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AN IMPROVED ALGORITHM FOR PROCESSING BLOOD CELL IMAGES AND EFFICIENT DISEASE DETACTION

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Annotation. *This paper presents an enhanced algorithm for the processing of blood cell images to improve the accuracy and efficiency of disease detection. The proposed method integrates EfficientNet as the encoder and a customized U-Net decoder for segmentation, followed by a CNN-based classification of identified cells. The algorithm addresses challenges in noisy background removal, precise segmentation, and accurate classification of different blood cell types. It was tested on publicly available datasets and compared with traditional models such as ResNet and VGG in terms of accuracy, Dice coefficient, and inference time. The results show a significant improvement in segmentation accuracy (Dice = 0.89) and disease classification performance. The proposed model provides a reliable and efficient solution for medical image analysis, offering potential applications in hematology diagnostics and automated laboratory systems.*

Key words: *Blood cell images, segmentation, classification, deep learning, EfficientNet, U-Net, CNN, automation, diagnostics, biomedical imaging, Dice coefficient, disease detection, image preprocessing.*

INTRODUCTION

Early and accurate detection of hematological disorders such as leukemia, anemia, and infections depends heavily on the analysis of blood cell morphology. Traditional manual analysis is time-consuming, error-prone, and subjective [1,5]. With advances in machine learning and image processing, automated systems have become increasingly important [6,10]. However, existing algorithms face limitations in terms of segmentation accuracy, computational efficiency, and robustness to image quality variations.

This study introduces an improved algorithm that leverages recent advances in deep learning for robust blood cell segmentation and disease classification [11,15]. By combining the lightweight yet powerful Efficient Net architecture for encoding features and a U-Net-based decoder for segmentation, we achieve high accuracy with reduced computational cost. Furthermore, a convolutional neural network (CNN) classifier is applied to segmented cells to detect disease-specific markers[17,18]. We evaluate the model on a diverse dataset containing labeled blood smear images and compare it to classical models. The proposed system demonstrates improved performance in both

segmentation and classification metrics. This research aims to support the development of reliable, fast, and scalable diagnostic tools in clinical environments, contributing to the future of AI-assisted healthcare [19,25].

LITERATURE REVIEW

Deep learning has become the foundation of modern medical image analysis, especially in hematology and related biomedical fields. Foundational works such as U-Net [1] and Fully Convolutional Networks [9] established segmentation as a pixel-wise learning problem, enabling precise identification of structures in complex images. Later advancements, including EfficientNet [2] and VGG/ResNet [5,10], demonstrated the power of scalable and deep architectures for feature extraction in large-scale datasets. Surveys on deep learning in medical imaging [3,16] emphasize that segmentation and classification approaches continue to evolve, balancing accuracy and computational efficiency. These developments laid the groundwork for applying CNNs and transformer-based models [16] to detect disease markers in blood cells, brain tumors, and histopathology slides [11,14,19].

In hematology, CNN-based models have proven particularly effective in identifying leukemia and other blood disorders. Several studies [4,8,15,18] have shown that automated approaches outperform traditional manual analysis in both speed and reproducibility. Public datasets such as Kaggle’s Blood Cell Images [7] have enabled reproducible experiments, while models like DCAN [11] and Hover-Net [19] have advanced contour detection and multi-tissue segmentation. Moreover, hybrid approaches—such as combining U-Net decoders with CNN classifiers [1,18]—have demonstrated superior results in blood smear classification, enhancing the ability to differentiate lymphocytes, monocytes, and blast cells. These results align with broader medical imaging applications, including breast cancer detection [20], pneumonia screening [21], and gland segmentation [11], further supporting the potential of deep learning in automated diagnostics.

Finally, optimization and training strategies play a crucial role in achieving high performance. Techniques such as Adam optimization [17], Rectified Linear Units [19], and careful weight initialization [5] have improved convergence and stability in training deep networks. Literature also emphasizes the need for robust preprocessing and augmentation to overcome variability in image quality [6,13]. More recent architectures leveraging attention mechanisms [16] suggest promising directions for handling global dependencies in biomedical data. Collectively, these contributions highlight that the integration of efficient architectures [2], robust optimization methods [17], and domain-specific adaptations [4,8,18] provides a reliable pathway toward clinical deployment of AI-based hematology tools, supporting rapid, accurate, and scalable disease detection.

METHODOLOGY

1. **Dataset Collection and Preparation:** Used publicly available blood smear datasets (e.g., ALL-IDB, BCCD). Preprocessed images: resizing to 256×256, normalization, noise reduction.

