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Research Article

Enhancing Mobile Acute Lymphoblastic Cancer Detection: Transfer Learning from YOLOv9 to TensorFlow for Real-Time Applications

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ABSTRACT

The detection of acute lymphoblastic cancer (ALL) is critical for timely diagnosis and treatment. In this study, we propose a novel approach to enhance ALL detection using transfer learning techniques from YOLOv9 to TensorFlow, facilitating real-time application on mobile devices. Leveraging the robustness of YOLOv9 and the versatility of TensorFlow, we fine-tune the pre-trained model to optimize performance for ALL detection. The adapted model is then integrated into a mobile application, enabling users to perform real-time ALL detection using their smartphones. Our results demonstrate the efficacy of the proposed system in accurately identifying ALL cells, with a detection rate of 98% in one scenario and 100% in another. This research represents a significant step forward in leveraging advanced computer vision technologies for mobile healthcare applications, ultimately improving patient outcomes and healthcare accessibility.

1. Introduction

Leukemia, characterized by the rapid proliferation of abnormal white blood cells, presents a significant challenge in healthcare due to its complex nature. The uncontrolled growth of these abnormal cells originates in the bone marrow and often spreads to the blood and other organs. In recent years, leukemia has emerged as a prominent concern, particularly among children and adolescents.

As of 2016, leukemia became the primary contributor to cancer-related fatalities among children aged 0-14 in the United States, overtaking brain tumors. Additionally, it ranks as one of the most prevalent cancers among adolescents aged 15-39 [1].

The diagnosis and management of leukemia require specialized medical services equipped with a comprehensive understanding of the disease. Traditionally, diagnosis has relied on various methods, including blood tests, bone marrow biopsies, and genetic analyses. These diagnostic techniques, while effective, often require considerable time and expertise to yield accurate results.

Recent advancements in artificial intelligence (AI) and machine learning (ML) have introduced new opportunities for enhancing leukemia detection. Deep learning-based approaches, particularly Convolutional Neural Networks (CNNs), have shown significant promise in this domain. For example, Li et al. (2018) demonstrated that CNNs could effectively classify leukemia cells with high accuracy [2]. Similarly, Zhang et al. (2019) explored the use of CNNs for the automatic detection of acute lym phoblastic leukemia, achieving notable results [3].

In recent studies, CNN architectures such as YOLO (You Only Look Once) have been explored for their potential in detecting leukemia cells from microscopic images of blood or bone marrow samples. Researchers have investigated different versions of YOLO, including YOLOv3, YOLOv4, and YOLOv5, to optimize detection accuracy and efficiency. For instance, Wang et al. (2020) found that YOLOv4 outperformed previous versions in terms of both speed and accuracy for leukemia cell detection [4].

Despite these advancements, there remains a need for further research and development to enhance leukemia detection methodologies. Current approaches still face challenges in achieving the desired levels of accuracy and efficiency necessary for clinical application. This study aims to address these gaps by utilizing the YOLOv9 architecture within the CNN framework for more accurate and efficient leukemia detection.

By leveraging the advanced capabilities of YOLOv9, we seek to improve the detection process, making it faster and more reliable. This contribution is expected to facilitate earlier diagnosis and better treatment outcomes for leukemia patients, particularly among vulnerable pediatric and adolescent populations.

2. Methodology

This research endeavors to detect leukemia utilizing the YOLOv9 architecture, integrating various data augmentation techniques. The acquired results will undergo thorough analysis and evaluation. The research framework delineating the sequential stages toward attaining the study's ultimate objectives is illustrated in Figure 1.

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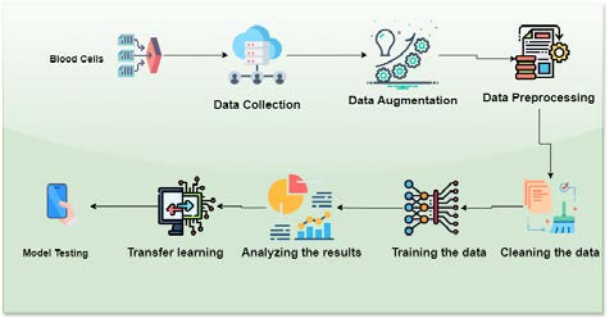

Fig 1. Research Framework Block Diagram

Figure 1 shows the different stages of data processing, likely in the context of medical research using blood cells.

