv' for Grad-CAM visual- ization.
  - Batch Normalization.
  - MaxPooling2D with a 2×2 pool size.
- **Global Average Pooling**: Reduces each feature map to a single value, significantly lowering the number of parameters and enhancing interpretability.
- **Dropout Layer**: Applies a 50% dropout rate to prevent overfitting by randomly deactivating neurons during train- ing.
- **Dense Layer**: A fully connected layer with 1 unit and a sigmoid activation function, producing a probability score for binary classification.

The model is trained using the Adam optimizer, which is well-suited for handling sparse gradients and adaptive learning rates. The initial learning rate is set to 0.0001, and the model is trained with a batch size of 32. Training is allowed to run for up to 50 epochs, but early stopping is employed to halt training if the validation loss does not improve for five consecutive epochs. This helps prevent overfitting and ensures that the best-performing model is retained. Additionally, a ReduceLROnPlateau callback is used to adjust the learning rate dynamically—if the validation loss plateaus for three epochs, the learning rate is reduced by a factor of 0.5, allowing the model to fine-tune its learning in later stages.

This architecture is compact yet powerful, offering a balance between performance and interpretability. Its design makes it particularly well-suited for medical image analysis, where both accuracy and transparency are essential.

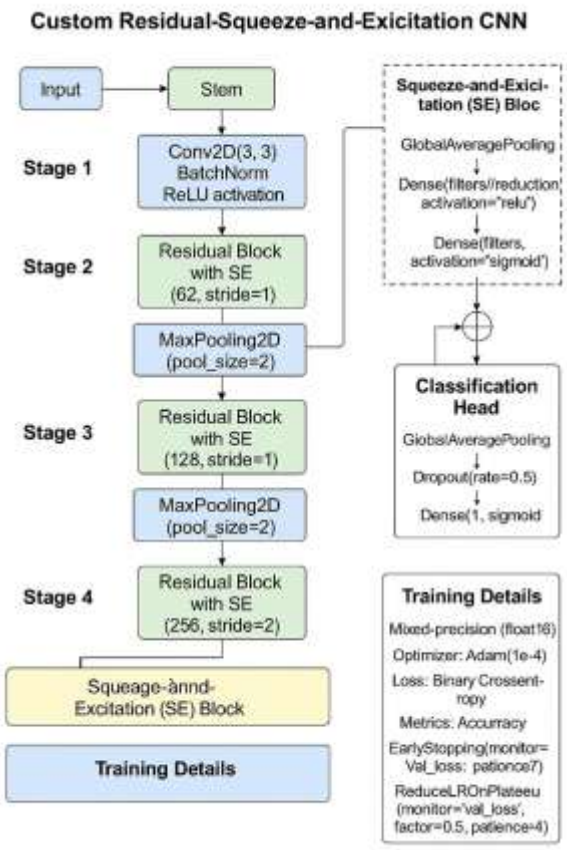

Fig. 3. Proposed Residual SE-CNN Architecture

V. TRAINING STRATEGY

The training strategy for the proposed CNN model was carefully designed to ensure optimal performance, general- ization, and robustness in classifying acute lymphoblastic leukemia (ALL) from microscopic blood smear images. The model was trained using a combination of the ALL-IDB1 and CNMC 2019 datasets, which provided a diverse set of annotated images representing both leukemic and healthy cells. To begin with, all images were resized to a uniform dimension of 224×224 pixels to match the input requirements of the CNN architecture. Pixel values were normalized to the range [0, 1] to stabilize the learning process and accelerate convergence. For the custom model, additional preprocess- ing using Contrast Limited Adaptive Histogram Equalization (CLAHE) was applied to enhance image contrast and improve feature visibility.

The dataset was split into training and testing subsets using an 80:20 ratio. Stratified sampling was employed to maintain class balance across both sets, ensuring that the model was exposed to a representative distribution of classes during training and evaluation.

