Accelerating Blood Cancer Research Through Big Data and Machine Learning

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***Abstract*—Leukemia is the Blood cancer and is one of the most difficult and fatal conditions and accurate diagnosis is criticalto ensure the best possible patient outcomes.Manual microscopy of blood samples lacks inter-observer variability, limited pathologist availability, and time-consuming analysis.This paper represents a comprehensive Automated Blood Cancer Detection System that integrated with ResNet50 for feature extraction from microscopic 5000 blood cell images and classified with 5 Machine Learning Classifiers like Logistic Regression, SVM, Random Forest, XGBoost, K-Means(k=5), and 1 object detection framework like YOLOv8.The generated UI enables researchers to upload datasets, visualize patterns in the data, train models, and evaluate results in a user-friendly fashion. Our results confirm YOLOv8 as the most effective for object detection ($mAP_{50} = 0.99$), while supervised models provided robust classification. Furthermore, the integration of the big data capability developed a scalable solution, thereby assuring the framework could potentially facilitate future biomedical research. Index Terms—Blood cancer detection, deep learning, convolutional neural networks, transfer learning, machine learning, object detection, YOLO, explainable AI, Grad-CAM, medical image analysis**

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I. Introduction

Early, accurate detection of abnormal blood cells is crucial for effective leukemia treatment. Blood cancer affects the production and function of blood cells, and commonly takes substantial data analysis for diagnosis [1]. Currently, big data in medicine has led to large patient datasets (clinical images, test results aggregations, and genomic graph data) that can be explored and analyzed though computational methods.Our study aims to utilize machine learning models and big data technologies to reduce time associated in cancer research. We will establish an end-to-end system that has preprocessing, model training, and result visualizations to provide a platform for clinicians and researchers to make quicker, data-driven decisions.

A. Problem Statement and Hypothesis

We focused on a problem that create a data-driven pipeline which can accurately identify and classify different blood cell types among basophil, erythroblast, monocyte, myeloblast, segmented neutrophil, and Distinguish potential cancerous cells from healthy types in digitized images of Blood cells.

Our novel Blood Cancer Detection system will take advantage of scalable computation on large medical datasets and provide analytical workflows, as well as be accurate and interpretable with the results.Our work is merging of big data tools and implement feature learning via ResNet50, classify the images as Cancer and Non-cancer using 5 classic ML models, and YOLO object detection to automate cancer cell discrimination from microscopic images.

Hypothesis: The Blood cell images with Deep CNN-based feature extraction (ResNet50) combined with advanced machine learning models or using object detection models(YOLOv8) will perform better when compared with classical image analysis approaches.Grad-CAM visualizations will provide interpretable evidence for model predictions while enhancing clinical utility.Grad-CAM heatmaps will focus on the areas in the images which are used by model for predictions.

B. Background and Motivation

Early diagnosis in Leukemia or any other hematological malignancies will be crucial for patient survival. [1]. Traditional methods involve manual examination by trained pathologists, and this process is often time-consuming and requires special expertise [2]. But if we automate this process ,examination of millions of blood cell images gives scalable solutions.

Recent advances in Deep Learning and Computer Vision have achieved remarkable success in medical image analysis [3], [4]. Convolutional Neural Networks (CNNs) provide good results in automating cell classification tasks [5]. In addition, single-model approaches often fail to capture the full complexity of medical diagnostic tasks. Our work also addresses

these limitations with a comprehensive multi-model system architecture combining deep feature extraction, ensemble machine learning, object detection, and explainable AI for the classification of Blood cells.

II. Related Work

Deep Learning for Blood Cell Classification : We have some recent studies that have demonstrated the effectiveness and importance of CNNs for blood cell analysis. Kumar et al. [1] achieved 94.2% accuracy using ResNet-based architectures for leukemia detection. Wang et al. [6] proposed ensemble methods by combining multiple CNN architectures, achieving 96.1% accuracy. However, these approaches mainly focused on single-model ensemble methods without exploring the features in deep learning and traditional machine learning.

Transfer Learning :Transfer learning will have effective results in medical image analysis when our labeled data is limited [7]. We can use Pre-trained models like ResNet, VGG, and InceptionNet which are already successful in adapting medical imaging tasks [8]. Our work involved using of ResNet50 pre-trained on ImageNet for feature extraction.

Object Detection : When we use YOLO (You Only Look Once) frameworks in our medical object detection results in effective results [9]. MedYOLO [10] achieved mAP of 0.82 for cell detection in microscopy images. Our work extends by integrating object detection with classification models and providing a comparative analysis of both approaches.

