Mathematical Modeling of Tumor Immune Interactions: A Closer Look at the Role of a PD-L1 Inhibitor in Cancer Immunotherapy

In this paper, we provide a mathematical framework comprising a system of differential equations, graphical representations, and simulations useful for analyzing the effects of anti-cancer treatments on tumor growth. Building upon a model constructed by Reuf et al., we interpolate new parameters to account for the PD1-PDL1 pathway and its significance on tumor growth. Following the literature surrounding the dynamics of anti-PDL1 and ibrutinib, we employ an exponential decay model to account for the sigmoidal behavior of the tumor growth when in interaction with the drugs. We exploit the fminsearch function in Matlab to fit essential parameters for curve fitting, namely d (maximum kill rate) and r (tumor growth rate). Using data extracted from Sagiv-Barfi et al. experiments, we run simulations in Matlab to delineate curve fitting results. From the results of the curve fitting iterations, we are able to validate our model and provide an in-depth analysis of the effects of treatments, such as anti-PDL1 and ibrutinib on tumor growth. Our results and analysis offer a promising approach for improved regulation in experimental cancer treatments on mice, with hopes of extension to human patients in the near future.