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Delay equations for the cell cycle of tumoral cells

Cancer is nowadays one of the most complex severe diseases in the world. To better understand it, mathematical biologists have been working for the last decades on the theoretical aspects of the disease.

In this work, we model a combined treatment of immuno- and chemotherapy and its effects on a solid tumor.

Many authors (e.g. Arino, Dyson et al.) suggested structured population models in the context of cancer biology. Here, we start with a tumoral cell population structured by age and introduce the effects of drugs and immunotherapy on the tumoral mass. For a better description of the effects of phase-specific drugs, we define three sub-populations for interphase, mitotic and quiescent cells. Effectors from the immune system work against every kind of tumor cells, whereas chemotherapy is assumed to be mitosis-specific only.

Following a similar approach to that of Bocharov and Hadeler (2000), we derive a system of delay differential equations equivalent to the original age-structured model. Although our results apparently resemble those of Villasana (2003) and Liu (2007), the model here is not deduced from the mass action kinetics principles. But our approach allows us to take care of all delayed and undelayed variables and to locate them at the right place in the equations, thus providing a better description of the biological phenomenon.

We investigate the delay model both from the analytical and the numerical point of view and focus on the stability of the cancer-free equilibrium. Inspired by the work of other authors (e.g. d'Onofrio, 2010), we simulate different kinds of immunotherapy and estimate their effects on the tumor growth. Our aim is to find conditions for the eradication of the tumor or for its reduction to a life-compatible size.

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