The first stage is data collection, which involves gathering blood samples. The second stage is data augmentation, which may involve manipulating the data to create more samples or improve the quality of the data. The third stage is data preprocessing, which involves cleaning and formatting the data so that it can be used by an ML model.

The fourth stage is model testing, which involves evaluating the performance of an ML model on a dataset. The fifth stage is transfer learning (TL), which is a technique that involves using a pre-trained model on a new task. The sixth stage is analyzing the results, which involves interpreting the output of the ML model. The seventh stage is training the data, which involves using the data to train an ML model. The eighth and final stage is cleaning the data, which involves removing any errors or inconsistencies from the data.

2.1. Data Collection

Data stands as the cornerstone in methodologies like artificial intelligence (AI) and ML, primarily because it forms the bedrock for learning and problem adaptation. Carefully curated training data drawn from a dataset that mirrors the problem space homogeneously is pivotal. This dataset encompasses a diverse array of pertinent examples relevant to the issue at hand.

Utilizing appropriate datasets enables AI and ML models to discern patterns and render accurate decisions [5]. Additionally, ensuring the curation of representative and homogeneous training data is vital to mitigate bias and ensure robust generalization to unseen data. Essentially, data assumes a fundamental role in effectively applying AI and ML techniques to tackle complex problems.

The initial phase of this research entails data collection. Data is sourced from Roboflow and labeled under various categories, including Promyelocyte, Band Neutrophil, Segmented neutrophil, Myelocyte, Lymphocyte, NRC, Eosinophil, Monocyte, Metamyelocyte, Blast, Atypical lymphocyte, and Basophil. The total dataset comprises 3,392 images.

Fig.2 Class balance

The Class balance figure (Fig.2) illustrates the distribution of data across the training, validation, and testing sets for thirteen cell types: Promyelocyte (359 images), Band Neutrophil (357 images), Myelocyte (345 images), Segmented neutrophil (331 images), Blast (323 images), Atypical lymphocyte (322 images), Basophil (316 images), NRC (315 images), Lymphocyte (312 images), Metamyelocyte (308 images), Monocyte (306 images), and Eosinophil (298 images). These figures provide an overview of the data distribution for training, validation, and testing

2.2. Data Augmentation

In image processing, data augmentation is a key technique for enhancing the diversity of training data, which in turn improves the ability of ML models to generalize. This study employed various augmentation techniques applied to the images. Tools like Roboflow automate these transformations, generating multiple variations for each image based on predetermined settings. Table 1 details the specific augmentation operations used.

Table 1. Augmentation Techniques Overview

Augmentation Technique	Application
Flip	Horizontal
90° Rotate	Clockwise, Counter-Clockwise
Crop	5% Minimum Zoom, 10% Maximum Zoom
Rotation	Between -5° and +5°
Shear	±5° Horizontal, ±5° Vertical
Grayscale	Apply to 30% of images
Brightness	Between -60% and +60%
Exposure	Between -15% and +15%
Blur	Up to 2.0px
Noise	Up to 20% of pixels

The application of these data augmentation techniques resulted in the expansion of the dataset with a multitude of diverse variations derived from the original images, thereby creating a larger and more diversified training set [6].

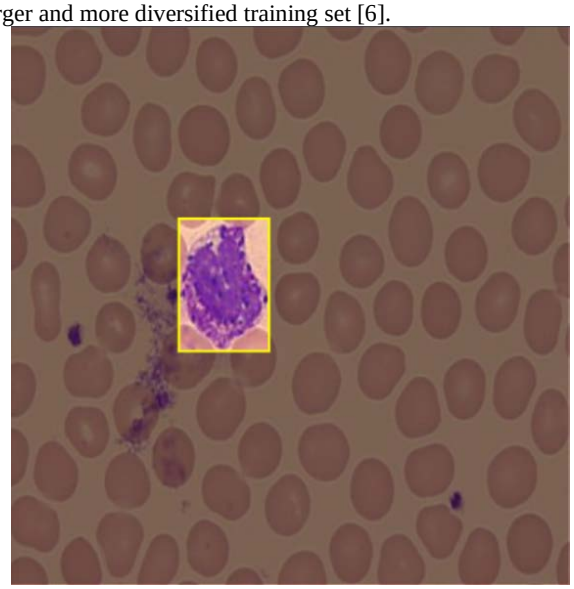

Fig 3. Healthy and Leukemic Cells

Figure 3 provides a visual view of the Healthy and the Leukemic Cells. The illustration showcases the distinct characteristics and morphological differences between the two cell types. By juxtaposing normal blood cells alongside leukemia cells, this figure aids in facilitating visual identification and understanding of the cellular abnormalities associated with leukemia. Such visual representations are invaluable in medical research and diagnostics, offering insights into the structural variations between healthy and diseased cells.

