

Mathematical modeling and simulation with deep learning methods of cancer growth for patient-specific therapy

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Numerous methods of tumor therapy have gained attention in recent decades for cancer treatment. Three of these methods include anti-angiogenic therapy, virotherapy, and immunotherapy, each of which attempts to inhibit cancer cell growth. While much research has focused on experimental techniques, there has been parallel developments to understand these methods through novel mathematical model. Often, these models are described by a system of coupled ordinary differential equations that include the interactions between constituent proteins, molecules, and drugs that impact the growth of the cancer cells. This study aimed to improve existing mathematical models by including new details to enhance our understanding of the disease dynamics. For anti-angiogenic therapy, Aspirin was utilized due to its protein-regulatory properties and its ability to induce apoptosis in cancer cells. For virotherapy, the effect of the immune system was included to enhance the interaction between the oncolytic virus and cancer cells. For immunotherapy, liposomes carrying IL-2 cells were introduced to enhance the dynamics of the model. Additionally, mathematical models of these therapies involve parameters corresponding to growth, death, diffusion, and inhibition rates, which are often hard to estimate experimentally. We employ sophisticated numerical and optimization techniques, including deep learning with neural networks, to estimate these parameters and predict model dynamics. Our computational results indicate that the enhancements to the models in this research have a significant impact on the cancer dynamics. Potential future applications also include the implementation of deep learning for predictive analysis of tumor growth and therapy stemming from patient-specific data in real-time.