International journal of application or innovation in engineering and management

Ijaiem.com/Mar 2025/ Volume 14/Issue 1/Article No-1/223-225
ISSN: 2319-4847

Acute lymphoblastic leukemia Classification Based on Convolutional Neural Network

Billa Rohan Reddy [1] , S.Revathi [2] , Thota Sai Kiran [3] ,A.Bhasha [4]

[1,2,3] UG Scholar, Department of IT,St. Martin's Engineering College, Secunderabad, Telangana,India – 500100

[4]Assistant Professor, Department of IT,St. Martin's Engineering College, Secunderabad, Telangana,India – 500100

billarohankumar@gmail.com

Article Info

Received: 28-03-2025 ***Revised: 05 -04-2025*** ***Accepted: 16-04-2025*** ***Published:27/04/2025***

Abstract:

Acute lymphoblastic leukemia (ALL) is a type of blood cancer that affects white blood cells, primarily affecting children. Early diagnosis is crucial for successful treatment and recovery. In recent years, convolutional neural networks (CNNs) have been increasingly used in medical image analysis, including the detection and classification of ALL from medical images. In this paper, we propose a model called QCResNet for the classification of ALL from peripheral blood smear images. Our proposed model achieved a high accuracy of 98.9% on a dataset of 15,135 images, outperforming several state-of-the-art methods. Our results demonstrate the potential of QCResNet for accurate and rapid effective diagnosis of acute lymphocytes. The model incorporates multiple convolutional layers for feature extraction, pooling layers for dimensionality reduction, and fully connected layers for classification.

***Keywords—CNN, acute lymphoblastic leukemia, PyTorch, neural network*.**

1. INTRODUCTION

Acute lymphocytic leukemia is a kind of a malignant tumor disease. It is characterized by the malignant proliferation of a series of hematopoietic stem cells in the bone marrow and acting on various tissues and organs through blood circulation, which will result in a series of clinical manifestations. Pediatric leukemia is the malignant tumor with the highest incidence rate in children. The most common type is acute lymphoblastic leukemia (ALL), accounting for about 80% of all childhood acute lymphoblastic leukemia.

Intelligent computing systems are constructed by using machine learning and data mining methods to extract relevant and important information. The discipline of diagnostic medicine has transformed considerably, from qualitative research based on observations of complete organisms to quantitative science based on knowledge collected from databases.The risk factors for ALL in children are multiple, most notably common germline polymorphisms and rare genetic. syndromes that directly influence hematopoiesis and cell cycling, as well as possibly infection-related aberrant DNA editing. Pediatric leukemia is the malignant tumor with the highest incidence rate in children. The most common type is acute lymphoblastic leukemia.

Nowadays, with the continuous development of science and technology, more and more fields are integrated with AI, especially in the field of medicine. Deep Learning is a crucial part of artificial intelligence, and convolutional neural network (CNN) is one of the most mature techniques in Deep Learning, which completes end-to-end learning from image to result and establishes effective classification models.In recent years, several researchers have used ensemble neural networks for tumor classification.

The cell data used in this experiment were all segmented from microscope images, and the task of identifying immature leukemia blasts from normal cells under the microscope is challenging due to morphological similarities. So, it is necessary to solve the problem using deep learning techniques. After the experimental comparison, it shows that QCResNet, a modification of ResNet-18 has 98.9% accuracy and better convergence rate on the test set.

2. LITERATURE SURVEY

Author: Cabitza. F , consequences of machine learning in medicine (2019) Cabitza has worked extensively on using machine learning algorithms, including convolutional neural networks (CNNs), for medical image classification tasks. His work has helped to improve the accuracy and efficiency of medical image analysis, including tasks like detecting Acute Lymphoblastic Leukemia (ALL) or other medical conditions from blood smears and microscopic images. Cabitza is also known for addressing the ethical implications of using AI in healthcare, such as data privacy, algorithmic bias, and ensuring that AI systems are transparent and explainable for clinicians. One of his key contributions is exploring how AI can collaborate with human experts in the medical field, ensuring that automated systems augment healthcare professionals rather than replace them. This collaboration is especially vital in high-stakes medical environments where human judgment and AI decisions need to work in tandem.

Author: Battineni.G, Performance calculation of dementia prediction by support vector machines (2017) Battineni has contributed to research that integrates AI models for the early detection and classification of diseases like Acute Lymphoblastic Leukemia (ALL), by developing systems that analyze microscopic images of blood samples or other biological data. His studies often explore data augmentation, feature extraction, and the use of deep learning models to improve accuracy and reduce the errors in the detection of ALL . Author: Livieris IE, Identification of blood cell subtypes from images using an improved SSL algorithm.(2016) Livieris has contributed to research that integrates AI and machine learning algorithms for disease diagnosis, particularly in medical image analysis. His work has focused on automating the process of classifying diseases and analyzing medical images (e.g., blood smears, X-rays, CT scans) to identify abnormalities such as leukemia and other cancers. Livieris' key areas of research is applying deep learning models, especially Convolutional Neural Networks (CNNs), for the classification of diseases from medical images. In his studies, he has demonstrated how CNNs can automatically learn features from images and classify them into different categories (such as healthy vs. ALL). This approach is highly relevant to your project, as CNNs are often employed for ALL detection in blood smear images. Livieris has worked on improving feature extraction and data preprocessing techniques in medical imaging. In the context of your project, these contributions are important because efficient feature extraction can enhance the performance of the machine learning model, especially when working with complex datasets like medical images of ALL. Techniques like data augmentation and the selection of relevant features are key to training robust models.

Author :M. C. O'Neill, Neural network (2014) O'Neill has worked extensively on evolutionary algorithms, particularly genetic algorithms and genetic programming, and their applications in healthcare. These algorithms can be used to optimize model performance and help automate the feature selection process, especially in complex medical datasets such as blood smear images for leukemia detection. M. C. O'Neill has explored the use of AI-driven pattern recognition techniques for medical image analysis. This is highly relevant to your project on ALL classification, asthe ability to identify subtle patterns in medical images (such as blood smears) is essential for accurately classifying different types of leukemia.

Author: alnazer i, bouurdon p, urruty The role of Israa Alnazer, Pascal Bourdon, and Thierry Urruty in the classification of acute lymphoblastic leukemia using convolutional neural networks is pivotal. Their research focuses on leveraging advanced AI techniques to improve the accuracy and efficiency of diagnosing this type of leukemia. By utilizing convolutional neural networks, they aim to enhance the detection and classification of leukemia cells in medical images, which can significantly aid in early diagnosis and treatment planning. Their collaborative efforts contribute to the development of innovative solutions in medical image processing, ultimately aiming to improve patient outcomes and advance the field of healthcare technology.

Author: Kaiming He, Xiangyu Zhang, Shaoqing Ren, Jian Sun Kaiming He, Xiangyu Zhang, Shaoqing Ren, and Jian Sun are renowned for their groundbreaking work in deep learning, particularly in the development of deep residual networks (ResNets). Their seminal paper, "Deep Residual Learning for Image Recognition," introduced a residual learning framework that significantly improved the training of very deep neural networks. They proposed a novel approach where layers learn residual functions with reference to the layer inputs, rather than learning unreferenced functions. This innovation helps in training much deeper networks by addressing the vanishing gradient problem. Their research demonstrated that networks could be trained with depths of up to 152 layers, which was a significant increase compared to previous models. This depth allowed for more complex and accurate representations.

PROPOSED METHODOLOGY

This proposed methodology focused on Deep learning uses artificial neural networks with multiple layers to solve complex problems. Convolutional neural networks (CNNs) are specifically designed for image classification and computer vision tasks. In 1979, Kunihiko Fukushima proposed the concept of Neocognitron, which aimed to create a network structure that can recognize features like the human brain and understand its workings. LeCun et al. introduced LeNet-5 in 1998, and since then, several other advanced networks have emerged, including AlexNet 2012, VGG 2014, and ResNet 2015. This section provides an in-depth analysis of CNNs and their applications.

