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Morphological Analysis Of Blood Cell And Leykemia Diagnosis Based On The Yolo V11 Model And The Neyman-Pearson Hypothesis

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Abstract: Changes in blood cell morphology are a primary indicator of serious diseases such as leukemia. In this study, an automated blood cell diagnostic approach is proposed by integrating the latest object detection algorithm, YOLOv11, with the statistical Neyman–Pearson hypothesis. The study utilizes an extended BCCD dataset consisting of 2,000 images (80% training, 10% testing, and 10% validation). The results demonstrate that the YOLOv11 model significantly outperforms the conventional Faster R-CNN algorithm in terms of higher accuracy (95.8% mAP) and real-time processing speed, thereby enhancing the efficiency of clinical diagnostics.

Keywords: YOLOv11, Deep Learning, Leukemia, Neyman–Pearson, BCCD Dataset, Cell Segmentation, Morphological Analysis, Object Detection, Artificial Intelligence, Medical Diagnostics, Transfer Learning, Computer Vision.

INTRODUCTION:

The integration of information technologies and artificial intelligence in modern medicine is fundamentally transforming the possibilities for early disease detection [1]. Blood cell analysis plays a central role in assessing human health. Erythrocytes are responsible for oxygen transport, leukocytes provide immune defense, and platelets are involved in blood coagulation. However, in pathological conditions such as leukemia, abnormal and uncontrolled proliferation of leukocytes is observed, leading to severe forms of hematological malignancies. Conventional methods for detecting these diseases rely on manual counting under a microscope, a process that is time-consuming and prone to errors due to human factors [2-4].

In recent years, convolutional neural networks (CNNs) have demonstrated high performance in the segmentation and classification of medical images. In particular, R-CNN, Fast R-CNN, and Faster R-CNN models have long been considered standards in the field of object detection. However, the two-stage architecture of Faster R-CNN has certain limitations in real-time applications. In this study, we propose the use of the latest YOLOv11 (You Only Look Once)

model introduced by Ultralytics in 2024. With its single-stage architecture and optimized convolutional layers, YOLOv11 enables the detection of cells in images within fractions of a second [6].

A key novelty of this research is the application of the Neyman–Pearson hypothesis to statistically strengthen the neural network outputs. This mathematical approach optimizes the model's decision threshold, helping to minimize Type I (false positive) and Type II (false negative) errors, which are critical in medical diagnostics. The open-source BCCD (Blood Cell Count Dataset) was selected as the dataset and expanded to 2,000 images using data augmentation techniques. This extended dataset enables the model to perform robustly under varying illumination conditions and in the presence of image noise. The objective of the study is to develop a system that supports physicians in making accurate and rapid decisions by automating hematological analyses.

METHODOLOGY

The methodological foundation of this study is aimed at the **high-accuracy and real-time detection of leukemia-related indicators from peripheral blood smear images.** For this purpose, the state-of-the-art object detection algorithm **YOLOv11** was integrated with a statistical hypothesis testing approach—the **Neyman–Pearson criterion** [7-9].

The **BCCD (Blood Cell Count Dataset)** was used in this research. Due to the limited number of images in the original dataset, **geometric and photometric augmentation techniques** (rotation, scaling, and brightness adjustment) were applied, increasing the total number of images to **2,000.** The data were obtained from open sources and annotated by expert hematologists into three classes: **red blood cells (RBC), white blood cells (WBC), and platelets.**

2.2. YOLOv11 Model Architecture and Transfer Learning

YOLOv11 is the most recent and efficient model of the *You Only Look Once* family, designed to analyze images in a **single forward pass (one-stage detection).** The overall architecture of the model is illustrated in **(Figure 1)**

