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Uncovering Low-Dimensional, miR-Based Signatures of Acute Myeloid and Lymphoblastic Leukemias with a Machine-Learning-Driven Network Approach

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ABSTRACT: MicroRNAs are a class of short noncoding RNAs that target messenger RNAs to regulate gene expression post-transcriptionally. Recent evidence has shown that the expression of microRNAs is altered in acute leukemias. Our goal is to find which and how many microRNAs are needed to build a reliable signature for each acute leukemia type. We introduce a method to build multi-microRNA signature networks based on machine-learning of microRNA expression datasets from cell lines and patient samples. This approach is systematic, quantitative, scalable, and unbiased; moreover, the predicted signatures are given in terms of small microRNA groupings, such as dyads and triads, which can readily be used to inform further laboratory experiments. This approach is not restricted to the analysis of microRNA expression, but also offers the potential to be applied to other kinds of biomedical data from measurements obtained in basic, translational, and clinical settings. For instance, this method could be used to identify small subsets of genes on a patient-specific basis, with the aim to provide more effective individualized diagnosis, prognosis, and treatment options.

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