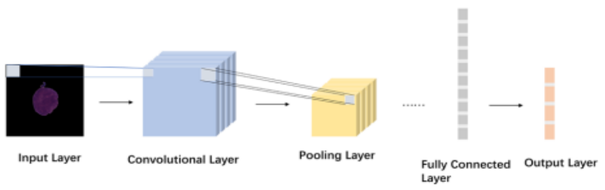
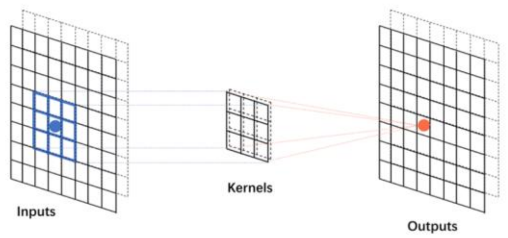


Figure 1: Structure of CNN

The proposed methodology typically includes the following key components:

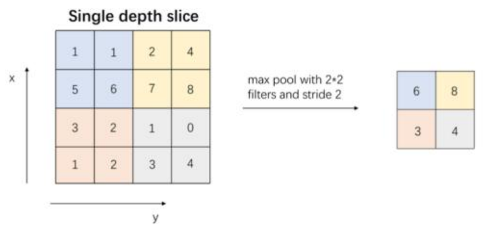
Convolutional Layers :

CNNs' core building blocks are convolutional layers with filters designed to detect specific features like edges or textures in images. Filters' weights are adjusted to minimize error during training.



Fully connected layer :

The fully connected layers are used to perform the layer is finally classification of the input data. They take the output of the previous of layers and transform it into a vector of class scores.
number of neurons in the fully connected layer corresponds to the number of classes in the classification task.

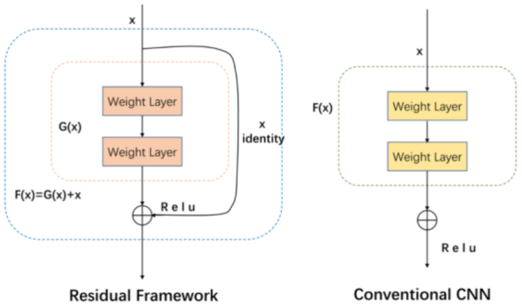


Ijaiem.com/Mar 2025/ Volume 14/Issue 1/Article No-1/223-225
ISSN: 2319-4847

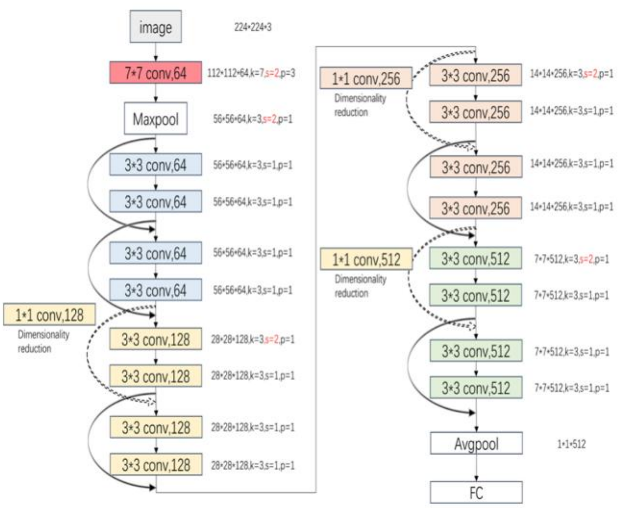
ResNet-18:

Resnet was proposed by Microsoft Research in 2015, and won the 1st places on the tasks of ImageNet detection, ImageNet localization, COCO detection, and COCO segmentation.The deep residual network (ResNet) architecture is composed of convolutional neural networks (CNNs) with shortcut links. These shortcut links enable identity mappings, as illustrated in Fig.4. Remarkably, these shortcuts can span multiple layers without introducing additional parameters or increasing computational complexity. This design ensures that the worst-case scenario of the model learning F(x) = 0, where no new knowledge is acquired, does not degrade the model's performance, allowing the network to maintain its performance.

