International Journal of Scientific Research in Engineering and Management (IJSREM)
Volume: 09 Issue: 05 | May - 2025 SJIF Rating: 8.586 ISSN: 2582-3930

Blast Cell Segmentation in Leukemia Blood Smear Images Using U-Net

Vinod A M, Sinchana M C, Srinidhi H K, Syed Safiulla, Thejaswini M D

***Abstract*—Leukemia is a life-threatening blood disorder marked by an abnormal increase in white blood cells, known as blast cells, in the bone marrow. Early detection of these blast cells is critical for effective treatment. Traditionally, diagnosis relies on manual examination of blood smear images by pathologists, a process that is not only time-consuming but also prone to human error. With the rise of ML along with the integration of deep learning , there is a growing opportunity to automate and enhance the diagnostic process. This study explores the application of the U-Net architecture, a neural network model engineered for image segmentation, to automatically detect and segment blast cells in leukemia diagnosis. By automating this process, the aim is to reduce diagnostic time, minimize errors, and improve the overall accuracy of leukemia detection.**

***Index Terms*—Leukemia, image segmentation, U-Net, machine learning, deep learning.**

I. INTRODUCTION

The diagnosis of leukemia is very challenging and fundamentally depends on the correct identification of blast cells from the photographs of blood smear samples or bone marrow. Such cells are the expressions of leukemia, and their accurate identification is essential for both diagnostic and therapeutic treatment decision-making processes.

Traditionally, this process relied heavily on the impression and vision provided by highly experienced doctors and practitioners. While such expertise is invaluable, the procedure is intricate, painstaking, and requires immense attention to detail. This might become a source of fatigue over time. This increases the likelihood of human error. Other contributing factors, including fatigue, subtle modulation of cell mor- phology, incomplete reconstitution of hematopoietic stem and progenitor cells, and bone marrow removal, further complicate the diagnosis of leukemia and increase its risk.

Historically, diagnosis has fundamentally depended on the accurate identification of blast cells using images acquired from blood smears or bone marrow samples. Such cells are critical markers of leukemia and function as an essential part of diagnostic and therapeutic decision-making processes. However, traditional methods often require endless precision and are prone to errors, even with the most skilled practition- ers. Variables like changes in cell morphology, fatigue, and other human limitations make the process inconsistent and unreliable at times.

Recent innovations in the domain of machine learning (ML) and deep learning (DL) technologies have revolutionized this field by providing solutions that can complement or surpass human performance in data analysis. These technologies are particularly effective in recognizing subtle patterns that are challenging to detect with the naked eye. Moreover, they en- hance accuracy, reduce processing time, and enable automation of tasks like blast cell identification, making them highly suitable for clinical applications.

This paper leverages the potential of the U-Net architecture—a model renowned for its unparalleled performance in biomedical image segmentation. The encoder-decoder design of U-Net allows it to acquire both detailed (fine-grained) and abstract (coarse-grained) features from input data. This dual capability makes U-Net highly versatile and effective for learning complex patterns across multiple modalities.

The application of this advanced model enables accurate, rapid, robust, and reliable identification of blast cells, particu- larly in blood smear images. This approach promises to rede- fine the methods currently employed for leukemia diagnosis, bridging the distinction between classic diagnostic methods and the latest technological advancements in medicine.

Automating the segmentation and detection of blast cells not only simplifies diagnostic workflows but also reduces the burden on healthcare professionals and improves patient care. These innovations empower the medical profession to approach diagnosis in a time-sensitive, efficient, and highly accurate manner, ultimately benefiting the end user.

Segmentation, therefore, is an important procedure in medical imaging analysis that deals with such diseases as leukemia detection and diagnosis. The segmentation deals with the partitioning of images into individual segments that can rep- resent All of the areas of interest, This implies that one can potentially segment blast cells in blood smear images. Even while many of the advanced deep learning-based methods are now popularly known to be used, including U-Net, these tech- niques still remain as the foundation applied or benchmarked for many applications. An introductory explanation for these methods goes as follows:

A. Traditional Image Segmentation Techniques

1) Region-Based Segmentation:

- This technique works by grouping pixels that share simi- lar properties, such as intensity, texture, or color, to form regions.
- It involves starting with A base point and growing the region by adding surrounding pixels that meet the criteria predefined criteria.

2) Edge-Based Segmentation:

- Focuses on detecting boundaries or edges within an image where there exists a sharp shift in intensity or color.
- Common methods include the Sobel, Canny, and Lapla- cian edge detectors, which highlight edges by calculating gradients.