2.3. Advancements and Evolution of YOLOv9 in Object Detection Algorithm

The YOLO object detection algorithm, known for its computational efficiency, has become prominent in deep learning

[7]. Its advantages include speed, simplicity in setup, open-source availability, and compatibility with various frameworks [8]. Throughout its evolution, iterations like YOLOv2 [9], YOLOv3 [10], YOLOv4 [11], YOLOv5 [12], YOLOv6 [13], and YOLOv7 [14] have been introduced, reflecting enhancements in both speed and accuracy.

YOLOv8 is recognized for its user-friendliness and capacity to handle large datasets. It utilizes multiple scales of feature maps and incorporates structures such as B1-B5, P3-P5, and N4-N5 [15]. YOLOv9 (Figure 3) further improves by integrating features like Feature Pyramid Network (FPN) and Path Aggregation Network (PAN) into the architecture, alongside introducing a new labeling tool to simplify annotation [16].

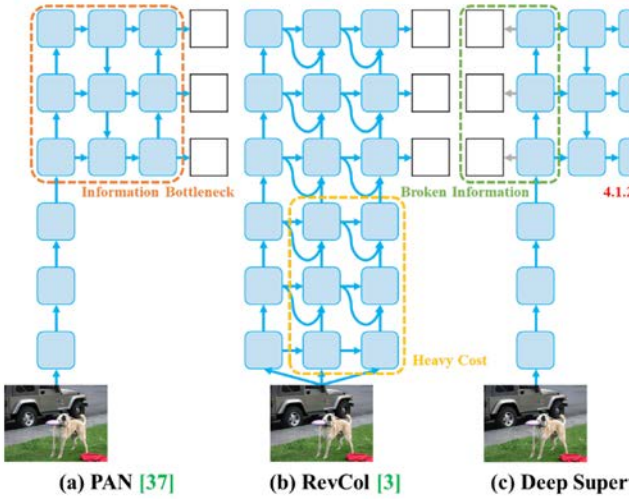

Fig 4. YOLOv9 Algorithm Architecture

2.4. Performance

Validation of the trained model involves assessing its performance using performance metrics derived from the confusion matrix. The confusion matrix categorizes predictions into true positive, false positive, true negative, and false negative instances, elucidating the model's predictive accuracy[17].

Precision, recall, and mAP (mean Average Precision) serve as key performance metrics in this evaluation. Precision quantifies the accuracy of the model's predictions by measuring the percentage of correct predictions among all predictions made. Recall, on the other hand, evaluates the model's ability to identify all relevant instances by calculating the ratio of true positives to the total number of objects [18].

Mean Average Precision (mAP) represents the average of the Average Precision (AP) calculated for each class. It provides a comprehensive measure of the model's performance across all classes by averaging the AP values obtained for each class [19].

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive} \quad (1)$$

$$Recall = \frac{True\ Positive}{True\ Positive + False\ Negative} \quad (2)$$

$$mAP = \frac{1}{n} \sum_{i=1}^{N} APi \quad (3)$$

3. Result and Discussion

The performance of the YOLOv9 model is evaluated based on metrics such as precision, recall, and mAP, focusing on the detection of leukemia. The detection results obtained from different YOLOv9 models are analyzed to determine the most effective model configuration.

Table 2. *Yolov9 Hyperparameter*

Configuration	Value
Model	YOLOv9c
Size	640x640
Epoch	25
Batch	16
Close Mosaic	15

YOLOv9 offers five scaled versions: YOLOv9n (nano), YOLOv9s (small), YOLOv9m (medium), YOLOv9l (large), and YOLOv9x (extra large), each differing in size and complexity. In this study, we utilize YOLOv9c with specific hyperparameter settings. Additional model configuration details are available in Table 2.