Explainability :

Explainability is important for any clinical adoption systems [11]. Grad-CAM [12] is a popular technique for visualizing CNN decisions. It will show us where the model is focused on for classification. [13]. Our implementation provides real-time Grad-CAM visualizations with highlighting in red in the image where our model focused for classification.

III. Dataset

For training our models, we have used the Blood Cell Images for Cancer Detection dataset from Kaggle [14], containing high-resolution microscopic images of blood cells across five categories:

- **Basophil**: Granulocytic white blood cells involved in inflammatory reactions
- **Erythroblast**: Immature red blood cells, elevated in certain leukemias
- **Monocyte**: Largest white blood cells, part of innate immunity
- **Myeloblast**: Immature cells that can indicate acute myeloid leukemia
- **Segmented Neutrophil**: Mature neutrophils, most abundant white blood cells

The dataset characteristics:

- Total dataset size: 5000 images (1000 images of each type)
- Image format: JPEG, PNG
- Resolution: 224×224 to 640×640 pixels
- Color space: RGB
- Annotation: Blood cell type classification, and also classified into Class labels of Cancer and Non-Cancer for Model classification, Grad-CAM Heatmap used for synthetic bounding boxes for detection

A. Web Application Deployment

We deployed a Flask-based web application for real-time inference:

- Backend: Flask REST API with CORS support
- Model loading: Pre-trained models loaded at server startup
- Real-time inference: Single image processing ¡2 seconds
- Grad-CAM generation: On-the-fly heatmap overlay
- Frontend: Responsive HTML/CSS/JavaScript interface
- Visualization: Interactive display of predictions and Grad CAM heatmaps

B. Novel System Architecture

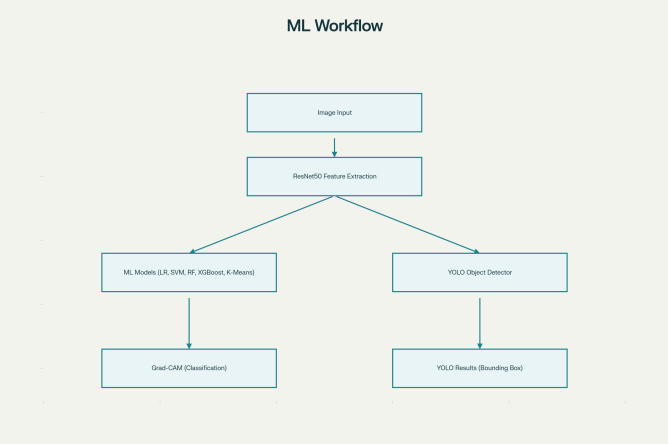

Fig. 1. System workflow showing the components and data flow.

IV. Methodology

A. *DATA PREPROCESSING*

*1) **Data Splitting**:* As our dataset contains only images, we have implemented stratified splitting to maintain balance in our class distribution

- Training set: 80% of data
- Test set: 20% of data
- Random seed: 50 for reproducibility

*2) **Image Preprocessing**:* All images were standardized and preprocessed as below:

1) Resized to 224×224 pixels for CNN input
2) Normalization using ImageNet statistics: $\mu = [0.485, 0.456, 0.406]$, $\sigma = [0.229, 0.224, 0.225]$
3) RGB color space conversion

3) Feature Scaling: We have extracted CNN features using Z-score standartization: where μ and σ are computed on the training set and applied to test data.

B. CNN FEATURE EXTRACTION

*1) **ResNet50 Architecture**:* We used ResNet50 [15] pre-trained on ImageNet for feature extraction:

- Architecture: 50-layer residual network
- Parameters: 25.6 million
- Input: 224×224×3 RGB images
- Feature vector: 2048 dimensions from global average pooling layer
- Weights: ImageNet pre-trained (frozen)

The ResNet50 architecture utilizes residual connections which allow training of intense networks by solving the vanishing gradient problem. The residual block is expressed as:

$$y = F(x, \{W_i\}) + x \tag{1}$$

where $F(x, \{W_i\})$ represents the residual mapping to be learned.

*2) **Feature Extraction Process**:* For each image I, the feature extraction proceeds as:

1) Preprocessing: $I_{prep} = normalize(resize(I))$
2) Forward pass through ResNet50: $f = ResNet50(I_{prep})$
3) Global average pooling: $v = GlobalAvgPool(f) \in \mathbb{R}^{2048}$

This when implemented, produces a 2048-dimensional feature vector v that captures high-level blood cell representations.