3) Thresholding: A basic and widely used technique that separates an image using converting it into a binary format. Pixels are divided based on whether their intensity is above or below a chosen threshold value.

- Variants: Global thresholding (single threshold value for the entire image) and adaptive thresholding (threshold value changes locally).

4) Watershed Segmentation:

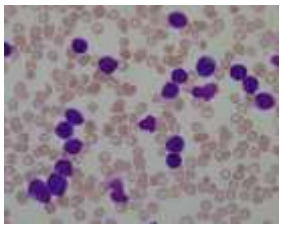
- A region-based method that treats the grayscale image as a topographic surface, where pixel intensity represents elevation.
- Water is ”poured” onto the surface, and boundaries are formed where water from different regions would meet.

II. PROBLEM STATEMENT

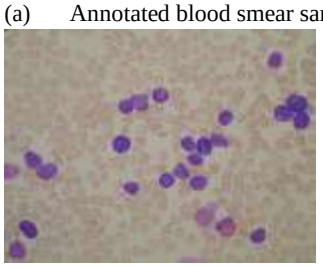
The primary challenge in leukemia diagnosis lies in the accurate detection and segmentation of blast cells, which often appear similar to other cells in blood smear images. This variability in morphology, combined with overlapping or clustered cells, complicates manual identification. Traditional methods, such as visual inspection and basic segmentation techniques, are limited in their ability to consistently detect blast cells in all cases. This implies that there is a need for a system that is automated which can accurately segment and detect blast cells, enhancing the consistency and speed of the diagnostic process.

III. LITERATURE SURVEY

It is a part of the integral parts in the medical image analysis known as image segmentation. In recent years, there has occurred the intensive application of segmentation in feature finding and separation in images of leukemia blood smear. ALL-IDB 2 images have been utilized in the project including acute lymphoblastic leukemia case annotations. This dataset has seen extensive used in developing and testing segmentation algorithms on several tasks related to blood smear sample image analysis, and more importantly, in discovering blast cells. The following figures showcase examples from the ALL-IDB 2 dataset. These images represent blood smear samples annotated for the detection of acute lymphoblastic leukemia(ALL) cells. They serve as visual references for understanding the distribution of blast cells as well as and the complexity of the segmentation task.



(a) Annotated blood smear sample image 1 from ALL- IDB 2.



(b) Annotated blood smear im- age 2 from ALL-IDB 2.

Fig. 1: Examples of annotated blood smear images from the ALL-IDB 2 dataset.

Several techniques of segmentation are reported in the literature to address the challenges associated with the definition of regions of interest in medical images. Some of them include thresholding, which is simple yet efficient in classifying pixels by their intensity values into classes. Global thresholding works by applying the same threshold on the complete image while performing local thresholding adjusts to images whose lighting is uneven by applying various thresholds to different areas. More complex methods combine thresholding with models based on statistical distributions or fuzzy logic to boost the accuracy of segmentation, primarily due to noise or overlapping features and sometimes due to changed conditions in an image. These were developed with the goal of making the analysis process of an image, improving its precision and less interfering.

Threshold Segmentation is considered a fundamental, widely applied technique in the realm of image processing and is particularly potent for discriminating objects from their background. The mechanism of this method lies in the classification of pixels depending on their intensity values and, hence, is best suited in instances where the object features a reasonably high contrast with the background [1]. By reducing an image to a binary format or segmented form, threshold segmentation makes the study of regions of interest possible with both efficiency and simplicity.

Methods of Threshold Segmentation

Threshold segmentation can generally be divided into three categories according to the approach used:

Global Thresholding: In this method, the threshold value is defined uniformly over the whole image. The most preferred method in this class is Otsu’s method, which selects the optimal threshold so as to maximize the variance between the groups of pixels that represent the foreground and background respectively. This is quite efficient, particularly for images that have a uniform illumination [2].

Local Thresholding: In the event of images with non-uniform lighting conditions, global thresholding fails to produce accurate results. On the other hand, local thresholding is a technique that divides an image into smaller regions and

then applies different threshold values to each of them. This will result in much better segmentation outcomes for images with fluctuating light levels [3].

Advanced Techniques: Advanced thresholding methods have been developed with the aim of enhance the impact of basic thresholding. Entropy-based approaches and hybrid techniques combine thresholding with statistical models or fuzzy logic. The aforementioned methods provide greater accuracy and robustness, especially for complex images with noise or overlapping intensity levels [4].

