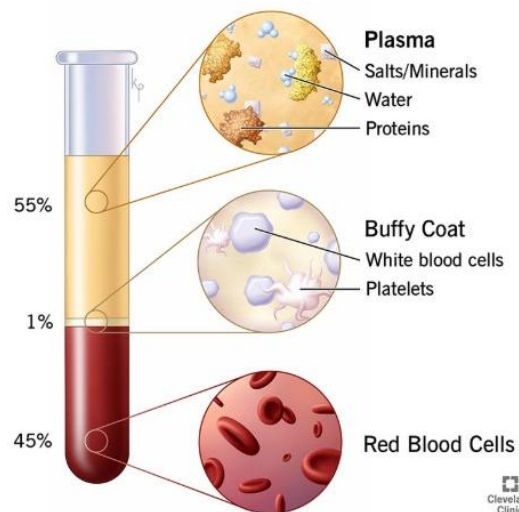
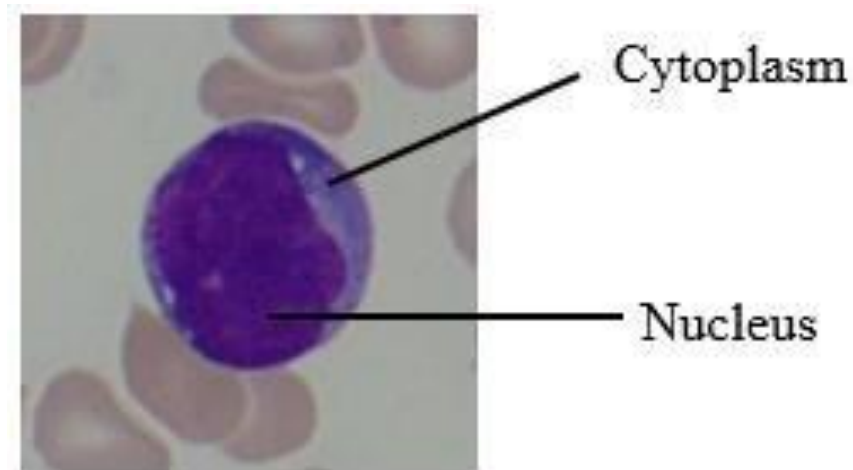


Segmentation of White Blood Cells from Unstained Microscopic Blood Smear Images

Hematology, the study of blood and its components, plays a fundamental role in understanding human health and disease. Blood is a vital fluid that circulates throughout the human body, performing essential functions required for survival. It delivers oxygen and nutrients to tissues, removes waste products, and plays a central role in the body's defense system. Blood is composed of three main components: **red blood cells (RBCs)**, which transport oxygen; **white blood cells (WBCs)**, which protect against infections; and **platelets**, which help in clotting and wound repair. Each of these components has a specialized function, working together to maintain overall health and ensure the proper functioning of the body.



White blood cells (WBCs) are essential components of the immune system, playing a critical role in defending the body against infections, foreign pathogens, and abnormal cells. Clinically, WBCs are evaluated not only by their count but also by their morphology, as changes in size, shape, or composition can indicate infections, blood disorders, or hematological malignancies such as leukemia. Structurally, each WBC consists of a nucleus and cytoplasm, with the nucleus often displaying distinctive shapes that help differentiate cell types.



Traditionally, WBC analysis is performed on stained blood smear images, where chemical stains enhance contrast, clearly highlighting the nucleus and cytoplasm for easier visualization and accurate identification. However, staining is labor-intensive, time-consuming, and can introduce variability due to differences in staining protocols. Unstained blood images, on the other hand, preserve the native morphology of the cells but exhibit low contrast, making it difficult to delineate the nucleus and cytoplasm directly. These images often show subtle light scattering and intensity variations that can act as markers for WBC localization. Segmenting WBCs from unstained images using annotated masks is therefore a clinically valuable task, enabling rapid, label-free analysis while maintaining cellular integrity, and providing a foundation for downstream applications such as classification or virtual staining

Overview:

In this project, students will implement a segmentation system to automatically identify white blood cells (WBCs) in unstained blood smear images using the provided masks. The model will take 128×128 pixel images as input and learn to predict masks that delineate both the nucleus and the cell boundary, effectively separating the WBC from the background. Students can use existing deep learning architectures for image segmentation, such as U-Net, DeepLabV3+, or Mask R-CNN, which are designed to learn spatial features and generate pixel-level predictions. The system will be trained using supervised learning with the annotated masks as ground truth, optimizing a combination of segmentation losses such as Dice loss or cross-entropy loss. Model performance will be evaluated using metrics like Dice coefficient, Intersection over Union (IoU), and visual inspection of predicted masks, ensuring accurate segmentation of both the nucleus and cytoplasm. The project encourages experimentation with preprocessing, data augmentation, and network hyperparameters to achieve robust performance on low-contrast unstained images.

Dataset Description

The dataset for this project consists of unstained microscopic blood smear images of size 128×128 pixels, along with corresponding annotations in JSON format. Each image contains a WBC roughly centered in the field of view, though some images may also include one or two additional cells. The annotations provide precise masks with two classes: ‘n’ for the neutrophil nucleus and ‘b’ for the boundary of the cell, including the surrounding cytoplasm. These masks serve as ground truth for supervised segmentation, enabling models to learn both the location and structure of WBCs in low-contrast unstained images. A subset of annotated images is provided for training, validation, and testing, allowing students to develop segmentation models that accurately delineate WBCs while preserving their morphological features, supporting downstream tasks such as classification or virtual staining. An example of a WBC and its corresponding mask is shown in the figure, where the white region represents the nucleus, the red region represents the cell boundary (cytoplasm), and the black region represents the background. The annotations are originally stored in JSON format, which can be converted into mask images for model training and evaluation.



Dataset Link:

<https://drive.google.com/drive/folders/1WFXZUG1jVvvtCiEmHuRjLRb7ir3zGJ26?usp=sharing>

Papers :

- Blood Cell Images Segmentation using Deep Learning Semantic Segmentation
- Fast and robust segmentation of white blood cell images by self-supervised learning
- Segmentation of White Blood Cell, Nucleus and Cytoplasm in Digital Haematology Microscope Images: A Review–Challenges, Current and Future Potential Techniques
- WBC-based segmentation and classification on microscopic images: a minor improvement

Final Requirements;

By the end of this project, students are expected to:

- i. Implement a segmentation system capable of accurately delineating the nucleus and cell boundary of white blood cells (WBCs) from unstained microscopic blood smear images.
- ii. Demonstrate model performance using quantitative metrics such as Dice coefficient, Intersection over Union (IoU), and visual inspection of predicted masks.
- iii. Provide visual results showing the predicted masks overlaid on test images to illustrate segmentation quality.
- iv. Submit a complete implementation, including code, preprocessing steps and documentation explaining the model architecture, training process, and evaluation strategy.
- v. Prepare a short report or presentation summarizing the dataset, methodology, results, and key observations from the experiments.