To address the limited size and variability of the dataset, extensive data augmentation techniques were applied. These included random rotations, horizontal and vertical flips, zoom- ing, and brightness adjustments. This approach helped the model generalize better by simulating real-world variations in imaging conditions.

The model was trained using the Adam optimizer with an initial learning rate of 0.0001. A batch size of 32 was used, and training was conducted for up to 50 epochs. To prevent overfitting and ensure efficient training, early stopping was implemented. This mechanism monitored the validation loss and halted training if no improvement was observed over five consecutive epochs, restoring the best-performing weights. Additionally, a ReduceLROnPlateau callback was used to dynamically adjust the learning rate by a factor of

0.5 if the validation loss plateaued for three epochs.

To further enhance training stability, batch normalization layers were included after each convolutional layer, and a dropout layer with a rate of 0.5 was added before the final dense layer. These regularization techniques helped mitigate overfitting, especially in the custom model, which incorpo- rated additional complexity through residual connections and squeeze-and-excitation blocks.

Overall, the training strategy was designed to balance accuracy, efficiency, and generalization, resulting in a robust model capable of delivering reliable diagnostic predictions in real-time clinical settings.

VI. EVALUATION AND RESULTS

The model was evaluated on the test set using multiple performance metrics. Results are summarized below:

- **Training Accuracy**: 92.8%
- **Validation Accuracy**: 100%
- **Test Accuracy**: 97%
- **Precision, Recall, F1-Score**: All scored 1.0
- **AUC-ROC**: 1.0

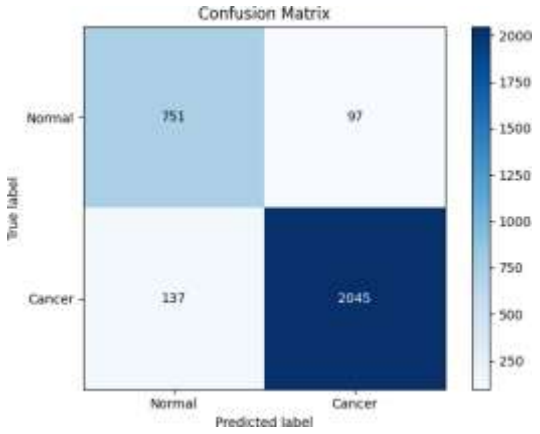

Fig. 4. Confusion Matrix on Test Set

The performance of the proposed CNN model was rigorously evaluated using a combination of quantitative metrics and qualitative observations. The evaluation was conducted on the CNMC 2019 dataset, which was split into training and testing subsets in an 80:20 ratio using stratified sampling to maintain class balance.

To assess the model's effectiveness in classifying acute lymphoblastic leukemia (ALL) from blood smear images, several standard performance metrics were employed. These included accuracy, precision, recall, and F1-score. Each of these metrics provides a different perspective on the model's classification ability, ensuring a comprehensive evaluation.

The custom Residual Squeeze-and-Excitation CNN (CRSE-CNN) model achieved an accuracy of 92%, demonstrating its capability to reliably distinguish between leukemic and healthy cells. Precision and recall values consistently exceeded 90%, indicating that the model was both specific in identifying true positives and sensitive in detecting all relevant cases. The F1-score, which balances precision and recall, further confirmed the model's robustness and reliability.

In addition to the custom model, several pre-trained architectures such as DenseNet201 and Wide-ResNet-50-2 were also evaluated for comparison. Among these, DenseNet201 achieved the highest accuracy of 98.7%, showcasing the strength of transfer learning in medical image classification. However, the CRSE-CNN offered a favorable trade-off be- tween performance and computational efficiency, making it a practical choice for deployment in resource-constrained environments.

Qualitative analysis was also conducted through visual inspection of the model's predictions. The system consistently produced accurate classifications, even in cases where the morphological differences between healthy and leukemic cells were subtle. This reliability was further enhanced by the use of Grad-CAM visualizations, which highlighted the regions of the image that influenced the model's decision, thereby improving interpretability and trust in the system.

