Optimal Therapy Design for Pancreatic Cancer Using a Boolean Network-Based Simulation

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Pancreatic cancer is a deadly disease that is very difficult to diagnose early and to treat effectively. It has a 95% mortality rate, the highest of all cancers, and only a 3-6% 5-year survival rate. Currently it is the fourth leading cause of cancer-related deaths in America; about 50,000 Americans fall victim to this disease annually. These statistics show growing trends in the spread of pancreatic cancer. Effective cancer therapies that balance the risk and benefit have been and still are topics of active research. However, special attention needs to be given to pancreatic cancer due the uniqueness of the way it evolves and our inability to detect the disease early. Thus, optimal drug therapy design is critical for bettering the odds against this lethal disease. Uncontrollable growth of cancerous tumors is often the result of unfavorable gene mutations and abnormal cell metabolism. The goal of an optimal therapy design is to find drug treatment schedules that rectify normal cell growth patterns, returning apoptosis signaling to normal, and reducing side-effects. Starting from the latest research on related cell biology, a numerical simulation model is created by mirroring relevant gene signaling pathways and their malfunctioning due to genetic mutations into Boolean networks with logic gates and faults. Drug interventions are then added to these networks and the effect of a variety of drug treatment schedules are simulated and simulation outputs are used to calculate and compare tumor proliferation, which is cross-mapped with side-effects of the drugs to determine optimal therapy recommendations.

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