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#### Abstract

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White blood cells (WBCs) provide a significant role in the immune system, and precise classification and quantification are critical for detecting a variety of diseases. This work employs the VGG16 model combined with transfer learning to improve WBC classification and counting in blood smear pictures. We utilized a dataset of 1,651 images, including samples from normal bone marrow and chronic myeloid leukemia (CML) cases, to train and evaluate the model. The workflow incorporates data augmentation, Otsu thresholding, and morphological operators to improve segmentation accuracy. The VGG16-based model achieved a high accuracy of 92.37%, with validation accuracy reaching 96.41%. Performance metrics were evaluated using accuracy, precision, recall, and F-measure, highlighting that eosinophils provided the highest accuracy, while neutrophils demonstrated the best precision. The model effectively distinguishes between normal and elevated WBC counts, as evidenced by the results from normal and CML blood smears. Despite these promising results, further refinement is suggested. Future work may focus on specific WBC types, such as monocytes or neutrophils, to improve precision and balance memory efficiency. This approach has the potential to advance diagnostic accuracy and efficiency in medical image analysis.

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