Implementation of a Machine Learning Tool for Better Resistance Prediction in Acute Myeloid Leukemia

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Since acute myeloid leukemia (AML) is a heterogeneous disease with respect to genetic mutations and clinical outcomes, identifying the best therapy treatment method for patients remains the principal problem for doctors. In a phase 3 trial of treatment, the therapeutic resistance outcome for patients with somatic mutations has not been systematically evaluated and used for predictive purposes. Hence, we present a machine learning tool, in WEKA, that analyzes 3700 patients' covariates independently associated with the ability to, or failure to achieve complete remission after therapy treatment. The significant increase in AUC of a bootstrap-corrected multivariable model predicting this outcome from 0.50 to 0.81 (bootstrapped = 0.92) indicates fair predictive ability. In a separate dataset, mutational analysis was performed on 18 genes in 398 patients who were randomly assigned to receive induction therapy with high-dose or standard-dose daunorubicin. For high-dose induction chemotherapy, only DNMT3A and NPM1 mutations and MLL translocations predicted an improved outcome in patients with AML. Our better ability to forecast resistance based on routinely available pretreatment covariates provides a rationale for doctors to no longer randomize therapy selection, and supports further examination of genetic and post-treatment data to optimize resistance prediction in AML. In addition, a web service was created to host the model and provides doctors the model's predicted remission outcomes for patients.

Awards Won:
Third Award of $1,000