Increased understanding of molecular mechanisms that mediate the pathogenesis of cancers is leading to careful manipulation of these pathways and the development of new cell-specific approaches to cancer therapy. At the same time, advances in cancer immunotherapy have led to the reemergence of their clinical use and effectiveness. Using data-driven computational models is a powerful and practical way to optimize novel combinations of these two very different therapeutic options for clinical cancer treatment. This talk will highlight a suite of multiscale mathematical models designed to optimize targeted drug treatment strategies, alone and in combination with immunotherapy. Together with existing and newly generated experimental data, these mathematical models are poised to improve the ability to combine promising drugs for clinical trials and reduce the time and costs associated with transitioning novel therapeutic approaches from "equations to bench to bedside."