ACE: Explainable Classification of Acute Myeloid Leukemia Subtypes Using Unlabeled Single-Cell Images

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Acute myeloid leukemia (AML) is the most common type of acute leukemia in adults, with ~22,000 new cases and ~11,000 deaths in the USA annually. AML subtypes require distinct treatment protocols, so rapid and accurate classification is vital. Current diagnostic standard, bone marrow biopsy, is highly invasive, painful, and poorly suited for continuous monitoring. This project introduces ACE, an AI-based framework for detecting AML and its subtypes using minimally invasive and easily accessible peripheral blood tests. Unlike traditional AI-based frameworks that function as “black boxes” and require labor-intensive manual cell labeling, ACE also provides cell-level explainability without requiring individual cell annotations. ACE utilizes Multiple Instance Learning (MIL) to classify AML subtypes using white blood cell images from each patient. For each patient, a convolutional neural network (CNN)-based encoder extracts cell feature vectors from unlabeled blood cell images. These cell feature vectors are aggregated via attention weights into a patient-level feature vector, which is then classified as one of the four AML subtypes or a control using a multilayer fully connected neural network. ACE achieved a macro-average F1-score of 0.91 across 189 patients, significantly outperforming the prior work (0.81). The learned attention weights quantify each cell’s contribution to patient-level classification, providing automated cell-level explainability. By training solely on patient-level labels, ACE eliminates the bottleneck of manual expert cell-by-cell annotation, making it highly cost-efficient and scalable. These results demonstrate that ACE is an effective computational framework for classifying AML and AML subtypes using minimally invasive blood tests.

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