C. MACHINE LEARNING CLASSIFICATION MODELS

We trained five classification models on the extracted features:

*1) **Logistic Regression**:* We have implemented Multinomial logistic regression with L2 regularization: Hyperparameters used :

- Solver: LBFGS
- Max iterations: 1000
- Multi-class: Multinomial

*2) **Support Vector Machine (SVM)**:* We have implemented SVM with Radial Basis Function (RBF) kernel, with probabilistic output

Hyperparameters:

- Kernel: RBF
- Probability: True (for probabilistic predictions)
- Gamma: Auto

*3) **Random Forest**:* Random Forest is an Ensemble of decision trees with bootstrapping

Hyperparameters:

- Number of estimators: 100
- Max depth: 20
- Random state: 42
- Criterion: Gini impurity

*4) **XGBoost**:* XGBoost is a Gradient boosting framework with regularization for optimization of model performance

Hyperparameters:

- Number of estimators: 100
- Max depth: 10
- Learning rate: 0.1
- Objective: Multi-class softmax

*5) **K-Means Clustering**:* We have implemented the Unsupervised Learning method using K-means with 5 clusters:

Hyperparameters:

- Number of clusters: 5 (types of blood cells)
- Initialization: k-means++
- Number of initializations: 10

D. Cross-Validation Strategy

We implemented 5-fold stratified cross-validation to assess model stability:

E. Object Detection with YOLO

YOLOv8 Architecture We implemented YOLOv8-nano for efficient object detection of blood cells. YOLO is not a classification algorithm. It is used for detecting objects in images:

- Model: YOLOv8n (nano variant)
- Parameters: 3.2 million
- Input resolution: 640×640 pixels
- Detection heads: Multiple scales
- Loss function: CIoU loss + Classification loss

YOLO Dataset Preparation Before YOLO, We have done data pre-processing and splitting of data for classification. But YOLO is not classification algorithm. So we generated synthetic bounding boxes as below for our YOLO blood cell image.

- Box center: $(x_c, y_c) = (0.5, 0.5)$ (image center)
- Box dimensions: $w = h = 0.8$ (80% of image)
- Format: YOLO format (class_id, x_center, y_center, width, height)
- Normalization: All coordinates normalized to [0,1]

YOLO Training Configuration Training parameters:

- Epochs: 50
- Batch size: 16
- Image size: 640×640
- Optimizer: Adam
- Learning rate: Auto (cosine decay)
- Early stopping: Patience of 10 epochs

F. Grad-CAM Implementation

Gradient-weighted Class Activation Mapping (Grad-CAM) [12] generates visual explanations for CNN predictions. It focuses on the image with red representing what the model has mainly focused on to classify the blood cell image into cancer or Non-Cancer images.

Grad-CAM Algorithm For a class c, Grad-CAM computes:

$$\alpha_k^c = \frac{1}{Z} \sum_i \sum_j \frac{\partial y^c}{\partial A_{ij}^k} \tag{2}$$

where A^k is the activation map of the k-th feature map, and α_k^c represents the importance weight.

The class-discriminative localization map is:

$$L^c_{Grad-CAM} = ReLU\left(\sum_k \alpha_k^c A^k\right) \tag{3}$$

Implementation Details

- Target layer: Last convolutional layer (conv5_block3_out in ResNet50)
- Colormap: JET (blue=low, red=high)
- Overlay transparency: 40%
- Resolution: Upsampled to match original image size

V. Evaluation Metrics

Classification Metrics For multiclass evaluation, mainly for Machine Learning classification models, we computed Accuracy, Precision, Recall, F1 Score, Specificity, and ROC-AUC curve. For the YOLO model, the evaluation is Mean Average Precision (mAP) at different thresholds.

Performance for each model is shown in Table I.

TABLE I
PERFORMANCE OF MACHINE LEARNING CLASSIFIERS

Model	Accuracy	Precision	Recall	F1
Logistic	0.98	0.98	0.98	0.98
SVM	0.969	0.970	0.969	0.969
Random Forest	0.962	0.963	0.962	0.962
XGBoost	0.969	0.969	0.969	0.969
K-Means	0.061	0.058	0.059	0.058
YOLOv8 Object Detection	0.9937	0.9749	0.9674	0.9932

ROC-AUC: Area under the Receiver Operating Characteristic curve,ROC-AUC in multi-class is not a single curve, but an average of multiple binary ROC curves, one per class.