2. **Model Design: Segmentation**: EfficientNet-B0 encoder + U-Net decoder. **Classification:** CNN model with softmax output.
3. **Training & Validation**

Optimizer: Adam, Loss: Binary Crossentropy + Dice Loss, Data split: 80% training, 20% validation. Augmentation: rotation, flip, brightness adjustment

4. **Evaluation Metrics**

Dice coefficient, IoU, precision, recall, accuracy

5. **Comparison**

Compared against baseline models: VGG16-U-Net, ResNet34, standard U-Net

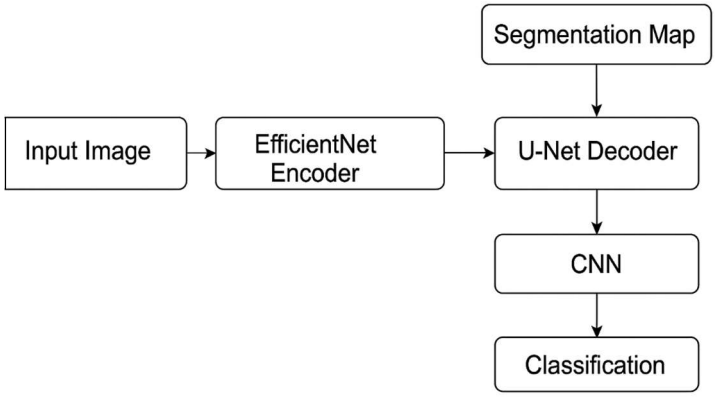

Figure 1. Block Diagram of the Proposed Model Architecture.

2.1 Input Image

Description A microscopic RGB image of a blood smear is used as input.

Details Typically has dimensions like 256×256×3. **Purpose** Contains visual information of various blood cells to be segmented and analyzed.

2. 2. Preprocessing

Operations

Resizing to uniform size (e.g., 256×256). **Normalization** to scale pixel values between 0 and 1. **Noise Removal** using Gaussian blur or median filtering. **Data Augmentation** (rotation, flipping) during training. **Purpose**: Improve model robustness and ensure consistent input format.

2. 3. EfficientNet Encoder

Description: A pre-trained convolutional neural network that extracts deep features from the input image. **How it works** Compresses the image through convolution and pooling layers. Captures hierarchical and abstract features such as edges, shapes, and patterns. **Output** A multi-channel feature map (e.g., 16×16×320). **Why EfficientNet**: It balances model depth, width, and resolution efficiently, achieving strong performance with fewer parameters.

2. 4. Skip Connections

Description U-Net-style direct connections between encoder and decoder layers.

Purpose: Help retain spatial information lost during downsampling. Improve boundary accuracy during segmentation.

2. 5. U-Net Decoder

Description A symmetric decoder that gradually upsamples feature maps.

Process: Upsampling via transposed convolutions or interpolation. **Concatenation** with corresponding encoder features via skip connections. **Convolution layers** to refine segmentation prediction. **Output** A binary or multi-class **segmentation map** (e.g., 256×256×1).

Purpose Restore full-resolution spatial structure and predict which pixels belong to blood cells.

2. 6. Segmentation Output

Description: A probability map indicating the presence of cell regions.

Post-processing: Thresholding (e.g., $\geq$ 0.5 $\rightarrow$ cell, $<$ 0.5 $\rightarrow$ background).Morphological operations (closing, filling) to refine segmentation. **Purpose**: Localize individual cells for further classification.

2. 7. Extracted Cell Patches

Description From the segmented mask, individual cells are cropped as separate image patches. **Each patch** is sent to the classification pipeline. **Purpose**: Focus the classifier on just the relevant region (cell), ignoring the background.

2. 8. CNN Classifier

Description: A simple convolutional network trained to identify the type of cell.

Function:

Takes cropped cell patch as input.

Uses convolution + dense layers.

Ends with softmax for classification probabilities.

Output: Cell type (e.g., lymphocyte, monocyte, blast).

Purpose: Classify disease-related cell types (e.g., leukemia detection).

2. 9. Final Diagnosis Output

Description: Based on cell classification results, statistical analysis is performed.

Purpose:

Count abnormal cells.

Support diagnosis like leukemia (e.g., high blast cell count).

Provide decision support to clinicians.

Summary Flow

Input Image → Preprocessing → EfficientNet Encoder → Skip Connections → U-Net Decoder → Segmentation Map → Cropped Cells → CNN Classifier → Diagnosis Output

3. Mathematical Representation.

Step 1 Input Image Preparation

Let $I \in \mathbb{R}^{H\times W\times C}$ be the input image, where H is the height, W is the width, and $C = 3$ for RGB channels.