ResNet-18 is a well-known and widely used variant of the ResNet architecture. In comparison to other popular network structures such as VGG and GoogLeNet, ResNet-18 is less complex and has fewer parameters. This makes it particularly difficult suitable for datasets with limited data, as it helps prevent overfitting while maintaining high accuracy. The residual structure of ResNet-18 allows for effective feature extraction and representation learning, leading to robust.



ResNet-18 architecture comprises 17 convolutional layers and 1 fully connected (FC) layer, with the convolutional layers organized into 5 blocks. The input to the model is a tensor of size (224, 224, 3), representing the image dimensions in height, width, and channels. Following the calculations through the convolutional layers, the classifier outputs the class probability of the image using the fully connected.



International journal of application or innovation in engineering and management

Ijaiem.com/Mar 2025/ Volume 14/Issue 1/Article No-1/223-225
ISSN: 2319-4847

EXPERIMENTAL ANALYSIS

Recent studies on Acute Lymphoblastic Leukemia (ALL) classification using Convolutional Neural Networks (CNN) have shown promising results. For instance, an attention-based CNN incorporating the Efficient Channel Attention (ECA) module with VGG16 achieved an accuracy of 91.1% on the C-NMC dataset. Another study designed a pyramid model CNN with varying kernel sizes, which resulted in an impressive accuracy of 99.17%, precision of 99.33%, and recall of 99% on the ALL-IDB2 dataset. These advancements highlight the potential of CNNs in accurately classifying ALL, aiding in early diagnosis and treatment planning.

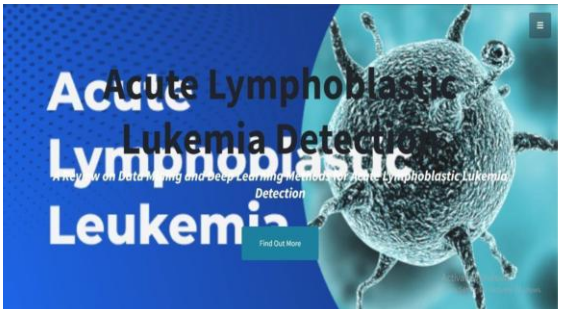


Figure 1:Home Page

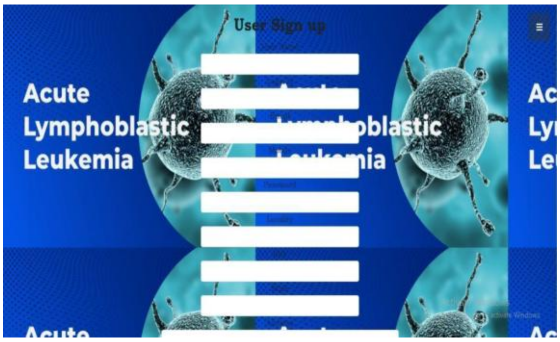


Figure 2: User Registration Page

Figure 3:Admin Login Page

Figure 4:User Login Form

Figure 5: Prediction Page

Compared with existing models,QCResNet has significant advantages over existing models for leukemia classification problems. First, by adding linear layers and LeakyReLU activation function, QCResNet can improve the depth, expressiveness and feature extraction ability of the model, thus better adapting to the complex leukemia classification task. Secondly, QCResNet has faster training convergence speed compared with other models, which can obtain more excellent training results faster and also can avoid the overfitting situation. In summary, QCResNet has higher accuracy and faster convergence speed than other classical convolutional neural networks in leukemia classification tasks and can effectively avoid overfitting. Therefore, QCResNet is a very promising and application-worthy deep learning model in the field of medical images.

3. CONCLUSION

This In this study, we built a residual neural network which named QCResNet to classify the cell images of Leukemia's dataset. First, we divide the training set, validation set and test set in a ratio of 8:1:1. Since the data distribution was unbalanced, we balanced the amount of each type of data and image enhancement was applied to the images. After feeding data to the neural network for iteration, the accuracy of QCResNet on the test set can reach 98.9%.The application of Convolutional Neural Networks (CNN) for the classification of Acute Lymphoblastic Leukemia (ALL) has demonstrated significant potential in enhancing diagnostic accuracy. The studies reviewed show that advanced CNN architectures, such as attention-based models and pyramid models, can achieve high accuracy, precision, and recall rates. These results underscore the importance of leveraging deep learning techniques in medical image analysis, which can lead to earlier and more accurate diagnoses, ultimately improving patient outcomes. Continued research and refinement of these models are essential to further optimize their performance and integrate them into clinical practice.

