OncoPharML: A Machine-Learning Approach for Cancer Biomarkers Identification and Multi-Omics-Based Targeted Cancer Drug Prediction

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The current practice of treating cancer with radiation, chemotherapy, and immunotherapy is a one-size-fits-all approach in which patients with the same type and stage of cancer receive the same treatment. Yet, with cancer being a highly heterogeneous disease, research has shown that this approach is ineffective 75% of the time. Recent research has focused on comprehending tumor heterogeneity by analyzing patient-specific biomarkers, like genetic mutations or microRNA, and leveraging these biomarkers to computationally predict targeted treatments. While these approaches demonstrate improved targeted drug prediction, they present some limitations; most use data from cancer cell lines and humanized mice models, not from real human patients, and focus on using one biomarker in isolation, known as single-omics. Single biomarkers, regardless of whether they come from genetic mutations or microRNA, are not precise enough to explain treatment responses given tumor heterogeneity, making multi-omics integration critical. Additionally, driver biomarkers must be identified computationally and validated through rigorous biological analysis. The focus of this research is to create a pan-cancer solution using machine learning to identify key genetic mutations and microRNAs as driver biomarkers of cancer, validate this selection through functional enrichment analysis and overall survival analysis, and predict targeted drugs based on these selected multi-omic biomarkers of cancer. This multi-omics approach of predicting targeted drugs with high accuracy based on drivers of oncogenesis of real patient data is superior to current research that narrowly focuses on monotherapy, relying only on computational biomarker identification, and single-omics approaches on cancer cell line data.

Awards Won: