PRPS-ST: A Protocol-Agnostic Self-training Method for Gene Expression–Based Classification of Blood Cancers


Précis: An algorithm overcomes the problem of gene expression-based classification portability across different methods and batches, improving lymphoma subtyping accuracy and enabling consolidation of patient classification from multiple sources.

Revealing the Impact of Structural Variants in Multiple Myeloma


Précis: Genome-wide analysis of structural variants and gene expression of a large well-annotated clinical cohort reveals new drivers and widespread impact of complex rearrangements on multiple myeloma development and outcomes.

See commentary, p. 221

Aging of Preleukemic Thymocytes Drives CpG Island Hypermethylation in T-cell Acute Lymphoblastic Leukemia


Précis: DNA methylation landscape of T-ALL identifies a developmental age signature suggesting long-lived thymocyte as a preneoplastic cell of origin in a subset of T-ALL.
Patients with hematologic malignancies are more vulnerable to infections, as the disease itself and its treatments impact immunity and homeostasis. In this issue, Malin Hultcrantz, Ola Landgren, and colleagues report real-life clinical data on the severity of SARS-CoV-2 in a large cohort of multiple myeloma patients hospitalized with the infection at the peak of the epidemic. This multicenter study encompasses a broad spectrum of patients across myeloma stages, comorbidities, and anticancer and COVID-19–mitigating treatments. The study associates elevated inflammatory markers with combined adverse endpoint. It also identifies significantly higher mortality rates among Black or Hispanic/Latino as compared to White patients. These findings provide groundwork to understanding vulnerabilities of patients with blood malignancies to COVID-19 and may inform prioritizing frontline COVID-19 therapies, as they become available, to those at highest risk. For details, please see the article on page 234 and the accompanying commentary on page 218.