Compared with existing models, QCResNet has significant advantages over existing models for leukemia classification problems. First, by adding linear layers and LeakyReLU activation function, QCResNet can improve the depth, expressiveness and feature extraction ability of the model, thus better adapting to the complex leukemia classification task. Secondly, QCResNet has faster training convergence speed compared with other models, which can obtain more excellent training results faster and also can avoid the overfitting situation. In summary, QCResNet has higher accuracy and faster convergence speed than other classical convolutional neural networks in leukemia classification tasks, and can effectively avoid overfitting. Therefore, QCResNet is a very promising and application-worthy deep learning model in the field of medical images.

However, due to the limitations of the dataset itself, we still need to find more stable datasets and other reasonable data enhancement methods to further improve the performance of the model.

REFERENCES

[1] Cabitza, F., Rasoini, R., & Gensini, G. F. (2017). Unintended consequences of machine learning in medicine. Jama, 318(6), 517-518.

[2] Battineni, G., Chintalapudi, N., & Amenta, F. (2019). Machine learning in medicine: Performance calculation of dementia prediction by support vector machines (SVM). Informatics in Medicine Unlocked, 16, 100200.

[3] Uribe, C. F., Mathotaarachchi, S., Gaudet, V., Smith, K. C., Rosa-Neto, P., Bénard, F., ... & Zukotynski, K. (2019). Machine learning in nuclear medicine: part 1-introduction. Journal of Nuclear Medicine, 60(4), 451-458.

[4] Livieris IE, Pintelas E, Kanavos A, Pintelas P (2018) Identifification of blood cell subtypes from images using an improved SSL algorithm. Biomed J Sci Tech Res. https://doi.org/10.26717/BJSTR.2018.09.001755

[5] Ajay Vora ,Childhood Acute Lymphoblastic Leukemia Switzerland: Springer International Publishin Switzerland,2017:2

[6] ALNAZER I, BOUURDON P, URRUTY T,et al.Recent advances in medical image processing for the evaluation of chronic kidney disease[J].Med Image Anal,2021,69:101960I. S. Jacobs and C. P. Bean, “Fine particles, thin films and exchange anisotropy,” in Magnetism, vol. III, G. T. Rado and H. Suhl, Eds. New York: Academic, 1963, pp. 271–350.

[7] XIE G, CHEN T,LI Y,et al.Artificial intelligence in nephrology: how can artificial intelligence augment nephrologist’ intelligence?[J]Kidney Dis (Basel),2020,6(1):1-6R. Nicole, “Title of paper with only first word capitalized,” J. Name Stand. Abbrev., in press.

[8] L. J. Veer, H. Dai, M. J. Vijver, Y. D. He, and A. A. Hart, et al., “Gene expression profiling predicts clinical outcome of breast cancer,” Nature, vol. 415, pp. 530-536, 2002.

[9] M. C. O'Neill and L. Song, “Neural network analysis of lymphoma microarray data: prognosis and diagnosis near-perfect,” BMC Bioinformatics, vol. 4, no. 13, 2003.

mir Ghahremani and Christoph Lofi, "ImECGnet: Cardiovascular Disease Classification from Image- Based ECG Data Using a Multibranch Convolutional Neural Network," Journal of Image and Graphics, Vol. 11, No. 1, pp. 9-14, March 2023.

[10] Kaiming He, Xiangyu Zhang, Shaoqing Ren, Jian Sun; Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR), 2016, pp. 770-778.

[11] Ioffe, Sergey; Szegedy, Christian (2015). "Batch Normalization: Accelerating Deep Network Training by Reducing Internal Covariate Shift". arXiv:1502.03167