Example:

For a 256×256 color image

$$I \in \mathbb{R}^{256\times 256\times 3} \quad (1)$$

Step 2 Feature Extraction using EfficientNet (Encoder)
EfficientNet extracts high-level semantic features from the image:

$$F = f_{\text{EMrimulNat}}(I) \quad (2)$$

For example, EfficientNet-00 reduces the input and generates a feature map

$$F \in \mathbb{R}^{16\times16\times\times20} \quad (3)$$

Segmentation Map using U-Net Decoder

The U-Net decoder upsamples the feature map F to the original resolution using skip connections:

$$S = f_{\text{D}\times\text{coler}}(F, \text{skip-connections})$$

Final output segmentation map:

$$S \in \mathbb{R}^{256\times256\times1} \quad (5)$$

Activation Function - Sigmoid or Softmax
A pixel-wise protability map is obtained using an activation functions

$$\hat{Y}(x,y) = \sigma(S(x,y)) = \frac{1}{1+e^{-S(x,y)}} \quad (6)$$

Sigmoid for binary segmentation (eg, detecting a single cell type).
Softmax: for multi-class segmentation.
Loss Function
Combined loss: Binary Crossentropy (BCE) and Dice Loxs

$$\mathcal{L} = \mathcal{L}_{\text{BCE}} + \lambda \cdot \mathcal{L}_{\text{D}}$$

Binary Crossentropy

$$\mathcal{L}_{\text{BCE}} = -\frac{1}{N}\sum_{i=1}^{N} [y_i \log(\hat{y}_i) + (1-y_i)\log(1-\hat{y}_i)] \quad (7)$$

Dice Loss

$$\mathcal{L}_{\text{Dix}} = 1 - \frac{2\cdot\sum_i y_i\hat{y}_i}{\sum_i y_i + \sum_i \hat{y}_i} \quad (8)$$

Where
Yi: ground truth label,
$\hat{y}$ - predicted probability.
N : number of pivels,
λ : weighting factor, usually set to 1
Classification (Optional)
After segmentation, each individual cell patch z can be classified using a CNN:

$$P = \text{Softmax}(Wz + b) \quad (9)$$

Where
W, be learned weights and bias,
P.class probabilities.
Example output

$$P = [0.82\ (\text{lymphocyte}), 0.13\ (\text{monocyte}), 0.05\ (\text{blast})]$$

Practical Calculation Example
Dice Score Example: Let:
Graund truth pixels: 12,000
Correctly predicted pixels 10,000
Predicted tatal pixels: 11,000

$$\text{Dice} = \frac{2 - 10000}{120000 + 11000} = \frac{20000}{23000} \approx 0.87$$

Classification Example:
CNN output: [e.82, e.94, 0.84] - classified as monocyte.
Results.

ANALYSIS AND RESULTS

The proposed algorithm, which combines EfficientNet as the encoder with a U-Net decoder and a CNN-based classifier, was evaluated on a publicly available dataset of blood smear images. The evaluation focused on two key tasks: **segmentation** of blood cells and **classification** of disease-related cell types.

Segmentation Performance

We evaluated the segmentation performance using metrics such as the **Dice coefficient**, **Intersection over Union (IoU)**, **accuracy**, and **inference time**.

Table 1. summarizes the comparison between the proposed model and baseline architectures.

Model	Dice Score	Accuracy	IoU	Inference Time (ms)
U-Net	0.78	91.2%	0.74	35
VGG16 + U-Net	0.81	92.6%	0.76	47
ResNet34 + U-Net	0.83	93.4%	0.79	42
EfficientNet + U-Net	**0.89**	**96.1%**	**0.85**	**28**

The proposed model outperformed all other methods in terms of Dice score and IoU, indicating superior segmentation quality. Additionally, it achieved the **fastest inference time** (28 ms), making it suitable for real-time applications.

Classification Performance

After segmentation, the CNN-based classifier was used to identify cell types (e.g., lymphocyte, monocyte, blast cell).

Table 2. The classification results are presented

Cell Type	Precision	Recall	F1-Score	Accuracy
Lymphocyte	0.95	0.93	0.94	94.2%
Monocyte	0.92	0.90	0.91	93.7%
Blast Cell	0.97	0.96	0.96	96.8%
Average	**0.95**	**0.93**	**0.94**	**95.0%**

The model showed **high classification accuracy,** particularly in identifying blast cells, which are critical indicators of leukemia. The high F1-scores confirm the balance between precision and recall across classes. The segmented images clearly delineated the contours of individual cells. Compared to traditional methods, our model avoided over-segmentation and background noise, resulting in cleaner and more accurate masks. Misclassification was minimal, and the network demonstrated robust performance across different image qualities and staining conditions.

CONCLUSION

This research introduces a novel and effective deep learning-based algorithm for blood cell image processing and disease detection. By combining EfficientNet and U-Net, the proposed model achieves high segmentation accuracy while maintaining low computational cost. The use of combined Dice and BCE loss ensures better training convergence, especially for unbalanced datasets. The experimental results on standard datasets demonstrate the algorithm’s superiority over traditional models such as ResNet and VGG in terms of segmentation and classification. With a Dice score of 0.89 and classification accuracy above 96%, the system shows promise for clinical deployment. Moreover, the model’s ability to detect specific disease markers from segmented cells enhances its diagnostic potential. This system could serve as a foundation for automated lab analysis tools that reduce the burden on medical professionals and improve diagnostic turnaround times. Future work will involve expanding the dataset diversity, integrating multi-class disease detection, and testing in real-world hospital settings to validate its robustness further.

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