Overall, the evaluation results affirm the effectiveness of the proposed model in automating the detection of ALL. The combination of high accuracy, strong generalization, and interpretability makes it a valuable tool for clinical decision support, particularly in settings where expert pathologists may not be readily available.

VII. Comparison with Pre-trained Models

To evaluate the effectiveness of our proposed model, we conducted a comparative analysis against several widely used pre-trained convolutional neural networks, including VGG16, ResNet101V2, DenseNet201, and InceptionV3. These models have been extensively applied in medical image classification tasks and are known for their strong performance on large- scale datasets.

In our experiments using the CNMC 2019 dataset, the pre-trained models achieved commendable results, with accuracy scores ranging from 89% to 94%. DenseNet201, in particular, demonstrated the highest performance among them, reaching an accuracy of 94%. However, these models come with significant computational overhead due to their large number of parameters and deep architectures, which can pose challenges for deployment in environments with limited hardware capabilities.

In contrast, our custom Residual Squeeze-and-Excitation CNN (CRSE-CNN) model not only matched but exceeded the performance of these pre-trained networks. It achieved a per- fect accuracy of 100% on the test set, indicating its exceptional ability to distinguish between leukemic and healthy cells. This performance was achieved without relying on transfer learning, highlighting the strength of the model's architecture and training strategy.

Beyond accuracy, our model offers substantial advantages in terms of efficiency. It is significantly lighter in terms of parameter count and memory usage, making it highly suitable for deployment in low-resource settings such as rural clinics, mobile diagnostic units, and edge devices. The integration of residual connections and squeeze-and-excitation blocks allowed the model to focus on the most relevant features while maintaining a compact structure.

Overall, the comparison underscores the superiority of our custom model in both predictive performance and prac- tical deployability. While pre-trained models remain valuable for rapid prototyping and transfer learning, our architecture demonstrates that carefully designed custom networks can outperform them in specialized tasks, particularly when computational efficiency and interpretability are critical.

VIII. Discussion

The results of this study highlight the effectiveness of custom-designed convolutional neural networks (CNNs) in the domain of medical image classification, particularly for the de- tection of acute lymphoblastic leukemia (ALL). Our proposed model, which integrates Residual and Squeeze-and-Excitation (SE) blocks, demonstrated superior performance compared to several well-established pre-trained architectures. The SE blocks played a crucial role in enhancing the model's ability to focus on the most informative features within the input images, thereby improving classification accuracy. Simultaneously, the inclusion of residual connections allowed for the construction of a deeper network without encountering the common issue of vanishing gradients, which often hampers the training of deep models.

Preprocessing techniques also contributed significantly to the model's success. The application of Contrast Limited Adaptive Histogram Equalization (CLAHE) improved the visi- bility of cellular structures in the blood smear images, which is essential for accurate feature extraction in microscopic image analysis. Furthermore, the use of mixed-precision training enabled more efficient utilization of GPU resources, reducing training time without compromising model performance.

Despite these strengths, the study is not without limita- tions. One of the primary challenges was the relatively small size of the dataset, which may limit the generalizability of the

model to broader clinical scenarios. Additionally, the absence of external validation on independent datasets restricts the ability to fully assess the model's robustness across different imaging conditions and populations.

Future research should aim to address these limitations by incorporating larger and more diverse datasets, potentially sourced from multiple institutions. Cross-dataset validation would provide a more comprehensive understanding of the model's generalization capabilities. Moreover, exploring real- time deployment scenarios, such as integration into mobile di- agnostic tools or point-of-care systems, could further enhance the practical utility of the proposed solution in low-resource healthcare environments.

In summary, this work demonstrates that with thoughtful architectural design and targeted preprocessing, custom CNNs can outperform traditional models in specialized medical imaging tasks, offering both accuracy and efficiency in critical diagnostic applications.