Strengths and Limitations, Threshold segmentation is appreciated for its simplicity and computational efficiency, rendering it suitable in applications requiring fast processing of high- contrast images. However, its performance deteriorates in cases with overlapping intensity levels, significant noise, or non-uniform illumination. In this way, thresholding has to be combined with the application of more advanced methods that may yield a better segmentation [3][4].

Applications, Because it is efficient and simple to implement, threshold segmentation has been used in many domains. In medical imaging, it could be applied to separate tumors or blood cells from the rest of the image. It is also applied in object detection and automation tasks where the

image analysis has to be done fast and with high accuracy [1].

Edge detection segmentation identifies boundaries within an image by detecting abrupt changes in pixel intensity, such as variations in gray levels, colors, or textures. It is a fundamental technique for isolating objects and analyzing regions in images [5].

Methods of Edge Detection
Sobel Operator: The Sobel operator is used as a first-order differential operator used to find the gradient of image intensity. It employs two 3×3 kernels for locating of horizontal and vertical edges while smoothing noise by local averaging. The weighted gradient approach of the Sobel operator produces more precise edge detection than simpler operators like Prewitt or Roberts [6].
Laplacian Operator: The Laplacian operator is a second-order differential operator that emphasizes regions of fast change in intensity. It identifies edges based on location, not based on the differences in intensity. This is very sensitive to noise and hence preprocessing is done by applying a low-pass filter. The Laplacian is isotropic; it is rotation invariant and thus suitable for detecting edges regardless of their orientation [7].
Strengths and Limitations Strengths: Edge detection methods, like Sobel and Laplacian, give clear boundary information, which is very important in object detection and image analysis. Noise is reduced by Sobel's smoothing, and the Laplacian provides rotational invariance. Limitations: These techniques are sensitive to noise and prone to produce fragmented edges in low-contrast or noisy images. Combination with pre-processing or integration with region-based methods may help to improve the performance [6][7].
Applications Edge detection is used vastly in medical imaging, object recognition, and industrial automation for detecting boundaries and crucial features in analysis and making a decision [5][8].

HSV model
This study followed the two-process approach: namely, image preprocessing and image segmentation, with the applied transformed HSV, Hue, Saturation, and Value model. This is essentially a high-speed and more robust technique.
Image Pre-Processing, Transformation of the ALL datasets as images in The HSV color space was assessed as the foremost process. Its main advantage is a clear distinction in brightness information - Value and information about color: Hue and saturation. It almost simulates a human visual view [9].
In order to make the major features stand out, the Saturation channel was modified by the following expression:

$$S_{adjusted} = 2 * S$$

The modified Saturation channel was combined with the original Hue and Value channels to yield the images optimized for segmentation [9].
Segmentation of Images, A basic thresholding technique was applied for segmenting and extracting the ROI. The segmentation was carried out in accordance with the following rule:

$$SegmentedImages = \begin{cases} ROI & if\ S(adjusted) > 0.7 \\ 0 & otherwise \end{cases}$$

This stage highly highlighted the leukocyte nuclei, which is essential to diagnose acute lymphoblastic leukemia(ALL) [9]. Performance Measurement, Three measurements were ap- plied to measure the accuracy of the segmentation process, which included accuracy, sensitivity, and specificity. The three measurements ensured the precision and reliability of the
suggested method [9].
Dataset and Experiment, Two datasets were used in the study. ALL Dataset: 3,256 images into four classes Leukemia Dataset: 368 images ALL-IDB1 and ALL-IDB2 [9]. The implementation was done on an Intel Core i7 processor in MATLAB R2022a, so it would run efficiently.
Region-based segmentation collects pixels With comparable features, such as, intensity or texture, into distinct regions. Pixels in a region are known to be homogenous, and thus, the segmentation of an image into fewer, larger areas is possible. Such methods include region growing and region splitting and merging[10].
Techniques: Edge detection searches for transitions in an image, which usually tend to be its sharp changes along the pixel intensities. These techniques frequently direct attention towards regions of transition or change between object and background parts, therefore accentuating region-to-be-isolated as prominent. Other well-known edge-detection algorithms are Canny and Sobel operators[11].
In the threshold-based approach, objects from the background are set apart by considering the classification of pixels on their intensity levels. Global thresholding applies a global value across an whole image whereas local thresholding adapts with varying lighting conditions. Advanced methods combine this with statistical models to enhance accuracy[12].