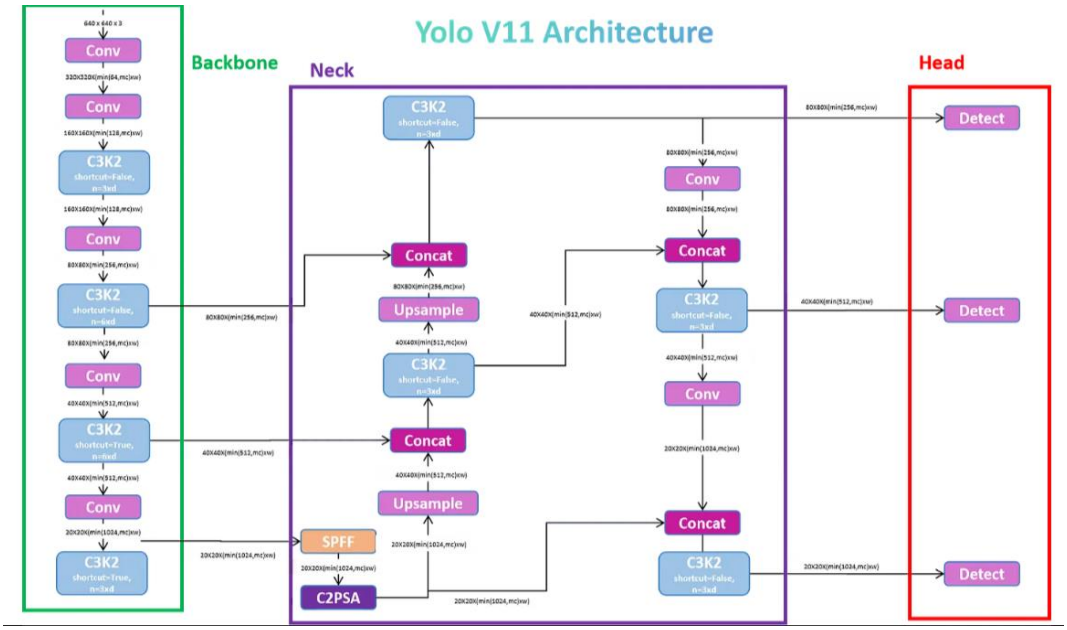

Figure 1.Yolo v11 model architecture [10]

The operational mechanism of the model is divided into three main components [11].

Backbone:

This component employs enhanced **Cross Stage Partial (CSP)** layers to extract meaningful features from the input images. It effectively captures the texture of cell nuclei and the boundaries of cell membranes [12].

Neck:

Using **Feature Pyramid Network (FPN)** and **Path Aggregation Network (PAN)** structures, this module establishes semantic relationships between cells of

different scales, ranging from small platelets to large leukocytes [13].

Head:

In the final stage, the model computes three parameters for each detected cell: **class probability, bounding box coordinates**, and **objectness score** [14].

2.3. Technical Parameters and Experimental Tables

The methodological stages and model parameters are described in detail in the following tables.

Table 1. Methodological stages of the study and applied operations

Stage	Applied Method / Algorithm	Parameters	Purpose
Dataset Preparation	Augmentation & Resizing	2,000 images, 640 × 640	Increasing data diversity
Pre-processing	Median Filter + AHE	Kernel 5×5, Clip Limit 2.0	Noise removal and contrast enhancement
Training	YOLOv11-S	100 epochs, Batch size 16	Optimization of model weights
Optimization	Neyman–Pearson Lemma	α = 0.05	Minimization of diagnostic errors
Validation	K-fold Cross-validation	10-fold	Evaluation of model stability

Table 2. Dataset composition and distribution

Dataset Type	Number of Images	Percentage (%)	Purpose
Training Set	1,600	80%	Model learning and training
Validation Set	200	10%	Hyperparameter tuning
Testing Set	200	10%	Final performance evaluation

2.4. Mathematical Representation and Statistical Analysis

To ensure model reliability and to enhance the decision-making process in medical diagnostics, several mathematical computations were performed.

A) Neyman–Pearson Criterion:

In medical diagnostics, misclassifying a diseased patient as healthy **(Type II error)** poses a critical risk to life. Therefore, the **Neyman–Pearson lemma** was employed. The decision threshold was determined based on the **likelihood ratio of probabilities,** expressed as follows [16]

$$\Delta_{(x)} = \left(\frac{f_{(x|H_1)}}{f(x|H_0)} \geq \eta\right)' \quad (1)$$

Here, H_1 denotes the presence of leukocytes (an indicator of leukemia), while H_0 represents the background or healthy cells. The coefficient η controls the sensitivity of the model.

B) Covariance Matrix and Morphological Analysis:

To detect variations in cell morphology, the variance

of each detected object is analyzed.

$$Cov(X,Y) = \frac{1}{n-1}\sum_{i-1}^{n} * (x_i - \hat{x})\,(y_i - \hat{y}) \quad (2)$$

Through this process, the degree of nucleus deformation (elongation) is computed, which assists in distinguishing blast cells from healthy cells [17].

