

HematoNet: Expert level classification of bone marrow cytology morphology in hematological malignancy with deep learning

Abstract

Automating the cytomorphological classification of bone marrow (BM) cells has long been a challenge due to the inherent complexity and variability of hematological cell morphologies. This study introduces HematoNet, a deep learning-based framework designed to achieve expert-level accuracy in the classification of bone marrow cytology for the diagnosis of hematological malignancies. The research utilizes a large-scale dataset comprising 171,375 cell images obtained from 945 patients at the MLL Munich Leukemia Laboratory, representing 21 distinct morphological classes of BM cells. To address class imbalance, extensive data augmentation was applied, involving random rotations, flips, translations, and zoom transformations, ensuring balanced training across underrepresented categories.

The proposed model, CoAtNet, integrates the strengths of convolutional neural networks (CNNs) and transformer-based attention mechanisms to enhance both generalization and representational capacity. CoAtNet's performance was benchmarked against two state-of-the-art CNN architectures, EfficientNetV2 and ResNeXt50, using accuracy, precision, and recall metrics. Experimental results demonstrated that CoAtNet achieved superior performance across most morphological classes, particularly in accurately distinguishing complex cell types such as blasts, promyelocytes, and erythroblasts. The attention mechanism of CoAtNet contributed to improved learning efficiency and robustness, especially in classes with limited data availability.

To ensure interpretability and clinical transparency, explainable AI (XAI) techniques—Grad-CAM and SmoothGrad—were applied to visualize model decision regions. These analyses confirmed that HematoNet effectively focused on diagnostically relevant cell regions (e.g., cytoplasm, nucleus) while minimizing background noise. The findings highlight the potential of hybrid CNN-attention models for high-precision cytology classification and suggest a pathway toward integrating deep learning into diagnostic hematopathology. Future work will focus on expanding datasets across multiple clinical centers and integrating multimodal diagnostic data, such as molecular and cytogenetic profiles, to further enhance the system's diagnostic capability and generalizability.

Guide name: Dr. Saravanan P

Designation: Assistant Professor

Department: Department of Computing Technologies

Batch No: B496

Student 1 Reg. No: RA2311003012188

Student 1 Name: Balaji G

Student 2 Reg. No: RA2311003012240

Student 2 Name: Sanjai Kumar R