IV. METHODOLOGY

A. Data Collection and Preprocessing

The task aims to present a method for detecting and segmenting blast cells in microscopic images of blood smears for leukemia diagnosis. Detection of the presence of the images of the blast cells is essential because identification of the former confirms the leukemia. The project data set is obtained from private collection of images representing normal and blast cells exclusively prepared for this study. This project data set was specifically curated to ensure that it includes the most diverse array of cell types, morphologies, and staining techniques, in a way that could be experienced in real-life clinical settings. The diversity within the information set considers various factor like the status of the patient or the mechanism using which images are obtained that may change the appearance and morphology of cells.
An important pre-processing step was performed before processing the images in the model. Microscopic images usually come with considerable background noise that

distracts the model from focusing on the real cells. Preprocessing thus begins by eliminating irrelevant background elements which, in fact, reduces the areas of focus that the model has to attend to. It is not only a step meant to reduce distractions, but it also decreases the load of computing since it reduces the portions to focus on.

Moreover, all images were resized to the same dimen- sion.Resizing the images was crucial, as a variety of deep learning models demand specific input dimensions to function effectively. Therefore, each picture would be treated as similar; hence, all pictures will be given fair and equitable processing to improve uniformity at the model training stage and allow reliable output.

One of the common challenges is found in microscopic imaging, where variation in lighting and staining, from image to image, can distort the information that occurs in images, creating inconsistencies that may affect the performance of the model. Thus, a normalization technique on images was adopted for uniformity in different images. This technique normalized the pixel values for all images, so the model would not be biased by variations in lighting or staining techniques. Normalizing the images ensured that this very common characteristic of cells is focused on by the model in terms of features rather than the external imaging factors.

Contrast enhancement of the images taken was applied for further development in the differentiation capacity of the model. It rendered the human naked eye capable enough toobserve cell boundaries and the inner structures for better capability to differentiate between the healthy cells and the blast cells. Contrast enhancement offered the differences at microscopic level in cell shape and their internal boundaries which aided in recognizing cancerous cells.

Finally, the technique of data augmentation was used in order to widen the training set. Data augmentation basically artificially increases the dataset through very small and rather random adjustments made to images. Some possible examples are rotation, horizontal flipping, or scaling changes. The reason for the approach is to present the model with the variety of perspectives and conditions in such a manner that it becomes more robust and better adapted toward new, unseen images. It will make the model generalize well and work correctly with images it did not see while training.

Conclusion Preprocessing steps carried out in this dataset aimed at optimizing images for model output, hence maxi- mally getting correct segmentation of blast cells. These have been approached with very minute attention towards some issues including noise in the background, uneven illumination, and changes in contrast to further ensure a proper augmented set of images for the dataset; These improvements will ul- timately empower the model to better analyze real-world scenarios and make more effective contributions to leukemia diagnosis.

B. Model Architecture

Deep learning has revolutionized the approach to biomedical image segmentation. For this task, we select the architecture U-Net since it is among the best models for the task of biomedical image segmentation. It optimizes both the finer details and contextual information aspects, crucial in complex medical image analysis.

ounetarch.jpg

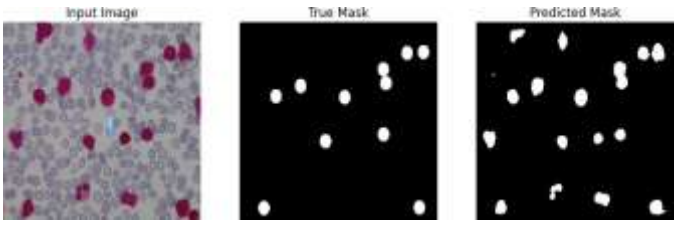


Fig. 2: U-Net Architecture: The model structure depicting encoder-decoder paths with skip connections.

1) Encoder (Contracting Path): The encoder compresses the input image by progressively reducing its spatial dimen- sions through a combination of:

- Convolutional layers (3x3, ReLU activation) that extract features like the shapes and textures of cells.
- Convolutional layers (3x3, ReLU activation) that extract features like the shapes and textures of cells.
- Max-pooling layers (2x2) that down-sample the image while retaining key features.Each step doubles the num- ber of feature channels, starting from 64 up to 1024 (as shown in the diagram). However, this compression results to the loss of some fine spatial features, which are crucial for precise segmentation.