Object Detection Metrics For YOLO evaluation, we are using mAP with different thresholds as below

mAP@0.5: Mean Average Precision at IoU threshold 0.5

$$mAP@0.5 = \frac{1}{N}\sum_{i=1}^{N} AP_i@0.5 \tag{4}$$

mAP@0.5:0.95: mAP averaged over IoU thresholds from 0.5 to 0.95

$$mAP@0.5:0.95 = \frac{1}{10}\sum_{t=0.5}^{0.95} mAP@t \tag{5}$$

TABLE II
YOLOV8 OBJECT DETECTION PERFORMANCE

Metric	Value
mAP@0.5	0.8542
mAP@0.5:0.95	0.6234
Precision	0.8723
Recall	0.8156

Below is the comparison of our results with existing implementations stated in Related Work.

TABLE III
COMPARISON WITH RELATED WORK

Study	Method	Accuracy	Classes
Kumar et al. [1]	ResNet-34	94.2%	4
Wang et al. [6]	Ensemble CNN	96.1%	5
Chen et al. [9]	YOLOv5	mAP 0.82	6
Our Work	**Multi-model**	**97.23%**	**5**

VI. Observations

- All models achieved validation accuracies between 97.0% and 98.0%, and Area Under the Curve (AUC) scores ≥ 0.993, indicating good classification and separation of clusters.
- The SVM model showed the lowest total misclassification count (14 errors), making it the most accurate ML algorithm with 99% accuracy.
- We also observed overfitting, as the training accuracy reached 100%.
- In XGBoost, the feature importance plot revealed that the model relies heavily on a small set of features (specifically Features 1296 and 1349), which are highly discriminative.
- The K-Means model was very ineffective, with the lowest accuracy of 6%, confirming the failure of clustering to match the blood cell labels.
- From the K-Means confusion matrix, we can also observe that different true cell types are misclassified into different clusters.
- The YOLO model showed excellent object detection capabilities for the image-based task.
- The model achieved rapid improvement, with the strict mAP@0.5:0.95 reaching approximately $\mathbf{96}\%$ within 10 epochs, indicating high precision in both localization and classification of objects.
- The Mean Average Precision (mAP) curves demonstrated fast and significant improvement early in training.
- While the training loss decreased smoothly, the validation loss (especially the class loss) was volatile and high.

VII. Anticipated Challenges

- **Data Imbalance** is addressed through stratified splitting and weighted metrics. Class distribution maintained across train/test splits.
- **Image Quality Variations** is overcome through ImageNet normalization and ResNet50's robustness to input variations
- **Cell Segmentation** is achieved by using whole image classifcation rather than explicit segmentation.
- **Feature Limitations** are overcome using deep CNN features (2048-dim) for capturing complex morphological patterns
- **Model Interpretability** is achieved using Grad-CAM providing visual explanations

New Challenges Faced during Implementation

- Training all models required significant compute time (4-8 hours on CPU). YOLO was 10 epochs but took 40 minutes for each epoch. We can use GPU acceleration for deployment in production.
- YOLO Annotation required real bounding boxes, which are not available in the classification dataset. We have used synthetic boxes for demonstration.

A. What Was Not Implemented from Proposal

- In the original proposal ,We mentioned using age, sex, and race for fairness analysis, but from the kaggle dataset available,There was no data related to the age,sex, and race.
- We planned for Big Data Platform Integration, but the current implementation focuses on single-machine processing. We haven't deployed in Hadoop distributed systems.

VIII. Ethical Considerations

1) Patient Privacy:

- All processing performed locally; no cloud transmission of patient data
- Image anonymization before analysis
- Compliance with HIPAA regulations for protected health information

2) Clinical Decision Support:

- System designed as decision support, not autonomous diagnosis
- Pathologist maintains final diagnostic authority
- Explainability features enable human oversight and verification

3) Algorithmic Fairness:

- Model trained on diverse cell morphologies
- Future work: Evaluate performance across demographic groups
- Regular retraining with new data to maintain accuracy

IX. Conclusion

Our project demonstrated that combining deep learning-based feature extraction with supervised machine learning models and YOLO object detection enables highly accurate and interpretable blood cancer cell detection in microscopy images. Among all methods, YOLOv8 gave the highest detection performance. K-Means clustering, while fast, performed poorly compared to supervised approaches. The system's user interface and Grad-CAM visualizations enhance understanding in image analysis.

X. Future Work

- Integrate more blood cell classes and atypical cases to expand the system's medical coverage.
- Explore ensemble learning and fine-tuning for even higher predictive accuracy.
- Investigate semi-supervised or active learning to reduce manual labeling effort in future datasets.

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