A Multimodal Precision Oncology Framework for Personalized Drug Suitability Scoring

Siddhi P. Jani, Mohammed Ali-Ani, Raghvendra Mall and **Halima Bensmail**
Qatar Computing Research Institute, HBKU, Doha, Qatar

Background: AML is compromised by therapeutic heterogeneity, where standard chemotherapies often yield suboptimal responses and significant toxicity due to diverse patient genomics and tumor biology.
Objective: We show that a machine learning framework that integrates multi-omics data can accurately predict individual patient drug suitability and identify optimal therapeutic strategies.
Design: Curated a cohort of patients over 10 years with the integration of ex vivo drug sensitivity, clinical annotations, DNA and RNA sequencing. Our machine learning model was trained on this dataset to predict drug suitability using somatic mutations, gene expression, drug representation and clinical features as inputs. We propose a computational framework that leverages the AML cohort to devise and validate machine learning models for predicting drug response in cancer patients. Our approach integrates clinical, genomic, and transcriptomic profiles to engineer unified vector representations of drugs, patients, and their oncogenic pathways. By modeling patient-specific drug-pathway interactions, cellular states and, the framework accurately estimates individual drug response, advancing personalized therapy for AML. Specifically, using contrastive learning, we also model patients and drugs as two modalities and learn embeddings that pull responding pairs together and push non-responding pairs apart, based on their full feature representations.
Results: Our model achieved strong predictive performance for well-characterized drugs, like Venetoclax. Feature importance analysis revealed novel biomarkers and confirmed the significant impact of tumor cell differentiation state on drug susceptibility. The model also successfully stratified patients into distinct risk groups with significantly different clinical outcomes.
Conclusions:
The path to personalized AML therapy is clear; the remaining challenge is implementation. Our model provides the clinical decision engine to make this a reality, transforming complex multi-omics data into simple, actionable directives to ensure the right drug is chosen the first time, for every patient.