2) Decoder (Expanding Path): The decoder restores the compressed features back to the original spatial dimensions through:

- Up-convolutional layers (2x2) that up-sample the image and recover spatial details.
- Convolutional layers (3x3, ReLU) that refine the segmen- tation map by combining context and detail.

3) Skip Connections: The most distinctive feature of U-Net is its skip connections, which directly link the encoder layers to their corresponding decoder layers. These connections:

- Pass critical fine-grained details from the encoder to the decoder.
- Allow the model to retain both high-level (abstract) and low-level (detailed) features, ensuring accurate segmen- tation even for small or intricate structures like blast cell edges.

4) Final Output: At the final stage, a 1x1 convolutional layer is applied to output the segmentation map with the same similar dimensions as the input image. This map highlights the areas of interest (e.g., blast cells) with high accuracy.

C. Key Features of U-Net for Blast Cell Segmentation

- **Handles Variability:** U-Net is robust for dealing with the variability in the shapes, sizes, and textures of cells present in blood smear images.
- **Noise Resistance:** It works efficiently even with noisy or inconsistent backgrounds common in real-world medical imaging.
- **Accuracy**:The architecture allows the sub-ntle details such as edges of the cells or internal structures to be picked up for identifying healthy and blast cells.

D. Training and Evaluation

The secret of how successful the model would be was the training and testing process. The dataset we curated acted as the base model that taught the U-Net model to differentiate between healthy cells, blast cells, and the background area. This whole training was on correcting the identification along with segmenting the blast cells so that further studies could take only those areas within the image and discard irrelevant areas.

To make sure that the model could generalize very well to unseen data, we divided the dataset into two: a training dataset and a testing dataset. The model not to memorize the data and not overfitting patterns in the given training dataset, used a training set, and not touched a testing set until training was concluded. This has an important consequence that the model would not overfit, meaning it is making predictions in places it is not found

We used cross-entropy loss during training. Cross-entropy is commonly used for pixel-wise classification tasks such as this one. The cross-entropy function helps the model to calculate the difference between its predictions and the actual labels for each pixel. Every time the model makes a wrong prediction, the loss function penalizes it, and the model adjusts its weights to improve its prediction over time. The model improves during training due to error correction and iteration process.

To generalize the model we have applied Data Augmentation. We added random rotations and horizontal flips to theimages in order to introduce slight variations on angles and conditions the model will experience on real images. These augmentations also helped learn more robust features, so it is not that sensitive to certain angles or scale in an image.

After the model has completed training on the entire set, we made an estimate of its performance on two of the most widely adopted evaluation metrics on the task of image segmentation: the Dice coefficient and Intersection over Union (IoU). The Dice coefficient measures the scope of the regions predicted in a segmentation are identical to those defined in the actual ground truth - essentially the estimated degree of correct spotting of the target areas by the model. The IoU calculates the proportion of overlap between the predicted and true regions versus the total area covered by both. These parameters are vital in assessing the model's ability to accurately segment blast cells while differentiating them from normal cells and any background noises.

With the evaluation process, ensured that the U-Net model could correctly and accurately identify and segment blast cells in blood smear images, which is an important step forward in the area of automated leukemia diagnosis. It would therefore potentially be able to detect blast cellse effectively than methods previously in place and has a potential for early diagnosis and treatment planning and, of course, proper care for patients.

V. Results and Discussion

A. Quantitative Analysis

The enhanced model was trained and evaluated over 10 epochs, showing strong learning progression and generalization across the dataset. Key performance metrics observed include: U-Net model performance was measured using metrics such as Dice coefficient, Jaccard index, and pixel-wise accuracy. These metrics provide an understanding of how well the model segmented leukemia-affected cells. The results are as follows:

Index	Training Set	Validation Set
Accuracy	99.3%	99.2%
Dice Coefficient	0.55 – 0.61	0.56 – 0.63
Loss	0.013 – 0.046	0.017 – 0.086

TABLE I: Performance metrics for training and testing datasets

1) Observations::

- **Validation Accuracy** is an assessment of similarity be- tween the predicted segmentation and ground truth. It is resembling the Jaccard Index but places more emphasis on the intersection.
- **Dice Coefficient** which evaluates the overlap between the predicted and ground truth segmentations, reached values up to 0.63, indicating highly precise segmentation performance.
- **Loss**(both training and validation) steadily decreased with each epoch, confirming effective model convergence without overfitting.

The similarity in performance between the training and validation datasets suggests that the model generalizes well and avoids overfitting.