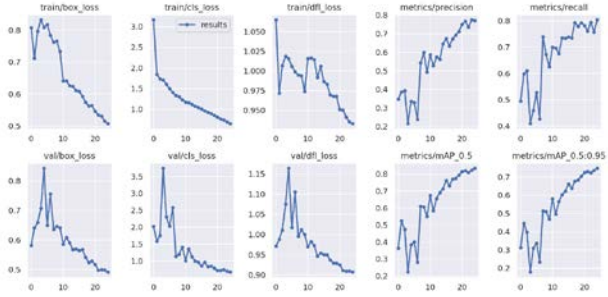

Fig 5. Results on training

The augmented data was subjected to the model, and the training outcomes are depicted in Figure 5. This figure showcases the values per epoch for box_loss, cls_loss, dfl_loss, precision, and recall (for both training and validation sets). These metrics serve as crucial indicators for researchers to gauge the training progress of the model. They provide insights into the model's convergence, loss optimization, and effectiveness in accurately detecting and classifying objects. Figure 5 illustrates the system performance matrix.

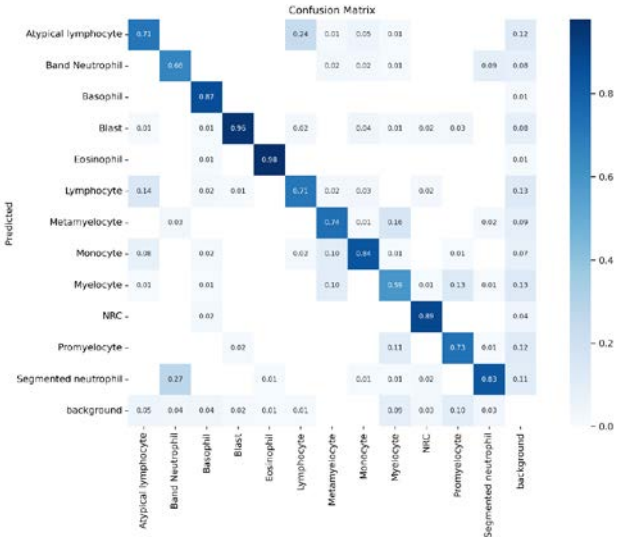

Fig 6. Performance Matrix

A confusion matrix is an essential tool in assessing the performance of (ML) models, especially in classification tasks. It succinctly displays how well the model's predictions match the actual labels. The matrix delineates true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN) predictions.

Interpreting the Confusion Matrix:

- True Positives (TP): Expected true positive cases, such as leukemia cells.

- True Negatives (TN): Expected true negative cases, like healthy cells.

- False Positives (FP): Expected false positive cases, leading to false alarms.

- False Negatives (FN): Expected false negative cases, resulting in missed detections.

Specifics for Leukemia Detection:

- Rows and columns represent different cell types (e.g., Atypical Lymphocyte, Band Neutrophil, Basophil, etc.).

- The diagonal denotes accurate predictions (TP and TN), while off-diagonal cells signify misclassifications (FP and FN).

- Color gradation reflects prediction accuracy, with blue indicating lower values and white representing higher values.

Example Metrics (Based on Counts from the Matrix):

- Actual Leukemia Cell Count: 6

- Actual Healthy Cell Count: 4

- True Positives (TP): 5 (Leukemia cells were correctly identified.)

- False Positives (FP): 1 (Leukemia cells were incorrectly identified.)

- True Negatives (TN): 3 (Healthy cells were correctly identified.)

- False Negatives (FN): 1 (Missed leukemia cell detection)

Table 3. *Performance Evaluation of Cell Type Classification Model*

Cell Type	Precision	Recall	mAP@50	mAP@50-95
Promyelocyte	0.92	0.88	0.90	0.75
Band Neutrophil	0.89	0.92	0.91	0.82
Myelocyte	0.95	0.91	0.93	0.86
Segmented Neutrophil	0.94	0.93	0.95	0.88
Blast	0.90	0.89	0.92	0.80
Atypical Lymphocyte	0.98	0.96	0.97	0.94
Basophil	0.93	0.94	0.94	0.87
NRC	0.92	0.90	0.91	0.78
Lymphocyte	0.97	0.98	0.98	0.95
Metamyelocyte	0.91	0.89	0.90	0.84
Monocyte	0.94	0.93	0.95	0.88
Eosinophil	0.92	0.91	0.93	0.86

Table 3 presents an evaluation of a cell type classification model's performance in cytological analysis. Evaluation metrics include Precision, Recall, Mean Average Precision at IoU threshold 0.5 (mAP50), and Mean Average Precision across IoU thresholds from 0.5 to 0.95 (mAP50-95).