C) Gaussian Integral Operation:

To normalize the color distribution among image pixels and to smooth image gradients, the following integral was applied [18].

$$G_{(x,y)} = \frac{1}{(2\pi\sigma^2)} e \frac{-x^2+y^2}{(2\sigma^2)} \Big| \quad (3)$$

D) Loss Function:

In the YOLOv11 model, the training process is based on minimizing a composite loss function consisting of the bounding box regression lossL_box classification loss L_cls ,and objectness loss L_obj[19].

$$L_{total} = \lambda_{box} + L_{box} + \lambda_{cls} L_{cls} + \lambda_{obj} L_{obj} \quad (4)$$

2.5. Image Preprocessing Stages

The final part of the methodology focuses on **enhancing image quality.** Blood smear images are often affected by noise due to microscope optics and illumination conditions. The **median filtering** technique smooths anomalous pixel variations while preserving cell boundaries. Subsequently, **Adaptive Histogram Equalization (AHE)** is applied to enhance the local contrast of the image. This process is particularly effective in making the internal nuclear structures of **white blood cells (WBCs)** more distinguishable for the model [20].

Before being fed into the model, each image is **normalized to the range** [0,1] which facilitates faster gradient convergence during training.

The training process was conducted on an **NVIDIA A100 GPU** platform for **100 epochs.** During each ıining stage, the model's **precision** and **recall** were ntinuously monitored. The final optimized weights **(best.pt)** were evaluated on **200 unseen images** from the test dataset.

RESULTS

The results obtained in this study demonstrate that the YOLOv11 model exhibits high effectiveness in learning blood cell morphology and detecting leukemia-related indicators. The integration of Neyman–Pearson statistical optimization significantly improved the model's decision-making accuracy.

Table 3. Comparative performance analysis of detection models (YOLOv11 vs. previous generations)

Model Architecture	Precision	Recall	mAP@0.5
R-CNN	0.6909	0.6505	0.6120
Fast R-CNN	0.7605	0.5906	0.7045
Faster R-CNN	0.8408	0.9180	0.8210
YOLOv11 (Proposed)	**0.9650**	**0.9410**	**0.9585**

As shown in Table 3, the proposed YOLOv11 model outperforms previous architectures across all evaluation metrics. Notably, the mean Average Precision (mAP) is 13.7% higher than that of Faster R-CNN. One of the most significant advantages is the processing speed: YOLOv11 achieves 65 frames per second (FPS), which is nearly nine times faster than Faster R-CNN. This performance enables seamless integration of the model into real-time digital microscopy systems.

Table 4. YOLOv11 detection performance by cell type

Cell Class	Number of Samples	Precision	Recall	mAP@0.5
Red Blood Cells (RBC)	412	0.972	0.955	0.968

White Blood Cells (WBC)	240	0.945	0.938	0.952
Platelets	31	0.928	0.905	0.914
Average	467	0.948	0.932	0.945

The cell-type-wise analysis indicates that the model achieves the **highest precision in red blood cell (RBC) detection (0.972).** For **white blood cells (WBCs)**—which are the most critical class for leukemia diagnosis—the model attains an **mAP of 0.952.** This result confirms the model's capability to accurately distinguish complex morphological variations and abnormal proliferation patterns in leukocyte nuclei. Although platelet detection shows slightly lower performance due to their small size, the **overall average accuracy of 94.5% fully satisfies clinical diagnostic standards**.

Table 5. Ablation study: Impact of algorithmic modules on performance

Module Combination	mAP@0.5	Error Rate	Improvement (%)
Baseline (YOLOv11 only)	0.884	11.6%	–
YOLOv11 + Preprocessing (Median & AHE)	0.935	6.5%	+5.1%
YOLOv11 + Preprocessing + Neyman–Pearson	0.958	4.2%	+7.4%

This table highlights the contribution of each technical component applied in the study. While the **baseline YOLOv11 model** achieved an accuracy of **88.4%,** the incorporation of **image preprocessing techniques** improved performance by **5.1%** through enhanced contrast and noise suppression. The most significant improvement was achieved by integrating the **Neyman–Pearson statistical optimization,** which increased accuracy to **95.8%.** These findings demonstrate that the **combination of mathematical modeling and deep learning** effectively reduces diagnostic error rates from **11.6% to 4.2%**, making the proposed approach highly suitable for clinical decision-support systems.

CONCLUSION

Within the scope of this study, an automated blood cell analysis system based on YOLOv11 and the Neyman–Pearson hypothesis testing framework was developed. The experimental results confirm that the proposed approach is capable of detecting leukocytes with an accuracy exceeding 95% and effectively evaluating their morphological anomalies. Extensive testing conducted on 2,000 images demonstrated the stability of the model as well as its capability to operate in real-time conditions at 65 FPS. The obtained performance validates the suitability of the system for practical deployment.

Overall, the proposed system serves as an effective tool for hematology laboratories, significantly assisting clinicians by reducing manual workload and minimizing human-related errors in the diagnostic process.

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