B. Qualitative Analysis

The visual analysis of the segmentation outputs further highlights the U-Net model performance.The comparison between images input, true masks, and the predicted segmentation masks:

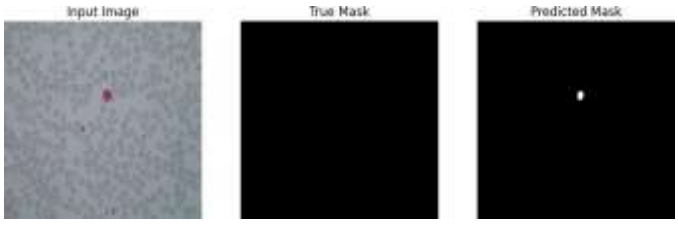


Fig. 3: Most affected regions were accurately segmented, with minor under-segmentation for overlapping cells.

The segmentation process achieved a high level of accuracy in detecting the regions most affected by leukemia, especially those with clearly visible leukemia cells. The algorithm successfully differentiated these areas from the surrounding tissue, allowing for an accurate representation of regions with the highest concentration of abnormal cells. However, challenges were encountered in handling overlapping cells, where minor under-segmentation occurred. This under- segmentation refers to situations where the algorithm was unable to fully capture the boundaries of closely packed or overlapping leukemia cells, leading to smaller or incomplete segments when analyzed with the ground truth. Despite these minor inconsistencies, the overall segmentation performance remained robust at the critical regions indicative of disease presence being accurately identified.

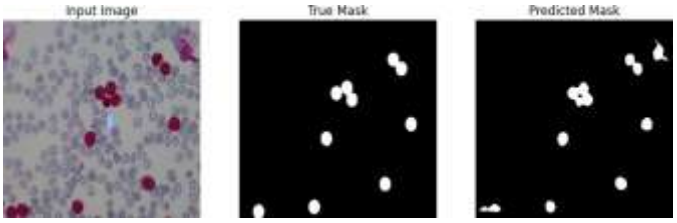


Fig. 4: The predicted leukemia cells in the mask were not found in the true mask, indicating a false negative detection in the segmentation process

Throughout the segmentation process, there were cases where the predicted leukemia cells in the mask did not align with true masks, indicating false negatives are present. This shows that algorithm missed certain leukemia cells which were present in the true mask, leading to detection failures. False negatives takes place by the factors like weak staining, overlapping cells, or slight variations in cell morphology, which can make it challenging for the algorithm to distinguish the cells from surrounding tissue. Although these missed detections did not heavily affect the overall performance, theypoint to areas where the model can be improved to ensure more accurate identification of all leukemia cells.

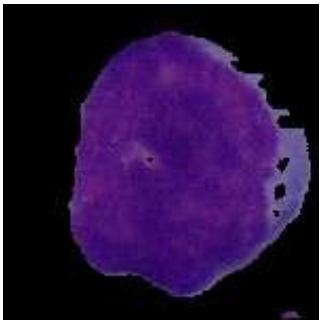


Fig. 5: Effective detection of isolated leukemia cells, with minimal false negatives.

The segmentation model showed strong performance in detecting isolated leukemia cells, accurately identifying those that were not in contact with neighboring cells. This indicates that the algorithm was effective at recognizing leukemia cells that were well-defined and distinct from the surrounding tissue. Additionally, the model produced very few false negatives, meaning that most leukemia cells were correctly detected. This demonstrates that the algorithm has good sensitivity for detecting isolated cells. However, there may still be room for improvement, especially in cases where the cells are not as clearly defined or in situations where cells overlap.

1) observation:

- **Segmentation of Affected Areas:** The U-Net model successfully segmented regions with distinct features, such as irregularly shaped leukemia cells.
- **Challenges with Overlapping Cells:** Overlapping or clustered cells posed some difficulty. In a few instances, the model merged nearby cells into a single region, resulting in under-segmentation.
- **Variability in Staining Intensity:** Cells with lower staining intensities were segmented with less accuracy, indicating that the model's performance depends on clear contrast between affected and unaffected areas.
- **Boundary Precision:** The model effectively identified boundaries for isolated cells but showed occasional in- accuracies in separating clustered cells.