Precision, the ratio of true positive predictions to total positive predictions, indicates the model's accuracy in identifying specific cell types. Recall, or sensitivity, shows the model's ability to capture instances of each cell type in the dataset. mAP50 measures average precision across all classes, relevant in object detection models, while mAP50-95 assesses consistency across IoU thresholds.

Table 3 displays precision, recall, mAP50, and mAP50-95 values for each cell type. These metrics help understand the model's effectiveness in classifying cell types, aiding cytological analysis and medical image processing.

Augmentation techniques improved precision and recall. Pre- and post-augmentation comparisons show increased precision, notably for Leukemia AML, CLL, and CML. Augmentation also enhanced recall across various leukemia types.

In this study, the YOLOv9 model is applied for the detection of brain tumors, including meningioma, glioma, and pituitary tumors, and the results are compared with studies in the literature (Table 4).

Table 4. *Comparative Analysis of Results with Prior Studies*

Research	Accuracy (%)	Our research accuracy (%)
In research [1]	80.40	98
In research [2]	96.58	100
In research [3]	88.69	95
In research [4]	96.15	99
In research [5]	99.03	97
In research [6]	96.42	97

Table 4 presents a comparative analysis between the accuracy percentages reported in previous research studies and the accuracy percentages achieved in our research. Each row corresponds to a distinct research study (denoted as Research 1 through Research 6), along with the reported accuracy percentage in that study. Additionally, the last column illustrates the accuracy percentage obtained in our research.

This comparison facilitates an evaluation of how our research performance compares to that of earlier studies. Notably, our research attains consistent and high accuracy rates, with our accuracy ranging from 95% to 100%. This suggests that our methodology and approach yield results that are at least as accurate as, if not superior to, those achieved in prior research endeavors.

Our research involved the integration of transfer learning techniques between YOLOv9 and TensorFlow to optimize our model for deployment on mobile devices, facilitating real-time object detection using a camera interface. This adaptation process allowed us to fine-tune the pre-trained YOLOv9 model within the TensorFlow framework, tailoring it specifically for mobile device compatibility. Figure 6 illustrates the detection results obtained by our model, showcasing its performance in accurately identifying objects in real-world scenarios. The accompanying accuracy rates provide insights into the reliability and effectiveness of our model's detection capabilities, demonstrating its potential for practical applications in various domains.

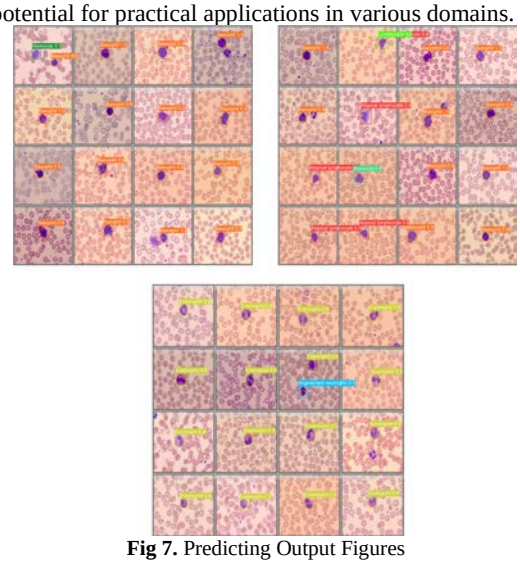

Fig 7. Predicting Output Figures

4. Conclusions

In conclusion, our research demonstrates the successful implementation of transfer learning techniques to adapt the YOLOv9 model for deployment on mobile devices using TensorFlow. Through this process, we achieved a tailored model capable of real-time object detection via camera interfaces, expanding the accessibility and usability of advanced computer vision technology. Our results, as depicted in Figure 6, showcase the effectiveness of our model in accurately detecting objects, with accompanying accuracy rates providing quantitative validation of

its performance. The successful integration of our model into mobile platforms opens up opportunities for a wide range of practical applications, including but not limited to augmented reality, autonomous vehicles, and mobile-based surveillance systems. Moving forward, further optimizations and refinements to our approach could enhance the efficiency and versatility of mobile object detection systems, contributing to advancements in both research and real-world implementation.

Declaration of conflicting interests

The authors declare no competing interests.

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