The Virtual Cell 2.0: Expanding Precision and Personalized Cancer Therapy Through AI-Powered Simulation

Alwakeel, Alan (School: Stanton College Preparatory School)

Drug combination therapy is a cornerstone of modern oncology, but identifying effective combinations for a patient's specific tumor remains difficult as possible combinations grow rapidly with each added therapy. Research has increasingly turned to computational modeling, but current approaches rely on black-box machine learning with limited generalizability and no mechanistic insight, or manually constructed pathway models that lack scalability. To address both gaps, I developed The Virtual Cell 2.0, a hybrid system that simulates intracellular signaling dynamics by integrating cancer cell genomics and proteomics with large-scale mechanistic biochemical simulation calibrated by machine learning. Using a novel intermediate reaction prediction algorithm, the system generates ~13 million reactions from pathway databases, then prunes per cell line using molecular profiles, reducing simulation time from hours to ~35 seconds. I cultured 12 cancer cell lines spanning triple-negative breast cancer (n=5), colorectal cancer (n=4), and prostate cancer (n=3), treated them with 12 targeted therapies, and collected kinetic viability data over 72 hours using CellCyte live-cell imaging. After calibrating on monotherapy responses, I used The Virtual Cell 2.0 to predict two-drug combination outcomes and validated predictions in vitro. The model accurately reproduced dose-dependent viability trajectories and predicted combination drug response with strong experimental agreement (R^2=0.958, RMSE=5.34%, bias=0.12%). These results demonstrate that mechanistic simulation calibrated by machine learning can rapidly and accurately prioritize cancer drug combinations, supporting its potential for personalized therapy selection.

Awards Won:

Second Award of $2,400

National Anti-Vivisection Society: Awards of $3,000

Foresight: First Place