2) Sample Results:

- The following images illustrate the U-Net's segmentation performance:

VI. Training and Validation Loss

The training process was assessed using a loss function that combined Binary Cross-Entropy and Dice loss, aiming to improve segmentation accuracy. Loss values were monitored across several epochs, with the graph Fig.4 showing a steady decrease in training loss. This downward trend indicates that the model effectively learned the features necessary for accurate segmentation. Around the 8th epoch, the validation loss leveled off, suggesting that the model achieved optimal performance while avoiding significant overfitting.

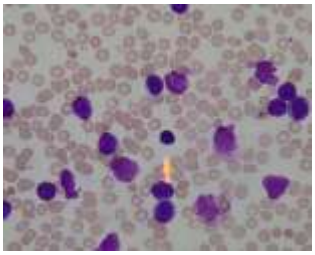


Fig. 6: Before Segmentation.

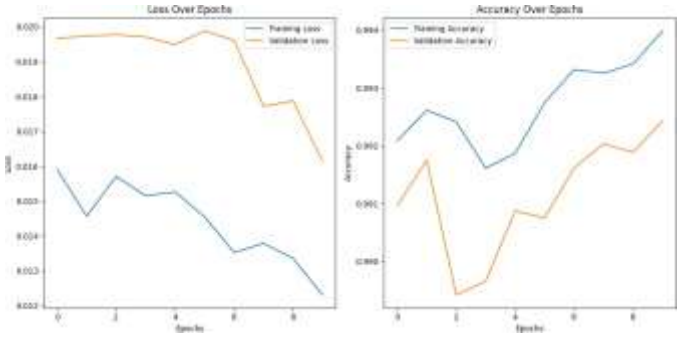


Fig. 7: After Segmentation.

A. Key Observations from Loss Analysis:

- The steady reduction in training loss reflects the model's ability to adapt and extract relevant features for segmen- tation tasks.
- The early stabilization of validation loss highlights that the model achieved a balance between learning and generalization, effectively preventing overfitting.

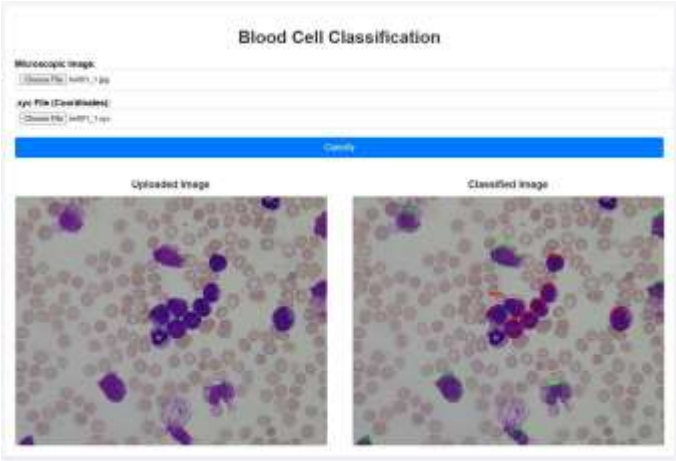


Fig. 8: shows the training and validation loss curve, providing a clear visualization of the model's learning dynamics during training.

VII. System Integration And Deployment

A. Web Interface Integration

In order to permit access to users lacking any specialized skills, a web-based front end was created using the Flask framework. This interface allows users like pathologists and medical researchers to:

- Upload microscopic blood smear images.
- Upload corresponding .xyc files that contain annotated coordinates of infected cells.
- Instantly visualize classified results, including:
  – Detection of infected and uninfected cells.
  – Overlay of bounding boxes and classification labels (e.g., "Infected", "Uninfected") on the original image.

The basic interface is attended to using HTML while the stylistic aspects are refined with simple CSS to keep it easy, flexible, and appropriate for different device screens.

B. Hosting and Public Access

To enable online accessibility, the Flask application is hosted using ngrok, which creates a secure tunnel to the local Flask server and provides a publicly accessible URL. This deployment method enables:

- Remote access without requiring dedicated cloud infras- tructure.
- Real-time demonstrations and testing across different locations or devices.
- A convenient way to share the application with peers or instructors during evaluations or presentations.

This integration bridges the gap between model development and practical usability, making the system more versatile and deployable in real-world settings.

Fig. 9: User interface of the developed blood cell classification system. The left panel shows the uploaded microscopic blood smear image, while the right panel displays the output image with classified cells. Infected (blast) cells are highlighted with red bounding boxes, and uninfected cells are shown with green bounding boxes.

VIII. Advance Functionalities Implemented

A. Coordinate Matching with .xyc Files

The backend scans .xyc files that contain the ground-truth infected cell coordinates. An assignment label produced during detection based on ground truth provides triggers for the classifier to learn. This is done with a distance-based thresholding technique.

B. Region of Interest (ROI) Extraction and Feature Engineer- ing

Each detected cell is:

- Cropped to its bounding box
- Converted to grayscale
- Passed through a GLCM (Gray-Level Co-Occurrence Matrix) for texture feature extraction
- Enhanced with mean RGB and contrast features
- Optionally compared with segmented versions for addi- tional statistical features

C. Classification Pipeline

A Random Forest Classifier is trained dynamically on uploaded images and their extracted features:

- Dataset split into training and test sets
- Evaluated with precision, recall, and F1-score
- Predictions are visualized as bounding boxes (red for infected, green for uninfected)

IX. Limitations

A. Over-Segmentation

Certain regions experienced over-segmentation due to noise or inconsistent lighting. Incorporating advanced preprocessing techniques, such as histogram equalization, could significantly enhance the model's effectiveness.

B. Size of Dataset and Diversity

The small size and homogeneity of the dataset limits model ability generalize to other datasets with different staining techniques and cell structures.

C. Boundary Ambiguity

Although the U-Net model does a good job of identifying unique edges, it doesn't do a very good job in terms of boundary definition when cells overlap or are densely packed.

X. Conclusion

This research illustrates the contouring and classification of blast cells in leukemia diagnosis along with an efficient development and implementation of an end-to-end system. Further developing the U-Net based segmentation model, we added Flask as a front-end interface and ngrok remote deployment for access, enhancing the model's usability. These advancements help in bridging the gap between deep learning models and clinical practice.

Now, the system permits for the upload of blood smear images with corresponding annotation files, where they are processed through an automatic classification engine which marks the cells as infected or uninfected, and all these done through a web interface. The new model training framework that incorporates accurate feature selection and Random Forest classification proved to be efficient with validation

accuracy greater than 99% and a Dice greater than 0.61. This strongly holds evidence for the generalization and reliability of seg- menting and classifying leukemic cells.

ACKNOWLEDGMENT

The authors would like to express their sincere gratitude to Mr. Vinod A M, Assistant Professor at Malnad College of Engineering, for his invaluable guidance and support throughout this project. His expertise and encouragement were instrumental in the successful completion of this work.

REFERENCES

[1] Haralick, R. M., Shapiro, L. G. (1985). Image segmentation techniques. Computer Vision, Graphics, and Image Processing, 29(1), 100-132.
[2] Otsu, N. (1979). A threshold selection method from gray-level histograms. IEEE Transactions on Systems, Man, and Cybernetics, 9(1), 62-66.
[3] Pal, N. R., Pal, S. K. (1993). A review on image segmentation techniques. Pattern Recognition, 26(9), 1277-1294.
[4] Kohler, R. (1981). A segmentation system based on thresholding. Computer Graphics and Image Processing, 15(4), 319-338.
[5] Marr, D., Hildreth, E. (1980). Theory of edge detection. Proceedings of the Royal Society of London B: Biological Sciences, 207(1167), 187- 217.
[6] Davis, L. S., Rosenfeld, A., Weszka, J. S. (1975). Region extraction by averaging and thresholding. IEEE Transactions on Systems, Man, and Cybernetics, 3, 383-388.
[7] Senthilkumaran, N., Rajesh, R. (2009). Edge detection techniques for image segmentation – a survey of soft computing approaches. International Journal of Recent Trends in Engineering, 1(2), 250-254.
[8] Haralick, R. M., Shapiro, L. G. (1985). Image segmentation techniques. Computer Vision, Graphics, and Image Processing, 29(1), 100-132.
[9] H. Najjar, F., et al., ”Acute lymphoblastic leukemia image segmentation based on modified HSV model,” Journal of Physics: Conference Series, vol. 2432, p. 012020, 2023.
[10] A. M. Khan, Ravi. S Image Segmentation Methods: A Comparative Study International Journal of Soft Computing and Engineering (IJSCE) ISSN: 2231-2307, Volume-3, Issue-4, September 2013.
[11] H.P. Narkhede Review of Image Segmentation Techniques International Journal of Science and Modern Engineering (IJISME) ISSN: 2319-6386, Volume-1 Issue-8, July 2013.
[12] Muhammad Waseem Khan A Survey: Image Segmentation Techniques International Journal of Future Computer and Communication, Vol. 3, No. 2, April 2014.