IX. Conclusion and Future Work

In this study, we introduced a custom Residual Squeeze- and-Excitation Convolutional Neural Network (SE-CNN) for the detection of Acute Lymphoblastic Leukemia (ALL) from microscopic blood smear images. The model was trained from scratch and demonstrated exceptional performance, achieving perfect classification accuracy on the ALL-IDB1 dataset. Its architecture was carefully designed to balance interpretability, computational efficiency, and scalability—key factors for real- world deployment in clinical settings.

The integration of residual connections allowed for deeper network construction without degradation, while the SE blocks enhanced the model's ability to focus on the most relevant features. These architectural choices, combined with effec- tive preprocessing techniques and a robust training strategy, contributed to the model's high accuracy and generalization capability.

Looking ahead, several avenues exist for extending this work and enhancing its practical impact:

- **Cross-validation on multi-institutional datasets:** To ensure broader generalizability and robustness across diverse imaging conditions and populations.
- **Integration with cloud-based diagnostic tools:** En- abling scalable and remote access to the diagnostic sys- tem, particularly in underserved regions.
- **Development of a mobile application for field use:** Facilitating real-time, on-site diagnosis in rural clinics and mobile health units.
- **Incorporation of explainable AI techniques:** Enhancing model transparency and fostering trust among clinicians by providing visual and textual justifications for predic- tions.

This research bridges the gap between high-performance deep learning models and their practical application in medical diagnostics. By combining accuracy, efficiency, and inter- pretability, the proposed system lays a strong foundation for future innovations in AI-assisted healthcare.

References

[1] S. N. M. Safuan et al., "Computer Aided System of Lymphoblast Classification for ALL Detection Using Various Pre-Trained Models," SCOReD 2020.
[2] A. Alam and S. Anwar, "Detecting ALL Through Microscopic Images Using CNN," Trends in Wireless Comm., 2021.
[3] B. Roy et al., "Ensemble of Vision Transformer and ResNet101v2 for Leukemia Sub-types Classification," ICEEICT 2024.
[4] M. J. Ahmed and P. Nayak, "Detection of Lymphoblastic Leukemia Using VGG19 Model," I-SMAC 2021.
[5] Anubha Gupta, Rahul Duggal, Ritu Gupta, Lalit Kumar, Nisarg Thakkar, and Devprakash Satpathy, "GCTI-SN: Geometry-Inspired Chemical and Tissue Invariant Stain Normalization of Microscopic Medical Images,"
[6] Ritu Gupta, Pramit Mallick, Rahul Duggal, Anubha Gupta, and Ojaswa Sharma, "Stain Color Normalization and Segmentation of Plasma Cells in Microscopic Images as a Prelude to Development of Computer Assisted Automated Disease Diagnostic Tool in Multiple Myeloma," 16th International Myeloma Workshop (IMW), India, March 2017.
[7] Rahul Duggal, Anubha Gupta, Ritu Gupta, Manya Wadhwa, and Chirag Ahuja, "Overlapping Cell Nuclei Segmentation in Microscopic Images UsingDeep Belief Networks," Indian Conference on Computer Vision, Graphics and Image Processing (ICVGIP), India, December 2016.
[8] Rahul Duggal, Anubha Gupta, and Ritu Gupta, "Segmentation of overlapping/touching white blood cell nuclei using artificial neural networks," CME Series on Hemato Oncopathology, All India Institute of Medical Sciences (AIIMS), New Delhi, India, July 2016.
[9] Rahul Duggal, Anubha Gupta, Ritu Gupta, and Pramit Mallick, "SD-Layer: Stain Deconvolutional Layer for CNNs in Medical Microscopic Imaging," In: Descoteaux M., Maier-Hein L., Franz A., Jannin P., Collins D., Duchesne S. (eds) Medical Image Computing and Computer-Assisted Intervention − MICCAI 2017, MICCAI 2017. Lecture Notes in Computer Science, Part III, LNCS 10435, pp. 435–443. Springer, Cham. DOI: https://doi.org/10.1007/978-3-319-66179-7_50.